MODULATION OF TRANSCRIPTION AND ALTERNATIVE SPLICING BY THE SPLICEOSOME-ACTIVATING NINETEEN COMPLEX (NTC) IN *ARABIDOPSIS THALIANA*

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ABBREVIATIONS AND SYMBOLS

°C	degree Celsius
µl	microliter
µM	micromolar
2,4-D	2,4-dichlorophenoxy acetic acid
A. thaliana	*Arabidopsis thaliana*
AA	alternative acceptor
ABA	abscisic acid
AD	alternative donor
AP	alternative position
AS	alternative splicing
ATPase	adenosine 5’-triphosphatase
BAP	6-benzylaminopurine
bp	base pair
BSA	bovine serum albumin
C	cytosine
CaMV	cauliflower Mosaic Virus
CBC	cap-binding complex
cDNA	complementary DNA
CHS1	chalcone synthase 1
Col-0	ecotype columbia-0 of *Arabidopsis thaliana*
CS	cell Suspension culture
CSM	cell Suspension culture Medium
Ct	threshold cycle
CTAB	cetyltrimethylammonium bromide
CTD	carboxyl-terminal domain
C-terminus	carboxyl terminus
DAPI	4,6-diamine-2-phenylindole dihydrochloride
DAS	differential alternative splicing
DDR	double-strand DNA repair
DE	differential expression
DMSO	dimethyl sulfoxide
DNA	deoxyribonucleic acid
dNTP	deoxyribonucleotide triphosphate
ds cDNA	double strand complementary DNA
DTT	dithiothreitol
E. coli	escherichia coli
ECL	enhanced chemiluminescence
EDTA	ethylenediaminetetraacetic acid
EJC	exon junction complex
ES	exon skipping
EtBr	ethidium bromide
EtOH	ethanol
FC	fold change
g	gram
GA	gibberellin
gDNA	genomic DNA
GFP	green fluorescent protein

GTC	guanidium thiocyanate
h	hour
H3	histone 3
HA	haemagglutinin protein of human influenza virus
hnRNPs	heterogeneous nuclear ribonucleoproteins
IAA	indole3-acetic acid
IR	intron retention
kb	kilobase
kDa	kilo dalton (1,000 Da)
l	liter
LB	lysogeny broth medium
LN	liquid nitrogen
M	molar
mA	milliampere
mg	milligram
min.	minute
ml	milliliter
mM	millimolar
mRNA	messenger RNA
NEB	new england biolabs
NMD	nonsense-mediated mRNA decay
nt	nucleotide
NTC	nineteen complex
N-terminal	amino terminal
O/N	overnight
OD	optical density
PAGE	polyacrylamide gel electrophoresis
PAL1	phe ammonia lyase 1
PCR	polymerase chain reaction
pH	negative logarithm of the proton concentration
PMSF	phenylmethylsulfonyl fluoride
PRL1	pleiotropic regulatory locus 1
PRL2	pleiotropic regulatory locus 2
Prp19	precursor RNA processing 19
PTCs	premature stop codons
PTMs	post transcriptional modifications
PVDF	polyvinylidene difluoride
RNA	ribonucleic acid
RNAP II	RNA polymerase II
RNase A	ribonuclease A
RNP	ribonucleoprotein
RPA	replication protein A
rpm	revolution per minute
RPs	ribosomal proteins
RT	room temperature
RT-PCR	reverse transcription polymerase chain reaction
SDS	sodium dodecylsulfate
SDS-PAGE	sodium dodecyl sulphate polyacrylamide gel
sec	second
SHR	shortroot

snRNAs	small nuclear RNAs
snRNPs	large nuclear ribonucleoprotein
SuR	sulfadiazine resistance
T	total
TAE	tris-acetate (40 mM); EDTA (1mM)
TBE	tris-borate-EDTA buffer
TBS	tris-buffered saline
TE	transcript expression
TE	tris.HCl (10mM); EDTA (1mM)
TEMED	N,N,N',N' tetramethylenethylendiamine
TF	transcription factor
Tris	Tris (hydroxymethyl) aminomethane
TUB	tubulin
U	unit
Ub	ubiquitin
UTR	untranslated region
UV	ultraviolet light
vol.	volume
wt	wild type
X-Gal	5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside

SUMMARY

Components of the spliceosome activating NTC (Nineteen Complex) are conserved in eukaryotes and their mutations in mammals result in early embryonic lethality. In *Arabidopsis*, the core PRL (PLEIOTROPIC REGULATORY LOCUS) NTC subunit is encoded by two closely related genes *PRL1* and *PRL2*. This provides the unique opportunity to study the regulatory roles of NTC using mutations of the PRL homologs. Whereas inactivation of *PRL1* results in dwarfism, early flowering, altered leaf development and hypersensitivity to low temperature, sucrose, ABA and cytokinin, the *prl2* mutations cause embryo lethality at the heart stage. Compared to *PRL1*, the *PRL2* mRNA level is about 10-fold lower in both wild type and *prl1* mutant seedlings. The viability of *prl1* mutant is thus likely maintained by partially overlapping function of PRL2, which secures reduced but still sufficient level of spliceosome activation. Main aim of this work was to characterize the roles of PRL1 and PRL2 in the regulation of transcription and alternative splicing. Deep RNA-Seq analysis identified 5,814 differential expression (DE) and alternative splicing (DAS) events indicating 5-fold higher representation of unspliced introns in upregulated versus downregulated mRNA isoforms in the *prl1* mutant compared to wt. About 25% of DAS events identified altered splice sites, and 30% changed mRNA's ORF removing either N-terminal organellar or secretion signal peptides, or increasing C-terminal distance between polyA and translational stop codons to enhance mRNA degradation by nonsense-mediated decay (NMD). 25% of DE mRNAs carried alternative 5' or 3' ends indicating that the *prl1* mutation also influences the positions of transcription start and polyadenylation/cleavage. Functional reannotation and GO analysis of dataset indicated upregulation of genes involved in cell division, UV response, DNA repair, iron uptake, anthocyanin biosynthesis, and ABA/oxidative stress responses, in contrast to downregulation of genes in cell elongation, vesicular transport, auxin signaling and redox-regulated pathogen defense and cell death pathways correlating with known phenotypic traits of the *prl1* mutant. In a subset of DE genes, we characterized the effect of *prl1* mutation on alternative splicing of ribosomal protein genes. To obtain *prl2* mutant cell populations, we used a conditional genetic complementation system for generation of genetic mosaics, in which the *prl2* mutant sectors were labelled by expression of the green fluorescent protein (GFP). Following enrichment of mosaic sectors in callus and cell suspension cultures, the GFP^{+} *prl2* and GFP^{-} wild type cell populations were separated by cell sorting and subjected to a similar deep RNA-Seq analysis. This study identified 6314 DE/DAS events, which were compared to those observed in *prl1*. This lead to the identification of numerous candidate genes implicated in meiotic recombination, fertilization, embryogenesis, DNA replication and post-embryonic development which are differentially downregulated in the *prl2* mutant. These data suggest that NTC complexes carrying PRL1 and PRL2 control transcription and splicing of mRNAs coding for both overlapping and distinct cellular functions.

ZUSAMMENFASSUNG

Komponenten des Spliceosome-aktivierenden NTC (Nineteen Complex) sind in Eukaryoten konserviert und ihre Mutationen in Säugertieren führen zu einer frühen embryonalen Letalität. In *Arabidopsis* wird die PRL (PLEIOTROPIC REGULATORY LOCUS) -NTC-Untereinheit durch zwei eng verwandte Gene PRL1 und PRL2 kodiert. Dies bietet die einzigartige Möglichkeit, die regulatorisch Bedeutung von NTC unter Verwendung von Mutationen der PRL-Homologen zu untersuchen. Während die Inaktivierung von PRL1 zu Zwergwuchs, frühem Blühen, veränderter Blattentwicklung und Überempfindlichkeit gegen niedrige Temperaturen, Saccharose, ABA und Cytokinin führt, verursachen die *prl2*-Mutationen eine Embryoletalität im Herzstadium während der Embryogenese. Im Vergleich zu PRL1 ist die PRL2-mRNA-Menge sowohl in Wildtyp- als auch in *pr11*-Mutantensämlingen etwa 10-fach niedriger. Die Lebensfähigkeit der *pr11*-Mutante wird daher wahrscheinlich durch teilweise überlappende Funktionen von PRL2 aufrechterhalten, was eine reduzierte, aber immer noch ausreichende Spleißosomaktivierung sicherstellt. Hauptziel dieser Arbeit war es, die Rolle von PRL1 und PRL2 in der Regulation von Transkription und alternativem Spleißen zu charakterisieren. Eine RNA-Seq Analyse identifizierte 5.814 differentiel expremierte (DE) und alternative gesplicte (DAS) Transkripte, die eine 5-fach höhere Repräsentation von ungespleißten Introns in hochregulierten gegenüber herunterregulierten mRNA Isoformen in der *prl1* Mutante im Vergleich zu wt zeigten. Etwa 25% der DAS-Ereignisse zeigten veränderte Spleißstellen und 30% änderten den mRNA-ORF, wobei entweder N-terminale Organell- oder Sekretionssignalpeptide entfernt wurden oder der C-terminale Abstand zwischen PolyA und Translationsstopcodons erhöht wurde, was den mRNA-Abbau durch Nonsense-vermittelten Abbau verstärkt. 25% der DE-mRNAs trugen alternative 5'- oder 3'-Enden, was darauf hinweist, dass die *pr11*-Mutation auch die Positionen von Transkriptionsstart und Polyadenylierung/Spaltung beeinflusst. Die funktionelle Re-Annotation und die GO-Analyse des Datensatzes zeigten eine Hochregulation von Genen, die an Zellteilung, UV-Reaktion, DNA-Reparatur, Eisenaufnahme, Anthocyanbiosynthese und ABA / oxidativen Stressreaktionen beteiligt sind, im Gegensatz zur Herabregulierung von Genen bei Zellverlängerung, vesikulärem Transport und Auxinsignalisierung und Redox-regulierter Pathogenabwehr und Zelltod, die mit bekannten phänotypischen Merkmalen der *prl1*-Mutante korrelieren. In einem Teil der DE-Genen charakterisierten wir den Effekt der *pr11*-Mutation auf das alternative Spleißen von ribosomalen Protein Transcripten. Um Zellpopulationen von *prl2*-Mutanten zu erhalten, verwendeten wir ein konditionales genetisches Komplementationssystem zur Erzeugung von genetischen Mosaiken, in dem die *prl2*-Mutantensektoren durch Expression des grün fluoreszierenden GFP Proteins markiert wurden. Nach der Anreicherung der Mosaiksektoren in Kallus- und Zellsuspensionskulturen wurden die Zellpopulationen von GFP^+ prl2 und GFP^- Wildtyp durch Zellsortierung getrennt und mit RNA-Seq untersucht. Diese Studie identifizierte 6314 DE / DAS-Ereignisse, die mit denen in *prl1* verglichen wurden. Dies führte zur Identifizierung zahlreicher Kandidatengene, die an meiotischer Rekombination, Fertilisation, Embryogenese, DNA-Replikation und postembryonalen Entwicklung beteiligt sind, und die in der *prl2*-Mutante differentiell herunterreguliert sind. Diese Daten legen nahe, dass NTC-Komplexe, die PRL1

und PRL2 tragen, die Transkription und das Spleißen von mRNAs steuern, die für überlappende sowie für unterschiedliche zelluläre Funktionen kodieren.

1. INTRODUCTION

1.1. Overview of pre-mRNA processing

In Eukaryotes, the molecular processes involved in the generation of mRNAs are the most complicated events in cell biology and biochemistry (Darnell, 2013). As for many years it’s been very difficult to understand the biological complexity of different organisms as there was no comparative information on the coding capacity of their genes. In humans, the genome is now recognized to contain about 21,000 protein-coding genes. The genome of nematode *Caenorhabditis elegans* with considerable simpler physiology has about ~19,000 protein coding genes, while the single-celled yeast *Saccharomyces cerevisiae* carries ~6000 protein coding genes (Pennisi, 2005; Gerstein et al., 2007). The elucidation of the so-called gene number paradox lead to the identification and in-depth understanding of the complicated mechanisms of transcription and RNA processing. Protein coding genes are transcribed by RNA polymerase II to pre-messenger RNAs (pre-mRNAs, Hurwitz, 2005). The pre-mRNA undergoes a series of biochemical modifications or maturation, which includes 5' capping, splicing, 3'-end processing and polyadenylation (Matlin et al., 2005). 5'-capping basically protects the transcript from degradation by exonuclease enzymes, it starts after the generation of the first 25 nucleotides of the transcript (Mandal et al., 2004). A guanine base and a ribose sugar are attached to the 5' end of the transcript, subsequently the guanine base is methylated. Capping is followed by or initiates splicing. Eukaryotic pre-mRNAs require extensive processing as they include intervening non-coding sequences called introns. Removal of intronic sequences is carried out by a large nuclear ribonucleoprotein (snRNPs) complex called the spliceosome, which is associated with numerous transcription regulatory and sequence specific RNA binding proteins including e.g. components of the so-called exon junction complex (EJC), heterogenous nuclear ribonucleoproteins (hnRNPs), TRE/THO mRNA export complex, exosome and polyadenylation/cleavage complex (Matlin et al., 2005). Splicing involves the precise removal of introns by RNA processing, and the exons are spliced together to produce the translatable mRNA. In the maturation final step, the 3' end of the pre-mRNA is defined by cleavage followed by addition of a poly(A) tail. The ultimate function of the poly(A) tail is to protect the RNA from degradation, and to assists in the RNA transfer to the cytoplasm for subsequent translation (Lutz, 2008). After RNA processing, the mature mRNA transcripts exit the nucleus and translated to protein by ribosomes in the cytoplasm. The mRNA export is highly dependent on correct processing, i.e. transfer through nuclear pores requires the recognition of a cap-binding complex (CBC) added during capping (Mandal et al., 2004). RNA editing allows generating multiple RNAs from genes across the whole genome and thus leading to the formation of the transcriptome. The generation of mRNA variants, which encode structurally and functionally different proteins, contribute to an expansion of the proteome (Nilsen and Graveley, 2010). Initially, mRNA processing was thought to happen post-transcriptionally. However, in reality transcription and processing are not consecutive, but simultaneous and interdependent (Neugebauer, 2002). It takes just several minutes to transcribe the gene of an average length. RNA sequencing studies with human B lymphocytes revealed that ~5 min after the start of transcription splicing was about 65% completed (Windhager et al., 2012). In addition, a wealth of other evidences demonstrates that mRNA processing is happening co-transcriptionally (Bentley, 2014). Alternative translation initiation and posttranslational modifications (such as phosphorylation, acetylation, methylation, ubiquitylation, sumoylation, glycosylation, palmitoylation and proteolytic clevage etc.) assist in the proliferation of protein coding capacity of the genome (Wilhelm et al., 2014). Alternative splicing acts as a major multiplication factor which contributes to the expansion of the proteome. In humans, around 95% genes are subjected to alternative splicing (Pan et al., 2008). Majority of the human genes generate two to three different mRNA isoforms (Djebali et al., 2012). Though, there are many expections, e.g., CD44, encoding human CD44 glycoprotein which can generate significantly more i.e., ~10 alternatively spliced exons, and might result in the production of more than 1000 alternative transcripts (Screaton et al., 1992; Bell et al., 1998).

1.2. Single gene derived multiple transcript isoforms

During initial sequencing of eukaryotic genes, one of the ground-breaking discoveries was the recognition that their coding sequences are often discontinuous and interrupted with non-coding intervening sequences called introns, which are absent from the mature transcripts derived from the corresponding genes. This discovery primed subsequent research on the mechanisms, which mediate intron removal from the primary pre-mRNA transcripts and splice together the remaining exon sequences into a continuous open reading frame of mature mRNAs. It was then soon uncovered that during transcription the eukaryotic pre-mRNAs undergo sequential 5’ capping, splicing and 3’ polyadenylation. The large molecular machine mediating pre-mRNA processing or “splicing” was subsequently identified and designated as spliceosome and found to correspond to a huge complex of five small nuclear RNAs (snRNAs) with over 200 proteins (Wahl et al., 2009). It became also evident that introns are not just disposable junk sequences retained through evolution, but they are linked to many cellular functions including the regulation of gene expression (e.g., by circular RNA formation) and generation of increased protein diversity via alternative splicing (Kriventseva et al., 2003; Russell et al., 2005; Stetefeld and Ruegg, 2005; Roy and Penny, 2006; Bulman et al., 2007).

The splicing reaction is driven forward by structure remodeling ATPases which control various spliceosomal rearrangements and the mode of proofreading of pre-mRNA substrates (Staley and Guthrie, 1998; Koodathingal and Staley, 2013). Depending on the signaling cues controlling the transcription rate, histone modifications, spliceosome activation and levels of various classes of RNA-binding factors, pre-mRNA processing by the spliceosome might result in altered mode of splicing generating novel combinations of exonic coding sequences. Alternative splicing (AS) represents a mechanism, which results in a huge variability of mature mRNA sequences that code for proteins with different combinations of functional domains. AS-mediated sequence changes considerably influence also the translation efficiency and stability of various mRNA isoforms (Barash et al., 2010; Nilsen and Graveley, 2010). AS is considered as an important mechanism controlling diverse physiological functions, such as cell division, cell differentiation, stress responses, cell lineage determination, as well as tissue-identity acquisition and maintenance, and organ development (Nicholson et al., 2010, Kalyna et al., 2012). Different transcript isoforms are generated by selection of alternative splice-sites in the pre-mRNAs (Nilsen and Graveley, 2010; Kelemen et al., 2013; Lee and Rio, 2015). AS leads also to the formation of mRNAs that differ in their untranslated regions (UTRs). Different modes of AS include exon skipping (the removal of specific exons, referred to as cassette exons), a choice between mutually exclusive exons, the use of alternative splice sites (i.e. different definition of boundaries between introns and exons) and intron retention. In summary, AS events consists of five fundamental groups: intron retention (IR), exon skipping (ES), alternative donor (AD), alternative acceptor (AA) and alternative position (AP).

1.3. Alternative splicing in eukaryotes

In plants and animals, the majority of intron-containing genes appear to undergo AS, which often shows cell type and tissue specific differences. Genome-wide studies indicate that 90-95% of pre-mRNAs derived from intron-containing genes are alternatively spliced in humans. About 15% of all AS events are caused by corrupted splicing: i.e., mutations affecting *cis*-acting pre-mRNA sequence elements (e.g., 5´ and 3´ splice sites, exon and intron enhancer or silencer sequences), altered expression of *trans*-acting splicing factors and other spliceosome components associated with human genetic diseases (Pan et al., 2008; Marquez et al., 2012). In humans, splicing disorders have been identified in about 60% of non-infectious diseases, which indicates that mutations in genes encoding components of the RNA splicing machinery lead to life-threatening diseases (Valadkhan, 2011; Wang et al., 2012). High-resolution mass spectrometry studies suggest that from the ~20,000 human protein coding genes about 37% are represented by multiple protein isoforms, indicating the contribution of AS to proteome complexity. In comparison, it has been estimated that >60% pre-mRNAs synthesized from multiple exon-containing Arabidopsis genes are subjected to AS (Marquez et al., 2012; Syed et al., 2012). In higher plants, AS is thought to act as a key regulator of gene expression because it was found that 60–70% of intron-containing genes are alternatively spliced (Marquez et al., 2012; Chamala et al., 2015). About 13–18% of alternatively spliced mRNAs serve as substrates for and destroyed by the nonsense-mediated mRNA decay (NMD) pathway (Kalyna et al., 2012; Drechsel et al., 2013). AS is proposed to play a major role in the regulation of growth and development, as well as responses to biotic and abiotic stresses (Mastrangelo et al., 2012; Filichkin et al., 2014). In *Arabidopsis*, AS is thought to play a major role in the control of flowering time, circadian clock, light signaling, seed dormancy, disease resistance and stress responses (Zhang et al., 2007; Li et al., 2016). AS often generates transcript isoforms with premature translation termination codons, which are selectively degraded by NMD (Lewis et al., 2003; Nicholson et al., 2010; Hug et al., 2016). Alternative splicing also generates mRNA isoforms with altered reading frames, resulting in the translation of different protein isoforms with diverse functions and/or localizations. Furthermore, alternative splicing events could lead to the production of noncoding RNAs which may modulate the stability of other coding RNAs or compete with their regulators.

Recently, de Almeida and Carmo-Fonseca (2014) reported on a functional cross-talk between chromatin modifications, transcription, and pre-mRNA processing. This and many other similar studies indicate that pre-mRNA splicing is a co-transciptional process, in which splicing factors are recruited to and act upon nascent pre-RNAs during their transcription by the RNA polymerase II (RNAP II) complex (Merkhofer et al., 2014). In coordination of splicing and transcription, the chromatin structure plays an important role by providing a recruitment platform for spliceosomal factors, as well as an environment to modulate the kinetics of transcription, which in turn influence both splice site recognition and kinetics of splicing (Gómez Acuña et al., 2013). Consequently, disruption of RNA polII-associated chromatin factors or change in their distribution leads to defects affecting both splicing efficiency and alternative splicing patterns (Naftelberg et al., 2015).

1.4. Intron retention and other alternative splicing events

Similarly to mammals, intron retention and alternative 5' and 3' splice sites comprise the most frequent AS events also in plants (Li et al., 2013). According to Wu et al. (2014), plants show significantly increased intron retention frequency during acclimatization to nutrient deficiencies and splicing patterns with increased complexity compared to standard optimal grown conditions. Regulatory consequences of alternative splicing resulting in e.g. retained introns with premature stop codons (PTCs) await rigorous investigations. It is possible that partially unprocessed pre-mRNAs are stored nuclearly as non-functional ribonucleoproteins during stress exposure but processed further by increasing the population of protein coding mature mRNAs during stress recovery. In that way non-functional (i.e. partially processed) pre-mRNAs might help to restore the levels of mature transcripts, and thereby the abundance of proteins with critical functions, by reactivation of splicing without recurrent induction of transcription of corresponding genes. For example, serine and arginine-rich SR splicing factors could either alleviate or repress the interaction of spliceosome with the subset of mRNAs, and thus modulate the shifting between the production of functional and PTC-containing transcripts. The probability of splicing events at particular splice junctions could also be analogously regulated by post-translational modifications of SR and mRNA-binding proteins (Vélez-Bermúdez and Schmidt, 2014). In addition, AS events in the 5'-UTR might also contribute to the control of mRNA translation. In plants, abiotic stress stimuli changes the translation efficiency, which leads to a massive bias in the pool of mRNAs that are actively translated affecting several plant developmental, metabolic and physiological programs (Mustroph et al., 2009; Juntawong et al., 2014).

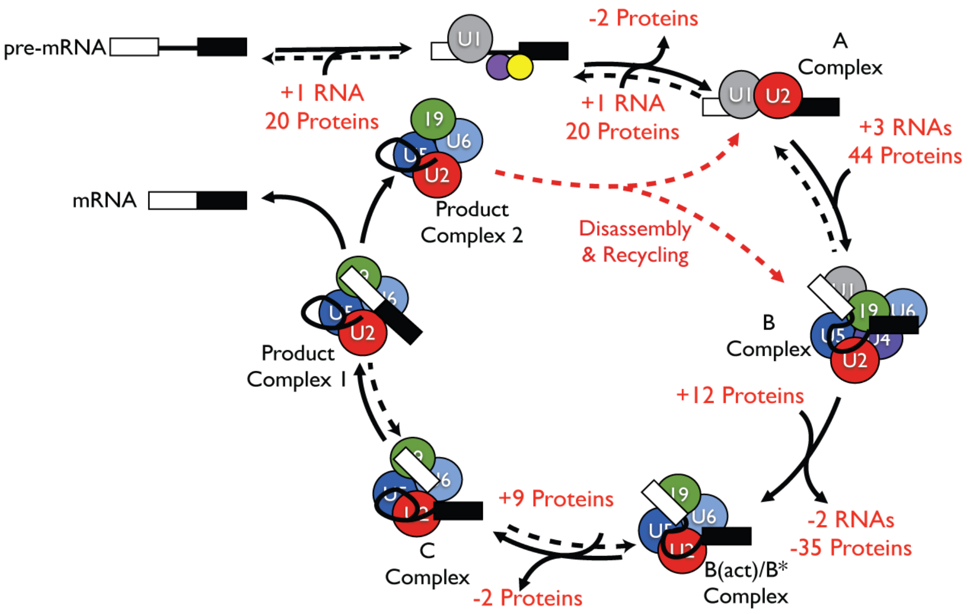
Intron retention (IR) is the most frequent type of AS, which occurs when an intron is not excised by the spliceosome and is preserved in the final mature mRNA. In *Arabidopsis*, IR represents about 64% of all AS events (Kalyna et al., 2012; Reddy et al., 2013; Wong et al., 2016) and might modulate development, stress responses, and tissue specific physiology (Wong et al., 2016; Jacob et al., 2017). Apparently, RNA Pol II might directly regulate intron retention because several trans-regulatory factors located near splice junctions modulate the rate of intron removal (Wang and Burge, 2008). In addition, lower DNA methylation levels near splice junctions have been linked to enhanced IR in human breast tissues (Wong et al., 2017). According to the kinetic model of co-transcriptional splicing, DNA methylation regulates IR by altering RNA Pol II processivity and splice-site recognition. IR is a conserved mechanism that regulates cell differentiation and plasticity in normal tissues and is implicated in diverse human cancers. Furthermore, it is suggested that introns determine the ratio of ribosomal protein isoforms and thereby modulate translation efficiency of ribosomes through asymmetric paralog-specific regulation of splicing.

1.5. Regulatory connections between splicing and translation

Ribosomes translate the genetic code encrypted in mRNAs into proteins. In eukaryotes, cytoplasmic ribosomes are composed of 60S and 40S subunits. The 60S subunit contains three rRNAs (28/25S, 5.8S and 5S) and 49 ribosomal proteins (RPs), whereas the 40S subunit contains a single 18S rRNA and 33 RPs (Panse and Johnson, 2010). Ribosome biogenesis requires stoichiometric amounts of RPs and rRNAs (Laferté et al., 2006). The *Arabidopsis* genome harbors about 1000 tandemly arrayed copies of the 5S rRNA gene and 570 to 750 copies of the 45S rRNA gene (Layat et al., 2012). The 81 RPs of *Arabidopsis* are encoded by more than 200 genes; each RP family comprising of 2-7 members. Ribosome function (i.e. translation efficiency) is a chief determinant of cell division and expansion. Consequently, mutations of RP genes result in developmental defects, such as deformed leaves, dwarfism, embryo lethality etc. (Rosado et al., 2012). Under limiting environmental conditions, the population of RPs shows a dynamic change in composition, which likely aids in tuning translational efficiency. In yeast, the majority of intron containing genes code for RPs. The yeast RP genes underwent evolutionary duplication, and then many of them some degree of subsequent functional specification (i.e., neofunctionalization). As expected, spliceosomal mutations results in overall splicing defects of intron-containing genes in yeast. However, given the fact that the majority of intron-containing yeast genes code for ribosomal proteins (Ares et al., 1999; Spingola et al., 1999; Juneau et al., 2006, 2007, 2009); spliceosome deficiencies dramatically reduce RP levels and consequently inhibit ribosome biogenesis, translation and related growth processes (Pleiss et al., 2007). However, not all spliceosomal mutations influence equally all RP genes indicating a specificity in the recognition of their intron sequences by the spliceosome. Moreover, deletion of whole introns or intronic hairpin structures of pre-mRNAs of some RP genes results in stress-related phenotypes indicating that splicing efficiency of RP pre-mRNAs determines the efficiency of ribosome assembly and translation under stress. Surprisingly, enhanced expression of one of the two paralogs of yeast RP genes results in feedback inhibition of transcription of the other paralog suggesting that certain RP isoforms play a role in regulation of transcription and splicing of pre-mRNAs of their paralogues (Parenteau et al., 2015; Petibon et al., 2016). The fact that Arabidopsis nucleolus was found to be enriched with alteranatively spliced mRNAs (Pendle et al., 2005), the majority of which code for RPs, raises the intriguing question whether similar regulatory mechanisms are involved in spliceosomal regulation of ribosomal function and translation in plants.

1.6. Spliceosome assembly and catalytic cycle

The removal (i.e., excison or splicing) of intronic sequences from unmature pre-mRNAs is catalyzed by the spliceosome through two sequential trans-esterification reactions. The spliceosome assembles on the pre-mRNA by sequential binding of different splicing factors, which recognize conserved RNA sequences within the introns and at exon-intron junctions. By removing the introns, the spliceosome precisely ligates the exons producing mature mRNAs for translation into proteins and is finally released for recycling after completion of these reactions (Matera and Wang, 2014). The spliceosome is a large macromolecular RNP (ribonucleoprotein) complex, the composition and conformation of which are very dynamic resulting in high fidelity and flexibility during splicing of a wide variety of pre-mRNAs (Will and Luhrmann, 2011). The spliceosome consists of five conserved U-rich small nuclear RNP (snRNP) particles and numerous non-snRNP factors (Bessonov et al., 2008; Fabrizio et al., 2009). Each snRNP contains a distinct set of splicing factors, interacting proteins and uridine-rich snRNAs, namely U1, U2, U4, U5, or U6 (Wahl et al., 2009; Hogg et al., 2010). The snRNAs orderly bind specific sets of interacting proteins to form the U-snRNP particles, which sequentially assemble to form distinct temporally changing forms of splicosomal complexes involved in base-pairing with pre-mRNAs, intron recognition and 5' and 3' cleavage of exon-intron junctions (Valadkhan and Jaladat, 2010; Hang et al., 2015).



Adapted from Fabrizio, et al., Mol. Cell, 2009.

Figure 1: **Stepwise spliceosome assembly from its U-snRNP components.**

The scheme is drawn according to Fabrizio et al. (2009) indicating the number of ribonucleic protein and small RNA. Exons are indicated by black and white boxes, while thin black lines show intron and intron lariat.

The U-snRNP-associated factors play well-defined structural, enzymatic, and regulatory functions (Jurica and Moore, 2003; Will and Lührmann, 2011), and sustain a dynamic interaction network by associating splicing with other stages of gene transcription (Alexander and Beggs, 2010; Bentley, 2014). The U-snRNPs assemble dynamically on the pre-mRNA along with other non-snRNP regulatory factors and catalyze two trans-esterification reactions sequentially producing mature mRNA after removal of the introns. Studies support and reveal that splicing is likely to be co-transcriptional and this includes deep sequencing of nascent transcripts (Khodor et al., 2011; Nojima et al., 2015; Nieto Moreno et al., 2015).

Multiple evidence links transcription and splicing. Deletion of the carboxyl-terminal domain (CTD) of RNA Polymerase II (RNAPII) results in inefficient splicing (McCracken et al., 1997). Alternative splicing is also modulated by numerous transcription factors (Kadener et al., 2001; Nogués et al., 2002; Kadener et al., 2002), and coactivators (Auboeuf et al., 2004), and other regulators with dual activity that act as both transcription and splicing factors (Kornblihtt et al., 2004). Likewise, chromatin remodelers, as well as factors that alter chromatin structure are involved in regulation of alternative splicing (Batsché et al., 2006; Luco et al., 2010; Saint-André et al., 2011; Schor et al., 2009). In order to recognize weak splice sites, several components increase the time window for the recognition which includes sequences that induce pauses on transcription (Roberts et al., 1998), as well as chromatin compaction factors that block RNAPII (Schor et al., 2009). Histones are proteins which are chief principal components of chromatin and play a critical role in gene regulation. Histones undergo post transcriptional modifications (PTMs) that alter chromatin structure and consequently affect regulation of cotranscriptional splicing. Histone PTMs include methylation, acetylation, phosphorylation, ubiquitination and sumoylation. Histone variants and histone tail PTMs impact gene expression by either silencing/activating which in turn influences alternative splicing, modulate chromatin structure and the recruitment of histone modifiers.

Assembly of the spliceosome is initiated by formation of pre-spliceosome complex A, which is composed of U1 and U2 snRNPs. Concommitantly with U1 snRNP-mediated recognition of conserved 5′ splice sites of exon-intron junctions through base-paring with the U1 snRNA, the U2 snRNP interacts with the conserved intronic branch-point sequence. During the first step of splicing (i.e. at 5’ intron junctions), binding of the U2 snRNP to branch-point sequences results in protruding of a conserved intronic adenosine residue, which serves as nucleophile centre for attacking the 5′ splice site in the first trans-esterification reaction. The branch-point adenosine performs a nucleophilic attack which leads to the formation of lariat intermediate (Burgess and Guthrie, 1993). Subsequently, a preformed tri-snRNP composed of U4, U5 and U6 snRNPs, in which the U4 and U6 snRNAs are extensively base-paired, joins the pre-spliceosome (complex A) to form the precatalytic spliceosome complex B. In this pentameric snRNP complex then a large structural rearrangement occurs: base-pairing interaction of pre-assembled U4/U6 snRNAs unwinds allowing U6 to form two mutually exclusive interactions with the 5′ splice site sequence and U2 snRNA, to form the activated spliceosome complex B^{ACT}. The latter conformational change is promoted by association of pentameric snRNP with the so-called spliceosome-activating nineteen complex NTC and associated NTC regulatory (NTR) factors, which promote destabilization and release of U1 and U4 snRNAs and formation of catalytic complex C (Chan et al., 2003). Complex C then catalyses the second trans-esterification reaction, in which the intron lariat is removed, and the two exons are ligated (Will and Lührmann, 2011).

1.7. Composition and regulatory role of spliceosome activating NineTeen Complex (NTC)

The first identified component of spliceosome activating NineTeen Complex (NTC) was human PSO4 and its functional otholog, the yeast E3 ubiquitin ligase subunit Prp19 (Precursor RNA processing 19). In addition to its role in spliceosome activation, during last decades the NTC was implicated in the regulation of transcription elongation, mRNA export, genome stability, protein ubiquitylation and lipid droplet biogenesis (Cheng et al., 1993; Chan et al., 2003; Chan and Cheng, 2005; Kuraoka et al., 2008; Hogg et al., 2010; Chanarat et al., 2011; Chanarat and Sträßer, 2013). As outlined above, the NTC plays an essential role in the assembly and catalytic activation of the spliceosome (Will and Lührmann, 2011). Consequently, core subunits and structure of the NTC are remarkably conserved throughout the eukaryotic kingdom. The core of NTC consists of eight subunits in *Saccharomyces cerevisiae*: Prp19, Prp46, Cef1, Syf1, Syf2, Syf3, Snt309, Isy1, Prp45 and Ntc20. Conserved orthologs of these NTC components were identified also in higher eukaryotes, including plants and animals (Fabrizio et al., 2009; Koncz et al., 2012). Affinity purification and proteomics studies of budding and fission yeast NTCs identified at least 26 Prp19-associated proteins (Ohi et al., 2002). Similar proteomics studies suggest the existence of three different human Prp19-like complexes. The core of purified human NTC complexes contains the PRP19, PRLG1(Prp46), CDC5L(Cef1), and SPF27(Stn309) subunits in association with at least 28 other factors, many of which are represented by orthologs in the yeast NTC and NTC-associated NTR complexes. Human NTC components have been identified in the spliceosome B, B^{act} and C complexes indicating their important roles in spliceosome assembly and activation. Following dissociation of complex C, components of the NTC remain bound to the core of U5 snRNP (Makarova et al., 2002; 2004; Behzadnia et al., 2007; Bessonov et al., 2008; Fabrizio et al., 2009).

In comparison to yeast and mammals, a unique feature of plants that several NTC components, such as the core subunits PRP19 and PRL1, are encoded by functionally equivalent or slightly divergent duplicated genes. NTC purified from *Arabidopsis* contains thus two PRL19 paralogs (MAC3A and B), PRL1(Prp46, MAC2), CDC5 (Cef1, MAC1) SKIP (Prp45, MAC6), SYF1 (MAC9), SNT309 (MOS4), ISY1 (MAC8), and SYF3 (MAC10) together with the NTR- factors ECM2-1a/b (MAC5A/B) and PRP17 (CDC40, MAC12), as well as complex B^{ACT} and C specific factors PRP2a (MAC15) and Aquarius (AQR/MAC7). In addition, *Arabidopsis* NTC co-purifies with several components of U5 snRNP including U5-220/Prp8 (MAC16), U5-200-2a/Brr2 (MAC14), U5-116-1a/Snu114 (MAC11), and the PRP8-binding WD-40 factor U5-40 (MAC17) (Palma et al., 2007; Monaghan et al., 2009). Purification of *in vitro* assembled human spliceosomal A, B, B^{ACT} and C complexes revealed association of NTC components with the U4/U6.U5 tri-snRNPs suggesting that NTC binds to the spliceosome either before or during unwinding of U4 from U6 snRNA (Fabrizio et al., 2009; Song et al., 2010). Therefore, NTC appears to be a key factor for transition of the spliceosome from the B to B^{ACT} complex assisting extensive remodelling of the U4/U6.U5 tri-snRNPs and. maintenance of stable association between pre-mRNA and specific parts of U6 and U5 snRNAs in the active spliceosome (Chan and Cheng, 2005). Mutations affecting the functions of non-essential NTC subunits enhance dissociation of U5 and U6 snRNPs from the spliceosome (Chan et al., 2003; Chan and Cheng, 2005).

Purified NTC components

Yeast	Human	Arabidopsis
Ppr19	**hPRP19SNEV/PSO4**	**Ppr19a/b_MAC3a/b**
Cef1/NTC85	**CDC5L**	**CDC5/MAC1**
Clf1/Syf3/NTC77	CRNKL1/SYF3	**CRN1c/MAC10**
Syf1/NTC90	XAB2	**Syf1/MAC9**
Syf2/NTC31	SYF2/GCIP p29	(SYF2)
Isy1/NTC30	ISY1/KIAA1160/SAP33	**Isy1/MAC8**
Snt309/NTC25	**BCAS2/SPF27**	**SPF27/MOS4**
NTC20	-	-
-	**CTNNBL1/NAP**	(CTNNNBL1)
-	**HSP73**	(HSC70-1/2)
Cwc2/NTC60	-	-
Prp46/NTC50/Cwc1	**PLRG1/PRL1**	**PRL1/MAC2**
Bud31/Cwc14	BUD31/G10	(BUD31)
Cwc15	**AD002/HSPC148**	AD-002
Yju2/Cwc16	CCDC130	(CCDC130)
Cwc21	SRRM2/Srm300	(SRM300-like)
Cwc22	KIA1606	(CWC22)
Cwc23	DNAJC17	-
Cwc24	RNF113A	(ZF-CCH 51)
Cwc25	CWC25/CCDC49	(CWC25)
Bud13/Cwc26	MGC13125	(CWC26)
Cwc27	NY-CO-10	(CWC27/SDCCAG10)
Prp17/CDC40/Slu4	CDC40	**PRP17-1/MAC12**
Prp22	hPRP22/DHX8	(PRP22-1/2/3)
Prp45	SKIP1/SNW1	**PRP45/MAC6**
Slu7	hSLU7	(SLU7-1a/b)
Ecm2	RBM22	**ECM2-1a/MAC5a**
Spp2	GPKOW/T54	(MOS2)
(Aim4p)	*WBP11, NPWBP; SIPP1*	-
-	*PRCC*	-
-	*PPIL1*	**PPIL1b**
(*Cwf11p*)	*Aquarius AQR*	**Aquarius/MAC7**
(Urn1)	(TCERG1; Urn1; CA150)	(PRP40C)
(*Cwf18*)	-	(CWF18)
(Prp2)	(DHX16)	**PRP2-1a/ESP3/MAC15**
(Prp8)	(U5-220)	**PRP8a/SUS2/MAC16**/PRP8b
(Brr2)	(U5-200/SNRNP200)	**Brr2/MAC14**
(Snu114)	(U5-116/EFTUD2)	**Snu114/CLO1/GFA1/MAC11**
(*Cwf17*)	(SNRNP40)	**U5-40/MAC17**

Figure 2: **Conserved components of NTC core and associated subunits detected in purified yeast, human, and *Arabidopsis* complexes**.

Proposed NTC core subunits are highlighted in bold, brackets indicate factors that are not present in purified NTC complexes but encoded by corresponding homologous genes in the yeast, human, and *Arabidopsis* genomes (Koncz et. al., 2012).

The role of NTC in spliceosome activation (Chan et al., 2003; Makarova et al., 2004; Fabrizio et al., 2009; Wahl et al., 2009; Chanarat and Sträßer, 2013) is particularly well illustrated by structural and functional studies of its essential subunit Prp45/SKIP in *S. cerevisiae, S. pombe, and H. sapiens* (Yan et al., 2015, 2016; Bertram et al., 2017). Cryo-electron microscopy studies of spliceosome structures show that Prp45/SKIP interacts with a number of proteins across the spliceosome, including its primary contact to Prp8, which occurs along the entire length of Prp45/SKIP. Dissociation of U1 snRNP from the pentameric complex B depends on the Prp45-interacting U5 snRNP factors Prp3 and Prp28, which play a key role in remodeling complex B^{ACT} to complex C before the second step of splicing. C-terminal domain of Prp45 also influences the association kinetics of U2/U5-U6 components of tri-snRNP, preferably enabling them to attain an association-competent state. In addition, through likely interaction with the C-terminal domain of RNA polII, Prp45 appears to be involved in early stages of co-transcriptional spliceosome assembly (Hálová et al., 2017). Therefore, the core NTC subunit Prp45/SKIP is an essential factor in the spliceosome assembly and splicing cycle (Albers et al., 2003; Chen et al., 2006). David et al. (2011) found that the U2 snRNP component U2AF65 is implicated in interaction with the RNA polymerase carboxy-terminal YSPTSPS heptapeptide repeat (CTD) domain and facilitates recruitment of NTC components to transcribing RNA polII. In fact, transcription elongation is critically affected by the interaction of NTC with RNAPII which implies further NTC interactions with the THO/TREX complex involved in nuclear export of messenger ribonucleoproteins (mRNPs) (Chanarat et al., 2011). Recently, Deng et al. (2016) reported that the *Arabidopsis* homolog protein arginine methyltransferase 5 (AtPRMT5), which is implicated in the regulation of flowering time, growth rate, leaf morphology, stress and circadian rhythm (Pei et al., 2007; Sanchez et al., 2010; Deng et al., 2010; Zhang et al., 2011), is required for the recruitment of specific first step and second step splicing factors mediating spliceosome activation. Though PRMT5 is widely conserved between plants and animals, and it was reported to interact with the U5 snRNP subunit PRP8 in *Arabidopsis*, thus far it has not been identified by proteomics and immunoprecipitation studies in affinity purified and *in vitro* assembled Drosophila, mice and human spliceosomal complexes (see for review Koncz et al., 2012). Rather, in human cells PRMT5 was identified as an interacting partner of the WD-40 protein WDR77 in the cytoplasmic 20S methylosome, which is responsible for symmetric arginine dymethylation of various spliceosomal proteins (Brahms et al., 2001; Friesen et al., 2001; Rengasamy et al., 2017). Thus, PRMT5 appears to play a role in post-translational modulation of the activity, stability and/or interaction of RNA-binding proteins. In any case, discrepancies in the definition of PRMT5's regulatory function do not change the emerging conclusion that NTC is directly involved in the regulation of RNAPII transcription and simultaneous co-transcriptional spliceosome assembly and activation (Perales and Bentley, 2009; Muñoz et al., 2010; Carrillo Oesterreich et al., 2011).

1.8. Components of the core PRP19 E3 ubiquitin ligase complex

Prp19 was first identified by a mutation in yeast (Henriques et al., 1989; Vijayraghavan et al., 1989) which blocks splicing at step I resulting in a cold temperature-dependent growth defect (Tarn et al., 1993; Song et al., 2010). Prp19 carries an N-terminal U-box/RING-finger domain with E3 ubiquitin ligase activity mediating the formation of ubiquitin K63 chain on Prp3, a component of U4/U6 snRNP, which plays a role in the recruitment of U5 snRNP to the U4/U6.U5 tri-snRNP and its subsequent conversion to the catalytic complex C (Chen et al., 1993; Grey et al., 1996; Song et al., 2010). In *Arabidopsis*, 37 genes are predicted to encode U-box-like factors, two of them represent homologues of

Prp19 (At1g04510 and At2g33340; for review see Azevedo et al., 2001). In addition to the RING E3 domain, Prp19 harbors a coiled-coil domain mediating tetramerization, and a WD-40 repeat domain involved in protein-protein interactions (Ohi et al., 2005; Grote et al., 2010). Human hPrp19 has been shown to homo-oligomerize *in vivo* (Grillari et al., 2005). The structure of Prp19 was defined using NMR spectroscopy (Ohi et al., 2003) and x-ray crystallography (Vander Kooi et al., 2006; 2010). Recently, de Moura et al. (2018) demonstrated that human PRP19 forms an autoinhibited tetrameric E3 ligase complex by interaction of its coiled coil domains. Activation of PRP19 E3 ligase requires sequential binding of the core NTC components SPF27 (Snt309, MOS4), CDC5L (Cef1, MAC1) and PLRG1 (PRL1, MAC2). In mice, PRP19 was identified to interact with the SUG1 regulatory subunit of the 26S proteasome (Sihn et al., 2007), whereas Prp19 was detected to bind *in vivo* the β7 catalytic subunit of 20S proteasome in both yeast and human cells. Hence, it was proposed that NTC is involved in PRP19-dependent ubiquitination and subsequent proteasomal degradation of various substrates including some NTC-associated factors (Löscher et al., 2005; Sihn et al., 2007). Mutation of PRP19 called SNEV in mice results in early embryonic lethality in the blastocyst stage indicating that Prp19/SNEV performs an indispensable and non-redundant function. By contrast, in *Arabidopsis* two PRP19 orthologues were identified which share about 83% of identity (Monaghan et al., 2009). However, in contrast to the observation of latter authors, *prp19a prp19b* double mutants in *Arabidopsis* are not viable due to lethality of haploid gametes.

It has been observed early on that NTC plays an important role in regulating DNA repair damage (Henriques and Moustacchi, 1980; Henriques et al., 1989). In fact, subsequent studies in mouse and human cells revealed that the core PRP19/CDC5/PRL1/SPF27 E3 ligase complex functions as DNA damage sensor in double-strand DNA repair (DDR) (Maréchal et al., 2014). The PRP19/SNEV undergoes K63 ubiquitination in response to DNA damage. The PRP19 complex was identified to ubiqutinate the single-strand DNA binding replication protein A (RPA) at DNA damage sites. In turn, ubiquitinated RPA recruits the ataxia telangiectasia and RAD3-related (ATR) phosphatidylinositol 3-kinase-related kinase, which is key regulator of the DNA repair cell cycle check-point. An alternative but similar PRP19 core E3 ligase complex carrying the NTC core subunit XAB2 (Syf1) has been analogously implicated in transcription-coupled DNA repair (Kuraoka et al., 2008). The third kind of PRP10 complex has been identified in lipid droplet associated form in the cytoplasm of adipocytes but found to carry no known NTC subunit.

1.9. Cell division cycle 5 (CDC5)

CDC5 has been identified by a mutation causing mitotic cell cycle arrest at G2/M and accumulation of unspliced pre-mRNAs in fission yeast (*Saccharomyces pombe*) by Ohi et al. (1994). Subsequently, Ohi et al. (1998) characterized the *CDC5* encoded Myb-related protein, and by a proteomics study demonstrated that it is a component of the NTC (Ohi and Gould, 2002). In parallel, several labs showed that CDC5 orthologs are widely conserved in other eukaryotes and can complement the fission yeast *cdc5* mutation (McDonald et al., 1999; Tsai et al., 1999; Ohi and Gould, 2002; Ohi et al., 2002; Hazbun et al. 2003). Subsequently, Burns et al. (1999) identified human CDC5L and Ajuh et al. (2000) confirmed that it also represents a core subunit of human NTC. Notably, Burns et al. (2002) demonstrated that cell cycle arrest of the yeast *cdc5* mutant can be suppressed by removal of a single intron from the α-tubulin (*tub1*) gene. Using complementation of the yeast *cdc5* mutant, the *Arabidopsis* CDC5 homolog was isolated by Hirayama and Shinozaki (1996), who demonstrated that AtCDC5Myb can act as sequence specific DNA-binding transcription factor *in vitro*. Through its C-terminal domain, CDC5 (Cef1) binds to the U-box domain of tetrameric PRP19 similarly to SPF27 (Snt309) and PRL1 (see below, Chen et al., 2002; Ohi and Gould, 2002; Grote et al., 2010; de Moura et al., 2018). At the same time, CDC5 interacts with the C-terminal WD-40 repeats of PRL1 (Prp46) (Ohi and Gould, 2002). In the PRP14/Pso4 DNA repair complex CDC5 interacts with ATR and is required for the activation of components of downstream S-phase checkpoint pathway arresting cell cycle progression (Willis and Rhind, 2009).

Snt309 was originally identified by screening for mutations enhancing the cold sensitive phenotype of the *prp19* mutant in yeast (Chen et al., 1998). Concurrently, Snt309p was found to be associated with the spliceosome (Chen et al., 1998) and, as it co-purified with NTC (Tarn et al., 1994), its interaction with Prp19 was further characterized by Chen et al. (1999). As mentioned above, Snt309/BCAS2 mediates stable interaction of Prp19 with CDC5. The BCAS2/SPF27 human homolog yeast Stn309 is an interactor and inhibitor of canonical tumor suppressor p53. Mutations of BCAS2 stimulates nuclear retention and phosphorylation of p53 leading to apoptosis (Kuo et al., 2009). It is thus intriguing that a mutation in the MOS4 *Arabidopsis* homolog of Snt309/BCAS2 was identified by screening for suppressors of constitutive activation of innate immunity pathway in the *snc1* mutant, which implies the induction of programmed cell death (Palma et al., 2007).

1.10. PLEIOTROPIC REGULATORY LOCUS 1 (PRL1) and its paralogue PRL2

The Pleiotropic Regulatory Locus 1 was first identified in *Arabidopsis* by characterization of a T-DNA insertion mutation, which caused highly pleiotropic defects including concomitant alterations in the regulation of root and leaf development, flowering time, sugar, cold, ethylene, cytokinin, and auxin responses (Németh et al., 1998). As another NTC mutants, the *Arabidopsis prl1* mutation conferred also cold sensitivity (i.e., seedlings displayed characteristically slower development under moderately low (14°C) temperature conditions (Németh et al., 1998).

In the first isolated insertion mutant allele of *PRL1* gene the T-DNA insertion removed part of the last C-terminal WD40 repeat coding region. The viability of this *prl1-1* mutant thus suggested that the mutation might have caused only a partial loss of function. This possibility was also supported by the observation that a T-DNA insertion mutation removing the C-terminal PRL1-binding domain of CDC5 resulted in a mutant phenotype undistinguishable from that of the *prl1-1* mutant (Palma et al., 2007). However, other genuine knockout mutations located in the coding sequence of CDC5’s SAINT DNA binding domain resulted in gametophytic lethality demonstrating that CDC5 is an essential NTC factor. This has strengthened the original conclusion of Németh at al. (1998) who found that PRL1 has a very close paralog PRL2 in *Arabidopsis* and suggested that these duplicated NTC subunits perform at least partly redundant functions. Both structural modelling of U5 snRNP in association with the NTC (Yan et al., 2016) and proposed structure of the NTC core (de Moura et al., 2018) indicate that NTC is located on the periphery of U5 snRNP and U4/U6.U5 tri-snRNP, as well as in the centre of core NTC formed by PRP19, SPF27 (Snt309) and CDC5L in close vicinity of SKIP (Prp45). The fact that the *prl1* mutation results in prominent activation of numerous abiotic stress induced genes (e.g., UV stress induced intronless genes of flavonoid biosynthesis; Németh et al., 1998) correlates with the observation that Prp45 (SKIP) was found in fission yeast to interact with the RNA polymerase II CTD-binding U2 snRNP factor U2AF35, which recruits very early on spliceosomal components to the transcription machinery (Ambrozková et al., 2001). On the other hand, the contact between PRL1 and SKIP (Prp45) also suggests that the *prl1* mutation likely inhibits spliceosome recycling (i.e. thereby reducing splicing efficiency) because SKIP (Prp45) is also required for recruitment of the Prp22 helicase mediating spliceosome dissociation (Gahura et al., 2009). From this point it is notable that transcription of *Arabidopsis* SKIP/Prp45 is stimulated by ABA and osmotic stresses and its overexpression confers osmotic stress tolerance (Lim et al., 2010), while the *prl1* mutation causes ABA and sugar hypersensitivity (Németh et al., 1998). The latter authors showed that PRL1 interacts with a specific member of the α-importin family, ATHKAP2/IMPA-3, which mediates likely its nuclear import. (Németh et al., 1998). Inactivation of IMPA-3 in the *Arabidopsis mos6* mutant was reported to suppresses constitutive activation of innate immunity by the *snc1* mutation similarly to the *mos4* (*snt309*), *cdc5* (*mac1*), and *prl1* (*mac2*) mutations (Palma et al., 2005, 2007). CDC5 in human cells is imported into the nucleus by the CTNNBL1 (catenin-β-like 1) armadillo repeat protein. CTNNBL1 remains then part of the human core NTC and mediates interaction with the PRP31 subunit of U4/U6 snRNP (Grote et al., 2010). It is remarkable that temperature sensitive mutations of fission yeast CDC5 and PRL1 homologs show synthetic lethality at permissive temperature (McDonald et al., 1999) indicating that the functions of these interacting NTC proteins are indeed required for cell viability. C-terminal deletions in CDC5 were observed to stimulate dissociation of PRL1 from the NTC in yeast (Ohi and Gould, 2002) but did not lead to complete loss of NTC function, which is consistent with the observations made in *Arabidopsis*. By contrast, RNAi-silencing of *Arabidopsis* CDC5 was suggested to result in a G2/M cell cycle defect by affecting the transcription of SHOOT MERISTEMLESS (STM) and WUSCHEL (WUS) (Lin et al., 2007). In comparison, knockouts of sole mouse and zebrafish PRLG1/PRL1 homologs result in dissociation of CDC5 from the NTC. Inactivation of PLRG1/PRL1 in animal cells leads to nuclear to cytoplasmic translocation of CDC5, stimulation of p53 and histone H2AX phosphorylation, and induction of apoptosis. Consequently, *prl1* knokcout mice embryos decay 1.5 days after fertilization (Kleinridders et al., 2009).

Due to lethality of *prl1* and *cdc5* null mutants in other multicellular organisms, the viability of *Arabidopsis* plants carrying different *prl1* mutant alleles provides a unique opportunity to study pathway specific regulatory functions of the NTC. Preliminary studies addressing this possibility however revealed that inactivation of the *Arabidopsis PRL1* paralog *PRL2* arrests embryo development during the early heart stage (Szakonyi, 2006). This observation indicates that PRL1 and PRL2 perform indeed only partially redundant functions. This might imply that they could replace each other in splicing-related functions of the NTC, whereas PRL2 could play a distict role in controlling embryo development through some DNA replication, repair or cell cycle related function. Although plants lack othologs of canonical mammalian p53 tumor suppressor, functional homologs of replication protein complex subunits, such as RPA and numerous factors involved in double-stranded DNA and transcription-coupled repair are conserved in *Arabidopsis*, including ATM (González Besteiro and Ulm, 2013). Further exploitation of *Arabidopsis prl1* and *prl2* mutations thus might provide valuable information about conserved functions of NTC in genome-wide regulation of transcription with and without implication of splicing defects casued by compromised function of NTC, as well as about roles of the NTC in DNA repair, replication, cell cycle and various other developmental pathways.

1.11. Regulatory interactions between chromatin modifications and alternative splicing

The paradigm of the kinetic model on coupling between transcription and alternative splicing predicts that histone modifications regulate transcriptional initiation and elongation rates which in turn affect alternative splicing (Luco et al., 2010; Naftelberg et al., 2015). During transcription initiation, Ser5 residues of heptapeptide repeats in the C-terminal domain of the RNAPII largest subunit are phosphorylated by the kinase module of TFIIH. The Ser5 CTD modification is recognized by numerous transcription activators, including homologs of yeast SET1/SETD and human MLL methyltransferases, which deposit histone H3K4me3 chromatin marks around the transcription start site potentiating transcription initiation (Zhang et al., 2015). The human MLL and yeast COMPASS histone H3 Lys4 methyltransferase complexes share functionally conserved subunits including ASH2L and its yeast homologs Cps40/Cps60. Mutations of ASH2L homologs deplete the H3K4me3 mark and reduce splicing efficiency immediately after transcription initiation (Dou et al., 2006; Steward et al., 2006; Sims et al., 2007; Shilatifard, 2008; Vermeulen et al., 2010). The H3K4me3 is recognized by so-called reader or adaptor proteins, such as the SNF2-related chromodomain DNA helicase CHD1, which interacts with and aids further recruitment of the U2 snRNP (Vermeulen et al., 2010). In yeast, the Sgf29 tudor domain subunit of the SAGA histone acetyltransferase (HAT) complex acts as H3K4me3 reader and targets SAGA to this histone mark during transcription initiation. Yeast Sgf29 and human CHD1 interact with U2 snRNP, thus promote assembly of spliceosomal complex A in a H3K4me3-dependent fashion (Vermeulen et al., 2010; Schneider et al., 2004; Bernstein et al., 2005; Barski et al., 2007; Heintzman et al., 2007; Guenther et al., 2007; Mikkelsen et al., 2007).

H3K4me3-dependent targeting of HATs result in histone H3 lysine 9/14 acetylation (H3K9/14ac), which is a hallmark of relaxed chromatin at active promoters (Zhou et al., 2010; Gates et al., 2017). In human cells histone deacetylase (HDAC) inhibitors increase H3K9ac levels and have an impact on alternative splicing patterns of both transiently expressed splicing reporter minigenes and at least about 700 endogeneous transcripts (Hnilicová and Staněk, 2011; Hnilicová et al., 2011). Apparently, histone acetylation preferentially modulates alternative splicing of genes that are rapidly activated or repressed in response to changing conditions. During neuronal cell depolarization, an increased exon skipping was observed in the NCAM (CD56, neural cell adhesion molecule 1) pre-mRNA following hyper-acetylation in H3K9. Schor et al. (2009) found that H3K9ac modulates alternative splicing in correlation with a higher elongation rate of RNAPII.

In the case of human fibronectin gene binding of the SRp40 (SRSF5) splicing factor to splicing enhancer sequences plays an important role in initial recruitment of U1 snRNP to the first functional 5' splice site in elongating pre-mRNA (Hnilicová et al., 2011). Subsequently, the U1snRNA becomes associated with the TFIID and TFIIH general transcription factor complexes, and by interacting with cyclin H enhances the phosphorylation of S5 residues in the heptapeptide repeats of RNA polymerase II largest subunit CTD by the cyclin H-dependent CDK7 protein kinase. The yeast histone acetyltransferase Gcn5, a component of the SAGA complex predominantly acetylates histones at promoters and acts as an anchor, which stabilizes the binding and regulates the recruitment of U2 snRNP to the transcription unit (Hassan et al., 2002; Baker and Grant, 2007; Gunderson and Johnson, 2009). The yeast Msl1 and its mammalian U2B bromodomain components of U2 snRNPs play a chief role in recognition of the H3K9ac mark promoting promoter proximal assembly of U1 and U2 snRNPs (Hassan et al., 2002). Consequently, the presence of a 5’ splice site near the promoter enhances the recruitment of transcription activators and the assembly of RNAPII elongation complex (Fong and Zhou, 2001; Furger et al., 2002; Nogués et al., 2002; Damgaard et al., 2008). In any case, splice site mutations result in Rrp6-dependent nuclear retention of unspliced pre-mRNAs and subsequent downregulation of splicing defective genes (Eberle et al., 2010).

After transcription initiation, recruitment of the positive transcription elongation factor b (P-TEFb) and CycK/CDK12 complex (corresponding likely to plant CDKCs) to Ser5 phoshorylated RNAPII CTD stimulates further phosphorylation of Ser2 residues of heptapeptide repeats. The Ser2 phosphorylated CTD is recognized by conserved SET2 type histone methyltransferases, which are loaded onto the RNAPII in interaction with the elongation and PAF complexes catalyzing the deposition of H3K36me3 marks on nucleosomes in gene bodies. Recognition of H3K36me3 mark by the yeast Eaf3 chromodomain subunits of Rpd3 histone deacetylase (HDAC), as well as by its human and Drosophila homologs MRG15 (MORF-related gene 15)/MORF4L1 (mortality factor 4 like 1) in association with the HDAC1 complex, prevents the deposition of H3K9ac mark in gene bodies inhibiting internal transcription reinitiation (Yochum and Ayer, 2002; Joshi and Struhl, 2005; Carrozza et al., 2005; Govind et al., 2010; Jelinic et al., 2011; Zhang et al., 2003; 2015). At the same time, these H3K36me3 readers recruit the splice site selecting factor PTB1 (polypyrimidine tract-binding protein 1), a component of U2 snRNP. In the human fibroblast growth factor receptor 2 (FGFR2) pre-mRNA, PTB1 is targeted to splicing suppressor squences of an alternative intron located closeby an alternative (exonIIIb) and thus regulates alternative splicing (Luco et al., 2010). Remarkably, MRG15 can also recognize the H3K4me3 mark and has been identified in a repressor complex together with the JmjC domain-containing H4K4me3 demethylase RBP2, which inhibits the histone deacetylase Rpd3 (Hayakawa et al., 2007; Lee et al., 2009). Knock-down of MRG15 influences alternative splicing of more than 180 genes independently of PTB. Thus, MRG15 appears to control alternative splicing also by a PTB-independent mechanism (Luco et al., 2010). Genome-wide ChIP-Seq studies indicate that the H3K36me3 histone mark is enriched on exonic nucleosomes, as well as that nucleosomes are preferentially positioned in exons (Schwartz et al., 2009; Andersson et al., 2009; Tilgner et al., 2009). A negative correlation between exon positioning, and histone marks versus the strength of certain splice sites suggests that histone marks might aid marking of exons that are flanked by weak splice sites (Tilgner et al., 2009; Spies et al., 2009).

In contrast to the activating histone marks discussed so far, the methylation of H3K27 and H3K9 residues, as well as ubiquitination of H2A(K119) are associated with transcriptional repression and mark silent loci. Data on cross-talk between repressive chromatin marks and alternative splicing are less numerous compared to histone marks involved in co-transcriptional regulation of splicing. The H3K27me3 mark is deposited by Polycomb Repressor Complex 2 (PRC2). In human cells, trimethylation of H3K27 close to an alternative exon was observed to stimulate alternative splicing, i.e., inclusion of exon E33 into the fibronectin pre-mRNA (Alló et al., 2009). H3K9 methylation plays a major role in silencing of heterochromatic loci (Vakoc et al., 2005, Barski et al., 2007; Hon et al., 2009). Saint-André et al. (2011) demonstrated that the recruitment of human chromodomain transcription repressor HP1γ to trimethylated histone H3K9me3 enhances inter-nucleosomal interactions and chromatin compaction, which decreases the RNAPII elongation rate favouring alternative splicing of pre-mRNA transcribed from the human CD44 gene. Recently, PTB, along with other splicing regulator hnRNP proteins (hnRNP A1, hnRNP L, hnRNP K, hnRNP A2/B1, hnRNP A/B), were identified to recognize H3K9me3 (Vermeulen et al., 2010). Surprisingly, Drosophila Heterochromatin Protein 1 (HP1a) was identified in different classes of heterogeneous nuclear ribonucleoproteins (hnRNPs) involved in RNA processing of over hundred of euchromatin genes (Piacentini et al., 2009). Both H3K9me2 and H3K9me3 marks are enriched at introns rather than exons (Spies et al., 2009; Dhami et al., 2010). The processivity of RNA polymerase II is decreased with induced heterochromatin formation near alternative exons, which enhances the inclusion of exons. This raises the possibility that that H3K9 methylation regulates splicing of certain genes directly through tethering of splicing factors, such as PTB and hnRNPs.

1.12. Aims of the present work

The PhD project presented here has four major goals aiming at:

i) Genome-wide analysis of *prl1* splicing defects and their pathway specific consequences
ii) Characterization of splicing defects of selected ribosomal protein genes in the *prl1* mutant
iii) Generation of viable *prl2* mutant cells by creating conditionally complemented genetic mosaics
iv) Analysis of differential genome expression and pre-mRNA splicing in *prl2* mutant cells isolated from genetic mosaics.

2. MATERIALS AND METHODS

2.1. Materials

2.1.1. Chemicals, enzymes and laboratory supplies

Company	Product
Abcam plc Ltd., Cambridge, UK:	Antibodies
Agrisera AB Ltd, Vannas, Sewden:	Antibodies
Enzo Life Sciences GmbH, Lorrach, Germany:	Antidoies
Merck Chemicals GmbH, Darmstadt, Germany:	ECL^{TM}Enhanced Chemiluminescence Kit
	Hybond^{TM}-N nylon membrane
Beckman Instruments Inc., Palo Alto, USA:	Centrifuge tubes
BIOMOL GmbH, Hamburg, Germany:	X-Gal(5-Bromo-4-Chloro-3-Indolyl-1-ß-D-galactopyranoside)
Bio-Rad, München, Germany:	Bradford Reagent
	Pre-stained Protein Standard
	Goat anti-Rabbit-HRP IgG (H+L)
Boehringer Mannheim, Germany:	RNase A
Calbiochem Corp., Darmstadt, Germany:	Ethidium bromide
Difco Laboratories, Detroit, USA:	Bacto-agar
	Bacto-peptone
	Bacto-tryptone
	Yeast Extract
Duchefa, Haarlem, the Netherlands:	ATP
	Carbenicillin Disodium Salt
	Cefotaxime sodium
	Phytoagar
	Ticarcillin/Clavulanic Acid
Eppendorf AG, Hamburg, Germany:	Safe-lock tubes (0.5, 1.5 and 2.0 ml)
	Single use pipette tips
Eastman Kodak Co., Rochester, USA:	Kodak X-Omat AR-5 Film
Cambrex Bio Science Inc., Rockland, USA:	Seakem® LE Agarose
Invitrogen GmbH, Karlsruhe, Germany:	1kb molecular mass marker
	Restriction endonucleases
	Taq DNA Polymerase
Greiner bio-one GmbH, Kermsmünster, Austria:	Petri dishes
	Falcon tubes (15 and 50 ml)
	Cellstar® Suspension culture plates

Heirler Cenovis GmbH, Radolfcell, Germany:	Milk Powder
Merck, Darmstadt, Germany:	2-propanol
	Chloroform
	Ethanol
	D-Glucose
	Glycine
	N, N-dimethylformamide
	General chemicals
Invitrogen, Thermo Fisher Scientific, Germany:	Oligonucleotides
Millipore, Bedford, USA:	Filter 0.025µm white VSWP
	Immobilon^{TM}-P (PVDF membrane)
	Sterivex^{TM} 0.22µM filter units
New England Biolabs, Frankfurt am Main, Germany:	Restriction Endonucleases
Qiagen GmbH, Hilden, Germany:	miRNeasy mini kit
	QIAquick® PCR purification kit
	RNeasy Plant Mini Kit
Macherey Nagel:	Nucleospin RNA plant
Agrisera AB Ltd, Vannas, Sewden:	Goat anti-Rabbit IgG, (H+L), HRP
	Rabbit anti-Chicken IgG, (H+L), HRP
Sigma-Aldrich Co., St. Louis, USA:	Calcium hypochlorite
ChromoTek GmbH, Martinsried, Germany:	anti-GFP
Carl Roth GmbH, Karlsruhe, Germany:	dNTP solutions
	Filter units 0.22µm
	Phenol
Serva Electrophoresis GmbH, Heidelberg, Germany:	Cellulose R-10
	Macerozyme R-10
	Bromphenol Blue-Na-salt
	Ponceau S solution
	Sarcosyl
	SDS
Sigma-Aldrich Co., St. Louis, USA:	Ammoniumpersulfate
	Antibiotics
	BSA
	CTAB (Cetyl-trimethylammonium bromide)
	DTT (Dithiothreitol)
	Goat anti-Rat IgG, (H+L), HRP
	Lithium acetate
	PMSF (Phenylmethylsulphonyl fluoride)

	PVP-40 (Polyvinyl pyrrolydone-40)
	β-mercaptoethanol
	Sucrose
	TEMED
	TritonX-100
	Tween-20
	General chemicals
Whatman, Maidstone, USA:	3MM paper
	Whatman circles

2.1.2. Bacterial Strains

2.1.2.1. *E. coli* strains

DH10B	Δ(*mrr-hsd* RMS-*mcr*BC) *mcr*A *rec*A1

2.1.2.2. *Agrobacterium tumefaciens* strains

GV3101 (pMP90RK)	C58C1, rif, pMP90RK (pTiC58ΔT-DNA), Gm^{r,} Km^{r} (Koncz and Schell, 1986)

2.1.3. Plant Material

2.1.3.1. *Arabidopsis thaliana*

Genotype	Ecotype	Obtained from
Wild-type	Col-0	Rédei, 1992
prl1	Col-0	Nemeth et al., 1998
prl2 GABI_228D02	Col-0	Rosso et al., 2003
prl2 KONCZ16136	Col-0	Rios et al., 2002
pPCV812-PRL1::GUS	Col-0/*prl1*	Szakonyi, 2006
pPCV812-PRL2::GUS	Col-0/*prl2*	Szakonyi, 2006

2.1.4. Oligonucleotides

2.1.4.1. Oligonucleotides for *PRL2gDNA-HS*

BastaF	5’-GAAGTCCAGCTGCCAGAAACCCAC-3’
pNOSR	5’-CCGTTTTACGTTTGGAACTGACAGAACC-3’
pNOSF	5’-GTGCTTAGCTCATTAAACTCCAGAAACCC-3’
CaMV35SF	5’-CACTATCCTTCGCAAGACCCTTCCTC-3’
CRT1F	5’-AAAGCTGTTTCAGGATCTGGGTGGC-3’

CRT1R	5’-CTGCTCAAGGTACGCAAAAATACGGTC-3’
PRL2F	5’-CAGGAAGAATGGCCGTGCTTTTG-3’
PRL2R	5’-GAACAGGGAGGTCGAAACTCAGTCAC-3’
Gal4VP16F	5’-GAAGCCGAAGTGCGCCAAGTGT-3’
Gal4VP16R	5’-CTCGTCAATTCCAAGGGCATCGG-3’
GFP5F	5’-CTGTCAGTGGAGAGGGTGAAGGTGATG-3’
GFP5R	5’-GTCTTCGATGTTGTGGCGGGTCTT-3’

2.1.4.2. **Oligonucleotides for *qRT-PCR Standard***

PDF2-5	5’-CAGTATCGCTTCTCGCTCCAGTAATG-3’
PDF2-3	5’-CCGTATCATGTTCTCCACAACCGCT-3’
TIP41L-5	5’-CGATTTTGGCTGAGAGTTGATGGTG-3’
TIP41L-3	5’-CAACTGGATACCCTTTCGCAGATAGAG-3’
UBQ5-F	5’-CCAGAAGGAATCGACGCTTCATCTC-3’
UBQ5-R	5’-CTGTTGTAGCGGTAGATCGATCCTTCTC-3’

2.1.4.3. **Oligonucleotides for PRL2HS::GFP *qRT-PCR***

PRL2XHS-qRTfor	5’-GCAACTTGAATCTTATGGCAGAGCCG-3’
PRL2E1516F	5’-GGTCACTGGAGGTGATAAAGGTGGCT-3’
PRL2E17R	5’-GTTTTGTCTCCCTCACACGTTACCAGC-3’

2.2. General Buffers, Stock Solutions and Growth Media

2.2.1. Solutions

Phenol/Chloroform/Iso-amylalcohol:	mix to a ratio of 25:24:1
TE:	10 mM Tris.HCl, 1 mM EDTA, pH 8.0
X-gluc	20 mg/ml in N, N-dimethyl formamide
β-estradiol	10 mM in DMSO
MG132	50mM in DMSO

2.2.2. Antibiotics

Antibiotics	Stock solution	working concentration
Ampicillin	50 mg/ml in water	50 mg/L
Basta	200 mg/ml	250 mg/L
Carbenicillin	50 mg/ml in water	50 mg/L
Cefotaxime/Claforan	200 mg/ml in water	200-400 mg/L
Hygromycin	15 mg/ml in water	15 mg/L

Kanamycin	50 mg/ml in water	50mg/L for bacteria; 100mg/L for plants
Rifampicin	25 mg/ml in methanol	100 mg/L
Spectinomycin	50 mg/ml in water	100 mg/L
Sulfadiazine	7.5 mg/ml in water	15 mg/L
Tetracyclin	10 mg/ml in water	12.5 mg/L

All antibiotics were filter sterilized and stored at -20°C.

2.2.3. Hormones and growth factors

Abscisic acid (ABA)	1 mg/ml in methanol
6-Benzylaminopurine (BAP)	1 mg/ml 1N NaOH
2, 4-dichlorophenoxyacetic acid (2,4-D)	1 mg/ml ethanol
Indole 3-acetic acid (IAA)	1 mg/ml in 1N KOH
Kinetin	1 mg/ml 1N NaOH
1-naphtylacetic acid (NAA)	1 mg/ml 1N KOH
Salicylic acid (SA)	0.5 M in ethanol
Estradiol	10 mM in DMSO

All hormone solutions were filter sterilized and stored at -20°C.

2.2.4. Culture media

2.2.4.1. Bacterial media

2.2.4.1.1. LB medium

Bacto-Tryptone	10g/L
Bacto-Yeast Extract	5g/L
NaCl	10g/L

Adjust pH to 7.5 with NaOH. For solid media add 20g/L Bacto-Agar. Autoclave for 20 min at 120°C.

2.2.4.1.2. YEB medium

Beef Extrect	5g/L
Bacto yeast extract	1g/L
Bactopeptone	1g/L
Sucrose	5g/L

Adjust pH to 7.4 with NaOH. For solid medium add 15g/L Bacto-agar. Autoclave for 20 min at 120°C and after sterilization 20ml/L of 0.1M $MgCl_2$ was added.

2.2.4.2. **Plant media**

2.2.4.2.1. Plant cell suspension culture medium

Cell suspension:	MS Basal Mix	4.3 g/L
	B5 vitamin (100X)	10 ml
	Sucrose	3%

Adjust pH to 5.8 with KOH, autoclave at 120°C for 15 min and before use add 2,4-D to final concentration of 1mg/L.

B5 Vitamin (100X)	Nicotinic Acid	1mg/ml
	Pyridoxin-HCl	1g/ml
	Myo-Inositol	100mg/ml
	Thiamine-HCl	10mg/ml
Photosynthetic cell suspension:	MSMO Salts	4.4 g/L
	Sucrose	3%

Adjust pH to 5.8 with KOH, autoclave at 120°C for 15 min and before use add 0.5mg/L NAA and 0.1mg/L kinetin pH adjusted to 5.8 with KOH

2.2.4.2.2. Plant culture medium

MSAR medium (Koncz et al., 1994)

Macroelements	25.0 ml/L
Microelements	1.0 ml/L
Fe-EDTA	5.0 ml/L
$CaCl_2\cdot 2H_2O$	5.8 ml/L
KI	2.2 ml/L
B5 vitamin	2.0 ml/L
Sucrose	5g/L

pH was adjusted to 5.8 with KOH and 0.6 g/L phytoagar was added.

2.2.5. Antibodies

2.2.5.1. **Primary antibodies**

Anti-HA:	Rat monoclonal antibody (clone 3F10) to a peptide derived from the hemagglutinin protein of the human influenza virus (Roche). Dilution: 1:1000.
Anti-PRL1:	Rabbit polyclonal antibody raised against a PRL1 specific peptide (Nemeth et al., 1998). Dilution: 1:1000.
Anti-tubulin:	Mouse monoclonal antibody to α-tubulin (clone DM 1A), purified chick brain tubulin was used as immunogen (Sigma). Dilution: 1:1,000 or 1:2000.

2.2.5.2. Secondary antibodies

Goat anti-Rabbit IgG, (H+L), HRP	Dilution: 1:10,000
Goat anti-Rat IgG, (H+L), HRP	Dilution: 1:10,000

2.2.6. Bioinformatic Resources

2.2.6.1. Softwares

- CLC Genomic Workbench
- R Studio
- puTTY
- iQ5 Bio.Rad
- Adobe Photoshop CS
- DNASTAR (Editseq, Primer Select, Protean, SeqMan)
- ImageJ version 1.6.0_24
- Leica Confocal Software LCS Lite version 2.61
- Microsoft Office 2013

2.3. Methods

2.3.1. General molecular biology methods

2.3.1.1. Preparation of plasmid DNA (modified Birnboim and Doly, 1979)

A single *E. coli* colony was inoculated in 2 ml of LB medium supplemented with appropriate antibiotics. Bacterial cultures were grown overnight at 37°C with vigorous shaking (250 rpm). Cultures were transferred into 2 ml Eppendorf tubes and pelleted at 13,000 rpm speed for 2 min in a tabletop centrifuge. Then, the supernatant was removed, and cells were resuspended by vortexing in 250 µl of ice-cold solution I (50 mM Tris.HCl - pH 8.0, 50 mM glucose, 10 mM EDTA). Bacterial cells were lysed by adding 250 µl of freshly prepared solution II (200 mM NaOH, 1% SDS), and the tubes were gently inverted few times in order to mix solutions. After 5 min incubation, 500 µl of ice-cold solution III (3 M NaOAc - pH 4.8 or 3 M KAc - pH 6.0) was added to neutralize the lysate and the mixture was kept at 4°C for 30 min. The cell debris was removed by centrifugation at 13,000 rpm for 10 min. 1 ml of the supernatant was transferred into a new Eppendorf tube and nucleic acids were precipitated with 0.7 ml of isopropanol at -20°C for at least 10 min. Nucleic acids were pelleted by centrifugation at 13,000 rpm for 10 min and the supernatant was removed. Dried nucleic acids were resuspended in 0.5 ml of 25 µg/µl RNase A solution and incubated at 37°C for 1 h. Subsequently, DNA was dissolved in 50 µl of water or TE buffer.

2.3.1.2. DNA sequencing

Plasmids and DNA fragments were sequenced in collaboration with the Automatic DNA Isolation and Sequencing (ADIS) service of MPIZ. For sequencing, an Applied Biosystems 3730XL Genetic Analyzer was used.

2.3.1.3. Purification of DNA by Phenol/Chloroform extraction

To remove contaminating proteins, DNA samples were supplemented with 1/10 volume of 3 M sodium acetate solution (pH 5.2) and then mixed by vortexing with an equal volume of phenol/chloroform solution (1:1, v/v) and centrifuged at 13,000 rpm for 5 min. The aqueous upper phase was collected in a new Eppendorf tube and the extraction step with phenol/chloroform was repeated until there was no more precipitated protein ring between the water and organic solvent phases. Then, to remove phenol traces from the solution, an equal amount of chloroform: iso-amyl alcohol (24:1) mixture was added and vortexed. Phases were separated by centrifugation and DNA was precipitated by 0.7 volumes of ethanol.

2.3.1.4. DNA precipitation

DNA was precipitated using ethanol or isopropanol. In the case of ethanol precipitation, 1/10 volume of 3 M sodium acetate (pH 5.4) and 2 volumes of absolute ethanol were added to DNA samples, mixed and incubated at -20°C for at least 30 min. DNA was pelleted by centrifugation at top speed for 10 min. The DNA pellet was washed with 70% ethanol and centrifuged again. For isopropanol precipitation, 0.7 volumes of isopropanol were added to the samples and incubated on ice for at least 15 min. Then, DNA was pelleted by high-speed centrifugation (13,000 rpm for 10 min). DNA pellets were washed with 70% -20°C ethanol and dissolved in water or TE buffer.

2.3.1.5. Digestion with restriction endonucleases

Digestion of DNA samples was performed with restriction endonucleases according to the manufacturers' instructions. Typically, reactions were carried out in 1.5 ml Eppendorf tubes in a final volume of 20 or 50 µl using 1-5 U enzyme/µg DNA. The duration of the digestion varied from 2 h to overnight.

2.3.1.6. PCR amplification

For amplification of DNA fragments and bacterial colony, *Taq* polymerase (Invitrogen) was used. A master mix was prepared for five reactions using the following components on ice: 10 µl of 10X PCR buffer, 2 µl of 10 mM dNTP mixture, 3 µl of 50 mM $MgCl_2$, 5 µl of primer mix (10 µM each), 5 µl of template DNA, 1 µl of Taq DNA polymerase (5 U/µl), and the final volume was made up to 100 µl with autoclaved distilled water. For the PCR amplification, a Byozym Multicycler PTC 240 Tetrad^{TM} 2 machine was used. The reactions were performed in 20 µl final volume and the conditions for the PCR reactions were as follows: initial denaturation at 95°C for 5 min followed by denaturation at 95°C for

30 sec, annealing for 30 sec (with specific temperature for each primer), extension at 68°C for 30 sec to 3 min depending on fragment length and final extension at 72°C for 5 min. Normally 35 cycles were performed and the samples were stored at 4°C before further analysis.

2.3.1.7. **Isolation of plasmid DNA from *Agrobacterium tumefaciens***

Agrobacterium culture (5 ml) was grown for 2 days with constant shaking at 28°C. Bacterial cells were pelleted and then resuspended in 150 µl of solution I. Subsequently 300 µl of solution II was added to the cells and lysis was performed at 55°C for 10 min. Then, 225 µl of solution III was added and the mixture was incubated on ice for 10 min. Cell debris was removed by centrifugation at 13,000 rpm for 10 min. Subsequently, DNA was precipitated with 2 volumes of 100% ethanol and centrifuged at 13,000 rpm for 10 min. Pellet was washed with 70% ethanol, centrifuged and dried. DNA was dissolved in 50 µl of water or TE buffer. Plasmids were either analyzed by PCR amplification or they were transformed into *E. coli* for further analysis after preparation of plasmid DNA.

2.3.1.8. **Transformation of bacterial cells**

2.3.1.8.1. Preparation of electrocompetent *E. coli* cells (Dower et al., 1998)

A single colony from 1-5 days old plate was inoculated in 10 ml of liquid LB and the bacterial culture was grown overnight at 37°C with constant shaking (200 rpm). The next evening, 1 ml of this culture was inoculated into 300 ml of liquid LB and incubated overnight at 37°C with shaking. In the morning, the bacterial culture was diluted to OD_{600} 0.1-0.2 and the cells were incubated at 16-20°C with shaking until the OD_{600} reached 0.5-0.6. From this step on the bacteria were kept on ice. All centrifugation steps were performed at 4°C in plastic tubes pre-chilled at -20°C. For washing, ice cold distilled water was used. Bacteria were pelleted by centrifugation in Sorwall GSA tubes at 5,000 rpm for 20 min and resuspended in 200 ml of cold water. The washing step was repeated 3 times to remove salts, the cells were resuspended in 50 ml of water and transferred into a 50 ml falcon tube and bacteria were spun down for 10 min at 5,000 rpm. The supernatant was removed completely, and the cells were resuspended in 800 µl of water and divided into 50 µl aliquots in Eppendorf tubes. Competent cells were frozen immediately in liquid nitrogen and kept at -70°C.

2.3.1.8.2. Preparation of electrocompetent *A. tumefaciens* cells

Electrocompetent *Agrobacterium tumefaciens* was prepared using a similar protocol as in case of *E. coli* cells. Agrobacteria were incubated in liquid YEB medium at 28°C. After a final washing step, cells were resuspended in sterile 10% glycerol solution.

2.3.1.9. **Transformation of *E. coli* cells by heat-shock method**

1-5 µl of plasmid DNA was added to 50 µl competent bacterial cells. Cells were incubated on ice for 30 min and then heat-shocked at 42°C for 0.5-1.5 min. Recovery was done at 37°C for 1 h by adding 1 ml of LB medium. The transformation mixture was plated onto selective LB plates.

2.3.1.10. Electroporation of bacterial cells

An aliquot of competent *E. coli* or *A. tumefaciens* cells was thawed on ice. Cells were mixed with 0.5-3 µl of either plasmid DNA or pre-dialysed ligation mixture and transferred into prechilled 0.2 cm electroporation cuvettes. The transformation was performed in a Bio-Rad Gene Pulser set to 2.5 kV voltage, 25 µF capacitance, and 200 Ω resistance. After electroporation, bacteria were suspended in 1 ml of liquid LB medium, transferred into a centrifuge tube and incubated for 1 h at 37°C. After recovery phase, cells were spread on solid LB media supplemented with antibiotics. In the case of *A. tumefaciens*, cells were incubated at 28°C and plated on selective YEB medium.

2.3.1.11. Determination of protein concentration

To determine the protein concentration of samples, the Bradford assay was used (Bradford, 1976). After extraction, 1 or 2 µl of protein sample was mixed with 1 ml BioRad Protein Assay Concentrated Dye Reagent, which was previously diluted 5 times in water. After 5 min incubation at RT, the OD_{595} value was measured with a spectrophotometer. The protein amount was determined by the help of a standard curve obtained previously using a series of dilutions of bovine serum albumin (BSA).

2.3.1.12. Western blotting

2.3.1.12.1. Transfer of proteins from SDS-PAGE gels onto membranes

In order to detect proteins with specific antibodies, proteins separated by SDS-PAGE were transferred and immobilized onto Polyvinylidene difluoride (PVDF) membranes (Towbin et al., 1979). The membrane was rinsed in 100% methanol for 30 sec and then incubated in transfer buffer (50 mM Tris, 50 mM Boric acid - pH 8.0). The stacking gel was removed from the separating SDS-PAGE gel and the gel was equilibrated in 1X transfer buffer for 5 min. Then, a transfer “sandwich” was assembled using the following components: sponge layer, 3x 3MM Whatman paper, SDS-PAGE gel, PVDF membrane, 3x 3MM Whatman and sponge layer. This sandwich was placed in a transfer apparatus such that the membrane facing the anode and the gel sandwich was fully submerged in transfer buffer. Protein transfer was performed either for 2-3 h at 25 V or overnight at 10 V.

2.3.1.12.2. Staining of PVDF membranes

To monitor successful protein transfer and/or to determine equal protein loading, membranes were stained in Ponceau staining solution (0.2% Ponceau S in 3% trichloroacetic acid) for 1 min and the unspecific stain was washed out with water or 1X TBS solution (137 mM NaCl, 2.7 mM KCl, 20 mM Tris.HCl - pH7.4) (Hughes et al., 1988).

2.3.1.12.3. Antibody Probing

After protein transfer, the PVDF membranes were blocked in blocking solution (5% milk powder in 1X Tris-buffered saline (TBS) with 0.05% Tween-20) for 1 h at room temperature or at 4°C overnight. Then, the primary antibody diluted in blocking solution was poured on the membrane and incubated for

2 h followed by washing the membrane 3 times for 10 min with washing buffer (1X TBS with 0.2% Tween-20). Subsequently, the filters were incubated for 1.5 h with a horseradish peroxidase-conjugated secondary antibody diluted in blocking solution. The membranes were then washed 3 times for 10 min with washing buffer.

2.3.1.12.4. Detection of chemiluminescent signal

To visualize the position of proteins using horseradish peroxidase-conjugated secondary antibodies, an enhanced chemiluminescence (ECL) detection kit was used. Freshly prepared 1:1 mixture of the two ECL reagents was applied onto the PVDF membranes. Light emission was captured on Hyperfilm^{TM} by autoradiography and the films were developed in Hyperfilm.

2.3.2. Plant tissue culture and transformation

2.3.2.1. Plant growth conditions in the greenhouse

Arabidopsis thaliana plants were grown in 7 x 7 cm plastic pots at 22ºC day and 18°C night temperature, 70% humidity in trays under either short day (8h light/16h dark) or long day conditions (16 h light/8 h dark) under 200 to 400 µEinstein $m^{-2}s^{-1}$ irradiance.

2.3.2.2. Maintenance of *Arabidopsis* cell suspensions

The basal salt mixture including vitamins (B5 basal medium 3.2 g/L; Murashige and Skoog basal medium 4.4 g/L) was dissolved in distilled water. The 3% sucrose was added and stirred on a magnetic stirrer. Then pH was adjusted to the 5,8 with 1 N KOH and made up to volume with distilled water. Sterilized in autoclave at 121°C for 15 min. The plant hormone stock solutions were prepared according to manufacturer's instructions and sterilized them by filtration through sterile 0.2 µm filter units. Stored at 4°C. The plant hormones were added in concentration 0.5 mg/L 2,4-dichlorc phenoxyacetic acid (2,4-D), 2.0 mg/L indole3-acetic acid (IAA), 0.5 mgL 6-(y,y-dimethylallylamino~purine riboside (IPAR) to the autoclaved (cooled down) culture medium. Each week, 10-15 ml from 50 ml one-week-old *Arabidopsis thaliana* cell suspension was subcultured in 35-40 ml cell suspension medium for culture maintenance (Mathur and Koncz, 1998). The cells were grown under constant agitation of 120-150 rpm at 18-22°C.

2.3.2.3. Sterilization of *A. thaliana* seeds

Seeds were placed in an Eppendorf tube and immersed in 80% ethanol + 0.2% sodium hypochlorite for 15 min on a rolling platform for 10 min. Seeds were then rinsed 3 times with 80% ethonal and allowed to dry in a sterile hood overnight. The seeds were plated on appropriate growth medium.

2.3.2.4. **Agrobacterium-mediated transformation of *A. thaliana* plants using vacuum infiltration**

For transformation (Clough and Bent, 1998), plants cultivated in 10 cm pots (10-12 plants/pot) were used. 300-500 ml overnight culture of *Agrobacterium* cells were pelleted at 5000 rpm for 10 min. Agrobacteria were resuspended in 300 ml of transformation medium (½ MS salts, 1X B5 vitamins, 5% sucrose, pH 5.7, 0.044 µM BAP, 0.005% Silwet L-77) and inverted plants into liquid solution till entire rosettes were submerged. A vacuum was given until bubbles form on leaf and stem surface and solution starts to bubble a bit, then released vacuum very rapidly. The plants were removed from beaker, laid them on their side into a flat plastic and covered with plastic wrap to maintain humidity. The next day, uncovered plants and positioned upright. The plants were grown approximately four weeks. Finally, when siliques on plants were dried and harvested seeds.

2.3.2.4.1. Selection under sterile conditions

Seeds were sterilized in 15 ml tubes and sawn on MSAR medium containing appropriate antibiotics supplemented with cefotaxime to kill *Agrobacterium*. Antibiotic-resistant transformants were transferred first onto non-selective media, then later into the soil. Plants were cultivated in the greenhouse and seeds were collected for further analysis.

2.3.2.5. **Crosses of *Arabidopsis* plants**

To perform crosses of *Arabidopsis* plants following bolting, mature flowers and siliques were removed from stems. Two to three flowers were emasculated with a pair of forceps by removing petals, sepals, and immature anthers. Pollen from a mature male plant was used to dust the stigma. Seed maturation was monitored regularly, and fully-grown siliques were collected.

2.3.2.6. **DNA extraction from plant material**

For isolation of DNA from plants, the cetyl-methyl-ammonium bromide (CTAB) method adapted from Rogers and Bendich (1985) was used. Plant material was collected into centrifuge tubes and frozen in liquid nitrogen. Tissue was ground using a plastic rod fitted into a drilling machine. 0.5 ml of preheated (65°C) CTAB 2X (2% (w/v) CTAB, 100 mM Tris.HCl, 20 mM EDTA, 1.4 M NaCl, 1% (w/v) polyvinylpyrrolidone) was added to grind the tissue. The crude extract was vortexed and incubated at 65°C for 5-30 min, and then placed on ice. 0.4 ml of chloroform was added, and the extract was vortexed and centrifuged for 5 min at 13,000 rpm. 700 µl from the upper water phase was withdrawn and added to 1/10 volume (70 µl) of preheated (65°C) CTAB 10X (10% (w/v) CTAB, 0.7 M NaCl). Subsequently, 400 µl of chloroform was added, the sample was mixed well and centrifuged for 5 min at 13,000 rpm. Then, 0.6 ml of DNA extract from the upper phase was added to 0.6 ml of CTAB precipitation buffer (1% (w/v) CTAB, 50 mM Tris-HCl, 10 mM EDTA, and then mixed and centrifuged for 10 min at 13,000 rpm. The supernatant was completely removed and the pellet was air-dried for few minutes. The pellet was dissolved in 0.3 ml of high salt TE buffer (10 mM Tris-HCl, 1 mM EDTA, 1 M NaCl), and thereafter 0.6 ml of 100% ethanol was added. DNA was precipitated at -20°C for 15 min, and then collected by centrifugation for 15 min. Finally, the DNA sample was washed with 70% ethanol and after brief drying dissolved in 50 µl of 0.1 x TE.

2.3.3. Cell biological methods

2.3.3.1. Confocal laser scanning microscopy

The localization of GFP-tagged proteins in fresh tissue samples were captured with the Leica SP5 (Leica, Bensheim, Germany) system. GFP was excited with the Argon laser at 488 nm and the emitted fluorescence was detected between 505 and 535 nm, the autofluorescence of chlorophyll was detected at 620-720 nm. Simultaneous brightfield images were documented by a transmission detector. Merging of images and calculations of 3D projections were performed with the Leica LCS software. Selected images were processed with Adobe Photoshop.

2.3.3.2. Cell sorting

For cell sorting, PRL2HS-GFP protoplasts were prepared from cell suspension culture in 20 mL protoplast medium (20 mM KCl, 10 mM $CaCl_2$, 0.1 g/L BSA, 20 mM MES (pH 5.7), 0.4M Mannitol), supplemented with 1.5% (wt/vol) cellulose R-10 and 0.4% (wt/vol) macrozyme R-10. Free-floating single protoplasts from superficial cell layers were separated from remaining explant tissue by filtration through miracloth (MerckMillipore) and were centrifuged at 500 rpm for 10 min at 4°C and resuspended in 2.0 mL W5 medium to concentrate the suspension. The GFP-positive (GFP+) and GFP-negative (GFP–) cells were immediately separated on a FACS Vantage SE (Becton Dickinson) sorter for a maximum period of 2 h (30,000 cells s^{-1} flow rate; 100 µm aperture). The FACS work was done in Max Planck Institute for Biology of Ageing, Cologne. The sorted cells were used for RNA isolation and qRT-PCR experiments.

2.3.4. RNA methods

2.3.4.1. RNA extraction

RNA was extracted from the plant tissue by the RNeasy Plant Mini Kit (Qiagen), according to manufacturer's instructions using 50 to 100 mg of plant material ground in liquid nitrogen. To isolate RNA from larger amount of plant tissue, a CsCl density gradient purification protocol was used according to McGookin (1984). Plant material (2-5 g) was ground to powder with liquid nitrogen using a mortar and pestle followed by addition of 8 ml of GTC buffer (Guanidiumthiocyanate 4 M, Na-citrate 25 mM, Sarcosyl 0.5 %, and DEPC-treated H_2O to final volume) and 160 µl of ß-mercaptoethanol. Samples were let to thaw in a fume hood, transferred to a 15 ml falcon tube and mixed by inversion for 30 min at RT. After incubation, the supernatant was cleared by centrifugation at 4000 rpm for 30 min in a falcon tube centrifuge. 3 ml of supernatant was transferred to a 5 ml ultracentrifuge tube, on top of a 2 ml CsCl cushion (CsCl 5.7 M, EDTA 100 mM, and DEPC-treated H_2O to final volume) and centrifuged for 16 h at 35,000 rpm at 20 °C. After carefully removing the CsCl cushion containing DNA and impurities, the pelleted RNA was dissolved in 200 µl of DEPC-treated water and then precipitated by addition of 0.1 vol of 3 M NaOAc (pH 5.2) and 2.5 vol of ethanol at −20°C for 30 min. The RNA was pelleted by centrifugation for 15 min, washed with 1 ml of 75 % ethanol, and dissolved in 100 µl RNase-free water.

2.3.4.2. **Quantitative real-time PCR**

Quantitative real-time PCR (QPCR) was performed to validate the results from the transcript profiling experiments. A Bio-Rad iCycler device coupled to an iQ™5 Multicolor Real-Time PCR Detection System and controlled by the Bio-Rad iQ5 2.1 Standard Edition Optical System Software was used. The reaction was set up using the iQ™SYBR® Green Supermix (Bio-Rad) following the manufacturer's instructions. The qPCR primers were designed in a specific manner to prevent the possible amplification of genomic DNA. The primers were designed either to span an intron in the 3' region of the target transcript or to overlap exon-exon splice junctions. T_m (i.e. melting temperature) of the primers was optimally adjusted to 60°C. qPCR primer pairs used in this work are listed above. The general qPCR programme included the following steps: denaturation at 94°C for 15 s, annealing: 60°C for 30 s, extension at 72°C for 1 min/kb, measurement at 78°C for 20 s, and the melting curve at 65°C to 95°C 35Å~ to 40Å~. As a control, a melting curve analysis was performed with each primer combination to test for possible formation of primer dimers or unspecific amplification. The threshold cycle (Ct), inversely correlates with the target mRNA levels, and it corresponds to the cycle number at which the SYBR® Green fluorescence emission increases above a fixed threshold level. Ubiquitin Ct was used to normalize and compare the abundance of different input RNA quantity across samples.

2.3.4.3. **RNA seq**

Total RNA was extracted from 2-week-old plants of wt and *prl1* with using RNeasy Plant Mini (Qiagen) according to the manufacturer's instructions. The single-end library preparation was conducted using NEBNext Ultra II DNA Library preparation kit (new, New England Biolabs, Inc.) and sequencing was done on the Illumina HiSeq 2000 platform. The sequencing libraries were prepared at MP-GC and library preparation steps were always adjusted according to the centre's current best practices or the sample concentration.

2.3.4.4. **RNA seq by Ovation RNA-Seq System V2 (Nugen)**

The preparation of sequencing libraries have been done at max-planck genome center. Total RNA was isolated from protoplast after separation of the prl2::GFP+ and PRL2::GFP- using the miRNeasy mini kit and treated with RNase-free DNase I. The RNA was prepared for RNA-Seq library construction using Ovation RNA-Seq System V2 (Nugen), which is an isothermal linear nucleic acid amplification system for whole-transcriptome sequencing with input total RNA as little as 50 pg. First, total RNA is subjected to the first strand cDNA synthesis through the reverse transcription reaction with a combination of random hexamers and a poly-T DNA/RNA chimeric primer. The resulting cDNA/mRNA heteroduplex contains a unique sequence at the 50 end. Then, a heating step is used to degrade the original RNA template. The second strand cDNA is synthesized with the first-strand cDNA as template, using DNA polymerase. The double-stranded cDNA is then purified and amplified using a single-primer, isothermal, linear amplification (SPIA) process. SPIA uses RNase H enzyme to degrade the RNA sequence that is complement to the unique sequence at the 50 end of the DNA/RNA heteroduplex double-stranded cDNA. This results in the exposure of a DNA sequence for the SPIA DNA/RNA chimeric primer to hybridize. Subsequently, DNA polymerase initiates replication at the 30 end of the primer by displacement of the existing forward strand. Once again, RNase H enzyme degrades the RNA portion at the 50 end of the newly synthesized ds-cDNA, and the hybridization of the SPIA chimeric to the exposed DNA, DNA polymerization, and strand displacement repeats. The SPIA product is then subjected to a sequencing library preparation process. The sequencing was done on the Illumina HiSeq 2000 platform.

3. RESULTS

3.1. Genome-wide analysis of DE and DAS in the *prl1* mutant

3.1.1. Considerations to transcript profiling of spliceosomal/NTC mutants

Since the first description of the *Arabidopsis prl1* mutant by Németh et al. (1998), which defined its highly pleiotropic traits, including hypersensitivity to sucrose/glucose, ABA, cytokinin etc., several transcript profiling studies exploited *prl1* as a tool to identify gene regulatory networks controlled by sugar, ABA and stress signaling. Our current knowledge on transcription networks is still mostly based on Affymetrix transcript profiling experiments. The Arabidopsis Affymetrix ATH1 chip carries about 22,500 oligonucleotides representing about 24,000 gene sequences, which have been annotated in 2000, just after the completion of the *Arabidopsis* genome sequence. The ATH1 chip fails to detect the majority of pri-microRNAs, siRNAs, long and circular RNAs, and genes which have been annotated later in the TAIR10 genome version, including 27,416 protein coding genes, 4827 pseudogenes or transposable element genes and 1359 ncRNAs (33,602 genes in all, 41,671 gene models). To improve the technology, the Affymetrix Tiling 1.0R arrays provided the whole genome sequence in form as 35nt oligonucleotides on chip, which permitted the detection of hybridization signals on the newly annotated genes. In 2010, the International *Arabidopsis* Information Consortium in collaboration with teams working on alternative splicing initiated improved annotation of transcript isoforms based on deep Illumina RNA-Seq analyses of samples. In 2017, this project succeeded the assembly of a Reference Transcript Dataset for *Arabidopsis* (AtRTD2), which identified 82,190 non-redundant transcripts from 34,212 genes (Zhang et al., 2017a). Although so far environmental effects known to modulate alternative splicing have not been covered, the new database indicated that over 60% of genes have 2 or more alternatively spliced (AS) transcript isoforms, about 18% of which represent substrates for degradation by the NMD pathway. Although several studies suggest nuclear retention of intron-containing transcripts, experimental evidence is still missing for identification of translated mRNA isoforms through large-scale mass spectrometry analysis of corresponding proteins. Given these facts, it is clear that neither Affymetrix ATH1 nor Tiling 1.0R chips can detect multiple transcript isoforms, which could code for protein isoforms with altered function (dominant negative or positive forms missing or carrying certain catalytic, DNA/RNA binding domains, or organellar/secretion signal peptides etc.). Furthermore, it is difficult to predict *a priory* how much increase in the distance between a premature translational stop codon and polyA-site will target a transcript for NMD degradation, and what are the effects of AS-mediated changes in the length of 5’-UTRs on translation, RNA export and stability.

As discussed by Zhang et al. (2017a), Illumina short read sequencing is not the best tool for quantitative RNA-Seq analysis of transcript isoforms, since the preciseness of isoform identification largely depends on the window size of sequence signatures, which serve as unique identifiers for measuring the quantity of specific transcript isoforms. The higher is the number of overlapping transcript isoforms per gene, with alternative 5’ or 3’ splice sites or transcript ends differing in only few nucleotides, the higher is the error rate of isoform identification and measurement. Consequently, the error of conventional RNA-Seq analysis using various mapping programs is estimated as high as 35 to 50%. A common approach is to perform unidirectional strand sequencing and mapping the reads between known gene boundaries and to sequences of so far known transcript isoforms. Commercial software packages, such as the CLC Bio Genomics Workbench RNA-Seq option (Qiagen) or NextGene, or Genious etc. use this approach with different algorythms and error rates. Unfortunately, CLC Bio employs a transcript isoform numbering, which is different from the latest TAIR10/Araport 11 annotation, as well as gene name abbreviations differing from the accepted TAIR conventions (i.e., based on the nomenclature of the Uniprot database). As the CLC annotation files are not available from Qiagen, one has to construct first a combined annotation file, which allocates the proper TAIR10/Arapot11 gene names and functions to the CLC Bio annotation list.

Mapping of short Illumina reads can be similarly performed by the TopHead2 and CLCBio or NextGene programs, whereas the assembly of transcripts is routinely achieved using Cufflinks, which allows the identification of new splicing isoforms in an unbiased fashion. In our study, we relied only on mapping the reads to known transcript isoforms present in the CLC Bio database, independently from the identification of novel transcript isoforms, which have been detected in the *prl1* mutant by Cufflink assembly (collaboration with Baixong Song, MPIPZ). The RNA-Seq analysis pipeline used in this work is depicted in Figure 3.

First, we mapped all reads to the genome sequence resulting in a CLC GE (Gene Expression) dataset, which measures the number of reads between gene boundaries represented by the outmost 5’ and 3’ ends of known cDNAs of a gene. Following the conventions, we named this dataset **DE** (**Differentially Expressed**) genes. In parallel, the reads were mapped to transcript isoforms using the TE (Transcript Expression) mapping option of CLC Bio. The TE data defined thus a list of **Differential Alternative Splicing** (**DAS**) events. The quality of triplicate samples was assessed using PCNA (Principal Component Analysis), and then the data was subjected to filtering for 2-fold DE and DAS values at $p<0.05$ standard error. Next, the list of DE genes was combined with the DAS list, which is only predictive (because of the above mentioned errors derived from the size limitation of transcript isoform-specific signature sequences versus the number of overlapping reads in the samples).

The combined DE-DAS list was sorted for DE genes matching to one or more DAS transcripts, which yielded also two outhanging groups: DE genes not matching to DAS transcripts (DE-alone), and DAS-alone transcripts, which did not match DE values corresponding to the cut off parameters 2-fold change and $p<0.05$ error. The unique DE-alone data represents genes, where the reads could be mapped to gene sequences but only partially to known transcript isoforms, suggesting that in the analysed mutant additional transcript isoforms might exist, which should be further identified. By contrast, the DAS-alone list, for which no corresponding DE values passed the filter, represents differentially (i.e., often contrastingly) regulated transcript isoforms with potentially different coding capacity. Differential up- or downregulation of these transripts in the population of all isoforms does not exceeed the 2-fold change of reads mapped to a gene yet could dramatically alter the ratio of transcript isoforms encoding wt and altered protein products.

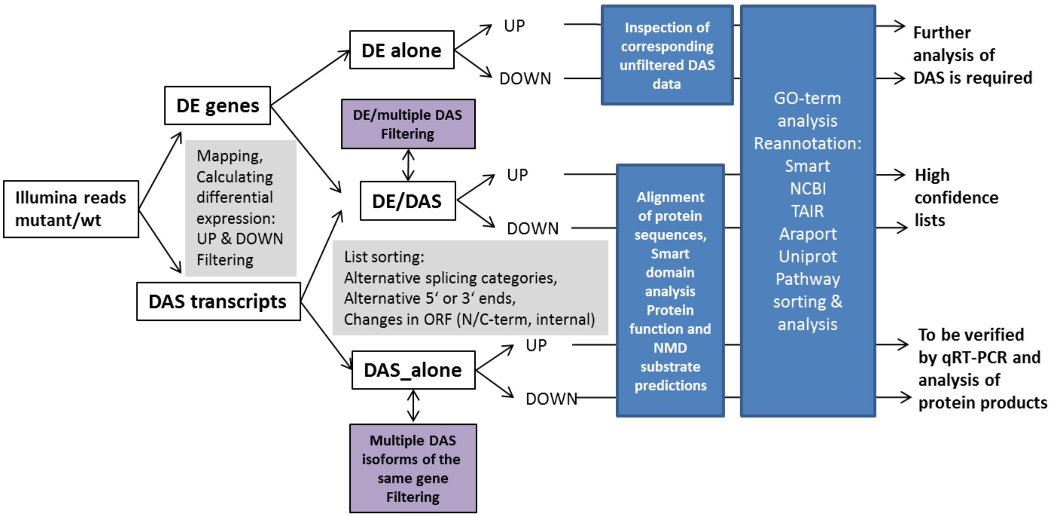


Figure 3: Pipeline of bioinformatics analysis of RNA-Seq data.

After mapping of sequence reads to genes and transcript isoforms, calculation of differential expression and filtering the data using the CLC Genomics Workbench RNA-Seq software, the data were processed as described in the text.

Those DE genes, where the up- or downregulation values matched with similar differential expression values of single DAS transcript isoforms represent the highest confidence class in the analysis. By contrast, DE genes rendered to multiple DAS transcript isoforms showing contrasting up- or downregulation defined the lower confidence class because currently it is difficult, if not impossible, to predict the final readout of differential expression of multiple mRNA isoforms with different coding capacity. Consequently, the DE/multiple DAS dataset was only taken into account, when all DAS transcript isoforms showed similar up- or downregulation as the corresponding DE gene value.

In the next step of analysis, all DAS transcript isoforms were classified for the type of alternative splicing event (i.e., retained introns; intron and exons corresponding to retained introns or exons compared to other transcript isoforms, respectively; exon skip; alternative 5’ and 3’ (or both) splice sites or transcript ends). In addition, each splicing event was classified whether it has changed the ORF (i.e., coding sequence). Subsequently, each DAS transcript isoform was individually translated to examine whether it codes for the predicted longest wild-type protein product or for an altered isoform carrying N- or C-terminal truncation or internal deletion. Following the alignment of wt and predicted altered protein isoform sequences, it was examined using the SMART protein domain database (http://smart.embl-heidelberg.de) whether alterations in the protein sequence influenced the presence of known functional domains (i.e., active sites of enzymes, DNA/RNA binding domains, sorting signals etc.). On this way, the predicted protein products were classified to carry: N-terminal deletions, internal deletions, and C-terminal truncations. In the case of N-terminal deletions, we specifically identified organelle targeted and secreted proteins, predicting a change in their cellular localization. Similarly, internal deletions in functional domains indicated a loss of normal function. Thus, e.g., upregulation of a transcript isoform coding for a functionally defective protein was predicted to decrease the ratio of wild type product, and thus, instead of enhancement, suggested an inhibition of the gene function (for downregulation *vice versa*). In the case of C-terminal truncations, which removed known functional domains or changed the 3' cDNA sequence by increasing the distance between a new stop codon and transcript end by more than 100 nucleotide, the transcript isoforms were predicted (in agreement with the Araport 11 database) to represent potential NMD substrates. Consequently, downregulation of such potentially degraded transcripts was predicted to lower the representation of nonfunctional transcript isoform by increasing the ratio of wt protein coding isoforms, and thus resulting in an enhancement of the gene function (for upregulation *vice versa*).

This analysis pipeline provided high confidence lists of up- and downregulated DE/DAS, the less confident DE-alone, and the least confident DAS-alone datasets based on the analysis of changes in the protein products and their functional domains, as well as NMD substrate prediction. Each gene in these filtered lists was rendered to a GO-term, if known, and then the up and downregulated gene lists were analysed for the enrichment of particular GO-terms using the GO Tools database (https://go.princeton.edu). Finally, the annotation of each gene was updated based on functional predictions derived from the SMART domain analysis, as well as identification of conserved orthologs of predicted proteins in other species and inspecting the relevant publications and curated informations in the NCBI, TAIR, Araport and Uniprot databases. For simplifying the classification of gene functions, we used a more general pathway classification in linkage with the GO terms and correlation with pathway-specific alterations detected previously in the examined mutants.

3.1.2. RNA-Seq analysis of differential gene expression and alternative splicing in *prl1-1* mutant seedlings

For the RNA-Seq analysis we used *prl1-1* mutant seedlings, which carried a tandem repeat of pPCV6NFluxF T-DNA insertion generating a deletion between exons 15 and 14, and thus causing a C-terminal truncation in the PRL1 coding domain. As described by Németh at al. (1998), this mutation removed the 6th and 7th WD40 domains of PRL1 and replaced the 3' end with T-DNA sequences providing an alternative polyadenylation site. Although the T-DNA tagged *prl1-1* mutant allele is transcribed, no truncated PRL1 protein is produced in the mutant probably due to effective proteolysis. Wild type and *prl1-1* mutant seedlings were grown in quadratic vertical Petri dishes on 0.5 MS medium on short day under 400 µEinstein $m^{-2}s^{-1}$ irradiance for two weeks, and then harvested in the middle of light period for RNA preparation from three independent biological replicates using RNeasy Plant Mini kit (Qiagen). Directional RNA libraries were prepared using a NEBNext Ultra II DNA Library preparation kit and subjected to deep sequencing on an Illumina HiSeq 2000 platform to obtain a total of 64,496,199 wt (21.59+21.34+21.56 Mio) and 64,032,802 (22.79+20.38+20.85) *prl1-1* sequence reads from triplicate samples. As outlined above, the reads were mapped using the CLC Bio Genomics Workbench RNA-Seq software to the genome and transcript isoform sequences, and then the calculated *prl1-1* versus wt differential expression values were filtered using 2-fold change and $p<0.05$ cut offs.

This yielded a primary list of 1997 DE genes and 3814 DAS transcript isoforms. Following the combination of DE and DAS list, it was sorted for up- and downregulated values to generate of overlapping DE-DAS, and unpaired DE-alone and DAS_alone lists. Next, each entry in these lists was examined for splicing changes and alternative splicing types, as well as for alteration of the ORF (coding domain) by the observed alternative splicing and transcription initiation/termination events. Subsequently, all DAS transcript isoforms were translated and compared to the longest wild type protein coding isoform using Clustal W alignments, to identify N-terminal and internal deletions and C-terminal truncations caused by the alternative splicing events. In parallel, the wild type protein sequences were blasted against the SMART database to identify functional protein domains affected by the splicing events. These informations were used to predict whether the observed splicing and ORF changes resulted in up- or downregulation of gene functions. Subsequently, all entries were removed from the DE_DAS and DAS-alone lists, which identified multiple DAS transcript isoforms. These have been inspected for consistent similar up or downregulation of all identified DAS isoforms to exclude events represented by contrasting changes in the levels of transcript isoforms. For pathway sorting, the resulting DE_DAS, DE-alone and DAS lists were examined for enrichment of specific GO-terms ($p<0.01$) and subjected to update their gene annotations as described above. The results of this analysis are summarized in Table 1 below.

Table 1: Identification of differentially expressed genes and differential alternative splicing of transcripts in the *prl1-1* mutant compered to wt.

After initial sorting, the DE and DAS lists passed a series of steps of curation by identification of alternative splicing events, ORF changes affecting protein functions and probability of transcript degradation by MND to generate three lists, which identify transcriptomic changes at different confidence levels.

DE_total	**1997**				
DE_UP_total	854			**DE_DOWN_TOTAL**	1143
DE_DAS_UP			**253**	**DE_DAS_DOWN**	**497**
no splicing change	no ORF change	DE_DAS>2	119	GE_TE<2	367
alt splicing	noORF change	DE_DAS>2	45	GE_TE<2	40
alt splicing	alt ORF	DE_DAS>2	89	GE_TE<2	90
DE_alone_UP			**439**	**DE_alone_DOWN**	**545**
no splicing change	no ORF change	DE_alone>2	224	DE_alone<2	390
alt splicing	noORF change	DE_alone>2	119	DE_alone<2	96
alt splicing	alt ORF	DE-alone>2	42	DE_alone<2	35
rest error			54		24
DE_DAS+DE_alone_UP_curated			**638**	**DE_DAS+DE_alone_DOWN_curated**	**1018**
predicted UP			559	predicted DOWN	969
predicted DOWN			83	predicted UP	49
DAS_alone UP				**DAS_alone DOWN**	

Unique DAS>2, DE<2			**1377**	Unique DAS<-2, DE>-2	**608**
predicted UP			666	predicted UP	188
predicted DOWN			702	predicted DOWN	417
error			9	error	3
DE genes represented by multiple DAS values			**609**		
predicted UP			99		
predicted DOWN			143		
miscellaneous			367		

Surprisingly, the results of RNA-Seq analysis identified alternative spliced transcripts only in 32 and 35% of up- and downregulated genes, and out of these only 24 and 4% altered the ORF of entries in the DE_DAS and DE-alone lists, respectively. By contrast, the uncurated primary DAS list, which showed changes in the level of transcript isoforms in the *prl1-1* sample, revealed an alteration of 5’ or 3’ termini (or both) in 20.9% and various splicing events in 65.6% of differentially regulated transcripts, while only 13.4% of these were represented by a single known isoform (Table 2). This data indicated that the *prl1-1* mutation altered the alternative splicing pattern of 3814, about 4.6% of currently annotated non-redundant transcripts. Consequently, the *prl1-1* mutant appeared to cause changes in the levels of specific transcript isoforms coding for altered protein products by affecting transcript initiation or termination, alternative splicing or transcript stability. However, most of these changes cannot be well detected by northern or Affymetrix chip hybridizations because they do not alter the total amount of transcripts per genes above the 2-fold threshold level.

Table 2: The distribution of alternative splicing events and change of 5’ and 3’ termini among DAS transcripts showing differential regulation in the *prl1-1* mutant.

Differential enrichment of specific classes in the up- and downregulated groups is highlighted.

splicing change	***ORF change***	***No.***		***ORF change +/-***		***ORF change***	***No.***		***ORF change +/-***	
no	no	135	5.78%		5.78%	no	378	25.58%		25.58%
alternative 5' and 3' ends	no	132	5.14%	252	10.79%	no	71	4.80%	155	10.49%
alternative 5' and 3' ends	yes	120	5.22%			yes	84	5.68%		
alternative 5' end	no	122	4.45%	226	9.67%	no	54	3.65%	87	5.89%
alternative 5' end	yes	104	0.94%			yes	33	2.23%		
alternative 3' end	no	22	1.16%	49	2.10%	no	18	1.22%	30	2.03%
alternative 3' end	yes	27	3.60%			yes	12	0.81%		
alternative 5' splice site	no	84	6.16%	228	9.76%	no	49	3.32%	143	9.68%
alternative 5' splice site	yes	144	3.17%			yes	94	6.36%		
alternative 3' splice site	no	74	8.01%	261	11.17%	no	55	3.72%	231	15.63%
alternative 3' splice site	yes	187	0.21%			yes	176	11.91%		
alternative 5' and 3' splice sites	no	5	0.98%	28	1.20%	no	3	0.20%	43	2.91%
alternative 5' and 3' splice sites	yes	23	0.21%			yes	40	2.71%		
exon skip	no	5	1.76%	46	1.97%	no	2	0.14%	33	2.23%
exon skip	yes	41	0.17%			yes	31	2.10%		
exons corresponding to exon skip	no	4	0.77%	22	0.94%	no	5	0.34%	25	1.69%
exons corresponding to exon skip	yes	18	10.19%			yes	20	1.35%		
retained intron	no	238	31.51%	974	41.70%	no	36	2.44%	123	8.32%
retained intron	yes	736	2.01%			yes	87	5.89%		
intron corresponding to retained intron	no	47	2.91%	115	4.92%	no	62	4.19%	230	15.56%
intron corresponding to retained intron	yes	68	0.02911			yes	168	11.37%		

The fact that mutation of a core subunit of spliceosomal activating NTC complex in *prl1-1* plants indeed compromised spliceosomal activity was indicated by 41.7% representation of transcripts carrying retained introns in the upregulated DAS sample. By contrast, the frequency of retained introns was about 5-fold lower (8.3%), whereas the occurrence of properly spliced introns was about 3 times higher (15.5 vesus 4.9%) in transcript isoforms, which were lower represented (i.e., downregulated) in the *prl1-1* mutant. Remarkably, the number of genes represented by single, often intronless short transcripts was 5-fold higher in the downregulated (i.e., compared to the upregulated) class of RNAs suggesting alteration of splicing-independent transcription regulatory (i.e., activating) functions in the *prl1-1* mutant. Consequently, the proportion of downregulated transcripts carrying no ORF change was higher (49.5%) compared to the upregulated transcript class (37.1%), whereas the latter showed higher representation of transcripts with altered ORFs.

3.1.3. Gene functions affected by differential expression in the *prl1-1* mutant

To verify the goodness of DAS mapping, we examined the positioning of reads at the *PRL1* locus as internal control (Figure 4).

Figure 4: Alignment of sequence reads to the PRL1 locus in the *prl1-1* mutant and wt.

This internal control illustrates that, when a gene is represented by a single transcript isoform, the fold value of differential expression detected in the genomic DE and transcript DAS lists is closely similar. In this case, the downregulation is likely due to the replacement of transcribed 3'-sequences by a T-DNA insertion in the *prl1-1* mutant. The value of fold change indicates that about half of the reads was mapped to this region in wt.

From the junction of T-DNA insertion in exon 15 reported by Németh et al. (1998) no reads were aligned to the *PRL1* transcript. Both DE and DAS lists indicated a 2.3-fold downregulation of transcript level as about half of the reads was located in the 3'-region, which was replaced by T-DNA sequences in the *prl1-1* mutant. The same approach was used to inspect all individual items in the DE and DAS lists.

A routine approach in current analysis of RNA-Seq data is to sort the DE and DAS data to overlapping DE/DAS, and unique DE_alone and DAS_alone groups, and then carry on with GO and pathway analyses (see e.g., Gallegos, 2018). An often used false approach is to combine the up- and downregulated classes for GO-term analysis, which eliminates the option to conclude about the final readout of alterations in pathway regulation. As discussed above, the omission of further filtering for the effects of alternative splicing might lead to completely false conclusions concerning the influence of these events on the gene functions. To illustrate this error, we examined the difference in prediction of GO-term enrichment in the overlapping DE-DAS list without (Figure 5) and with applying the filters for predicting the effects of alternative splicing events.

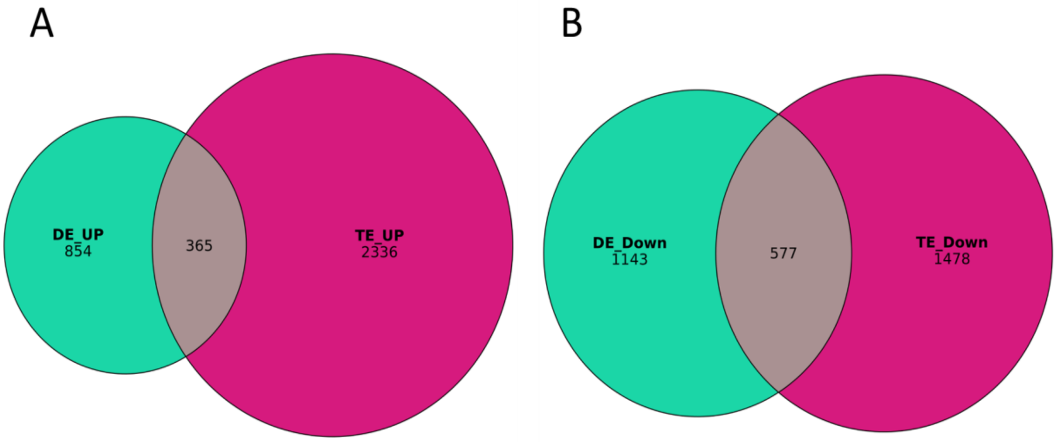


Figure 5: Venn diagram of overlapping DE-DAS, and unique DE_alone and DAS_alone upregulated (A) and downregulated (B) differentially expressed gene sets before filtering for the effects of alternative splicing events on gene functions.

Comparison of GO-term enrichment data of 365 upregulated entries defined by the overlap of GE and DAS lists without filtering to the upregulated class of 201 entries obtained by the filtering and prediction procedures is depicted in Table 3.

Table 3: Comparison of GO-term enrichment of DE_DAS overlaps without and with application of filtering for predicted effects of alternative splicing on regulation of gene functions.

377 Upregulated, no filters applied: Terms from the Process Ontology of gene_association.tair with p-value <= 0.01			
Gene Ontology term	**Cluster frequency**	**Genome frequency**	**Corrected P-value**
response to UV	11 of 319 genes, 3.4%	122 of 31767 genes, 0.4%	3.68e-05
response to karrikin	11 of 319 genes, 3.4%	135 of 31767 genes, 0.4%	0.00010
cellular response to iron ion starvation	4 of 319 genes, 1.3%	7 of 31767 genes, 0.0%	0.00027
response to stimulus	107 of 319 genes, 33.5%	6897 of 31767 genes, 21.7%	0.00053
response to UV-B	8 of 319 genes, 2.5%	74 of 31767 genes, 0.2%	0.00064
iron ion homeostasis	7 of 319 genes, 2.2%	57 of 31767 genes, 0.2%	0.00132
organic cyclic compound metabolic process	88 of 319 genes, 27.6%	5477 of 31767 genes, 17.2%	0.00204
cellular response to stimulus	57 of 319 genes, 17.9%	3051 of 31767 genes, 9.6%	0.00269
cellular response to stress	28 of 319 genes, 8.8%	1072 of 31767 genes, 3.4%	0.00370
cellular aromatic compound metabolic process	85 of 319 genes, 26.6%	5343 of 31767 genes, 16.8%	0.00485
microtubule-based movement	7 of 319 genes, 2.2%	71 of 31767 genes, 0.2%	0.00592
movement of cell or subcellular component	8 of 319 genes, 2.5%	103 of 31767 genes, 0.3%	0.00788
heterocycle metabolic process	82 of 319 genes, 25.7%	5165 of 31767 genes, 16.3%	0.00819
Filtering predictions-> 201 Upregulated: Terms from the Process Ontology of gene_association.tair with p-value <= 0.01			
Gene Ontology term	**Cluster frequency**	**Genome frequency**	**Corrected P-value**
cellular response to iron ion starvation	4 of 201 genes, 2.0%	7 of 31767 genes, 0.0%	3.37e-05
response to UV	8 of 201 genes, 4.0%	122 of 31767 genes, 0.4%	0.00073
response to karrikin	8 of 201 genes, 4.0%	135 of 31767 genes, 0.4%	0.00156
cellular response to stress	21 of 201 genes, 10.4%	1072 of 31767 genes, 3.4%	0.00315
response to UV-B	6 of 201 genes, 3.0%	74 of 31767 genes, 0.2%	0.00485

As expected, application of the filtering procedure resulted in a considerable reduced list of GO terms. This is because the filtering procedure essentially reduces the list only to those genes, which are represented either by intronless transcripts or by single known transcript isoform. According to Zhang et al. (2017a) this class includes about 40% of *Arabidopsis* genes in the latest genome annotation. Consequently, for these genes the results of northern RNA and Affymetrix chip hybridizations are expected to be comparable to the RNA-Seq data after filtering. In fact, for example, the “response to UV/UV-B” GO-terms in the curated list identified genes acting in the biosynthesis of UV-protecting phenylpropanoids/flavonoids, from which the *CHS1* (*CHALCONE SYNTHASE 1*) and *PAL1* (PHE AMMONIA LYASE 1) genes have been shown using RNA filter hybridizations by Németh et al. (1998) to be upregulated in the *prl1-1* mutant.

In addition to the overlapping DE-DAS entries, the DE-alone list (Table 1) identified 906 genes, 91.5% of which were represented by either intronless transcipts or transcripts in which splicing alterations did not modify the ORF. In part of this class, similar additive changes in the levels of transcript isoforms increased the numbers of reads above the 2-fold threshold, while the levels of individual isoforms remained below of the threshold. As mentioned above, in other part of DE_alone data the number of reads mapped to genes was higher than those mapped to transcripts suggesting either some discrepancy in the annotation of gene boundaries or the existence of yet unknown transcript isoforms with different 5’ and 3’ ends. Although the DE_alone class was considered to provide predictions at a lower confidence, we decided to combine it with the overlapping DE-DAS class because the DE_alone class contained numerous genes, which have been reported to show similar differential regulation in Affmetrix transcript profiling and promoter-reporter gene expression studies. These included, for example a set of auxin-induced genes that were observed to be downregulated, as well as several cell cycle-related genes coding for G_0/S and G2/M phase specific cyclins, which were reported to be down- and upregulated respectively correlating with root developmental defects in the *prl1* mutant (Szakonyi, 2006; Ji et al., 2015). In any case, further curation of the combined DE-DAS+DE_alone list based on ongoing identification of novel transcript isoforms in the *prl1-1* mutant will help proper filtering of this list for potential errors. The combined curated DE-DAS + DE_alone list (Table 1) contained 559 upregulated and 969 downregulated genes (Table 8 in the Appendix), for which the corresponding GO-term enrichment values are show in Table 4. It is important to emphasize that 97.5% of genes in this list were represented by transcripts in which the ORF was not changed by alternative splicing, and about 65% of entries were not associated to any alternative splicing event. Consequently, the combined DE-DAS + DE-alone list mostly identified splicing-independent transcription changes caused by the *prl1-1* mutation.

Table 4: GO-terms showing an enrichment in the combined DE-DAS+DE_alone dataset

DE-DAS+DE_alone_UP: Terms from the Process Ontology of gene_association.tair with p-value <= 0.1			
Gene Ontology term	**Cluster frequency**	**Genome frequency**	**Corrected P-value**
cell cycle	44 of 559 genes, 7.9%	672 of 31767 genes, 2.1%	1.01e-10
cell cycle process	33 of 559 genes, 5.9%	497 of 31767 genes, 1.6%	9.24e-08
microtubule-based movement	13 of 559 genes, 2.3%	71 of 31767 genes, 0.2%	3.00e-07
DNA recombination	18 of 559 genes, 3.2%	185 of 31767 genes, 0.6%	5.49e-06
microtubule-based process	19 of 559 genes, 3.4%	222 of 31767 genes, 0.7%	1.72e-05
cellular response to iron ion starvation	5 of 559 genes, 0.9%	7 of 31767 genes, 0.0%	3.28e-05
movement of cell or subcellular component	13 of 559 genes, 2.3%	103 of 31767 genes, 0.3%	3.31e-05
DNA metabolic process	33 of 559 genes, 5.9%	634 of 31767 genes, 2.0%	3.86e-05
meiotic cell cycle	17 of 559 genes, 3.0%	203 of 31767 genes, 0.6%	0.00013
nuclear chromosome segregation	13 of 559 genes, 2.3%	123 of 31767 genes, 0.4%	0.00027
cell division	21 of 559 genes, 3.8%	331 of 31767 genes, 1.0%	0.00051
meiotic chromosome segregation	9 of 559 genes, 1.6%	62 of 31767 genes, 0.2%	0.00130
chromosome segregation	13 of 559 genes, 2.3%	141 of 31767 genes, 0.4%	0.00133
heterocycle metabolic process	134 of 559 genes, 24.0%	5165 of 31767 genes, 16.3%	0.00134
reciprocal meiotic recombination	9 of 559 genes, 1.6%	63 of 31767 genes, 0.2%	0.00149
homologous recombination	9 of 559 genes, 1.6%	63 of 31767 genes, 0.2%	0.00149
nucleic acid metabolic process	114 of 559 genes, 20.4%	4303 of 31767 genes, 13.5%	0.00403
cellular aromatic compound metabolic process	135 of 559 genes, 24.2%	5343 of 31767 genes, 16.8%	0.00498
nuclear division	16 of 559 genes, 2.9%	239 of 31767 genes, 0.8%	0.00585
meiotic nuclear division	11 of 559 genes, 2.0%	118 of 31767 genes, 0.4%	0.00773
cellular response to stress	40 of 559 genes, 7.2%	1072 of 31767 genes, 3.4%	0.00784
synapsis	6 of 559 genes, 1.1%	29 of 31767 genes, 0.1%	0.00944
nucleobase-containing compound metabolic process	123 of 559 genes, 22.0%	4822 of 31767 genes, 15.2%	0.00967
meiosis I	9 of 559 genes, 1.6%	79 of 31767 genes, 0.2%	0.01015
organic cyclic compound metabolic process	136 of 559 genes, 24.3%	5477 of 31767 genes, 17.2%	0.01115
meiotic cell cycle process	13 of 559 genes, 2.3%	173 of 31767 genes, 0.5%	0.01272
meiosis I cell cycle process	9 of 559 genes, 1.6%	85 of 31767 genes, 0.3%	0.01850
chromosome organization involved in meiotic cell cycle	7 of 559 genes, 1.3%	51 of 31767 genes, 0.2%	0.02893
homologous chromosome segregation	6 of 559 genes, 1.1%	36 of 31767 genes, 0.1%	0.03490
RNA modification	21 of 559 genes, 3.8%	443 of 31767 genes, 1.4%	0.04518
DNA repair	18 of 559 genes, 3.2%	349 of 31767 genes, 1.1%	0.05348
organelle fission	16 of 559 genes, 2.9%	287 of 31767 genes, 0.9%	0.05523
iron ion homeostasis	7 of 559 genes, 1.3%	57 of 31767 genes, 0.2%	0.06032
DE-DAS+DE_alone_DOWN: Terms from the Process Ontology of gene_association.tair with p-value <= 0.1			

Gene Ontology term	Cluster frequency	Genome frequency	Corrected P-value
response to hormone	105 of 969 genes, 10.8%	1905 of 31767 genes, 6.0%	3.13e-06
response to endogenous stimulus	105 of 969 genes, 10.8%	1923 of 31767 genes, 6.1%	5.15e-06
response to chemical	152 of 969 genes, 15.7%	3171 of 31767 genes, 10.0%	1.17e-05
response to organic substance	116 of 969 genes, 12.0%	2268 of 31767 genes, 7.1%	2.88e-05
response to stimulus	281 of 969 genes, 29.0%	6897 of 31767 genes, 21.7%	3.88e-05
biological_process	320 of 969 genes, 33.0%	8068 of 31767 genes, 25.4%	4.18e-05
response to stress	171 of 969 genes, 17.6%	3910 of 31767 genes, 12.3%	0.00063
lipid transport	22 of 969 genes, 2.3%	212 of 31767 genes, 0.7%	0.00063
hormone-mediated signaling pathway	55 of 969 genes, 5.7%	888 of 31767 genes, 2.8%	0.00066
response to oxidative stress	36 of 969 genes, 3.7%	483 of 31767 genes, 1.5%	0.00096
lipid localization	23 of 969 genes, 2.4%	245 of 31767 genes, 0.8%	0.00206
cellular response to hormone stimulus	59 of 969 genes, 6.1%	1018 of 31767 genes, 3.2%	0.00222
cell redox homeostasis	15 of 969 genes, 1.5%	118 of 31767 genes, 0.4%	0.00315
cellular response to endogenous stimulus	59 of 969 genes, 6.1%	1037 of 31767 genes, 3.3%	0.00393
protein complex oligomerization	10 of 969 genes, 1.0%	54 of 31767 genes, 0.2%	0.00464
response to auxin	31 of 969 genes, 3.2%	439 of 31767 genes, 1.4%	0.01566
cellular response to chemical stimulus	70 of 969 genes, 7.2%	1364 of 31767 genes, 4.3%	0.01685
response to oxygen-containing compound	86 of 969 genes, 8.9%	1778 of 31767 genes, 5.6%	0.01709
response to drug	39 of 969 genes, 4.0%	637 of 31767 genes, 2.0%	0.03564
cellular response to organic substance	61 of 969 genes, 6.3%	1191 of 31767 genes, 3.7%	0.06197

The *prl1-1* mutant is semi-dwarf due to inhibition of hypocotyl and root elongation. Inhibition of cell elongation, resulting in smaller cells especially in meristemic tissues, is compensated by an increase of cell number in correlation with upregulation of 22 genes related to the control of cell division. This group contains 3 genes of G2/M phase sepefic cyclins CYCLIN B1, 2 and 3, and several other induced genes controlling chromosome segregation/condensation and cell plate (i.e., phragmoplast) formation, and the EBE AP2/ERF transcription factor, an activator of cell cycle-related genes during axillary meristem formation. In parallel, genes encoding inhibitors of cell cycle kinase CDKA, such as SIAMESE-RELATED 5 and 9, and CKS1, as well as G_0/S phase specific CYCLIN Ds are downregulated in *prl1-1*. The cell elongation defects correlate with lower expression of 44 genes encoding cell wall loosening enzymes (e.g., xyloglucan endotransglucosylases, pectinase and xylanase inhbitors), various functions in lignin, pectin, and suberin synthesis; Casparian strip and arabinogalactane proteins, and bHLH136/PRE1 (PACLOBTRAZOL RESISTANCE1), a key TF involved in transcriptonal control of cell size and elongation (Ikeda et al., 2012). It is striking that genes coding for 6 CLAVATA, 6 Rapid Alkalinization Factor (RALF) and 9 DVL (DEVIL, ROTUNDIFOLIA like) growth factor peptides involved in meristem differentiation are downregulated in *prl1-1* along with 64 other genes that encode short peptides with yet unknown functions. This suggests a general reprogramming of peptide growth factor signaling. In addition, 45 from the 58 known SAUR (Small Auxin UpRegulated) genes are repressed in *prl1-1* indicating a severe compromise of their functions in regulation of cell expansion and growth in response to different hormonal and environmental cues (Ren and Gray, 2015). Repression of auxin-inducible SAUR genes coincides with upregulation of MAX4 (MORE AXILLARY BRANCHING 4; ATCCD8; carotenoid cleavage dioxygenase 8), which acts in the synthesis of a strigolactone/karrikin inhibitor of auxin signaling and shoot branching (Sorefan et al., 2003). GO-term enrichment analysis of the DE-DAS list confirms differential upregulation of a set of strigolactone/karrikin induced genes in the *prl1-1* mutant (Table 3). A disturbance of auxin homeostasis is further suggested by upregulation of UGT74E2 indole-3-butyric acid UDP-glucosyltransferase, which plays a chief role in modulating growth and stress responses by inactivation of auxin hormone derivatives (Tognetti et al., 2010). Nonetheless, the tomato BLIND homolog MYB84/RAX3 (REGULATORS OF AXILLARY MERISTEMS 3; Müller et al., 2006), a positive regulator of shoot branching, showed simultaneous upregulation in *prl1-1*, providing an example for a compensatory event. By mentioning the latter example, we have to remember that the combined DE-DAS+DE_alone list represents only a part of transcription changes, which are largely independent of the effects of alternative splicing events in the *prl1-1* mutant. Thus, subsequent assessment of differential alternative splicing (DAS_alone) could extend the list of predicted pathway specific alterations.

The *prl1-1* mutant shows enhanced ABA and sucrose/glucose sensitivity in seed germination and root elongation assays (Németh et al., 1998). This appears to correlate e.g., with upregulation of MYB15, which is reported to increase ABA sensitivity (Ding et al., 2009), and with lower expression of the ABA-induced PP2C gene 1 (HAI1, SAG113), an inhibitor of ABA signaling (Zhang et al., 2012). However, downregulation of genes coding for *XERICO* (RING E3 ligase) and its E2 ubiquitin-conjugating enzyme partner AtUBC8 (representing known activators of ABA synthesis; Ko et al., 2006), the ABA receptor PYL5/RCAR8, or the root and stomatal ABA transporter ABCG40 suggests possible negative feedback regulation of several functions in the ABA signaling pathway. Whereas sucrose/glucose feeding stimulates ABA synthesis and senescence in leaves, these sugars are necessary to promote the growth of sink organs, such as roots. Remarkably, along with downregulation of root meristem growth factor RGF2, the root auxin transport regulator ROSY1, the nitrate-dependent root growth regulator ANR1 (AGAMOUS-like 44) TF and numerous other functions related to root growth, the SWEET2, 4 and 16 sugar transport facilitators, as well as ATL31 ubiqutin ligase controlling sugar and nitrate sensitivity, show lower expression in the *prl1-1* mutant. Similarly, to *prl1-1*, mutations of e.g. *SWEET2* and *ATL31* confer enhanced sensitivity sugar excess by inhibiting root elongation (Sato et al., 2009; Chen et al., 2015a). In comparison, enhanced cytokinin sensitivity of *prl1-1* mutant could reflect e.g. an upregulation of genes of the cytokinin-activating enzyme LONELY GUY 5 and root-to-shoot cytokinin translocator ABCG14 (Kurakawa et al., 2007; Ko et al., 2014) or lower expression of the type A negative response regulator ARR5 (To et al., 2004) and the AtMYB2 repressor of cytokinin synthesis at late stages of development (Guo and Gan, 2011). Yet, these events also coincide with a repression of some upstream or independently acting positive regulators, such as the CRF1 (CYTOKININ RESPONSE FACTOR 1; Rashotte et al., 2006).

Intriguingly, in the case of sugar and cytokinin inducible co-regulated genes of flavonoid biosynthesis pathway [PAL1, CHS1, CHI1 (CHALCONE-FLAVANONE ISOMERASE) and FLS1 (FLAVONOL SYNTHASE 1)] the data indicate simultaneous downregulation of two KISS ME DEADLY genes of Kelch-repeat F-box proteins (KFB20/KMD1 and 50) of SCF E3 ubiquitin ligases that control proteasomal degradation of both PAL1 and type B positive response regulators of cytokinin signaling (Kim et al., 2013; Zhang et al., 2013a). A similarly repressed gene of a third Kelch-repeat F-box protein KFB is involved in the degradation of CHS1 (Zhang et al., 2017b). Together with reduced expression of several genes involved in incorporation of phenylpropanoid compounds into cell wall lignin, these data predict an accumulation of UV-protecting compounds in *prl1-1* plants. Activation of the UV-induced DNA repair pathways is marked by the induction of genes coding for the XPB/Rad25 and XPG exonuclease components of TFIIH; TAN (TANMEI) and DDB2 (DAMAGE-SPECIFIC DNA BINDING PROTEIN 2) component of TFIIH interacting CUL4-DDB1 ubiquitin ligase; the human BRCA1 homolog, PARP2 (POLY(ADP-RIBOSE) POLYMERASE) and 21 other genes implicated in DNA repair and recombination.

Another GO-term showing significant enrichment in the DE-DAS dataset identified a set of upregulated genes controlling transcription responses to iron starvation. Remarkably, all four genes of currently known positive transcription regulators of iron uptake - BHLH 38, 39, 100 and 101 - were upregulated in *prl1-1* together with genes of iron-chelating nicotianamine synthase 2, root specific ferric chalate reductase FRO2, and phloem specific iron transporter OPT3, which is essential for systemic iron signaling (Wang et al., 2013; Zhai et al., 2014).

Although the mentioned bHLH TFs are known to be activated by both chloroplast and mitochondrial ROS signaling and predicted to play a role in controlling photooxidative stress tolerance, the exact mechanism linking iron signaling and oxidative stress defense is still unknown (Vigani et al., 2013; Noshi et al., 2018). Baruah et al. (2009) demonstrated that the *prl1* mutation suppresses the lethality conferred by the *flu* mutation. The FLU (FLUORESCENT IN BLUE LIGHT) gene encodes a chloroplast membrane-associated tetratricopeptide repeat protein, which is a suppressor of Mg^{2+}-protoporphyrine IX (ProtoIX) synthesis. The *flu* mutant accumulates protoporphyrine IX and protochlorophyllide resulting in generation of singlet oxygen ($^1O_2$) triggering cell death. Notably, a HEMA3 gene of glutamyl-tRNA reductase catalyzing the first rate-limiting step of protoporphyrine synthesis is upregulated in *prl1-1*, despite induction of the ELIP2 repressor of this pathway. At the same time, AtOEP16 required for chloroplast import of protochlorophyllide reductase A and genes of several jasmonate (JA) induced transcription activators (e.g., NAC055, ERF8, MYB2 etc.) of chlorophyll degradation are repressed. In *Chlamydomonas*, a bilin-dependent nuclear gene network stimulated by retrograde signaling via degradation of ProtoIX intermediers is involved in detoxification of reactive oxygen species (ROS), and this pathway is dependent on iron acquisition (Duanmu et al., 2013). The fact that the *prl1* mutation also suppresses the lethality of other chlorophyll deficient mutants, such as *ch42/cs*, which is impaired in the ATP-binding CHLI subunit of Mg^{2+}-protoporphyrine chelatase (Koncz et al., 1990, personal comm.), suggests that a similar ProtoIX/bilin signaling system might exist also in *Arabidopsis*, and is enhanced by the *prl1* mutation along with inhibition of ROS-stimulated cell death.

Palma et al. (2007) reported that a *mos4* (Modifier Of *snc1, 4*) mutation of the NTC subunit SPF27/BCAS2 (Breast Cancer-Amplified Sequence 2), as well as mutations of *PRL1* and *CDC5* suppress pathogen resistance conferred by the *snc1* mutation. The dominant *snc1* (*SUPPRESSOR OF NPR1-1*) mutation activates the salicylic acid (SA) signaling pathway in the absence of NPR1 in an EDS1-dependent fashion without induction of cell death (Li et al., 2001). In a flurry of papers, the same laboratory reported on that mutations of several other subunits of spliceosomal NTC and NTC-associated NTR complexes confer similar suppression of *snc1*-conferred basal resistance, thus defining the NTC as a major regulatory hub in pathogenic defense signaling. Recently, they reported on RNA-Seq transcript profiling of a *prl1prl2* double mutant (Jia et al., 2017) using an unfiltered conventional approach, which placed the pathogen defense pathway to the topmost enriched GO-term. In our combined DE_DAS+DAS_alone list of 1528 entries 13 upregulated and 66 repressed items were allocated to pathogen defense-related functions. However, the GO-term analysis did not indicate a specific enrichment of these functions even when lowering the cutoff value to $p<0.1$. Nevertheless, among the upregulated genes we identified CPR1/CPR30, which encodes an F-box protein substrate receptor of an SCF E3 ubiquitin ligase involved in proteasomal degradation of SNC1 (Gou et al., 2012), as well as WRKY48, a repressor of PR gene expression and basal resistance to the bacterial pathogen *P. syringae* (Xing et al., 2008). Intriguingly, a PR1 (PATHOGENESIS RELATED 1, AT4G337209) described Németh et al., 1998), FRK1 (FLG22-INDUCED RECEPTOR-LIKE KINASE 1) and flg22-induced RMG1 (Resistance Methylated Gene 1) NB-LRR receptor genes were also among the few upregulated pathogenesis-related entries in *prl1-1*. The larger, downregulated pathogen defense-related list include numerous genes of PR, antimicrobial Dirigent and Knottin domain proteins, as well as PLANT NATRIURETIC PEPTIDE A and PROPEP 2, 4 and 7 peptides, and Lipid-derived azelaic acid (AZA) binding transporter proteins representing known mediators of systemic acquired resistance (SAR). This indicates that, in addition to suppression of *snc1*, the *prl1-1* mutation alteres transcription regulation of a larger group of genes involved in the SA-related pathogen defense parthway. Suppression of ROS-induced cell death and SA-related pathogen responses by the *prl1-1* mutation also coincides with downregulation of 41 genes that encode thioredoxins, cupredoxins, plastocyanins, peroxiredoxins and glutaredoxins acting in redox regulation. From these, 14 of 21 known members of ROXY monothiol glutaredoxin genes are repressed in *prl1-1*. These include e.g, the *GRX480/ROXY19* redox regulator of TGA-NPR1 TF complex, which negatively controls a group JA/ethylene induced genes in pathogenic signaling (Ndamukong et al., 2007). Another 6 ROXYs (2, 3, 4, 12, 17 and 19) were reported to interact with TGA2 to repress EIN3-regulated genes in the ethylene-branch of defense pathways (Zander et al., 2012).

Jia et al. (2017) and two other papers from the same team (Zhang et al., 2013b, 2014) reported on a surprising correlation between transcription changes and expression of microRNAs and silencing siRNAs in the *prl1* and *cdc5* NTC subunit mutants. However, our entire dataset contained no entries of differentially regulated known microRNAs or siRNAs. Our data identified 6 induced and 21 repressed noncoding RNAs including some known natural-antisense (natsi) transcripts and 7 differentially regulated long noncoding RNAs, which were not detected by the GO-term enrichment analysis. Whereas our data failed to indicate a requirement of PRL1 NTC function for small RNA biogenesis, 10 genes of NTC, NTC-associated NTR, U5 and U2 snRNP complexes showed compensatory upregulation in the *prl1-1* mutant.

According to Németh et al. (1998), who noted that the *prl1-1* mutation results in an enhanced cold sensitivity similarly to the yeast NTC mutants, 14 genes allocated to the cold response pathway were downregulated in our dataset. These included CBF1/DREB1B_1, one of the central transcription activators of cold-induced genes (Novillo et al., 2007), DREB1F (DDL, DWARF AND DELAYED FLOWERING 1) from the same CBF/DREB TF family, which has a broader function in the regulation of cold, drought and heat acclimation (Kang et al., 2011), and DREB2D acting in the drough response pathway. Whereas overexpression of DREBF/DLL results in delayed flowering by upregulating the gibberellin oxidase GAOX7, overexpression of CBF1 and its homologs upregulate the *FLOWERING LOCUS C* (*FLC*), a central repressor of flowering (Seo et al., 2009). In fact, *FLC* and HUB2 (HISTONE H2 MONOUBIQUITINATION 2) required for FLC expression (Xu et al., 2009) are simultaneously downregulated, correlating with day-length independent early flowering trait of the *prl1-1* mutant.

3.1.4. Gene functions affected by differential alternative splicing in the *prl1-1* mutant

Compared to the above described DE-DAS+DE_alone list (total curated 1528: UP 559 and DOWN 969), the DAS_alone list, predicting differential alternative splicing (DAS) events, contained a total of 1973 items corresponding to 854 upregulated and 1119 downregulated entries (Table 1). As discussed, this class represented the lowest confidence group of RNA-Seq experiment. GO-term analysis of the DAS_alone data defined much fewer and broader pathways compared to the DE-DAS+DE_alone list (Table 5 and complete list in Table 9 in the Appendix).

Table 5: GO-term enrichment analysis of DAS_alone dataset.

DAS_alone_predicted UP_GO: Terms from the Process Ontology of gene_association.tair with p-value <= 0.01

Gene Ontology term	Cluster frequency	Genome frequency	Corrected P-value
response to abiotic stimulus	107 of 854 genes, 12.5%	2262 of 31767 genes, 7.1%	1.16e-05
response to stimulus	248 of 854 genes, 29.0%	6897 of 31767 genes, 21.7%	0.00030
cellular component organization	125 of 854 genes, 14.6%	3108 of 31767 genes, 9.8%	0.00452
response to chemical	127 of 854 genes, 14.9%	3171 of 31767 genes, 10.0%	0.00459
cellular process	463 of 854 genes, 54.2%	14842 of 31767 genes, 46.7%	0.00735

DAS_alone_predicted DOWN_GO: Terms from the Process Ontology of gene_association.tair with p-value <= 0.01

Gene Ontology term	Cluster frequency	Genome frequency	Corrected P-value
cellular process	631 of 1119 genes, 56.4%	14842 of 31767 genes, 46.7%	4.15e-08
metabolic process	566 of 1119 genes, 50.6%	13558 of 31767 genes, 42.7%	5.78e-05
cellular metabolic process	498 of 1119 genes, 44.5%	11680 of 31767 genes, 36.8%	6.11e-05
phosphate-containing compound metabolic process	119 of 1119 genes, 10.6%	2190 of 31767 genes, 6.9%	0.00250
defense response to bacterium	36 of 1119 genes, 3.2%	441 of 31767 genes, 1.4%	0.00498
phosphorus metabolic process	119 of 1119 genes, 10.6%	2236 of 31767 genes, 7.0%	0.00676
organic substance metabolic process	500 of 1119 genes, 44.7%	12178 of 31767 genes, 38.3%	0.00931

In the evaluation of DAS_alone data, we primarily searched for such DAS events, which could influence the functions of key regulators of those pathways that were identified in the DE-DAS+DE_alone list in relation to known phenotypic traits of the *prl1-1* mutant. The DAS-alone list was inspected for the number of sequence reads that were mapped to individual transcript isoforms in comparison to the number of reads mapped to genes (i.e., covering all transcript isoforms). A ratio of these reads estimates the proportion of a particular mRNA isoform among all known DAS transcript isoforms in the *prl1-1* mutant compared to wild type. The higher is the ratio of a mRNA isoform coding for a protein isoform with altered function in the *prl1-1* mutant compared to wt, then the higher is the probability that differential accumulation of the mRNA isoform compromises the gene function (e.g., the opposite is true for transcript isoforms predicted to encode functionally wt protein isoforms). From the total 1377 upregulated DAS mRNA isoforms 866 were not detected by any reads in wild type, whereas from the total of 608 downregulated isoform 365 were not represented by any read in *prl1-1*. Thus, about 62% of all DAS isoforms the fold-change values (e.g. *prl1-1*/wt) calculated by the CLC Bio software were artificially high or low. From the view point of predicted effects of DAS changes on gene functions, the critical parameter is the proportion of a DAS mRNA isoform, which encodes either an altered or wt protein product, among all mRNA isoforms synthesized from a gene. By working with bulk RNA samples from seedlings, it should be realized that the detected isoforms are most likely not synthesized from the gene in the same cells but represent cell type specific differential splicing of transcripts in wt and the *prl1-1* mutant. Consequently, in certain cell types the effects of observed DAS changes could have a much higher proportion and dramatic effect on the gene function but these effects are not identified well in the low resolution analysis of total seedling RNA. Compared to a clear increase or decrease of transcript amounts in the DE-DAS+DE_alone dataset, the DAS_alone list represents changes in the amounts of mRNA isoforms below 1 and above 0, where value 1 corresponds to the total amount of all transcripts from a gene. This fine and probably cell type specific regulation by altered splicing is thus principally different from the “course” regulation of total transcription rate. In this dataset, it is especially interesting to identify changes in the ratio of DAS events, which alter either the function of predicted protein products or the stability of mRNA isoforms. The higher is the ratio of such DAS isoforms among all transcripts from a gene, the more likely is its predicted effect on the gene function. Therefore, the DAS-alone list was filtered by removing entries in which the proportion of DAS mRNA isoform in the amount of total mRNA isoforms was lower than 20%.

In the filtered list of 488 DAS events (Appendix Table 7), for example, a mRNA isoform of TCP20 TF with an altered 3’ splice site not affecting the ORF was predicted to be upregulated 20-fold in *prl1-1*. This isoform represents 38.3% of total TCP mRNA isoforms in *prl1-1* but only 1.4% in wild type suggesting a fine uptuning of wild type TCP20 levels in *prl1-1*. Intriguingly, this data is in line e.g., with the observations of Li et al. (2006; 2007), who used Affymetrix profiling observed upregulation of several TCP TFs in *prl1-1* and predicted their binding to TELO sequence motives in the promoters of glucose-regulated genes involved in ribosome biogenesis and cell cycle (e.g. CYCB1;1). Similarly, a cyclin CYCA2;1 mRNA isoform with altered 3’ splice site and alternative 5’ and 3’ ends are not detected in wt but represents 51% of total CYCA2;1 transcript isoforms in *prl1-1*, while the total number of reads on the corresponding gene is comparable in *prl1-1* and wt (ratio 1.1). Yet, in this case the calculated 65-fold increase of wt CYCA2;1 mRNA isoform is questionable due to relatively low number of total reads, which reflects low representation of meristem specific CYCA2;1 mRNAs in the seedling total RNA. In addition, the DAS_alone list predicted NMD-mediated degradation of mRNA isoforms of several other cell cycle regulators (e.g. CYCB2;2).

In the auxin response pathway, the filtrated DAS-alone list suggested upregulation of ARF5 (MONOSPTEROUS) TF, but downregulation of the LAX1 auxin influx carrier required for proper establishment of embryonic root cell organization and root development (Ugartechea-Chirino et al., 2010), as well as ARF18, which controls cell division, elongation and petal growth in interation with the BIGPETAL bHLH TF (Varaud et al., 2011). Further examination of these candidate genes appears to be relevant because *prl1-1* shows highly aberrant root development and an apetala-like phenotype with short rudimentary petals under short day condition. At the same time, the level of TAS3 siRNA involved in the control of leaf polarity and development by silencing of ARF2, 3 and 4 is decreased in *prl1-1*, which shows aberrant leaf development. This also correlates with enhanced expression of an ARF3 (ETTIN, Simonini et al., 2017) mRNA isoform, which endoces a truncated protein lacking 152 N-terminal amino acids.

ABA3/LOS5 involved in the conversion of ABA-aldehyde to ABA and the GATA TRANSCRIPTION FACTOR 8 (BLUE MICROPYLAR END 3-ZINC FINGER; BME3-ZF) regulating seed germination were identified among the few potentially upregulated candidates in the ABA response pathway. Enhancement of chlorophyll biosynthesis pathway coincided with downregulation of the function of ABCC2 vacuolar transporter of chlorophyll catabolites through increased production of a mRNA isoform coding for a truncated protein product with 302aa N-terminal deletion of 5 transmembrane domains. The list of upregulated candidate genes in the iron uptake pathways was extended by predicted upregulation of the FRO3 (ferric reduction oxidase 3) in the DAS_alone list. In parallel with observed downregulation of cold response regulator CBF1, a remarkable accumulation of a mRNA isoform encoding a dominant negative form of CBF1 co-activator ADA2A without its N-terminal zinc-finger domain was detected in *prl1-1*. In addition, the functions of several histone mark readers (e.g., GT3, ALF6), HPC2 activator of histone gene transcription and expression of histone H4 are predicted to be compromised. Other DAS events suggest upregulation of heterochromatin silencing functions, including RDM12 (RNA-DIRECTED DNA METHYLATION 12), SUVR4 (histone H3K3 methyltransferase), and NRPD2 subunit of RNA polymerase IV, as well as several mediator subunits of RNA polymerase II.

The DAS_alone list also fails to identify SNC1, which is believed to be a PRL1-dependent alternative splicing target but suggests upregulation of ATNFXL1 transcription repressor of basal resistance responses (Asano et al., 2008) and parallel uptuning the functions of flagellin receptor kinase FLS2; EFR LRR receptor kinase of EF-Tu PAMP, ZAR1 HOPZ-ACTIVATED RESISTANCE 1 and ENHANCED DOWNY MILDEW 2 TF activator of RPP7. Improper splicing of the SNC1 pre-mRNA (i.e., alternative splicing of intron 5) was observed by Copeland et al. (2013) in the *mos2* and *mos2h* mutants affecting the functions of NTC-associated NTR proteins GPKOW/Spp2 and its homolog. In fact, the RNA-Seq analysis identifies the described alternative splicing events (Figure 6) but indicates contradictory up and down regulation of three different mRNA isoforms without a significant change in the number of sequence reads on the SNC1 gene in *prl1-1* and wt. Similarly, to all entries in the DAS_alone list, it is therefore obligatory to rigorously examine *SNC1* and all similar cases in the RNA-Seq analyses whether the observed changes in the levels of DAS mRNA isoforms indeed alter the level of wild type gene product. Alternatively, enhanced pathogen sensitivity of the *prl1-1* mutant could be explained either e.g., by upregulation of CPR1/CPR30 F-box protein of the SNC1 SCF E3 ubiquitin ligase, or induction of WRKY48 and ATNFXL1 repressors of basal resistance, which should also be further verified experimentally.

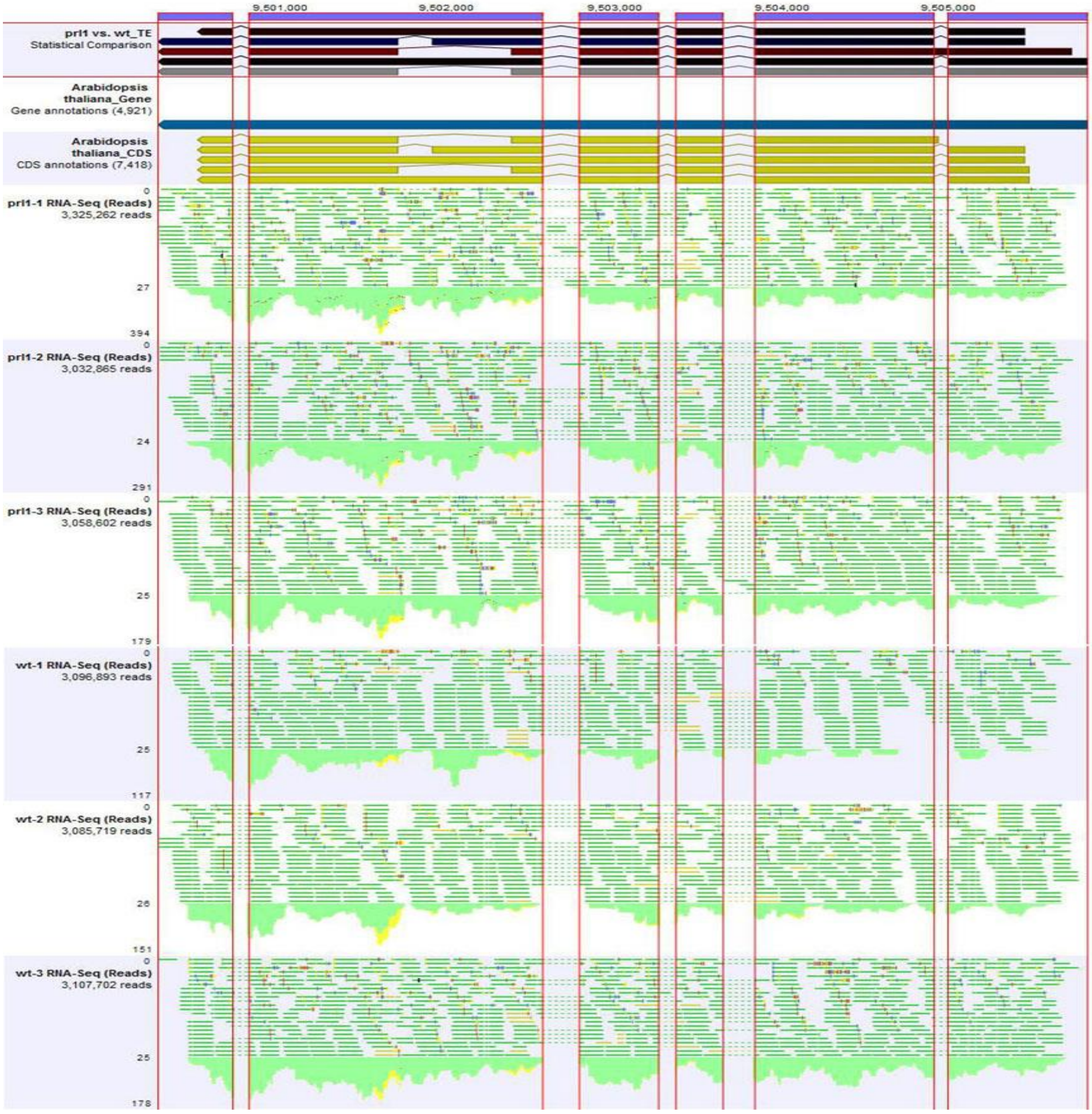


Figure 6: Mapping of RNA-Seq reads to SNC1.

The second versus first and third isoforms marked by blue and red colors at the top of the figure indicates mRNA isoforms with alternative 5' splice sites, showing -8.38-fold downregulation and 2.28 and 15.68-fold upregulation, respectively.

3.2. Generation of viable *prl2* mutant cells by creating conditionally complemented genetic mosaics

3.2.1. Are there viable *prl2* null mutants?

In the literature, there is an unfortunate disagreement concerning the effects of NTC subunit mutations on plant (i.e., gametophyte) viability. Monaghan et al. (2009) purified the NTC complex, which was renamed MOS4 (*Modifier Of snc1, 4*)-associated complex (MAC). These authors reported that combined mutations of duplicated PRP19A/MAC3A and PRP19B/MAC3B subunits suppress the *snc1*-

mediated autoimmunity (i.e., basal resistance) similarly to the *prl1* and *cdc5* mutations. Despite further confounding the already complex nomenclature of NTC subunits, a problem with the latter report is that the combinations of genuine null mutations of *prp19a* and *prp19b* are lethal according to our studies (i.e., cannot be obtained, Koncz personal comm.). From the same laboratory, Weihman et al. (2014) isolated a dominant *prl1* suppressor mutation, a single nucleotide exchange located at position -58 upstream of the ATG codon in the *PRL2* gene, which increased *PRL2* transcript levels about 2-fold conferring full complementation of *prl1* developmental defects and pathogen sensitivity trait. Recently, Jia et al. (2017) reported on RNA-Seq analysis of the above mentioned *mac3a*, *mac3b* double mutant from Monaghan et al. (2009), and an apparently viable *prl1*, *prl2* double null mutant. According to these authors, the *prl2* mutants are viable and display wild type phenotype. Consequently, they believe that PRL2 is a lower expressed paralog of PRL1, which performs completely redundant functions (see Weihman et al. 2014).

In our laboratory, Szakonyi (2006) isolated and characterized two T-DNA insertion mutations in *PRL2*. In the Koncz_16136/*prl2-4* mutant a tandem inverted repeat T-DNA insertion of pPCV6NFHyg vector caused a target site deletion between exon 9 and intron 9 sequences, whereas in the GABI_228D02 line the T-DNA insertion was located in intron 2 of the *PRL2* gene (Figure 7).

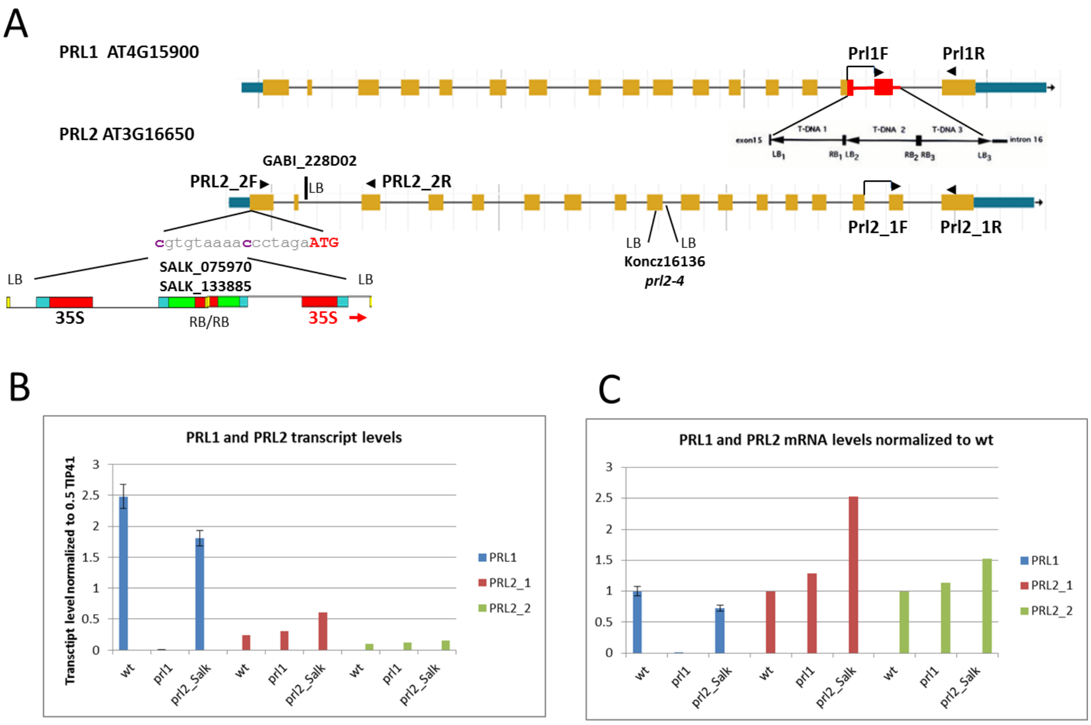


Figure 7: Quantitative real-time PCR measurement of PRL1 and PRL2 transcript levels in wt, *prl1-1* and SALK_075970 *prl2* insertion mutant seedlings.

A) Schematic map of *PRL1* and *PRL2* genes. Yellow boxes indicate exons, blue boxes mark 5’ and 3’ UTRs, and black lines correspond to introns. The positions of T-DNA insertions and primer pairs are indicated. In case of *PLR1* and *PRL2* primer pairs designed to the 3’ end, one of the primers spanned exons 15 and 16 to exclude detection of potential DNA contamination. LB and RB mark the left and right boder juntions of T-DNA inserts. B) *PRL1* and *PRL2* transcript levels in total RNA samples isolated from wt, *prl1-1* and *prl2* SALK_075970 seedlings nomrlaized to mRNA levels of control TIP41 (TAP42 INTERACTING PROTEIN OF 41 KDA) gene. C) *PRL1* and *PRL2* mRNA levels in the *prl1-1* amd *prl2* SALK_075970 mutants normalized to *PRL1* and *PRL2* mRNA levels in wild type.

Segregation analysis of 20 T2 families of the *prl2-4* mutant resulted in 1397 hyromycin resistant and 727 sensitive progeny indicating 2:1 segregation of the T-DNA carrying and wt progeny (χ^2 10.373, Homogeneity 10.208, 93% probability). Similar analysis of 20 T2 lines of the GABI_228D02 mutant yielded 2414 sufadiazin resistant and 1090 sensitive progeny indicating similarly a segregation ratio of 2:1 (χ^2 7.812, Homogeneity 10.96, probability 89%). In both lines, all resistant T2 progeny proved to be hemizygous for the T-DNA insertions and segregated in their siliques ¼ portion of white seeds, which underwent early abortion. In her work, Szakonyi (2006) demonstrated that abortion of the white seeds, carrying the *prl2* null mutations in homozygous form, resulted from early embryo lethality at the heart stage.

In their work, Jia et al. (2017) used the SALK_075970 *prl2* mutant allele, which they considered as null mutant because the T-DNA insertion was located only 7 nucleotides upstream of the translational start codon ATG (Figure 7). Our laboratory has also characterized earlier the SALK_075970 line, which proved to be identical with the SALK_133885 mutant and showed that an inverted tandem repeat of pROK vector T-DNA, facing the plant DNA junctions with its left border (LB) sequences, generated a small target site deletion of 10 bp indeed 7 bp upstream of ATG. T2 families of both SALK_075970 and SALK_133885 lines segregated at the expected 3:1 ratio viable homozygous progeny, which was indistinguishable from wild type. This indicated that the *PRL2* gene was likely expressed in these lines from a 35S promoter located upstream of the left boder junction facing the gene in the pROK T-DNA insertion.

To demonstrate this unequivocally, we have measured the *PRL2* transcript level in the homozygous SALK_075970 mutant and compared it to wt and *prl1* mutant seedlings. As control, we used the *prl1-1* mutant and parallel measurement of *PRL1* transcript levels in wt, *prl1-1* and SALK-_075970 seedlings. The *PRL1* and *PRL2* gene specific primers were placed upstream and downstream of the T-DNA insert boundaries of the *prl1-1* insertion mutation, where *PRL1* and *PRL2* sequences provided suitable mismatch regions. In addition, a second primer pair flanking the GABI_228D02 T-DNA insertion in intron 2 was used as control to estimate the amount of close to full-length cDNAs synthesized from the *PRL2* transcript using RNA templates from wt, *prl1-1* and SALK_075970 seedlings. As illustrated in Figure 7, the *PRL1* mRNA level is about 10-fold higher compared to *PRL2* in wt seedlings. As expected, the *PRL1* mRNA is not detectable in the *prl1-1* mutant, but surprisingly somewhat (about 25%) lower in the *prl2* SALK_075970 mutant. By contrast, the *PRL2* mRNA levels are comparable in wt and the *prl1-1* mutant but increased by about 2.5-fold in the SALK_075970 line. This demonstrates that the *prl2* SALK_075970 line is not a *prl2* null mutant, rather a *PRL2* overexpression line, in which *PRL2* transcription is likely driven by the CaMV 35S promoter located upstream of the ATG. Measurements with the second set of PRL2 gene specific primer pair, detecting the 5’ end of *PRL2* transcript, provided closely similar results, indicating at least 1.5-fold increase of *PRL2* transcription in the SALK_075970 line. Given the fact that Weihman et al. (2014) claimed that in the *prl1* suppressor mutant about a two-fold increase of *PRL2* transcript level was sufficient to confer genetic complementation of the *prl1* mutant traits, we have to assume that this occurs similarly in the *prl1*, *prl2* SALK_075970 double mutant used for RNA-Seq study by Jia et al. (2017). If fact, a series of promoter swap studies by Szakonyi (2006) demonstrates that ectopic expression of *PRL2* using 35S and other organ and tissue specific plant promoters complements either all or parts of pleiotropic mutant traits of the *prl1-1* mutant. Consequently, it is rather unclear how Jia et al. (2017) could detect transcription changes relevant to the *prl1* and *prl2* mutations using a combination of *prl1* and *prl2* SALK_075970 insertion mutations.

3.2.2. Conditional genetic complementation of *prl2* mutation and generation of plants carrying *prl2*/wt genetic mosaic sectors

To study the regulatory functions of SCARECROW(SCR) and SHORTROOT (SHR) in *Arabidopsis*, Heidstra et al. (2004) created a conditional genetic complementation system. The complementing wild type gene is cloned downstream of an *Erwinia uredovora* CTR1 carotenoid biosynthesis gene conferring resistance to the herbicide norflurazon, which is flanked by two *lox* sites in the pCB1 vector (Figure 8).

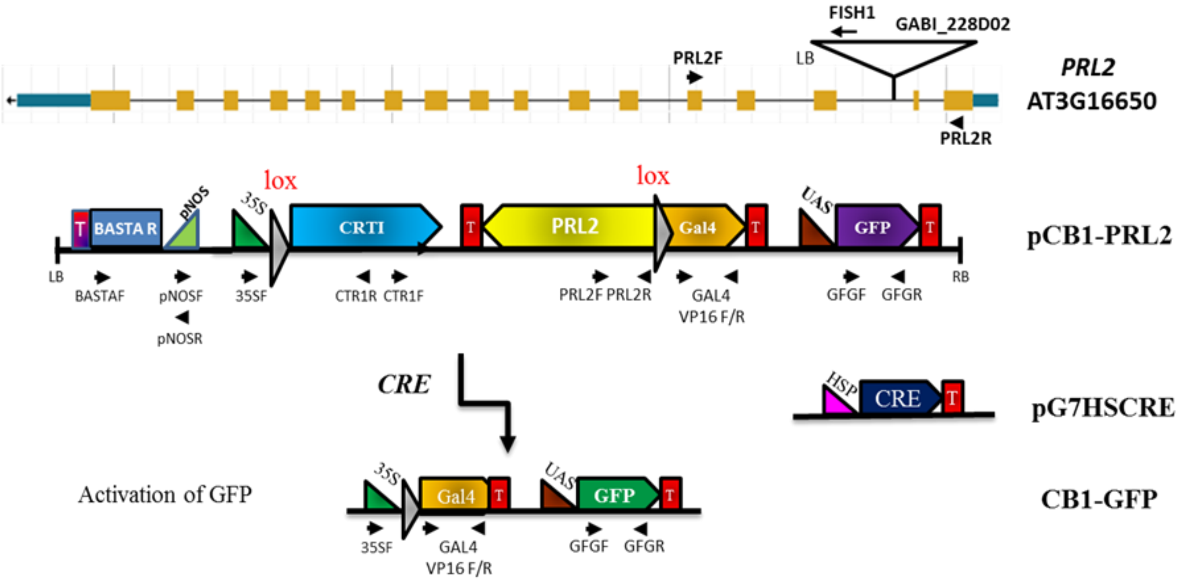


Figure 8: Schematic presentation of conditional genetic complementation system used for creation of genetic mosaics in the *prl2* GABI_228D02 mutant.

The pCB1-PRL2 vector carrying the wild type *PRL2* gene was transformed into the *prl2/+* plants carrying the PG7HSCRE T-DNA in homozygous form. F3 progeny carrying the CB1-PRL2 T-DNA (100% BASTA^R) was screened for homozygous status of the *prl2* mutation by screening for 100% sulfadiazine resistance. The positions of PCR primers used for verification of excision of complementing *PRL2* gene are indicated by arrows.

The *lox*-CTR1-complementing gene-*lox* cassette is flanked by a CaMV35S promoter upstream and a *GAL4VP16* gene downstream. The complementing pCB1 vector is introduced into the homozygous mutant, which is previously transformed with a second vector *pG7HSCRE* conferring heat-inducible expression of the Cre endonuclease driven by the *HSP18.2* heat shock promoter. Induction of Cre results in excision of the *lox*-CTR1-complementing gene-*lox* cassette by fusing the 35S promoter to the *GAL4VP16* gene. This mediates the expression of an ER-targeted green fluorescence protein (GFP) reporter gene, which is driven by a promoter carrying binding sites (UAS) for the GAL4VP16 transcription activator. Homozygous mutant cells, which have lost the complementing gene cassette during the Cre-lox excision become thus marked by GFP, which remains inactive in the genetically complemented "wild type" cells.

The conditional genetic complementation systems appeared to be also suitable for rescuing embryo lethal mutations providing the unique possibility for visualization of their so far undetectable phenotypic traits by generating genetic mosaic sectors in vegetative and reproductive organs of viable plants using the Cre-lox excision system. Therefore, Villacorta (2010) introduced the *PRL2* gene into the pCB1-PRL2 vector and transformed it into the *prl2/+* GABI_228D02 line, which carried the pG7HSCRE vector (conferring plant hygromycin resistance) in homozygous form. Upon selecting for the Basta resistance marker of pCB1 and sulfadiazine resistance (SuR) marker of *prl2* mutation, SuR progeny homozygous for the BastaR marker was isolated, and then screened for homozygous status of the *prl2* mutation in the next generation (all selfed progeny of F2 lines showing 100% SuR). Seeds carrying the *prl2*, pCB1 and pG7HSCRE vector T-DNAs in homozygous form served as starting material for our experiments.

First, the heat shock treatment was optimized by determining the time of treatment causing 50% lethality (LD_{50}). Four days old wild type seedlings grown on 0.5MSAR medium in Petri dishes were exposed to various times to 42°C heat-shock treatment in two different incubators and then subjected to recovery and grown for another 10 days under normal conditions to score for the number of dead and surviving seedlings. As shown in Figure 9, the LD_{50} value was reached after about 24 to 48 hrs of incubation of seedlings at 42°C.

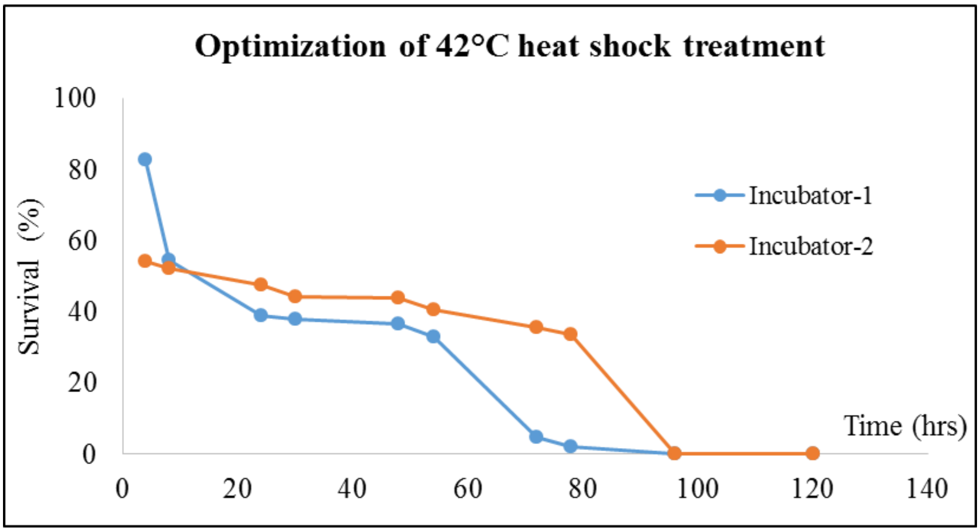


Figure 9: Determination of LD50 value of 42°C heat treatment of 4 days old *Arabidopsis* seedlings. The time of treatment causing 50% seedling lethality slightly varied but the survival rate sharply dropped after 60 to 70 hr treatment.

To induce excision of the complementing *PRL2* gene from the CB1-PRL2 T-DNA in the homozygous *prl2* mutant, seedlings were exposed to 42°C heat shock for 24h, and after recovery were inspected for activation of the GFP reporter by confocal microscopy. About 80-85% of examined plants revealed GFP signal in various tissue sectors and a large proportion of these produced GFP expressing F2 seed. The F2 plants were all wild type and displayed homogeneous 35S promoter driven GFP expression in all examined tissues (Figure 10).

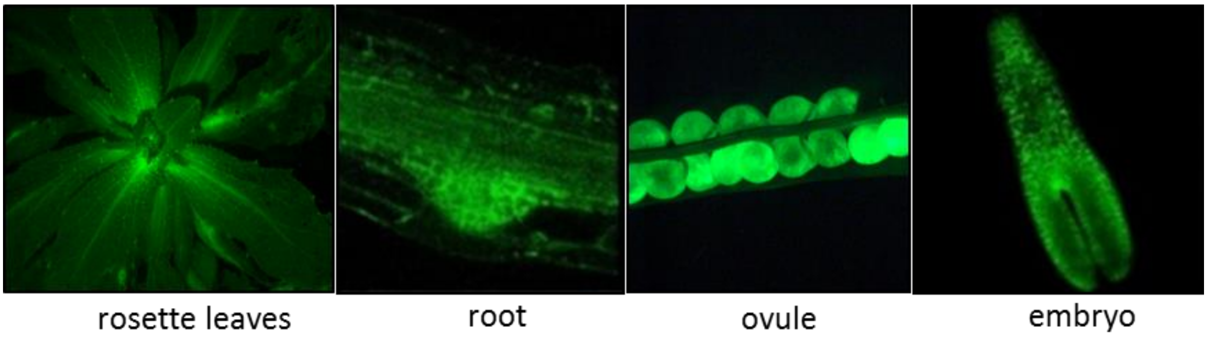
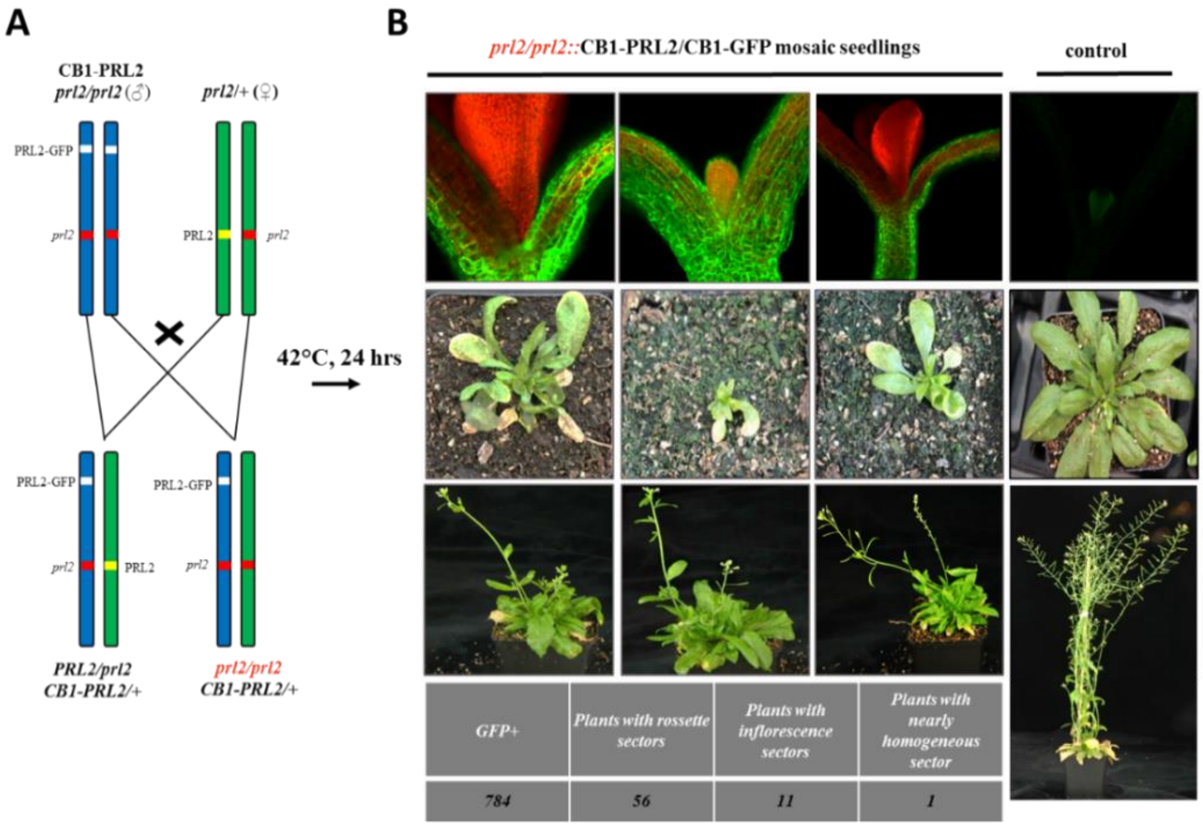


Figure 10: Expression of GFP marker in heat-shock treated *prl2* homozygous mutant carrying the CB1-PRL2 and pG7HSCRE vector T-DNAs in homozygous forms.
Wild type phenotype of all GFP expressing offspring indicated that heat-shock induced Cre expression was sufficient to remove only one of the two complementing wild type *PRL2* gene copies.

Because all selfed progeny displayed norflurazon resistance and carried a wild type *PRL2* gene copy detected by the gene specific PCR primers PRL2F and R (Figure 8), it became evident that Cre-mediated excision removed only one of the two complementing *PRL2* gene copies from the CB1-PRL2 T-DNAs resulting in plants with a *prl2*, *prl2, PRL2* genotype.

To reduce the number of complementing *PRL2* gene copies to one and keep one copy of the Cre encoding pG7HSCRE T-DNA, we crossed the original line carrying all components (i.e., *prl2* mutation, CB1-PRL2 and pG7HSCRE T-DNAs) in homozygous form with a *prl2/*+ mother. Half of the F1 hybrids remained thus homozygous for the *prl2* mutation and were expected to show mosaic GFP expressing *prl2* mutant sectors in *prl2, prl2*; *CB1-PRL2/*+ and pG7HSCRE/+ individuals. By contrast, the other half of F1 plants corresponding to the *prl2/*+; *CB1-PRL2/*+ and pG7HSCRE/+ progeny was expected to be wild type bearing only wt GFP expressing sectors (Figure 11). Following heat-shock treatment, 784 seedlings showing GFP expressing sectors were planted into soil for inspecting the appearance of aberrant organ sectors and their potential extension into the developing inflorescence. From 56 plants displaying larger GFP expressing sectors in quickly senescing narrow rosette leaves and shoot meristems, 11 produced aberrant inflorescence branches (Figure 11).



GFP+	Plants with rossette sectors	Plants with inflorescence sectors	Plants with nearly homogeneous sector
784	56	11	1

Figure 11: Identification of plants carrying GFP expressing *prl2* mutant and complemented wt sectors after reduction of the copy number of complementing CB1-PRL2 T-DNA to one by backcross with *prl2/+*.
A) Backcross with a *prl2/+* mother was used to reduce the copy number of complementing CB1-PRL2 T-DNA and Cre-encoding G7HSCRE construct to one by maintaining the *prl2* mutation in homozygous status in half of the F1 plants. B) *Upper row:* After heat shock and 6 days recovery, seedlings carrying larger GFP expressing sectors (green color) were identified using confocal microscopy. Red color corresponds to chlorophyll autoflorescence in the genetically complemented wt sectors. *Middle row:* Plants carrying larger *prl2* mutant sectors developed aberrant rossettes with narrow asymmetric leaves showing early senescence. *Lower row:* Following partial normalization of rossettes carrying increasing size of wt sectors, GFP expressing aberrant inflorescences were observed in 11 from 56 mosaic plants. The left panel shows confocal image of a Col-0 wt seedling, wt rosette and inflorescence.

The GFP expressing inflorescence branches were distinguished by their yellow green color and carried tightly placed flowers due to reduction of the internode length (Figure 12). The sepals of flowers had white or yellow color, indicating fast senescence. All flowers were open and contained rudimentary short sepals and stamens, and somewhat shorter pistils compared to wild type, which were freely exposed. The flowers produced siliques, which were somewhat shorter compared to fruits of a *prl2/+* control. Most siliques on the mutant sectors carried only decayed small brown seeds but occasionally one or two normal seed was also observed in them (Figure 12).

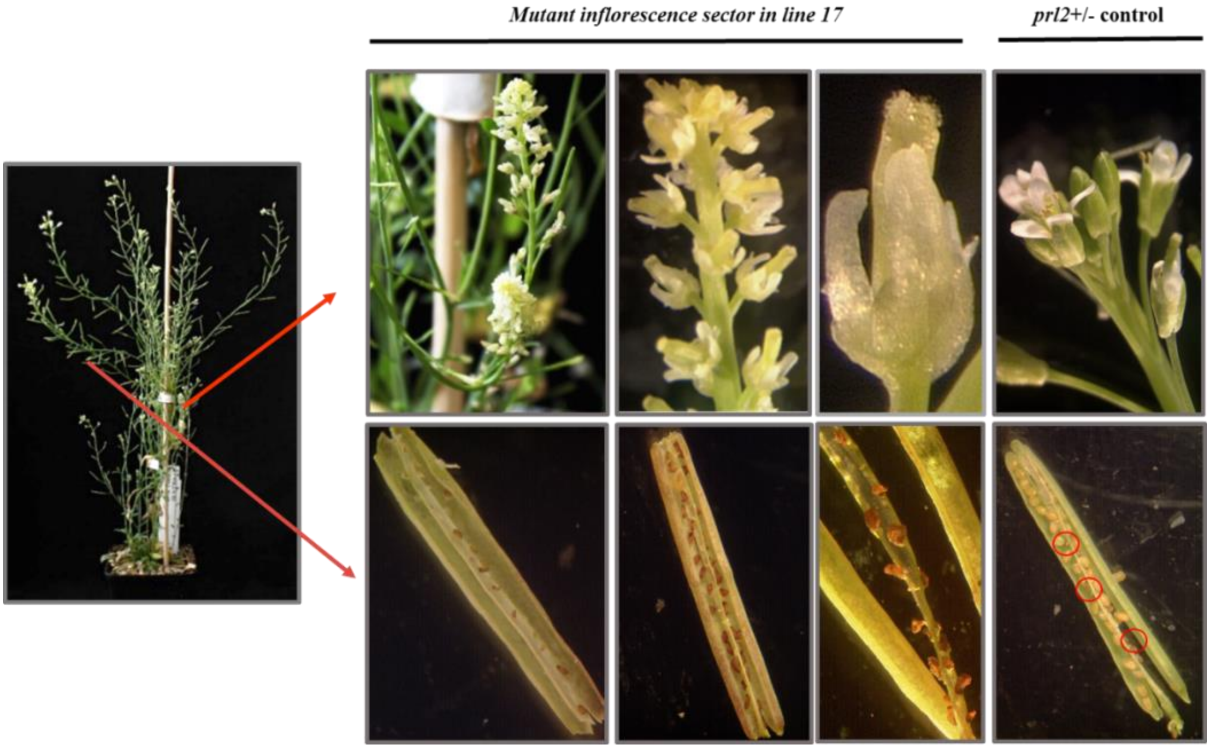


Figure 12: Inflorescence and flower phenotype of a mosaic plant (line 17), which carried nearly homogeneous mutant sector in several inflorescence branches examined by PCR amplification of complementing PRL2 gene.

The upper row shows dense distribution of flowers and shortening the internode length on the mosaic inflorescence, a close up of flowers in the mutant sector, and control *prl2/+* flowers for comparison. The lower section displays the seed content of siliques of three different mosaic inflorescence sector compared to a silique of a *prl2/+* plant.

To monitor excision of the complementing *PRL2* gene, DNA samples isolated from sections of aberrant inflorescences were subjected to PCR analysis using the combination the CaMV35SF and GAL4VP16R primers (Figures 8 and 13). From 10 examined plant lines, one (line 17) carried barely detectable wt cells in its inflorescence sector, which was indicated also by a lack of PCR product from the complementing *PRL2* gene in the first test. This line was next rigorously examined by PCR confirmation of the presence of DNA fragments corresponding to the left junction of *prl2* GABI_228D02 T-DNA insertion, GFP reporter gene, predicted excision product CB1-GFP between the pNOSF and 35SF and Gal4VP16R primer sites, and a segment of complementing *PRL2* gene. In addition, expression of the GFP reporter protein was detected by western blotting in all segments. Astonishingly, the results indicated that in 4 out of 5 segments of aberrant inflorescence of plant 17 the complementing *PRL2* gene was indeed absent, but one segment still carried it indicating that this inflorescence was still a genetic mosaic of *prl2* and complemented wt cells.

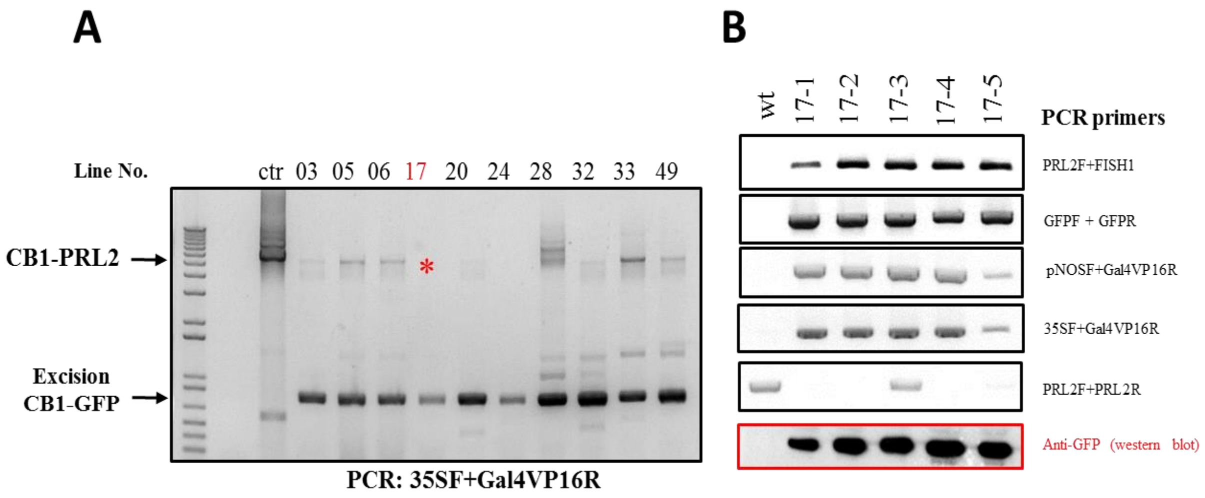


Figure 13: PCR detection of Cre-induced excision of complementing PRL2 gene in mosaic inflorescences and five consecutive inflorescence segments of plant no. 17, which carried a nearly homogeneous GFP expressing *prl2* mutant inflorescence segment.

A) Screening for the presence of complementing *lox-CTR1-PRL2-lox* cassette of CB1-PRL2 T-DNA and its excision, reconstrucing the 35S-GFP reporter gene in the excision product CB1-GFP by PCR amplification of DNA samples isolated from 10 mosaic inflorescences using the 35SF and Gal4VP16 primers (Figure 8). Ctr: PCR product amplified from the CB1-PRL2 vector. B) PCR amplification of the left border junction of *prl2* GABI_228D02 T-DNA insertion (PRL2F+FISH1), GFP reporter gene segment (GFPF+GFPR), excision products between pNOSF, 35SF and Gal4VP16R primer positions, and a segment of complementing *PRL2* gene using DNA templates prepared from five consecutive inflorescence segments of plant line 17, which carried a nearly homogeneous GFP expressing *prl2* mutant sector. The last raw in panel B shows a western blot confirmation of the presence of GFP reporter protein in the examined inflorescence mosaic segments.

3.2.3. Separation of GFP marked *prl2* mutant and genetically complemented wild type cells by fluorescence activated cell sorting (FACS)

To maintain the identified mosaic inflorescence sectors, tissue segments were sterilized and converted to callus tissues by cultivating them in MS-agar medium containing 2,4-D (0.5-3.0 mg/l) and NAA (0.5-2.5 mg/l). As control, wt and *prl2/+* inflorescence segments were treated similarly. Compared to the controls, callus initiation from mosaic inflorescence segments of line 17 was slower but upon one month resulted in visible tissue proliferation on all explants. After two-three months, sufficient amount of callus material was enriched for initiation of a cell suspension as described by Mathur and Koncz (1998). Prior establishment of cell suspension, the calli were inspected for maintenance of GFP expressing *prl2* mutant cells. As illustrated in Figure 14, luckily most cell clumps released from the calli contained some GFP expressing cells. This, together with the fact that no homogeneous *prl2* mutant sectors could be identified in any mosaic plants indicated that the presence of wild type cells is likely essential for maintenance of *prl2* mutant cells by metabolic or hormonal (or both) cross-feeding. Similarly, inspection of the established cell suspension by confocal microscopy indicated that about half of the cells carried the GFP reporter marking the non-complemented *prl2* mutation (Figure 14).

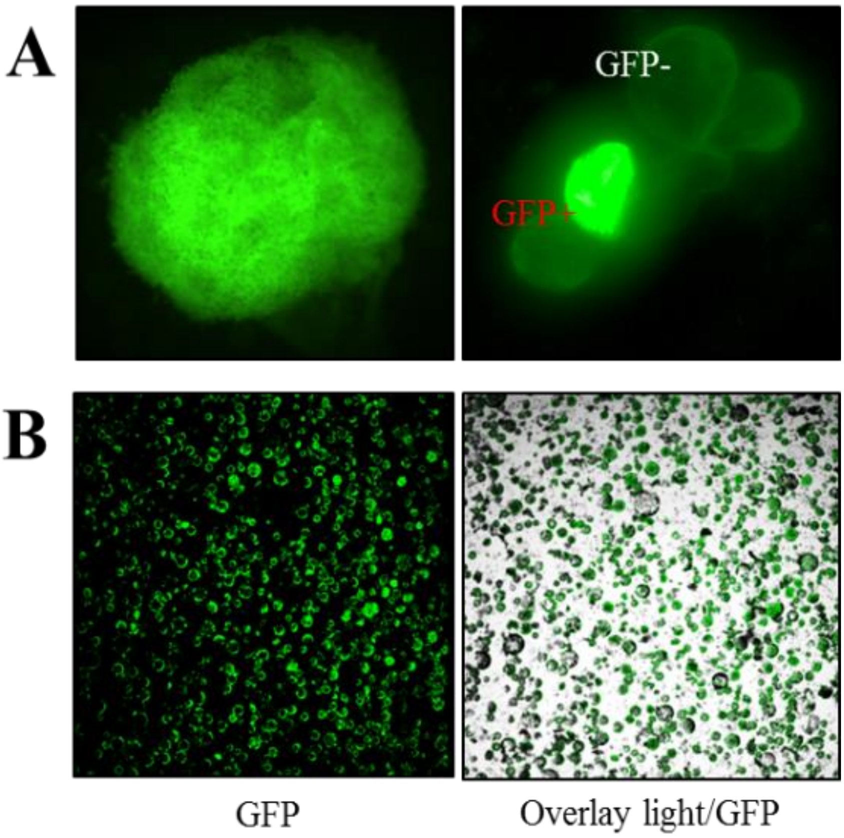


Figure 14: Calli and cell suspension obtained from genetic mosaic inflorescence sections contained a mixture of GFP expressing *prl2* mutant and GFP- wild type cells.

A) Confocal image of a compact callus and a detached cell clump. B) GFP image and overlay of light and GFP images of single cell protoplasts prepared from a cell suspension derived from genetic mosaic calli.

To separate the GFP expressing *prl2* and GFP$^-$ wild type cells, protoplasts were prepared from the cell suspension using macerozyme and cellulase as described (Yoo et al., 2007) and subjected to fluorescence activated cell sorting (FACS) using a BD Aria equipment (BD Biosciences, San Jose, CA at the Cologne Max-Planck Institute of Aging in collaboration with Prof. Christian Kukat and Mrs. Kat Folz-Donahue). A representative scatter graph showing the separation of GFP+ and GFP− protoplasts is depicted in Figure 15. Each of the three independent FACS separations yielded on an average 84ng/10,000 GFP$^+$ and 78ng/10,000 GFP$^-$ protoplasts. The samples were then normalized prior to cDNA synthesis and RNA-Seq library preparation. Control quantitative qRT-PCR assays indicated that the *prl2* GFP$^+$ did not carry any *PRL2* RNA with sequences between the PRL2F and PRL2R primer positions flanking the position of GABI_228D02 T-DNA insertion. Compared to the unsorted protoplast sample, the PRL2 transcript level was about two-fold higher in the FACS-isolated GFP$^-$ fraction of “wild type” (i.e. genetically complemented *prl2* mutant) cells (Figure 15).

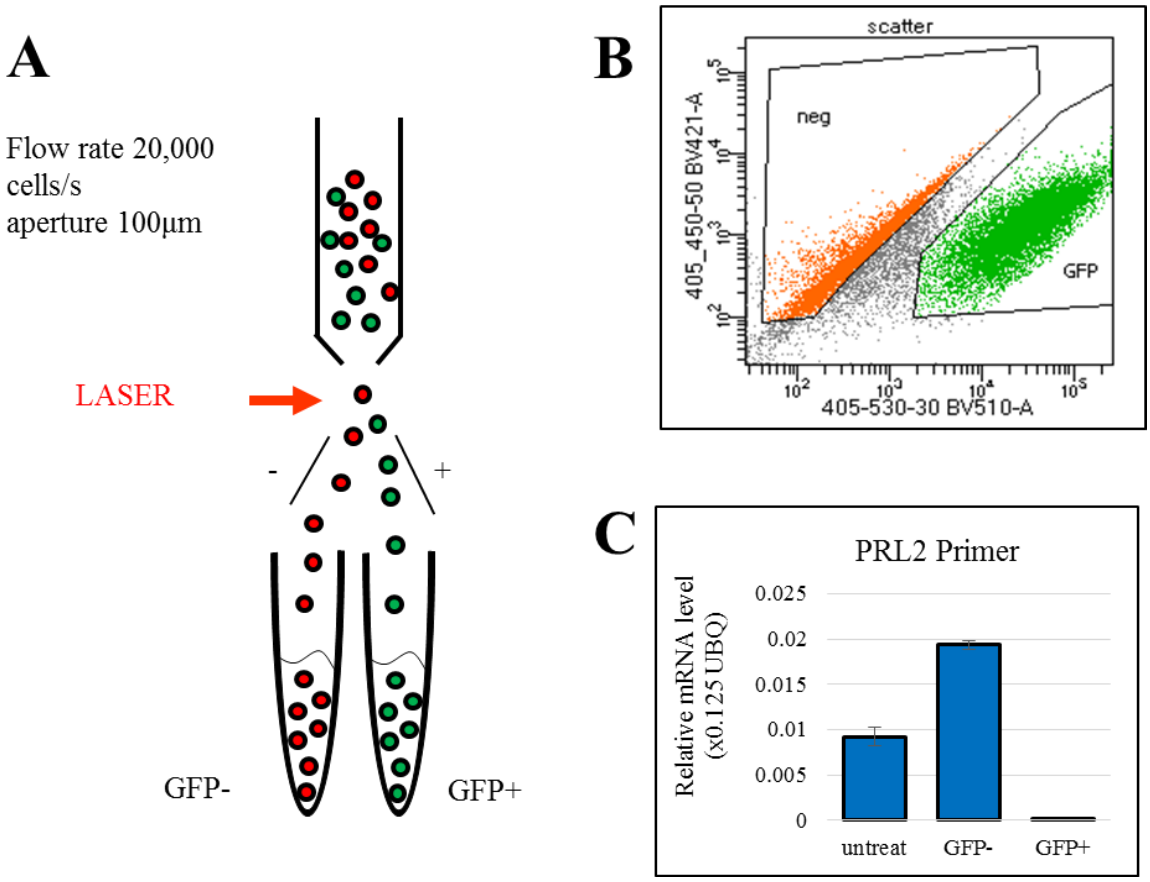


Figure 15: FACS separation of GFP expressing *prl2* mutant and GFP- wild type cells.

A) Schematic representation of cell sorting. B) Scatter plot showing the efficacy of cell sorting. C) Quatitative real-time PCR measurement of *PRL2* RNA levels in the unseparated protoplast mixture (untreated), and sorted GFP$^-$ wt versus GFP$^+$ *prl2* cells using the PRL2F+PRL2R primer pair (Figure 8) flanking the position of the GABI_228D02 T-DNA insertion in the *prl2* mutant.

3.2.4. RNA-Seq transcript profiling of FACS sorted *prl2* cells

From the FACS purified GFP$^+$ *prl2* and GFP$^-$ wt cell samples represented by three independent replicates, RNA was isolated using a miRNeasy mini kit (Qiagen, Valencia, CA). Because of the low amount of RNA yield, the library preparation was performed using the Ovation RNAseq systemV2 (Nugen) pipeline followed by Illumina HiSeq3000 sequencing at the Max-Planck Genome-Zentrum. The sequence reads (67,862,244 GFP$^-$ wt [23,844,010+20,510,551+23,507,683] and 61,704,290 GFP$^+$ *prl2* [20,547,696+20,707,880+ 20,448,724]) were mapped to genomic loci and transcript isoform sequences using the CLC Genomic Workbech (version 11.01) software as described in section 3.1.3. Table 6 below summarizes the number of differentially expressed genes (DE) and transcript isoforms showing differential alternative splicing (DAS), including mRNAs with alternative 5’ and 3’ ends.

Table 6: Identification of differentially expressed genes and differential alternative splicing of transcripts in GFP+ *prl2* mutant cells compared to genetically complemented GFP- wt cells.

After mapping, the DE and DAS lists passed a series of steps of curation by identification of alternative splicing events, ORF changes affecting protein functions and probability of transcript degradation by MND to generate three lists, which identify transcriptomic changes at different confidence levels. Stars indicate that the annotation of upregulated DAS_alone list and the category of genes, which are represented by multiple DAS mRNA isoforms is still in progress.

DE_total	**2724**				
DE_UP_total	1588			**DE_DOWN_TOTAL**	1138
DE_DAS_UP			**771**	**DE_DAS_DOWN**	**458**
no splicing change	no ORF change	DE_DAS>2	448	GE_TE<2	264
alt splicing	noORF change	DE_DAS>2	142	GE_TE<2	98
alt splicing	alt ORF	DE_DAS>2	121	GE_TE<2	80
multiple transcripts	alt ORF	DE_DAS>2	60	GE_TE<2	16
DE_alone_UP			**697**	**DE_alone_DOWN**	**487**
no splicing change	no ORF change	DE_alone>2	428	DE_alone<2	350
alt splicing	noORF change	DE_alone>2	70	DE_alone>2	59
alt splicing	alt ORF	DE-alone>2	62	DE_alone<2	29
multiple transcripts	alt ORF	DE-alone>2	137	DE_alone<2	49
DE_DAS+DE_alone_UP_curated			**1468**	**DE_DAS+DE_alone_DOWN_curated**	**945**
predicted UP			1344	predicted DOWN	886
predicted DOWN			124	predicted UP	61
DAS_alone UP				**DAS_alone DOWN**	
Unique DAS>2, DE<2			**1470**	Unique DAS<-2, DE>-2	**652**
predicted UP			*	predicted UP	248
predicted DOWN			*	predicted DOWN	404
DE genes represented by multiple DAS values			**765**		

As illustrated by values in Table 6, despite lower amount of RNA input form the FACS sorted cell samples, the RNA-Seq analysis identified higher number of differentially regulated genes in the *prl2* mutant compared to *prl1-1*. Inspection of number of reads mapped to DE and DAS entries indicated that about half of the reads in both *prl2* and wt cell samples were represented by less than 20 reads, which defined a potential internal error in the analysis. Following the filtration steps shown in Figure 3, the curated combined DE-DAS+DE_alone lists were analyzed for enrichment of specific GO terms (Table 7). When accounting the identified GO terms for subsequent pathway sorting, the lists were further filtrated by ignoring entries with lower than 20 reads. Whereas the GO-term enrichment analysis identified at a probability of $p<0.01$ only few upregulated genes acting in the conversion of phenylpropanoid/flavonoid compounds into cell wall suberin, the list of down-regulated genes revealed an enrichment of terms related to embryonic development, post-embryonic tissue and organ differentiation, and control of DNA replication.

Table 7: GO terms showing enrichment in the DE-DAS+DAS_alone lists of *prl2* RNA-Seq study. Genes represented by the color coded GO terms are highlighted in Table 10 in the Appendix.

DE-DAS+DE_alone 1468 UP: Terms from the Process Ontology of gene_association.tair with p-value <= 0.01			
Gene Ontology term	**Cluster frequency**	**Genome frequency**	**Corrected P-value**
suberin biosynthetic process	8 of 1468 genes, 0.5%	20 of 31767 genes, 0.1%	0.00226
DE-DAS+DE_alone 945 DOWN: Terms from the Process Ontology of gene_association.tair with p-value <= 0.01			
Gene Ontology term	**Cluster frequency**	**Genome frequency**	**Corrected P-value**
regulation of developmental process	46 of 945 genes, 4.9%	750 of 31767 genes, 2.4%	0.00477
post-embryonic development	91 of 945 genes, 9.6%	1904 of 31767 genes, 6.0%	0.00744
DNA replication initiation	7 of 945 genes, 0.7%	25 of 31767 genes, 0.1%	0.00777
tissue development	42 of 945 genes, 4.4%	678 of 31767 genes, 2.1%	0.00984

Functions identified by the latter GO terms thus suggested that early embryonic lethality of *prl2* homozygous seeds and poor viability of *prl2* mutant sectors in the absence of wt cells probably reflects respectively a downregulation of genes essential for the formation of embryo, and differentiation or growth of organs, as well as potential defects in the regulation of cell cycle and DNA replication.

3.2.5. Differentially expressed genes in *prl2* mutant cells

Most of the 120 differentially regulated genes identified by the GO-term enrichment in the downregulated DE-DAS+DE_alone list was previously found to be essential for embryogenesis and differentiation of leaf and inflorescence meristems by studying the corresponding gene mutations (Table 7). In addition, many more genes allocated to these pathways were identified following updated annotation of the DE-DAS+DE-alone lists. Upon examination of splicing alterations, from 945 downregulated entries only 81 revealed predictable upregulation of gene functions by decreased ratio of mRNA isoforms that code for defective gene products.

Inhibition of DNA replication in the *prl2* cells was indicated by downregulation of genes encoding the MCM2 (MINICHROMOSOME MAINTENANCE 2), MCM3 and MCM7 3' to 5' DNA helicase, MCM4, DNA polymerase α-interacting CDC45, ORC1B (Origin Recognition Complex subunit 1b), PCNA (Proliferating Cell Nuclear Antigen 1) and DNA ligase I components of the DNA replication initiation complex. Whereas e.g., mutation of *MCM2* causes very early block of embryogenesis (Ni et al., 2009), the ORC1 PHD-finger protein acts also as a histone H3K4me3 mark reader controlling transcription initiation (de la Paz Sanchez and Gutierrez, 2009) and its mutation results in an *une13* (UNFERTILIZED EMBRYO SAC 13) defect. A further gene repressed in *prl2* cells is *ICU2* (*INCURVATA 2*), which codes for the catalytic subunit of the DNA polymerase α. ICU2 interacts genetically with components of the Polycomb Repressor Complex 2 (PRC2; e.g., TERMINAL FLOWER 2/LHP1; and CURLY LEAF) controlling the deposition of repressive H3K27me3 chromatin mark, telomere stability and DNA replication, as well as the expression of genes in the flowering time, floral organ identity, embryogenesis, redox, ABA and SA signaling pathways. In *prl2* cells, the mRNA levels of EMF1 (EMBRYONIC FLOWER 1) are also lower. EMF1 acts in histone ubiquitin ligase PRC1 complexes with several BAH (bromo-adjacent homology domain) proteins, which recognize both H3K4me3 and H3K27me3 chromatin marks in many of the double imprinted genes acting in flower and embryo development, and thus represents a key regulator of reproduction (Li et al., 2018a; Yang et al, 2018). Intriguingly, the SWC4 Myb TF, which recruits the SWR1-C transcriptional repressor and NuA4 acetyltransferase complexes to promoters is induced, while the interacting ARP5 component of these complexes, which functions also in the INO80 complex in DNA repair, is downregulated in *prl2* cells. Simultaneous upregulation of RAD51C, RAD51C-interacting RING-finger protein 113A1, RAD9, DNA repair DNA photolyase and numerous other factors in DNA excision repair and recombination suggest simultaneous induction of compensatory DNA repair mechanisms.

A hallmark for defective regulation of cell division (as well as DNA replication & repair and meristem maintenance) in *prl2* is the downregulation of RBR1 (RETINOBLASTOMA-RELATED 1) human tumor suppressor homolog, which controls nuclear proliferation in the female gametophyte (Zhao et al., 2017). Similarly, to RBR1, MAIN (MAINTENANCE OF MERISTEMS), ALY1 encoding a DIRP (Domain in Rb-related Pathway) protein, and genes of the RBR1 regulated E2FC and E2FD TFs are repressed in *prl2* cells. Deficiency of MAIN abolishes the maintenance of stem cells inducing premature differentiation and cell death (Wenig et al., 2013), whereas deficiency of E2FD/DEL2 enhances the expression of genes coding for repressors of cell division (Sozzani et al., 2010). Similarly, *prl2* cells show a parallel repression of *TANMEI/EMB2757*, which encodes a WD40-repeat substrate receptor of a CUL4-DDB1 ubiquitin E3 ligase required for embryo development and control of the DNA damage cell cycle checkpoint by ATR (ATAXIA TELANGIECTASIA-MUTATED AND RAD3-RELATED; Yamagishi et al., 2005; Nezames et al., 2012).

Downregulation of at least 50 or more other functions might confer embryo lethality in the *prl2* mutant. Among these we find e.g., *WRKY2*, which controls unequal cell division and polar patterning in the embryo; the PHD-finger protein TTA2/OBE4 (TITANIA 2/OBERON 4) required for MONOPTEROUS (MP) dependent embryonic root meristem initiation; the ORTHRUS 4 (VARIANT IN METHYLATION 4) zinc-finger factor involved in endosperm imprinting; the TT6 (TRANSPARENT TESTA16, AGL38) MADS TF specifying the identity of endothelial layer in the ovule; and the BRM (BRAHMA; CHA2; CHR2; CHROMATIN REMODELING 2) ATPase subunit of SWI/SNF chromatin remodeling complex required e.g., for activation of CUC genes during the formation of embryo boundary cells.

In addition to transcription regulatory factors, the lethality of *prl2* embryos could also derive from repression of many other functions in ribosome biogenesis, vesicular, metabolite and hormone transport, metabolism or organelle to nucleus communication. Examples for the latter pathways include: e.g., *EDA19/SWA1* (*EMBRYO SAC DEVELOPMENT ARREST 13*/*SLOW WALKER1*; Shi et al., 2005), which encodes a WD40 protein involved in 18S rRNA processing and control of cell cycle progression during female gametogenesis; the RPF1 (RIBOSOME PRODUCTION FACTOR 1) homolog MEE49

(MATERNAL EFFECT EMBRYO ARREST 49); the embryo integumentum sucrose efflux transporter SWEET15 (SAG29, SENESCENCE-ASSOCIATED GENE 29; Chen et al., 2015b); the embryo-specific nitrate transporter NPF5.5 (Léran et al., 2015); the ARF GTPase guanine-exchange factor GNOM-LIKE1/ERMO1 required for biogenesis of endoplasmic reticulum and membrane recycling (Du et al., 2013) or the *GURKE* long-chain fatty acid acetyl-CoA carboxylase 1 (ACC1; EMB22; EMBRYO DEFECTIVE 22; GK; GLOSSYHEAD 1; GSD1; PAS3; PASTICCINO 3; SENSITIVE TO FREEZING 3; SFR3), which is required for proper cell division patterning and cold acclimation of the embryo (Baud et al., 2004). These examples illustrate that the *prl2* mutation results in coordinating downregulation of numerous functions required for embryo viability, including various metabolic functions. The list of downregulated genes involved in ribosome biogenesis identifies at least another 10 functions, which are likely essential for normal growth and/or viability (Table 9).

Dramatically altered phenotype of *prl2* mosaic sectors in leaves and inflorescences indicates a much wider range of defects in differentiation of leaf and flower meristems. Parts of these defects are likely related to coordinate downregulation of auxin efflux carriers PIN2, PIN3, PIN7 and PILS2, which play a key role in regulation of polar growth and cell differentiation not only in the embryo but also in shoot, intercalary and root meristems. Alteration of leaf and petal shape in *prl2* sectors could reflect reduced expression of *ASL1* (ASYMMETRIC LEAVES 2-like 1; Chalfun-Junior et al., 2005), which controls proximal-distal symmetry of leaves and petals, apical dominance and lateral organ differentiation; *DOT1* (*DEFECTIVELY ORGANIZED TRIBUTARIES 1*; Petricka et al., 2008) and *SCARFACE* (SFC, AGD3; ARF-GAP DOMAIN3; ASCULAR NETWORK DEFECTIVE 3; Deyholos et al., 2000) acting in vein patterning; and HB16 (homeodomain-leucine zipper class I (HDZip I) protein; Wang et. al., 2003), HAT3 (class II homeodomain-leucine zipper (HD-ZIPII) transcription factor; Bou-Torrent et al., 2012) and BOP1 (BLADE ON PETIOLE 1; Jun et al., 2010) regulators of leaf development. On the other hand, fast induction of leaf senescence in the *prl2* mosaic sectors correlates with enhanced expression of e.g., ethylene induced ERF1B, ERF2, and ERF8 transcription factors (Koyama et al., 2013); LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4, Takeda et al., 2011) PPD1 (PEAPOD 1, White, 2006) and GeBP (GL1 enhancer binding protein, Curaba et al., 2003) repressors of leaf development.

A disturbance of shoot and root meristem differentiation in *prl2* is suggested e.g., by repression of *CRN1* (CORYNE; SOL2; SUPPRESSOR OF LLP1 2 receptor kinase) which acts in the CLAVATA signaling pathways to repress WUS (Nimchuk et al., 2011); *CLV2* (CLAVATA 2), which regulates both meristem and organ development by stabilizing the CLA1 receptor kinase (Jeong et al., 1999); and DLL (DAWDLE) involved in DCL1-mediated processing of pri-microRNAs (Morris et al., 2006). Intriguingly, in the *prl2* mutant and wt cells derived from the mosaic inflorescence sectors relatively high RNA levels of several flowering time regulators were detected. Among these, mRNA levels of ELF5 (EARLY FLOWERING 5, Noh et al., 2004), LD (LUMINIDEPENDENS, Aukerman et al., 1999), FLK (FLOWERING LOCUS KH DOMAIN, Mockler et al., 2004), FTIP4 (FT INTERACTING PROTEIN 4, Liu et al., 2018), FHA2 (FORKHEAD-ASSOCIATED 2; Ahn et al., 2013), AP3

(APETALA 3, Wuest et al., 2012), SPL5 (SPL5 SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 5, Jung et al., 2016) and PTL (PETAL LOSS, Kaplan-Levy et al., 2014) are lower in *prl2* cells. PTL is a trihelix repressor of petal growth, AP3 specifies petal and stamen identity together with PISTILLATA, and FHA2 is required for stamen elongation. As a read out of PTL/AP3/FHA2 downregulation, the *prl2* mosaic flowers display reduced size petals and rudimentary stamen (Figure 12). FTIP4 represses the function of SHOOTMERISTEMLESS (STM), FLK is a negative regulator of FLC flowering time repressor, LD stimulates flowering as an activator of LEAFY, whereas ELF5 is a FLC-independent repressor of flowering and SPL5 acts as a regulator of LFY, AP1 and FRUITFULL in the aging pathway. Apparently simultaneous downregulation of ELF5, LD and SPL5 caused only a minimal (if any) delay in appearance of *prl2* mosaic inflorescences, whereas downregulation of *LD* and *SPL5* did not result in *leafy* flower phenotype. Rather the flowers in the *prl2* mosaic sectors carried rudimentary and fast senescing sepals, probably due to independent repression of a number of other functions affecting leaf development.

3.2.6. Comparison of changes in the regulation of different pathways in the *prl1* and *prl2* mutants

The comparison of *prl1* and *prl2* transcript profiling experiments is largely illegitimate because we try to relate transcriptomic changes detected in seedlings to altered gene expression observed in single cell protoplasts of an inflorescence-derived cell culture. Nevertheless, it is interesting to mention that the overlap between the DE-DAS+DE_alone lists of the two transcription profiling experiments (*prl1* 1656 and *prl2* 2413 curated entries) is represented by only 385 genes. Of these, 84 are upregulated and 86 are downregulated in both samples, whereas 75 genes show induction in *prl1* but repression in *prl2*, while 141 display the opposite contrasting regulation. As the GO term analyses of these categories fail to identify any significant enrichment, it is more worth to inspect the common pathways, which show altered regulation in both datasets. One of the striking differences is that the *prl1* mutation results in compensatory upregulation of several genes encoding subunits of the U5 snRNP, which serves as binding platform for the NTC, while the *prl2* mutation results in a repression of CDC5 PRL1-binding MYB TF NTC subunit, as well as two core subunits of the U5 snRNP, the BRR1 RNA helicase and STABILIZED 1 (STA1). BRR1 is also named EMBRYO DEFECTIVE 1507, whereas the synonym of STA1 is EMBRYO DEFECTIVE 2770 as their inactivation results in early embryo lethality similarly to null mutations of CDC5 and PRL2. The *prl1-1* mutation, like other NTC subunit mutations result in cold sensitivity and downregulation of *CBF1* and several other modulators of cold tolerance. It is thus interesting that the *prl2* mutation increase the expression of *CBF2*, which acts as a repressor of CBF1 and CBF3 positive regulators of cold acclimation (Jia et al., 2016). Thus, the *prl2* mutation is predicted to enhance cold sensitivity similarly to *prl1*.

A further intriguing observation is that several SAUR genes (e.g. SAUR8, 9, 38, 53 and 76) and a number of other auxin-induced genes show upregulation in the *plr2* mutant compared to a repression 45 other SAUR genes in the *prl1* mutant. Furthermore, the major root to shoot cytokinin transporter ABCG14, which appears to account for cytoninin hypersensitivity of the *prl1-1* mutant (Ko et. al., 2014), and several functions in the control of cell cycle and DNA replication (e.g. MCM2, MCM3, TANMEI etc.) are upregulated in *prl1-1* but repressed in *prl2* cells. The same is true for the BRAHMA ATPase of SWI/SNF chromatin remodeling complex, the histone H3K4me3/H3K27me3 reader BAH domain components of Polycomb 1, Polycomb 2 associated ICU2, the phloem specific iron transporter OPT3 etc. On the other hand, the *prl2* mutation does not appear to affect e.g. redox regulation of salicylic acid pathway by modulation of transcript levels of glutaredoxins. Defective transcript isoforms of e.g. *SNC1*, which appear to be enriched in *prl1-1* show downregulation in *prl2* cells. In contrast to *prl1-1*, genes of several pathogen defense PROPEP and defensin peptides are induced in *prl2*. However, the overlap between *prl1-1* and *prl2* affected genes in the pathogen defense pathways are minimal. The same is true for the phenylpropanoid biosynthesis pathway. While *prl1-1* upregulates genes involved in early steps of flavonoid biosynthesis, the *prl2* mutation leads to analogous upregulation of genes that code for late enzymes in the same pathway acting in cell wall suberin synthesis. In conclusion, mutations of the two PRL1 homologs in *Arabidopsis* appear to affect many common pathways but modulate the functions of largely distinct gene sets, with the exception a few common target genes. In the latter exceptional cases, the common target genes show contrasting regulation in *prl1-1* mutant seedlings compared to *prl2* mutant cells derived from calli of inflorescence origin.

4. DISCUSSION

4.1. Duplication of PRL1 homologs in plants

Blastp searches for *Arabidopsis* PRL1 homologs in the NCBI database indicate that PRL1 (XM_001698422.1) is encoded by a unique gene in the unicellular *Chlorophyta* algae species *Chlamydomonas reinhardtii* similarly to fungi and animals. Using the *Chlamydomonas* protein sequence in Blastp searches, two closely related PRL2 homologs are found however in *Marchantia polymorpha* (common liverwort, MARPO_0016s0006/ AXG93_3545s1000) and *Physcomitrella patens* (spreading earthmoss, XP_024376360.1/XP_024398749.1), which primarily differ in their N-terminal sequences upstream of the C-terminal seven conserved WD40 repeats. Duplication of PRL1 genes during evolution thus seems to coincide with the appearance of multicellular plant species and separation between the vegetative diploid sporophyte and reproductive haploid gametophyte generations. In higher plants, the size of haploid gametophytes represented by egg cells hidden in the ovary of flowers, and sperm and vegetative cell nuclei of pollens is largely reduced. In addition, a double fertilization of haploid egg cell and diploid central cell in the ovule is necessary for maintenance of the embryo developing from the fertilized egg cell by triploid endosperm tissues differentiating from the fertilized central cell. Kleinridders et al. (2009) elegantly demonstrated that knockout of mouse PRL1 and silencing of its homolog in the zebrafish *Danio rerio* results in very early embryo lethality. In the mouse knockout mutant, inactivation of the *PRL1* homolog called *PRLG1* leads to cytoplasmic translocation of its interacting partner CDC5 and activation of DNA damage repair responses by increased phosphorylation and stabilization of p53 tumor suppressor, which stimulates apoptosis in both embryonic and vegetative tissues. This observation indicates that in animals inactivation of PRL1 does not prevent egg cell formation but stimulates a decay of fertilized embryo by induction of cell death. In the case of *Arabidopsis prl2* mutation, we observe a very similar effect. During transition from the globular to the heart stage, the positions of two cotyledon primordia are specified. The decay of heart stage *prl2* embryos thus suggests that PRL2 is specifically required for cell differentiation of embryonic apical shoot meristem and possibly also the root meristem. By contrast, inactivation of the *PRL2* homolog *PRL1* does not have any effect on embryogenesis but rather influences the development of sporophytic vegetative organs through reducing the rate of cell elongation and stimulation of compensatory cell divisions in parallel with complex alteration of hormonal and stress responses. Nonetheless, the *plr1* mutation also affects differentiation of both apical and root meristems of seedlings, which is indicated by the early flowering and short root phenotypic traits. Diversification of the functions of duplicated PRL1 homologs could imply that they might interact with different regulatory factors during the process of co-transcriptional splicing. It will be therefore important to determine whether the two PRL1 homologs form distinct NTC complexes, which are distinguished by their embryonic functions in higher plants.

4.2. Genetic and functional analysis of NTC mutants

The *PRL1* gene was first identified by Németh at al. (1998) in an *Arabidopsis* T-DNA insertion mutant, which displayed complex, so-called pleiotropic alterations including organ developmental defects, increase of sugar (i.e., sucrose and glucose), ABA, cytokinin and cold sensitivity accompanied by upregulated expression of a battery of sugar, cytokinin and stress-regulated genes. At the same time, Ohi et al. (1998) and Burns et al. (1999) characterized the yeast CDC5/Cef1 and human CDC5L Myb-related proteins, and then Ajuh et al. (2000) and Ohi et al. (2002) purified the human and yeast CDC5 complexes, respectively. It became thus clear that CDC5 is an interacting partner of human (PLRG1) and yeast (*S. cerevisiae* Prp46; *S. pombe* Prp5) homologs of *Arabidopsis* PRL1. The purified CDC5 complex carried duplicated paralogs of the Prp19 ubiquitin ligase and 19 other subunits, mutations of which were found to cause splicing defects. The PRL1-CDC5 -PRL19 complex was therefore named the Nineteen Complex (NTC). Subsequent systematic purification of *in vitro* assembled human spliceosome complexes revealed that NTC becomes associated with the pentameric spliceosomal B-complex and is required for activation of both 1st and 2nd steps of splicing, as well as final dissociation of the spliceosome (see for review Koncz et al., 2012). Recent structural models of different spliceosomal complexes provide a detailed map on the localization of different NTC subunits relative to the U5 snRNP, Sm core and more distant U2 snRNP subunits (see e.g., Yan et al., 2016).

In their study, Németh et al. (1998) used northern RNA and nuclear run-on transcript hybridization experiments to demonstrate that the *Arabidopsis prl1* mutation results in constitutive activation (i.e., de-repression) of numerous ABA, light, salicylic acid, pathogen and oxidative stress induced genes, implying that some of these genes are controlled at the levels of transcription initiation. They also provided evidence that sucrose and cytokinin enhance the activation of several *prl1* regulated transcripts in correlation with the sucrose, ABA and cytokinin oversensitivity traits of the *prl1* mutant. These observations primed further research using the *prl1* mutant as a tool for identification of sugar (i.e., sucrose and glucose), ABA, cytokinin, cold etc. regulated *Arabidopsis* gene sets. For example, Li et al. (2006; 2007) used Affymetrix transcript profiling to demonstrate that the *prl1* mutation modulates sucrose-dependent regulation of gene networks, which are responding to either ABA or activated by the MURUS4 (MUR4) gene involved in arabinose synthesis. A highlight of these studies was the identification of TELO motives in the promoters of glucose-regulated ribosomal protein and cell cycle genes, which are recognized by the TCP transcription factor family.

In parallel, it was recognized that the *prl1* mutation acts as a suppressor of the *flu* mutation and alleviates pathogen resistance conferred by the *snc1* (*SUPPRESSOR OF NPR1-1*) mutation leading to pathogen sensitivity. The *FLU* (*FLUORESCENT IN BLUE LIGHT*) gene encodes a chloroplast membrane-associated tetratricopeptide repeat protein, which is a suppressor of Mg^{2+}-protoporphyrine IX synthesis. The *flu* mutant accumulates protoporphyrine IX resulting in generation of singlet oxygen ($^1O_2$) triggering cell death (Baruah et al., 2009). On the other hand, the dominant *snc1* mutation activates the salicylic acid (SA) signaling pathway in the absence of *NPR1* in an EDS1-dependent fashion without induction of cell death (Li et al., 2001). Palma et al. (2007) showed that a *mos4* (*Modifier Of snc1, 4*) mutation of the NTC subunit SPF27/BCAS2 (Breast Cancer-Amplified Sequence 2), as well as mutations of PRL1 and CDC5 suppress pathogen resistance conferred by the *snc1* mutation. Subsequently, Monaghan et al. (2009) found that combined mutations of the duplicated PRP19A/MAC3A and PRP19B/MAC3B NTC subunits also suppress the *snc1*-mediated autoimmunity (i.e., basal resistance). As mentioned in section 3.1.3., the problem with this report is that the combination of the same *prp19a* and *prp19b* T-DNA insertion mutations never yielded a viable homozygous progeny in our laboratory. Similarly, Copeland et al. (2013) observed that a combination of *mos2* and *mos2h* mutations, which abolish the functions of duplicated *Arabidopsis* homologs of GPKOW/Spp2 NTC-associated NTR protein, also confer gametophyte lethality. In the case of *Arabidopsis* CDC5, which is encoded by a single gene, our laboratory observed an interesting difference between the examined mutant alleles (Szakonyi, 2006). The GABI 278B09 *cdc5-1* mutant, in which a T-DNA insertion in exon 4 removed only a 3’ segment of the coding domain resulting in a deletion of 17 C-terminal amino acids, displayed a phenotype indistinguishable from the *prl2* mutant. By contrast, the KONCZ_76101 *cdc5-2* mutant, in which the T-DNA insertion in exon 2 resulted in a deletion of coding sequence for 289 C-terminal amino acids could not be recovered in homozygous form. This suggested that a partial loss of function of the *cdc5-1* mutant probably affected the interaction of CDC5 with PRL1 without compromising the function of PRL2. By contrast, in the *cdc5-2* mutation appeared to alleviate the PRL2 function by deleting the binding site for both PRL homologs and destabilizing the NTC complex. In conclusion, these data suggested that PRL2 can partially compensate the loss of PRL1, while PRL1 cannot replace the function of PRL2 required for proper embryo development.

Szakonyi (2006) demonstrated that the promoter regions of *PRL1* and *PRL2* genes extend into their coding sequences until the boundary of intron 2 and exon 3 but include only short segments of 5’-UTRs. A truncated PRL1 promoter carrying only 65 nucleotide sequence with the TATA-box upstream of ATG but extending 3’-downstream to exon 3 conferred nearly full-strength promoter activity. Subsequently, Villacorta (2010) replaced the 3’-segment of *PRL1* gene from exon 3 with corresponding sequences of *PRL2* cDNA and created a similar domain swap construct using the PRL2 promoter and 3’ end of *PRL1* cDNA. After introducing these constructs into the *prl1-1* and *prl2* GABI mutants, it was observed that the PRL1 promoter-PRL2 domain swap complemented all mutant traits of *prl1-1*, while the PRL2 promoter-PRL1 domain swap construct resulted only in partial complementation e.g., of *prl1* root elongation defect. By contrast, in 2 out of 40 examined *prl2/+* transformants a complementation of embryo lethal phenotype was observed by the PRL2 promoter-PRL1 domain swap, while the PRL1 promoter-PRL2 domain swap construct failed to rescue the *prl2* embryo lethality. This suggested that either the *PRL1* promoter does not confer high enough expression in the embryo or, which is more likely, the N-terminal domain of PRL1 cannot interact with some embryo specific regulatory factors that recognize the divergent N-terminal domain of PRL2. In any case, these studies did not answer the question whether the *prl1* mutation is a general cell death suppressor or affects the oxidative stress/cell death and pathogen defense pathways through independent mechanisms (e.g., regulating differential expression/transcription or alternative splicing (or both) of different target transcripts).

In contrast to Villacora (2010), Weihman et al. (2014) reported on the isolation of a dominant *prl1* suppressor mutation, a single nucleotide exchange located at position -58 upstream of the ATG codon in the *PRL2* gene. This point mutation was found to increase the *PRL2* transcript level to about 2-fold and claimed to confer complementation of all *prl1* developmental defects and pathogen sensitivity trait. Based on their results, Weihman et al. (2014) concluded that *PRL2* is a lower expressed paralog of *PRL1*, which performs an identical function. Recently, Jia et al. (2017) described RNA-Seq analysis of a surprisingly viable *prl1, prl2* double mutant, as well as that of the enigmatic *mac3a, mac3b* double mutant from Monaghan et al. (2009). In their report they emphasize that the NTC is a central hub in the SNC1-regulated pathogenic signaling pathway based on comparative analysis of RNA-Seq data. Jia et al. (2017) also emphasize that according to their RNA-Seq data the *prl1, prl2* double mutation results in downregulation of numerous pri-microRNA transcripts, which supports some other results suggesting that PRL1 interacts with the HYL1 and SERRATE subunits of DCL1 microprocessor complex that controls microRNA biogenesis (Zhang et al., 2013; 2014).

In section 3.2.1 we examined the putative *prl2* null mutation in the SALK_075970 line described by Jia et al. (2017). In fact, we confirmed that in this line a T-DNA insertion was located exactly 7 nucleotides upstream of the ATG codon as reported by these authors. Because the T-DNA insertion from the SALK pROK tagging vector carries a CaMV35S promoter upstream of the left T-DNA border, and in the SALK_075970 mutant a T-DNA inverted repeat facing with its left border the *PRL2* gene was identified, we examined the *PRL2* transcript levels in this mutant. The performed qRT-PCR measurements clearly show that in the SALK_075970 *prl2* mutant used by Jia et al. (2017) the *PRL2* mRNA level is at least 2-fold higher than in wt seedling. Consequently, the reported *prl1, prl2* double mutant is a *PRL2* overexpressing line. Given the fact that Weihman et al. (2014) from the same laboratory showed that 2-fold increase of *PRL2* mRNA level in their promoter point mutant *prl1* suppressor line confers full complementation of the *prl1* mutation, it is currently unclear how to evaluate the RNA-Seq results and derived conclusions of Jia et al. (2017).

4.3. RNA-Seq transcript profiling of the *prl1-1* mutant

All known mutations located in the *PRL1* gene result in the same phenotypic alterations as the first *prl1-1* mutation described by Németh et al. (1998). The mutants are characterized by their semi-dwarf growth habit in the light and show also shortened hypocotyl length in the dark. Németh et al. (1998) showed that in the hypocotyl epidermis of the *prl1* mutant the number of cells per unique distance is 2-3-fold compared to wild type, which indicates that the defect of cell elongation is compensated by enhanced cell division. Accordingly, GO analysis of RNA-Seq data indicated an enrichment of the term “cell division”, which was represented by 22 genes. Among these, several previously upregulated candidate genes, such as CYCLIN B1, 2, and 3 were identified (see e.g., Szakonyi, 2006) along with numerous genes of cell cycle kinase inhibitors (e.g., SIAMESE-RELATED 5 and 9, and CKS1), and G_0/S phase specific CYCLIN Ds, which are downregulated in *prl1-1*. The cell elongation defects in *prl1-1* correlate with lower expression of 44 genes coding for various cell wall loosening enzymes and the bHLH136/PRE1 (PACLOBTRAZOL RESISTANCE1) activator of these genes (Ikeda et al., 2012). At the same time, numerous genes coding for peptide growth factors and 45 out of the 58 known SAUR (Small Auxin UpRegulated) genes involved in the control of growth and cell expansion (Ren and Gray, 2015) showed lower transcript levels in *prl1-1*. The increased ABA sensitivity trait of *prl1-1* correlated with induction of MYB15 (Ding et al., 2009), and with lower expression of the ABA-induced PP2C gene 1 (HAI1, SAG113), an inhibitor of ABA signaling (Zhang et al., 2012). In addition to defective cell elongation and disturbance of auxin signaling, inhibition of root growth in *prl1-1* correlated with downregulation of root meristem growth factor RGF2, the root auxin transport regulator ROSY1, the nitrate-dependent root growth regulator ANR1 (AGAMOUS-like 44) TF, the SWEET2, 4 and 16 sugar transport facilitators, and the ATL31 ubiqutin ligase, which controls both sugar and nitrate sensitivity. Similarly, to *prl1-1,* mutations of e.g., *SWEET2* and *ATL31* were reported to confer enhanced sugar sensitivity (Sato et al., 2009; Chen et al., 2015a). At the same time, higher transcription of induction of genes coding for the cytokinin-activating enzyme LONELY GUY 5 and root-to-shoot cytokinin translocator ABCG14 (Kurakawa et al., 2007; Ko et al., 2014) and lower expression of the type A negative response regulator ARR5 (To et al., 2004) and AtMYB2 repressor of cytokinin synthesis (Guo and Gan, 2011) could provide an explanation for increased cytokinin sensitivity of *prl1-1*.

A nice example for coordinate regulation of positive and negative functions in a pathway is illustrated by upregulation of sugar and cytokinin inducible genes of flavonoid biosynthesis pathway and simultaneous downregulation of KISS ME DEADLY ubiquitin ligase F-box proteins that mediate proteasomal degradation of two rate-limiting enzymes of this pathway, CHS1 and PAL, as well as proteolysis of type B positive response regulators of cytokinin signaling (Kim et al., 2013; Zhang et al., 2013a). Upregulated synthesis of UV protecting flavonoids coincided with the activation of several key genes of the UV-induced DNA repair pathways (e.g., XPB/Rad25 and XPG exonuclease components of TFIIH; TAN (TANMEI) and DAMAGE-SPECIFIC DNA BINDING PROTEIN 2, BRCA1, PARP2 (POLY(ADP-RIBOSE) POLYMERASE) and 21 other genes involved in DNA repair and recombination.

We also observed a remarkable upregulation of all 4 known transcription activators of iron starvation response BHLH 38, 39, 100 and 101 along with their target genes (e.g., iron-chelating nicotianamine synthase 2, root specific ferric chelate reductase FRO2, phloem specific iron transporter OPT3) (Wang et al., 2013; Zhai et al., 2014). In relation to *flu*-induced cell death suppressing effect of the *prl1* mutation, our data indicated an upregulation of *HEMA3* gene of glutamyl-tRNA reductase catalyzing the first rate-limiting step of protoporphyrine synthesis along with a repression of AtOEP16 involved in chloroplast import of protochlorophyllide reductase A and several other genes of jasmonate (JA) induced transcription activators (e.g., NAC055, ERF8, MYB2 etc.) of chlorophyll degradation. It remains to be determined whether differential gene regulation affecting iron uptake and chlorophyll biosynthesis and degradation reflects the existence of a retrograde signaling pathway, which acts through the degradation products of ProtoIX activate nuclear genes involved in the detoxification of reactive oxygen species (Duanmu et al., 2013).

In contrast to the report of Jia et al. (2017), the GO analysis of our RNA-Seq data failed to detect a significant enrichment of pathogen defense related pathways at a probability $p<0.01$. However, we found that the CPR1/CPR30 gene, which encodes an F-box protein substrate receptor of an SCF E3 ubiquitin ligase involved in proteasomal degradation of SNC1 (Gou et al., 2012), as well as the WRKY48 repressor of PR gene expression and basal resistance to the bacterial pathogen *P. syringae* (Xing et al., 2008) are remarkably upregulated in the *prl1* mutant. The list of over 80 downregulated entries in the pathogen defense pathway include genes coding for PR, antimicrobial Dirigent and Knottin domain proteins, PLANT NATRIURETIC PEPTIDE A, PROPEP 2, 4 and 7 peptides, and Lipid-derived azelaic acid (AZA) binding transporter proteins representing known mediators of systemic acquired resistance (SAR). Taken together, the reported *prl1*-mediated suppression of basal resistance conferred by the *snc1* mutation correlates with altered transcription of numerous genes involved in the SA-related pathogen defense pathway. Furthermore, suppression of ROS-induced cell death and SA-related pathogen responses by the *prl1-1* mutation is likely closely related to remarkable downregulation of 14 out of the 21 known members of ROXY monothiol glutaredoxin genes in *prl1-1*. Among these, we find the *GRX480/ROXY19* redox regulator of TGA-NPR SA-receptor complexes (Ndamukong et al., 2007) and ROXY2, 3, 4, 12, 17 and 19, which interact with TGA2 to repress EIN3-dependent induction of genes in the pathogen defense pathways (Zander et al., 2012). In contrast to Jia et al. (2017), we failed to detect in any alteration in the levels of pri-microRNA transcripts, so could not confirm that PRL1 is a key regulator of microRNA biogenesis (Zhang et al., 2013b, 2014).

Finally, the RNA-Seq data indicated that the *prl1* mutation results in compensatory upregulation of 10 genes coding for components of the NTC, NTC-associated NTR, and U5/U2 snRNP complexes. Cold sensitivity of the *prl1* mutant correlated with lower transcript levels of 14 genes in the cold response pathway, including CBF1/DREB1B_1 (Novillo et al., 2007) and DREB1F (DDL, DWARF AND DELAYED FLOWERING 1) representing key transcription regulators of cold and drought acclimation (Kang et al., 2011). Overexpression of DREBF/DLL was reported to delay flowering though induction of GAOX7 gibberellin oxidase expression, whereas CBF1 and its homologs mediate upregulation of the flowering time repressor *FLC* (Seo et al., 2009). Consistently, we found that *FLC* and HUB2 (HISTONE H2 MONOUBIQUITINATION 2) required for FLC expression (Xu et al., 2009) are downregulated in the *prl1* mutant, which displays day-length independent early flowering.

4.4. Construction of conditional genetic mosaic for complementation of the *prl2* mutation and isolation of mutant cells by FACS for RNA-Seq transcript profiling

A Cre-lox conditional genetic complementation system established by Heidstra et al. (2004) was exploited to rescue the embryo lethal *prl2* mutation, and then to generate genetic mosaic plants carrying GFP marked mutant sectors. First, *prl2* GABI_228D02/+ plants were transformed with the *pG7HSCRE* vector, which carried a heat-inducible *Cre* gene driven by a *HSP18.2* promoter and a hygromycin resistance (HygR) plant selectable marker gene within its T-DNA. T3 offspring showing 100% HygR and 2:1 segregation of the sulfadiazine resistance (SuR) marker of the *prl2* GABI_228D02 T-DNA insertion was then identified. The complementing *PRL2* gene was inserted 3’ downstream of a norflurazon resistance gene (CTR1), which was flanked by *lox* cleavage sites of the Cre endonuclease in the T-DNA of vector pCB1 and transformed into T3 *plr2/+* plants carrying the T-DNA of vector *pG7HSCRE* in homozygous form. Subsequently, T3 progeny was tested for homozygous status of the pCB1 T-DNA, which carries both Basta and norflurazon plant resistance markers, as well as for homozygous status of the SuR marker of the *prl2* GABI_228D02 T-DNA insertion.

Efficient Cre-lox excision of the complementing *PRL2* gene required an optimization of heat shock treatment, which varied greatly between different growth chambers. Therefore, the time required for reaching a half lethal dose (LD_{50}) of heat treatment was determined in two different illuminated growth chambers set to 42°C. Heat-induced excision of the lox-CTR1-*PRL2*-lox complementing gene cassette from the pCB1 T-DNA fuses an upstream CaMV35S promoter to coding sequences of Gal4VP16 transcription activator, the expression of which then activates a GFP reporter gene driven by a promoter carrying Gal4VP16 binding sites. Heat treatment of 4 days old seedlings carrying the *prl2* GABI_228D02, pCB1 and *pG7HSCRE* vector T-DNAs in homozygous form at 42°C for 24h resulted in appearance of GFP^+ sectors in about 60-80% of surviving heat-shocked plants. However, GFP^+ progeny of these plants still showed 3:1 segregation of the CTR1 norflurazon resistance gene, which marked the complementing wt *PRL2* gene in the lox excision cassette. This indicated that only one of the two complementing *PRL2* gene copies was removed by the Cre-lox excision. Therefore, we crossed the *prl2* GABI_228D02, pCB1 and *pG7HSCRE* homozygous line with a *prl2/+* mother to obtain in 50% of *prl2*, *prl2* F1 progeny carrying only one T-DNA copy of complementing pCB1 and HSP18.2-Cre *pG7HSCRE* vectors. Upon heat-shock, over 700 seedlings were inspected for the presence of GFP^+ sectors in the rosette and apical meristem, and 56 of these were planted to soil. Most of the GFP^+ plants carried aberrant narrow and curling leaf sectors, which showed fast senescence. 11 from these produced also aberrant GFP^+ inflorescence stem sectors, which were then examined for the presence of wild type cells by PCR amplification of a segment of complementing wt *PRL2* gene. The mosaic sectors also showed senescence, a yellowish color indicating fast chlorophyll degradation, and bared tightly packed flowers due to shortening the internode length. In the flowers the sepals were bleached, the petals shorter than wt, the stamens very short rudimentary, and the pistils had also a reduced size. The flowers produced siliques, however most of these contained only brown aborted seeds.

One line showing an apparent loss of complementing *PRL2* gene was then carefully examined by PCR amplification of DNA isolated from 5 different mutant inflorescence sectors. In 4 out of the 5 sectors the PCR test indicated an apparent loss of the complementing *PRL2* gene and homozygous status of the *prl2* mutation. These apparently homogeneous mutant inflorescence sectors were converted to calli on auxin containing medium and examined by confocal microscopy whether indeed all cells express the GFP marker indicating homozygous status of the *prl2* mutation. The fact that the calli still contained

GFP$^-$ wild type cells suggested that *prl2* mutant cells might require a metabolic or hormonal cross-feeding from wt cells for their proliferation. Subsequently, the mosaic calli were converted to a fine cell suspension and subjected to fluorescence activated cell sorting (FACS), which yielded about equal amounts of purified GFP$^+$ *prl2* and GFP$^-$ wt cell populations.

The above described procedure could theoretically be applied to rescuing any embryo lethal mutation by generation of mosaic organs, tissues and visualization of developmental effects of these mutations in somatic tissues. The FACS separation also provides the possibility to isolate somatic cells carrying the embryo lethal mutations in homozygous status for transcriptomics studies. This is illustrated by the RNA-Seq analysis of mRNA samples which were isolated from three biological replicates of sorted *prl2* and wt cells.

The results of RNA-Seq analysis exclusively identified about 120 genes, which corresponded to enrichment of GO terms of embryogenesis, postembryonic organ development and DNA replication. The latter GO term included numerous essential components of DNA replication initiation complex (MCM2 (MINICHROMOSOME MAINTENANCE 2), MCM3 and MCM7 3' to 5' DNA helicases, MCM4, CDC45, ORC1B, PCNA (Proliferating Cell Nuclear Antigen 1) and DNA ligase I, null mutations of which cause either cell or very early embryo lethality. Further prominent downregulated genes were e.g., *ICU2* (*INCURVATA 2*), which codes for the catalytic subunit of the DNA polymerase α, and EMF1 (EMBRYONIC FLOWER 1), which is a core component of histone ubiquitin ligase PRC1 complexes. Defective control of cell division was indicated by repression *RBR1* (*RETINOBLASTOMA-RELATED 1*), which is essential for nuclear proliferation in the female gametophyte (Zhao et al., 2017), *MAIN* (*MAINTENANCE OF MERISTEMS*), and the RBR1 regulated *E2FC* and *E2FD* TF genes in *prl2* cells. Deficiency of MAIN was reported to abolish the maintenance of stem cells (Wenig et al., 2013), whereas lower expression of E2FD leads to induction of several repressors of cell division (Sozzani et al., 2010). Similarly, *prl2* cells showed simultaneous downregulation of *TANMEI/EMB2757* WD40-repeat substrate receptor of CUL4-DDB1 ubiquitin E3 ligase, which controls the DNA damage cell cycle checkpoint (Yamagishi et al., 2005; Nezames et al., 2012); *WRKY2* specifying unequal cell division and polar patterning in the embryo; the PHD-finger protein TTA2/OBE4 (TITANIA 2/OBERON 4) required for MONOPTEROUS (MP) dependent embryonic root meristem initiation; ORTHRUS 4 (VARIANT IN METHYLATION 4) involved in endosperm imprinting; the TT6 (TRANSPARENT TESTA16, AGL38) determining the identity of endothelial layer in the ovule; and the BRM (BRAHMA; CHA2; CHR2; CHROMATIN REMODELING 2) SWI/SNF chromatin remodeling ATPase required e.g., for differentiation of embryo boundary cells. The impressive list of genes required for embryogenesis included also *EDA19/SWA1* (*EMBRYO SAC DEVELOPMENT ARREST 13*/*SLOW WALKER1*; Shi et al, 2005), acting in 18S rRNA processing and cell cycle control during female gametogenesis; *RPF1* (*RIBOSOME PRODUCTION FACTOR 1/MATERNAL EFFECT EMBRYO ARREST 49*); the embryo integumentum sucrose efflux transporter SWEET15 (SAG29, SENESCENCE-ASSOCIATED GENE 29; Chen et al., 2015b); the embryo-specific nitrate transporter NPF5.5 (Léran et al., 2015); GNOM-LIKE1/ERMO1 required for biogenesis of endoplasmic reticulum (Du et al., 2013) and *GURKE* (long-chain fatty acid acetyl-CoA carboxylase 1, EMBRYO DEFECTIVE 22) involved in cell division patterning and cold acclimation of the embryo (Baud et al., 2004).

Among the functions affecting both embryogenesis and organ differentiation, we found the canonical auxin influx carriers PIN2, PIN3, PIN7 and PILS2, which showed simultaneous downregulation in *prl2* cells. Alteration of leaf and petal shape in *prl2* mosaic sectors correlated with reduced expression of *ASL1* (ASYMMETRIC LEAVES 2-like 1; Chalfun-Junior et al., 2005), *DOT1* (*DEFECTIVELY ORGANIZED TRIBUTARIES 1*; Petricka et al., 2008) and *SCARFACE* (SFC, ASCULAR NETWORK DEFECTIVE 3; Deyholos et al., 2000), HB16 (homeodomain-leucine zipper class I (HDZip I) protein; Wang et. al., 2003), HAT3 (class II homeodomain-leucine zipper (HD-ZIPII) TF; Bou-Torrent et al., 2012), BOP1 (BLADE ON PETIOLE 1; Jun et al., 2010) , the ethylene induced ERF1B, ERF2, and ERF8 transcription factors (Koyama et al., 2013); LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4, Takeda et al., 2011) PPD1 (PEAPOD 1, White, 2006) and GeBP (GL1 enhancer binding protein, Curaba et al., 2003) regulators of meristem differentiation and leaf development. A disturbance of shoot and root meristem differentiation was suggested e.g., by repression of *CRN1* (CORYNE; SOL2; SUPPRESSOR OF LLP1 2 receptor kinase) repressor of WUS (Nimchuk et al., 2011); *CLV2* (CLAVATA 2) partner of the CLA1 receptor kinase (Jeong et al., 1999); and DLL (DAWDLE) involved in DCL1-mediated processing of pri-microRNAs (Morris et al., 2006).

The *prl2* mutant and wt cells isolated from the mosaic inflorescence sectors contained relatively high amount of transcripts coding for several regulators of flowering time and floral organ identity. Among these, repression of PTL (PETAL LOSS, trihelix repressor of petal growth, Kaplan-Levy et al., 2014), AP3 (APETALA 3, specifies petal and stamen identity together with PISTILLATA, Wuest et al., 2012), and FHA2 (FORKHEAD-ASSOCIATED 2; required for stamen elongation, Ahn et al., 2013) correlated with size reduction of petals and inhibition of stamen elongation detected in flowers of *prl2* mosaic sectors.

Compared to the *prl1* transcript profiling data, the *prl2* RNA-Seq analysis revealed thus a unique repression of a large set of candidate genes required for embryogenesis. At the same time, only about 10% of the genes showing differential regulation were common in the *prl1* and *prl2* datasets. Surprisingly, more than half of common candidate targets showed contrasting regulation in *prl1* seedlings and *prl2* cells, among them numerous subunits of NTC and NTC associated NTR and U5/U2 snRNP complexes. In conclusion the results of *prl1* and *prl2* transcriptomics studies suggest that PRL1 and PRL2 might form distinct NTC complexes, which modulate the expression and splicing of largely different set of genes in similar pathways. In particular, PRL2 appears to be essential for proper expression of numerous genes, which are essential for embryogenesis, whereas PRL1 affects a larger number of genes in developmental, hormonal, stress signaling and metabolic pathways during seedling development.

5. OUTLOOK

The analysis of differential alternative splicing events in *prl2* is still in progress. However, due to the relatively low number of reads, about half of the entries will have to be removed by extra filtering. Preliminary evaluation of the *prl2* DAS_alone lists suggests that, similarly to the *prl1* mutation, inactivation of *PRL2* also results in a change in the representation of alternatively spliced isoforms. As discussed in section 3.1.1., following recent update of the *Arabidopsis* database of alternatively spliced transcript isoforms (Zhang et al., 2017a), the transcriptomics studies are faced with a new challenge. Namely, the database update revealed that about 60% of *Arabidopsis* genes produce at least two alternatively spliced transcript isoforms or transcripts with different 5' or 3' ends (or both) and could considerably differ in their encoded ORFs. Consequently, all previous Affymetrix chip transcriptomics studies ought to be re-evaluated because the conclusions are only valid for those genes that are represented by single transcripts or transcript isoforms carrying the same ORF. In all other cases differential expression of mRNA isoforms coding for wt and defective gene products has to be examined and verified because e.g., overexpression of a defective gene product might downregulate the gene function instead of the predicted stimulatory effect. However, Illumina short read sequencing and the routinely used downstream analysis tools are error prone as the preciseness of identification of differentially spliced transcripts is dependent on the size of signature sequences of unique mRNA isoforms, as well as on the number of reads carrying these sequences. This is why even the most careful conclusions estimate the error of Illumina RNA-Seq studies as high as 40 to 50%. In our work, we documented these problems on the example of *prl1* RNA-Seq study. Even by implementing a careful filtering and curation protocol, the value of predictions derived from the analysis of differential alternative splicing of mRNA isoforms (i.e., DAS-alone lists) remains at the level of low confidence.

A potential solution to this problem is suggested e.g., by Abdel-Ghany et al. (2018) who used single molecule long read sequencing on a Pacific Bioscience equipment to identify over 11,000 transcript isoforms of sorghum. Whereas this approach is very promising, it remains a problem that it is not always simple to predict which splicing isoforms will be targeted for NMD mediated degradation and which will be translated despite of e.g. alternative splicing events in their 5'-UTRs. A solution to this problem is offered by the so-called Ribosome Profiling technology, which aids exclusive sequencing of translated mRNA isoforms that are isolated in association with polysomes (see for review Brar and Weissman, 2015). Clearly a combination of ribosome profiling and long-read single molecule sequencing is a future solution for assessment of how differential alternative splicing modulates the gene functions. However, this approach also requires long read sequencing of total RNA samples alone, if one needs to examine the regulation of genes of non-coding long and short silencing RNAs and pri-microRNAs. In addition, in the latter case it is necessary to sequence the so-called degradome, the class of short regulatory RNAs. Even after this remains a problem that the analysis will not cover the class of circular RNAs, which are generated by alternative, i.e. back-splicing (Li et al., 2018b).

We have also discussed the problem how to relate the observed changes in alternative splicing and representation of different transcript isoforms to cell type, tissue, organ or developmental phase specific gene regulatory events, since it is likely that the various mRNA isoforms are produced in different cells in response to different stimuli. Several elegant technologies were recently published, which allow transcript profiling of single cells e.g., in immobilized and fixed tissues (Giacomello et al., 2017). However, these approaches heavily rely on massive *in situ* PCR amplification of cellular polyA-mRNAs and use Illumina short read sequencing. In the human transcriptomics projects cell surface antigens or fluorescence labelling is used for enrichment of homogeneous cell populations to increase the sample size. These approaches are analogous to the FACS enrichment approach exploited in our work. Given the availability of so-called enhancer-trap *Arabidopsis* lines, which express GFP in different cell types (DeBlasio et al., 2010) it is feasible to apply FACS for isolation of different cells followed by transcript profiling using single long-read sequencing. As we showed, the conditional genetic complementation (i.e., genetic mosaic) system of Heidstra et al. (2004) and its combination with cell type specific promoter driven GFP reporters, would even allow to compare the transcriptomes of mutant and wild type cell types. However, as for the release of cells from the different organs cell wall digesting enzymes are used and the resulting protoplasts are sorted in a solution, which contains 0.4M mannitol as osmolyte, it will be necessary to determine carefully how these treatments affect the observed transcriptomic changes. Our experiments used wt cells from the same mosaic tissues as reference, so the detected transcriptomics changes are specific to the *prl2* cells. Last but not least, the amount of certain cell types, such as egg cells or pollen are minimal, and some of them hard to prepare even by upscaling the cell isolation approaches. So, it remains a real challenge to perform e.g., egg cell or early embryo transcript studies using Ribosome profiling and single full length RNA sequencing.

Finally, concerning further characterization of functional differences between PRL1 and PRL2, the logical next step is the isolation and characterization of PRL1 and PRL2 NTC complexes. This will answer the question whether the two PRL homologs occur in different spliceosome complexes, which act in different cell types or during different developmental phases (sporophyte for PRL1, embryo for PRL2) or they interact with different cell type specific transcription regulators.

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7. APPENDIX

Table 8: DE-DAS+DE-alone list of differentially regulated genes in the *prl1-1* mutant

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
CYP707A1	AT4G19230	-				CYP707A1	2.1078	up	ABA 8'-hydroxylase activity, involved in ABA catabolism	up
NCED3	AT3G14440	-				NCED3	-2.113	down	ABA biosynthesis chloroplast 9-CIS-EPOXYCAROTENOID DIOXYGENASE; ATNCED3; nine-cis-epoxyca	down
CYS4	AT4G16500	CYS4_1	-2.64	3.87E-04	down	CYS4	-2.693	down	ABA drought heat tolerance DREB activated phytocystain cysteine protease inhibitor	down
ERF053	At2g20880	-				ERF053	-2.19	down	ABA drought induced AP2/ERF TF	down
DTX50	AT5G52050	-				DTX50	-2.159	down	ABA efflux DTX/MATE-type transporter mutant is ABA hypersensitive	down
MYB15	AT3G23250	-				MYB15	2.2255	up	ABA enhanced sensitivity MYB15 TF	up
ATDI19	AT1G56280	ATDI19_2	-2.4	1.90E-03	down	ATDI19	-2.432	down	ABA induced CPK11 phosphorylated zinc finger TF regulator of PR1/2/5	down?
LTP4	AT5G59310	-				LTP4	-2.181	down	ABA induced LTP4 lipid transfer protein 4	down
CML37	AT5G42380	-				CML37	-5.726	down	ABA JA pathogen positive regulator Ca2+/calmodulin CML37 calmodulin like 37	down
ZFP6	AT1G67030	ZFP6_1	-2.005	0.03562	down	ZFP6	-2.03	down	ABA light GA cytokinin signalling trichome development regulating ZFP6 zinc finger protein 6	down
AT3G28580	AT3G28580	-				AT3G2858	4.433	up	ABA oxidative stress induced unknown membrane ATPase	up
PYL5	AT5G05440	PYL5_1	-2.599	2.95E-04	down	PYL5	-2.628	down	ABA receptor PYL5 RCAR8; regulatory component of ABA receptor 8	down
AT4G29190	AT4G29190	AT4G29190_1	-2.499	1.56E-04	down	AT4G2919	-2.522	down	ABA salt signaling Oxidation-related Zinc Finger 2 ZnF_C3H1 domain	down
SAG113	AT5G59220	SAG113_2				SAG113	-2.072	down	ABA signaling negative regulator HAI1 PP2C protein phosphatase	down
ABCG40	AT1G15520					ABCG40	-3.981	down	ABA stomatal root ABA transporter uptake	down
XERICO	AT2G04240	XERICO_1	-2.048	0.01522	down	XERICO	-2.031	down	ABA synthesis positive regulator interacting partner of UBC8	down
UBC8	AT5G41700	UBC8_3	-2.336	2.97E-03	down	UBC8	-2.329	down	ABA synthesis regulation XERICO interacting ubiquitin conjugating enzyme 8	down
ERF018	At1g74930	ERF018_1	-8.077	7.94E-03	down	ERF018	-8.102	down	ABA, JA synthesis ORA47 AP2 TF	down
AT1G43910	AT1G43910	AT1G43910_1	3.2769	2.66E-03	up	AT1G4391	3.2538	up	ABA-induced phosphorylation unknown DNA replication DnaC domain	up
AT1G69890	AT1G69890					AT1G6989	-2.225	down	actin cross-linking protein (DUF569)	down
PRO5	At5g56600	PRO5_1	-2.015	0.02149	down	PRO5	-2.039	down	actin filament profilin3	down
NET2D	AT2G22560	-				NET2D	2.535	up	actin membrane anchor PRK1, a receptor-like kinase interacting KIP domain protein Networked	up
NET1C	AT4G02710	-				NET1C	2.7964	up	actin membrane anchor PRK1, a receptor-like kinase interacting KIP domain protein Networked	up
SCAR3	AT1G29170	SCAR3_1	2.046	0.04959	up	SCAR3	2.0967	up	actin WAVE complex, cell elongation	up
SSL7	At3g51450					SSL7	-2.13	down	alkaloid biosynthesis from tryptamine strictosidine synthase	down
GDU5	AT5G24920	GDU5_1	-2.91	0.03785	down	GDU5	-2.944	down	amino acid export GDU5 glutamine dumper 5	down
GDU1	AT4G31730	GDU1_1	-2.225	0.0247	down	GDU1	-2.265	down	amino acid Glu secretion plasma membrane GDU1 glutamine dumper 1	down
AT2G40420	AT2G40420	AT2G40420_1	-2.21	2.65E-03	down	AT2G4042	-2.235	down	amino acid permease Trp_Tyr_perm domain protein	down
AT4G03600	AT4G03600	-				AT4G0360	-2.53	down	amino acid proline degradation P5CR pyrroline-5-carboxylate reductase	down
IPSP	At5g04120					IPSP	-3.749	down	amino acid Ser synthesis	down
TAT3	AT2G24850	TAT3_1	-11.51	0.03883	down	TAT3	-11.34	down	amino acid, TYR metabolism tyrosine aminotransferase 3	down
TIP2-1	At3g16240	TIP2-1_1	-2.555	1.51E-03	down	TIP2-1	-2.591	down	ammonium transporter vacuolar	down
PDC1	AT4G33070	PDC1_1	3.1008	0.01018	up	PDC1	3.0899	up	anoxia, pyruvate decarboxylase1 acetaldehyde	up
DFC	AT3G10160	DFC_1	-4.135	7.11E-03	down	DFC	-4.183	down	anthocyanin, mitochondrial tetrahydrofolate synthesis, N-utilization, folylpolyglutamate synth	down
ATG8C	AT1G62040	ATG8C_1	-2.094	8.55E-03	down	ATG8C	-2.067	down	autophagy APG12 homolog	down
AT4G34800	AT4G34800					AT4G3480	-3.166	down	auxin SAUR4; SMALL AUXIN UPREGULATED RNA 4	down
AT4G27280	AT4G27280	AT4G27280_1	-2.174	0.01001	down	AT4G2728	-2.206	down	auxin Ca2+ signaling karrikin induced homolog of PINOID (PID)-binding protein containing putati	down
SMAP1	AT4G13520	SMAP1_2	-2.029	5.61E-03	down	SMAP1	-2.068	down	auxin COP9 signalosome component Neddylation of CUL1	down
IGMT1	AT1G21100	IGMT1_1	-2.529	2.85E-04	down	IGMT1	-2.547	down	auxin glucosinolate indole glucosinolate O-methyltransferase 1	down
IGMT5	AT1G76790	IGMT5_1	-2.608	1.19E-03	down	IGMT5	-2.626	down	auxin glucosinolate Indole Glucosinolate O-Methyltransferase 5	down
IAA34	AT1G15050					IAA34	-2.079	down	auxin IAA34	down
IGMT3	AT1G21110	IGMT3_1	-2.223	8.40E-03	down	IGMT3	-2.236	down	auxin indole glucosinolate O-methyltransferase IGMT3	down
CYP81F4	AT4G37410	CYP81F4_1	-2.315	1.37E-03	down	CYP81F4	-2.338	down	auxin indole glucosinolate biosynthesis CYP81F4	down
ARGOS	AT3G59900					ARGOS	-2.315	down	auxin induced cell elongation organ size controlling ARGOS transmembrane protein	down
AIR1B	AT4G12545	AIR1B_1	-5.508	0.01005	down	AIR1B	-5.534	down	auxin induced lipid transfer / seed storage protein / trypsin-alpha amylase inhibitor domain AIR	down
SAUR19	AT5G18010	SAUR19_1	-6.469	4.05E-03	down	SAUR19	-6.525	down	auxin induced SAUR PP2C inhibitor controlling cell hypocotyl elongation	down
SAUR20	AT5G18020	SAUR20_1	-2.268	0.02085	down	SAUR20	-2.303	down	auxin induced SAUR20 cell expansion	down
SAUR21	AT5G01830	SAUR21_1	-2.787	2.19E-03	down	SAUR21	-2.828	down	auxin induced SAUR21 U-box E3 ARM repeat protein	down
SAUR22	AT5G18050	SAUR22_1	-6.223	1.94E-04	down	SAUR22	-6.18	down	auxin induced SAUR22 cell expansion	down
SAUR23	AT5G18060	SAUR23_1	-6.389	5.51E-04	down	SAUR23	-6.294	down	auxin induced SAUR23 cell expansion	down
SAUR24	AT5G18080	SAUR24_1	-3.204	1.05E-03	down	SAUR24	-3.246	down	auxin induced SAUR24 cell expansion	down
AT5G50760	AT5G50760	AT5G50760_1	-2.4	0.01157	down	AT5G5076	-2.433	down	auxin induced SAUR55	down
SAUR63	AT1G29440	SAUR63_1	-2.076	0.03411	down	SAUR63	-2.106	down	auxin induced SAUR63 cell elongation	down
SAUR64	AT1G29450					SAUR64	-2.021	down	auxin induced SAUR64	down
SAUR66	AT1G29500					SAUR66	-2.031	down	auxin induced SAUR66	down
SAUR67	AT1G29510	SAUR67_1	-2.633	0.01802	down	SAUR67	-2.668	down	auxin induced SAUR67	down
AT1G29460	AT1G29460	AT1G29460_2	-2.501	0.03156	down	AT1G2946	-2.426	down	auxin induced transmembrane SAUR65; SMALL AUXIN UPREGULATED RNA 65	down?
AT1G29420	AT1G29420	AT1G29420_2	-62.1	0.0467	down	AT1G2942	-3.779	down	auxin indued SAUR61; SMALL AUXIN UPREGULATED RNA 6	down
CCD8	AT4G32810	-				CCD8	2.1464	up	auxin inhibitor synthesis shoot branching ATCCD8; carotenoid cleavage dioxygenase 8; MAX4; M	up
AIL7	AT5G65510	-				AIL7	5.4272	up	auxin meristem regulator of PIN1 AINTEGUMENTA-like 7; PLETHORA 7; PLT7	up
NPY4	AT2G23050	-				NPY4	2.6554	up	auxin NPY4 Phototropic-responsive NPH3 regulator of PIN exocytosis	up
MAM3	AT5G23020	MAM3_1	2.3344	1.39E-03	up	MAM3	2.319	up	auxin pathogen indole-glucosinolate synthesis	up
CYP81F1	AT4G37430	CYP81F1_1	2.1882	0.04707	up	CYP81F1	2.1632	up	auxin pathogen indole-glucosynolate synthesis	up
CYP705A5	AT5G47990	CYP705A5_1	-2.987	1.84E-04	down	CYP705A5	-3.01	down	auxin root flavonoid triterpene thalianol synthesis, auxin transport gravitropism	down
AT2G21220	AT2G21220					AT2G2122	-2.068	down	auxin SAUR12, SMALL AUXIN UPREGULATED RNA 12	down
AT4G38825	AT4G38825	-				AT4G3882	-3.587	down	auxin SAUR13; SMALL AUXIN UPREGULATED RNA 13	down
AT3G03850	AT3G03850					AT3G0385	-2.332	down	auxin SAUR26 SAUR-like auxin-responsive protein	down
AT3G03820	AT3G03820					AT3G0382	-2.688	down	auxin SAUR29 SAUR-like auxin-responsive protein	down
AT3G03840	AT3G03840					AT3G0384	-2.532	down	auxin SAUR29 SAUR-like auxin-responsive protein	down
AT4G34790	AT4G34790					AT4G3479	-3.402	down	auxin SAUR3, SMALL AUXIN UPREGULATED RNA 3	down
AT3G61900	AT3G61900					AT3G6190	-2.71	down	auxin SAUR33, SMALL AUXIN UPREGULATED RNA 33	down
AT4G22620	AT4G22620					AT4G2262	-3.172	down	auxin SAUR34, SMALL AUXIN UPREGULATED RNA 34	down
AT2G37030	AT2G37030					AT2G3703	-4.002	down	auxin SAUR46 SMALL AUXIN UPREGULATED RNA 46	down
SAUR50	AT4G34760					SAUR50	-2.024	down	auxin SAUR50, SMALL AUXIN UPREGULATED RNA 50	down
AT3G53250	AT3G53250	AT3G53250_1				AT3G5325	-5.632	down	auxin SAUR57, SMALL AUXIN UPREGULATED RNA 57	down?
AT1G20470	AT1G20470					AT1G2047	-2.25	down	auxin SAUR60 SMALL AUXIN UPREGULATED RNA 60	down
CNX7	AT4G10100					CNX7	-2.109	down	auxin sirtinol Molybdopterin- synthase small subunit) (MOCS2A) (MOCO1-A)	down
AT4G35160	AT4G35160	AT4G35160_1	-2.619	0.01574	down	AT4G3516	-2.641	down	auxin Trp metabolism N-Acetylserotonin O-methyltransferase conversion of 5-hydroxy-indoleac	down
TSBtype2	AT5G38530	TSBtype2_1	2.5513	5.45E-04	up	TSBtype2	2.5321	up	auxin, amino acid Trp biosynthesis tryptophan synthase beta type 2	up

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UGT74E2	AT1G05680	UGT74E2_1	2.1452	6.66E-03	up	UGT74E2	2.119	up	auxin, ROS induced IBA glucosylase	up
AT5G66580	AT5G66580	AT5G66580_1	-2.783	5.96E-04	down	AT5G6658	-2.817	down	auxin, unknown SAUR19/22/23/24 interacting DUF4228 domain protein	down
BHLH150	AT3G05800	BHLH150_1	-3.347	9.46E-03	down	BHLH150	-3.358	down	BR signaling activation by bHLH150 TF AIF1 AtBS1(activation-tagged BRI1 suppressor 1)-interacti	down
MSBP1	AT5G52240	MSBP1_1	-2.018	5.03E-03	down	MSBP1	-2.04	down	BR signaling hypocotyl elongation light HY5/HYH activated inhibitor	down
CML16	AT3G25600	CML16_1	-2.482	9.80E-03	down	CML16	-2.513	down	Ca2+ CAM signaling CALMODULIN LIKE 16, CML16 EF-hand repeat protein	down
CPK22	AT4G04710					CPK22	2.4471	up	Ca2+ signaling CPK22 calcium-dependent kinase	up
ECA2	AT4G00900	ECA2_2	2.7139	4.28E-03	up	ECA2	2.4223	up	Ca2+ transport Ca2+ ATPase mediating efflux of calcium from the cytoplasm	up
CML18	AT3G03000	CML18_1	-2.137	0.03477	down	CML18	-2.158	down	Ca2+ vacuole Na+/H+ antiporter binding calmodulin	down
PCR1	AT1G14880	PCR1_1	-94.04	0.02542	down	PCR1	-94.9	down	cadmium/zinc transport, plasma-membrane PLANT CADMIUM RESISTANCE 1	down
CYCB1-1	AT4G37490	CYCB1-1_1	3.3587	0.02812	up	CYCB1-1	3.3408	up	cell cycle G2/M, DNA repair	up
AT5G01660	AT5G01660	-				AT5G0166	2.2367	up	cell death DCD (Development and Cell Death) domain and Kelch repeat protein	up
BAP2	AT2G45760	-				BAP2	-5.187	down	cell death inhibitor BONZAI1-binding protein BAP1	down
anac028	AT1G65910					anac028	3.4254	up	cell death NAC028 TF	up
AT2G01810	AT2G01810					AT2G0181	11.395	up	cell division MALE MEIOCYTE DEATH 1 homolog	up
ERF114	At5g61890	-				ERF114	2.5812	up	cell division axillary meristem stimulation EBE/ERF114 AP2 TF	up
SMC2-1	At5g62410	SMC2-1_1	2.1085	0.04623	up	SMC2-1	2.0948	up	cell division chromosome condensation condensin SMC2	up
ATSMC2	AT3G47460					ATSMC2	2.2167	up	cell division chromosome condensation SMC	up
SMR9	At1g51355					SMR9	-3.051	down	cell division cyclin-dependent kinase inhibitor SMR3-like protein	down
ALY1	AT5G27610					ALY1	2.052	up	cell division DIRP (Domain in Rb-related Pathway) motive containing MYB TF	up
SMR5	AT1G07500	-				SMR5	-2.002	down	cell division DNA damage checkpoint CDKA inhibitor SIAMESE-RELATED 5; SMR5	down
CYCD4-2	AT5G10440	CYCD4-2_2				CYCD4-2	-2.541	down	cell division DNA synthesis Cyclin-D4-2	down
AT5G42710	AT5G42710	AT5G42710_1	85.237	0.02809	up	AT5G4271	2.4458	up	cell division G2/M TON1 Recruiting Motif 30	up
APC2	AT2G04660					APC2	2.0736	up	cell division G2/M anaphase promoting complex subunit 2	up
CYCB1	AT1G34460	CYCB1_2	73.363	0.03406	up	CYCB1	15.501	up	cell division G2/M cyclin B1;5/CYC3	up?
CYCB2-3	AT1G20610					CYCB2-3	2.109	up	cell division G2/M cyclin B2;3	up
AT3G58650	AT3G58650	-				AT3G5865	2.7948	up	cell division G2/M DUF4378 TON1 RECRUITING MOTIF 7, TRM7	up
CYCB3	AT1G16330	-				CYCB3	3.6439	up	cell division G2/M meiosis Cyclin B3	up
MAP65-4	AT3G60840					MAP65-4	2.5397	up	cell division kinetochore MAP65-4 microtubule-associated protein 65-4	up
DYAD	AT5G51330	-				DYAD	3.5665	up	cell division meiosis sister chromatid cohesion SWITCH1	up
ZYP1A	AT1G22260	-				ZYP1A	2.5866	up	cell division meiotic synaptosomal filament protein	up
ZYP1B	AT1G22275	-				ZYP1B	2.195	up	cell division meiotic synaptosomal filament protein	up
SEC1B	AT4G12120	-				SEC1B	2.0102	up	cell division microtubule vesicular transport syntaxon binding KEULE Sec1B protein	up
AT4G22860	AT4G22860					AT4G2286	2.3029	up	cell division microtubule associated TPX2_importin domain protein	up
MAP65-3	AT5G51600					MAP65-3	2.1948	up	cell division mitosis MICROTUBULE-ASSOCIATED PROTEIN 65-3; PLEIADE	up
EDE1	AT2G44190					EDE1	2.2081	up	cell division mitotic nuclear microtubule associated protein	up
CYCU4-1	AT2G44740	CYCU4-1_1	-2.391	0.02817	down	CYCU4-1	-2.419	down	cell division phosphate CDKA interaction PHO8/cyclin P	down
AT5G27330	AT5G27330	AT5G27330_1	2.4224	0.01941	up	AT5G2733	2.41	up	cell division Smc (COG1196) chromosome segregation protein SMC domain	up
KIN7A	At1g18370	KIN7A_1	2.866	0.01646	up	KIN7A	2.8602	up	cell division, cell plate expansion	up
CKS1	AT2G27960	CKS1_1	-2.058	7.49E-03	down	CKS1	-2.082	down	cell division, endoreduplication CDKA inhibitor CKS1	down
KIN12A	At4g14150	KIN12A_1	3.1145	0.04551	up	KIN12A	3.0969	up	cell division, male meiosis Microtubule motor kinesin PAKRP1/Kinesin-12A	up
MYB3R4	At5g11510	MYB3R4_4	6.0337	0.03773	up	MYB3R4	2.1641	up	cell division, pathogen G2/M phase-specific transcription factor MYB3R4	up
PRE1	AT5G39860	PRE1_1	-2.419	0.03805	down	PRE1	-2.457	down	cell elongation BR/GA response regulator bHLH136/PRE1	down
XTH21	AT2G18800					XTH21	-2.867	down	cell elongation XTH21 xyloglucan endotransglucosylase/hydrolase 21	down
DVL3	AT1G67265	DVL3_1	-4.786	8.01E-04	down	DVL3	-4.821	down	cell elongation, inhibitory transported oligopeptide	down
ARL	AT2G44080	ARL_1	-2.37	1.45E-03	down	ARL	-2.394	down	cell expansion organ growth BR induced transmembrane ER protein	down
AT4G24370	AT4G24370	AT4G24370_1	-2.459	5.61E-03	down	AT4G2437	-2.493	down	cell expansion organ growth endosomal excort complex	down
CNGC18	AT5G14870					CNGC18	3.6762	up	cell polarity elongation CNGC18, CYCLIC NUCLEOTIDE-GATED CHANNEL 18	up
ICR2	At2g37080	ICR2_1	4.7392	1.21E-05	up	ICR2	2.3519	up	cell polarity, pollen tube growth auxin-induced ROP interactor	up
ATROPGEF10	AT5G19560	ATROPGEF10_	46.581	0.04873	up	ATROPGEF	2.9031	up	cell polarity, root hair Ferronia_ROP GEF	up
TPD1	AT4G24972					TPD1	-2.01	down	cell specification tapetum LRR kinase EMS1 kinase subtrate TAPETUM DETERMINANT 1, TPD1	down
AGP24	AT5G40730	AGP24_1	-2.964	5.69E-04	down	AGP24	-3.013	down	cell wall AGP24 arabinogalactan protein 24	down
CSLA9	AT5G03760	CSLA9_1	2.0781	7.19E-03	up	CSLA9	2.0531	up	cell wall ANAC041, bZIP1 and MYB46 regulated mannan synthase	up
AGP12	AT3G13520	AGP12_1	-2.249	0.01483	down	AGP12	-2.284	down	cell wall arabinogalactan protein 12	down
AGP13	AT4G26320	AGP13_1	-4.014	4.07E-03	down	AGP13	-4.083	down	cell wall arabinogalactan protein 13	down
AGP14	AT5G56540	AGP14_1	-4.735	7.55E-07	down	AGP14	-4.817	down	cell wall arabinogalactan protein 14, inhibition of root hair elongation	down
AGP21	AT1G55330	AGP21_1	-2.616	2.73E-03	down	AGP21	-2.657	down	cell wall arabinogalactan protein 21	down
AGP22	AT5G53250	AGP22_1	-5.97	0.01229	down	AGP22	-6.052	down	cell wall arabinogalactan protein 22	down
SCPL46	AT2G33530	SCPL46_1	2.0472	0.02777	up	SCPL46	2.0221	up	cell wall associated serine carboxypeptidase	up
AT5G12960	AT5G12960					AT5G1296	5.769	up	cell wall Beta-L-arabinofuranosidase	up
KOR3	AT4G24260	KOR3_3	46.587	0.04869	up	KOR3	2.0547	up	cell wall cellulase nematode induced ATGH9A3; AtKOR3; glycosyl hydrolase 9A3	up
CSLG2	AT4G24000					CSLG2	-2.903	down	cell wall cellulose synthase like G2	down
FAR3	AT4G33790	-				FAR3	3.9637	up	cell wall cuticular wax synthesis CER4 ECERIFERUM 4; FAR3; FATTY ACID REDUCTASE 3	up
AT5G01075	AT5G01075	AT5G01075_1	-2.463	0.01322	down	AT5G0107	-2.493	down	cell wall cuticule formation, secreted 81aa oligopeptide with signal peptide, TWISTED SEED1, TW	down
ERF107	At5g61590	ERF107_1	-2.002	9.68E-03	down	ERF107	-2.017	down	cell wall cuticule synthesis inhibitor DEWAX AP2 ERF107 TF	down
DEGP3	AT1G65630					DEGP3	3.1177	up	cell wall DegP3; degradation of periplasmic proteins 3	up
XTH25	AT5G57550	XTH25_1	-3.583	0.02894	down	XTH25	-3.627	down	cell wall elongation xyloglucan endotransglucosylase/hydrolase 25	down
CASP2	AT3G11550	CASP2_1	-2.206	0.04799	down	CASP2	-2.232	down	cell wall endodermis lignin CASP2, CASPARIAN STRIP MEMBRANE DOMAIN PROTEIN 2	down
AT4G20390	AT4G20390	AT4G20390_1	-3.823	6.29E-06	down	AT4G2039	-3.867	down	cell wall endodermis lignin Casparian Strip CASP-LIKE PROTEIN 1B2, CASPL1B2	down
AT3G06390	AT3G06390	AT3G06390_1	-2.6	1.59E-03	down	AT3G0639	-2.623	down	cell wall endodermis lignin Casparian Strip CASP-LIKE PROTEIN 1D2, CASPL1D2	down
CASP4	AT5G06200					CASP4	-2.815	down	cell wall endodermis lignin Casparian strip membrane domain protein 4	down
CASP5	AT5G15290					CASP5	-2.589	down	cell wall endodermis lignin Casparian strip membrane domain protein 5, CASP5	down
AT5G54980	AT5G54980	AT5G54980_1	-2.189	7.90E-03	down	AT5G5498	-2.224	down	cell wall endodermis lignin CASP-LIKE PROTEIN 2D1, CASPL2D1	down
EXPA16	AT3G55500	EXPA16_1	-2.506	0.0274	down	EXPA16	-2.527	down	cell wall expansin with DPBB_1 domain and signal peptide	down
AT5G41050	AT5G41050	AT5G41050_1	-2.03	0.02062	down	AT5G4105	-2.063	down	cell wall extensine Pollen proteins Ole e I like	down
AT4G17215	AT4G17215					AT4G1721	-2.237	down	cell wall extensine Pollen proteins Ole e I like	down
AT5G26730	AT5G26730	-				AT5G2673	-10.44	down	cell wall extracellular adhesion FAS1 domain protein	down
AT5G38240	AT5G38240	-				AT5G3824	2.7046	up	cell wall galacturonan-binding transmembrane kinase	up
AT1G22460	AT1G22460					AT1G2246	7.1739	up	cell wall Golgi membrane bound O-fucosyltransferase	up
AT5G46950	AT5G46950	AT5G46950_1	-50.93	0.04304	down	AT5G4695	-48.24	down	cell wall invertase/pectin methylesterase inhibitor	down

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AT5G62340	AT5G62340	AT5G62340_1	-7.037	1.15E-03	down	AT5G6234	-7.03	down	cell wall invertase/pectin methylesterase inhibitor	down
AT5G62360	AT5G62360					AT5G6236	-3.126	down	cell wall invertase/PECTIN METHYL-ESTERASE INHIBITOR 13, PMEI13	down
GXM1	AT1G33800					GXM1	-2.309	down	cell wall lignin synthesis glucuronoxylan(GX)-specific 4-O-methyltransferase	down
CYP84A4	AT5G04330					CYP84A4	-2.232	down	cell wall ligning biosynthesis CYTOCHROME P450 84A4	down
LAC12	AT5G05390					LAC12	5.1947	up	cell wall ligning biosynthesis LACCASE 12	up
AT3G23470	AT3G23470					AT3G2347	2.1338	up	cell wall lipochitin oligosaccharide methylase NodS domain protein	up
AT1G24880	AT1G24880	AT1G24880_1	-5.048	3.43E-03	down	AT1G2488	-2.325	down	cell wall lipopolysaccharide synthesis LPXC2 UDP-3-O-acyl-N-acetylglucosamine deacetylase	down
JAL12	At1g52120					JAL12	18.602	up	cell wall mannose-binding jancalin lectin domain protein	up
JAL8	At1g52050	JAL8_1	-5.233	0.04671	down	JAL8	-5.264	down	cell wall mannose-binding lectin	down
JAL9	At1g52060	JAL9_1	-5.752	6.62E-03	down	JAL9	-5.768	down	cell wall mannose-binding lectin	down
AT4G20460	AT4G20460					AT4G2046	2.0852	up	cell wall MUR4 UDP-D-Xylose to UDP-L-Arabinose epimerase homolog	up
GAUT5	AT2G30575	-				GAUT5	2.025	up	cell wall pectin LGT5 los glycosyltransferase 5 homogalacturonan galacturonosyltransferase	up
AT4G24430	AT4G24430					AT4G2443	2.0123	up	cell wall pectin Rhamnogalacturonate lyase	up
AT4G25260	AT4G25260	AT4G25260_1	-2.259	3.83E-03	down	AT4G2526	-2.287	down	cell wall phytochorome/shade avoidance induced Plant invertase/pectin methylesterase inhibi	down
FUT6	AT1G14080	-				FUT6	2.0008	up	cell wall salt sensitivity xyloglucan fucosyltransferase 6	up
CESA9	AT2G21770	-				CESA9	2.5663	up	cell wall secondary wall CESA9 cellulose synthase A9	up
AT5G19120	AT5G19120	AT5G19120_1	-2.601	6.84E-04	down	AT5G1912	-2.628	down	cell wall secreted Xylanase inhibitor with signal peptide, 2h interacting partner of PXL1 LRR rece	down
AT2G22790	AT2G22790					AT2G2279	-2.55	down	cell wall SMI1_KNR4 domain regulator of 1,3-beta-glucan synthase activity and cell-wall formati	down
AT5G55110	AT5G55110					AT5G5511	-4.587	down	cell wall Stig1 cysteine rich stigna specific protein	down
GPAT2	AT1G02390					GPAT2	-2.215	down	cell wall suberin cutin biosynthesis sn-glycerol-3-phosphate 2-O-acyltransferase	down
AT4G27480	AT4G27480					AT4G2748	2.1132	up	cell wall transmembrane beta-1,6-N-acetylglucosaminyltransferase enzymes, I-branching enzyr	up
AT3G09035	AT3G09035					AT3G0903	-2.005	down	cell wall transmembrane lectin with signal peptide	down
JAL10	At1g52070	JAL10_1	-3.489	0.01481	down	JAL10	-3.516	down	cell wall unknown mannose-binding jancalin lectin domain protein	down
GRP3S	AT2G05380	GRP3S_3	-2.007	0.0149	down	GRP3S	-2.003	down	cell wall WAK1 kinase interactor	down
WAKL9	At1g69730					WAKL9	2.2382	up	cell wall WAK-like kinase WAKL9	up
AT1G06350	AT1G06350	-				AT1G0635	2.27	up	cell wall wax cutin AtADS4; delta 9 desaturase 4	up
AT5G19110	AT5G19110					AT5G1911	-2.96	down	cell wall Xylanase inhibitor	down
AGP30	AT2G33790	AGP30_1	-7.941	0.03101	down	AGP30	-7.769	down	cell wall, root elongation, arabinogalactan protein 30	down
HEMA3	AT2G31250	HEMA3_1	7.0704	0.04563	up	HEMA3	7.0303	up	chlorophyll biosynthesis, 1ts rate-limiting step	up
OEP161	At2g28900	OEP161_1	-2.458	0.03342	down	OEP161	-2.459	down	chloroplast cold induced AtOEP16, a 16-KDa plastid outer membrane protein involved in import	down
ELIP1	AT3G22840	ELIP1_1	6.4736	4.69E-04	up	ELIP1	6.3427	up	chloroplast EARLY LIGHT-INDUCABLE PROTEIN, ELIP, ELIP1	up
AT2G45180	AT2G45180	AT2G45180_1	-2.719	2.86E-04	down	AT2G4518	-2.745	down	chloroplast lipid transfer protein AII domain with sigal peptide	down
PSBN	ATCG00700					PSBN	3.1177	up	chloroplast PHOTOSYSTEM II REACTION CENTER PROTEIN N, PSBN	up
RPS11	ATCG00750	RPS11_1	2.7549	5.10E-03	up	RPS11	2.7459	up	chloroplast 30S RIBOSOMAL PROTEIN S11, RPS11	up
RPS8	ATCG00770	RPS8_1	2.3681	6.93E-03	up	RPS8	2.3565	up	chloroplast 30S RIBOSOMAL PROTEIN S11, RPS11	up
RPS3	ATCG00800	RPS3_1	2.23	7.38E-03	up	RPS3	2.2209	up	chloroplast 30S ribosomal protein S3	up
RPL14	ATCG00780	RPL14_1	2.156	0.01218	up	RPL14	2.1431	up	chloroplast 50S RIBOSOMAL PROTEIN L14, RPL14	up
RPL22	ATCG00810	RPL22_1	2.3712	8.70E-03	up	RPL22	2.3622	up	chloroplast 50S RIBOSOMAL PROTEIN L22, RPL22	up
RPL29	At5g65220	RPL29_1	-2.183	5.71E-03	down	RPL29	-2.209	down	chloroplast 50S ribosomal protein L29	down
RPL33	ATCG00640					RPL33	-2.464	down	chloroplast 50S ribosomal protein L33	down
AT1G63300	AT1G63300					AT1G6330	2.5382	up	chloroplast blue light movement protein-like with guanylate-binding protein 1, NT-C2 domain ar	up
ELIP2	AT4G14690	ELIP2_1	13.438	3.90E-07	up	ELIP2	13.214	up	chloroplast chlorophyll biosynthesis regulation UV induced	up
AT5G23240	AT5G23240					AT5G2324	-2.274	down	chloroplast DNAJ protein with 4Fe-4S single cluster domain of Ferredoxin I	down
AT3G59840	AT3G59840	AT3G59840_1	-2.298	3.88E-03	down	AT3G5984	-2.324	down	chloroplast envelop unknown protein	down
ACC2	AT1G36180	ACC2_2	3.3737	2.24E-03	up	ACC2	3.3614	up	chloroplast fatty acid biosynthesis acetyl-CoA carboxylase 2	up
BOLA1	AT1G55805	BOLA1_1	-2.083	7.08E-03	down	BOLA1	-2.11	down	chloroplast glutaredoxin interacting BolA domain protein	down
GBSS1	AT1G32900	-				GBSS1	2.3391	up	chloroplast granule bound starch synthase 1	up
CLPB3	AT5G15450	CLPB3_1	2.4068	7.03E-03	up	CLPB3	2.3795	up	chloroplast heat tolerance HSP101 ALBINO AND PALE GREEN 6, APG6, ATCLPB3, CASEIN LYTIC PRO	up
AT4G38490	AT4G38490	-				AT4G3849	-2.004	down	chloroplast inner envelop translocase SECE subunit	down
TIM22-2	At4g26670	TIM22-2_1	-3.153	0.01986	down	TIM22-2	-3.15	down	chloroplast inner envelop transporter	down
NEET	AT5G51720	NEET_1	-2.165	7.05E-03	down	NEET	-2.195	down	chloroplast iron metabolism redox	down
AOC2	AT3G25770	AOC2_1	-2.768	7.45E-05	down	AOC2	-2.799	down	chloroplast JA biosynthesis AOC2 allene oxide cyclase 2	down
TGD5	At1g27695	-				TGD5	-2.417	down	chloroplast lipid import from ER	down
AT1G12150	AT1G12150					AT1G1215	7.1163	up	chloroplast movement actin weak chloroplast movement under blue light protein (DUF827)	up
NDHH	ATCG01110	NDHH_1	2.314	0.04172	up	NDHH	2.2972	up	chloroplast NAD(P)H DEHYDROGENASE SUBUNIT H, NDHH	up
AT3G63160	AT3G63160	AT3G63160_1	-2.829	0.01917	down	AT3G6316	-2.832	down	chloroplast OEP6 outer envelope membrane protein	down
TOC75-IV	AT4G09080	TOC75-IV_1	106.07	0.01775	up	TOC75-IV	2.6059	up	chloroplast outer envelope translocation channel subunit	up
ENO1	AT1G74030	ENO1_1	2.1609	9.44E-03	up	ENO1	2.1459	up	chloroplast phosphoenolpyruvate enolase cytokinin-induced affects trichome development	up
PSAE2	At2g20260	PSAE2_1	-2.117	5.94E-03	down	PSAE2	-2.141	down	chloroplast photosystem I subunit E-2	down
AT1G51400	AT1G51400	AT1G51400_1	-2.08	0.01835	down	AT1G5140	-2.112	down	chloroplast Photosystem II 5 kD protein	down
PSBA	ATCG00020	PSBA_1	-2.055	6.65E-03	down	PSBA	-2.071	down	chloroplast photosystem II reaction center protein A	down
PSBK	ATCG00070					PSBK	-2.361	down	chloroplast PHOTOSYSTEM II REACTION CENTER PROTEIN K PRECURSOR, PSBK PSII K protein	down
PSBR	AT1G79040	PSBR_1	-2.262	4.32E-03	down	PSBR	-2.292	down	chloroplast photosystem PSII-R subunit	down
AT2G17880	AT2G17880	AT2G17880_1	-2.889	5.70E-05	down	AT2G1788	-2.912	down	chloroplast protein folding Chaperone DnaJ-domain protein	down
FKBP13	AT5G45680	FKBP13_1	-2.102	2.81E-03	down	FKBP13	-2.125	down	chloroplast protein folding immunophilin	down
HSP17.8	At1g07400	HSP17.8_1	-3.206	0.03181	down	HSP17.8	-3.27	down	chloroplast protein import/folding AKRA2 interacting heat-shock protein	down
AT5G17280	AT5G17280	AT5G17280_1	-2.41	1.50E-03	down	AT5G1728	-2.439	down	chloroplast protein with Oxidored-like domain	down
PSBTN	AT3G21055	PSBTN_2	-2.077	7.61E-03	down	PSBTN	-2.079	down	chloroplast PSBTN photosystem II subunit T	down
LHB1B1	AT2G34430	LHB1B1_1	-2.15	4.31E-03	down	LHB1B1	-2.166	down	chloroplast PSII LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX II SUBUNIT B1	down
AT3G20680	AT3G20680	AT3G20680_1	-2.026	5.01E-03	down	AT3G2068	-2.05	down	chloroplast PSII assembly DUF1995 domain protein	down
LQY1	AT1G75690	LQY1_1	-2.128	4.78E-03	down	LQY1	-2.153	down	chloroplast PSII protection from photodamage	down
ATJ11	AT4G36040	-				ATJ11	-2.005	down	chloroplast redox DNAJ chaperone DJC23, DNA J PROTEIN C23, DNAJ11, J11	down
NUDT19	At5g20070	NUDT19_1	2.0512	0.01779	up	NUDT19	2.0298	up	chloroplast redox NADPH	up
TRXF1	AT3G02730	TRXF1_1	-2.135	5.45E-03	down	TRXF1	-2.16	down	chloroplast redox regulation of carbon metabolism ATF1 Trxf	down
SUFE2	AT1G67810	-				SUFE2	-2.286	down	chloroplast redox SUFE2 iron-sulfur cluster assembly protein	down
RPS16-1	At4g34620	RPS16-1_1	-2.51	1.35E-03	down	RPS16-1	-2.54	down	chloroplast ribosomal protein S16	down
RPOC1	ATCG00180					RPOC1	2.3288	up	chloroplast RNA polymerase beta' subunit-1	up
RPOA	ATCG00740	RPOA_1	2.1971	5.86E-03	up	RPOA	2.1857	up	chloroplast RNA POLYMERASE SUBUNIT ALPHA, RPOA	up
RBCX1	AT4G04330	RBCX1_1	-3.157	0.04706	down	RBCX1	-3.146	down	chloroplast Rubisco chaperonin RBX1	down

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CRS1	AT5G16180	CRS1_1	2.1014	0.02867	up	CRS1	2.0164	up	chloroplast splicing factor	up
CFM3A	AT3G23070	CFM3A_1	2.0797	1.00E-02	up	CFM3A	2.0668	up	chloroplast splicing of group IIB introns	up
PSAJ	ATCG00630					PSAJ	-2.866	down	chloroplast subunit J of photosystem I	down
AT4G19390	AT4G19390	AT4G19390_1	-3.075	3.27E-03	down	AT4G1939	-3.024	down	chloroplast unknown envelop membrane protein with UPF0114 domain	down
AT4G13500	AT4G13500	AT4G13500_1	-2.261	1.86E-03	down	AT4G1350	-2.292	down	chloroplast unknown membrane protein	down
LON4	AT3G05790	LON4_1	59.099	0.042	up	LON4	2.7384	up	chloroplast/mitochondrion LON4 protease	up
AT5G02950	AT5G02950	-				AT5G0295	2.1256	up	chromatin assembly complex MSI/FCE binding PWWP domain protein	up
HMGB6	AT4G23800	HMGB6_2	2.2962	6.54E-03	up	HMGB6	2.2959	up	chromatin HMG factor	up
AT1G31760	AT1G31760					AT1G3176	-2.089	down	chromatin remodelling SWB/MDM2 p53 binding domain protein	down
CLSY3	AT1G05490					CLSY3	3.4479	up	Chromatin remodelling SWI/SNF ATPase CHR31	up
PIE1	AT3G12810	PIE1_2	2.137	0.01194	up	PIE1	2.1087	up	chromatin remodelling,DNA repair flowering time ATPase of ISWI complex	up?
AT5G66840	AT5G66840					AT5G6684	2.6011	up	chromatin unknown SAP domain protein	up
AT1G69710	AT1G69710	-				AT1G6971	10.756	up	chromosome condensation RCC1 repeat protein with phosphatidylinositol 3-phosphate (PI3P) b	up
SMC6A	AT5G07660					SMC6A	2.0432	up	chromosome condensation, DNA repair recombination Smc5/6 complext	up
AT1G79890	AT1G79890	AT1G79890_4	10.765	0.02898	up	AT1G7989	2.4577	up	chromosome segregation, sister chromatic cohesion yeast Chl1 homolog	up
ELF4	AT2G40080	ELF4_1	-5.69	0.04664	down	ELF4	-5.568	down	circadian clock evening complex	down
EFL3	AT2G06255					EFL3	-2.325	down	circadian clock venening complex ELF4-L3 ELF4-like 3	down
HVA22E	AT5G50720	-				HVA22E	-2.016	down	cold ABA drought salt upregulated TB2/DP1 (deleted in polyposis) domain protein	down
BCB	AT5G20230	BCB_1	-2.076	4.80E-03	down	BCB	-2.092	down	cold ALU tolerance, cell wall lignin BCB plastocyanin-like Cu2+-binding protein enhancer of Phen	down
RAV1	AT1G13260	RAV1_1	-2.157	4.63E-03	down	RAV1	-2.169	down	Cold induced AP2/B3 TF activator of senescence	down
CSP2	AT4G38680					CSP2	-2.002	down	cold induced GRP2 glycine rich protein 2 chromatin protein COLD SHOCK PROTEIN 2; ATCSP2	down
AT4G33980	AT4G33980	AT4G33980_1				AT4G3398	-2.778	down	cold induced unknown protein of COLD-REGULATED GENE 28, COR28	down?
CSP4	AT2G21060	CSP4_1	-2.062	0.01083	down	CSP4	-2.076	down	cold response RNA binding CSP Cold Shock domain protein with ZnF_C2HC zinc fingers	down
AT4G30660	AT4G30660	AT4G30660_1	-4.288	1.24E-03	down	AT4G3066	-2.814	down	cold salt induced Pmp3 Proteolipid membrane potential modulator	down
ZAT12	AT5G59820					ZAT12	-2.187	down	cold tolerance C2H2-type zinc finger activatpr of CBF and cold responsie genes	down
COR413IM2	AT1G29390	COR413IM2_2	-2.227	2.70E-03	down	COR413IM	-2.256	down	cold tolerance chloroplast inner membrane protein	down
DREB1B	AT4G25490	DREB1B_1	-18.2	0.04975	down	DREB1B	-17.63	down	cold tolerance, ABA CBF1	down
AT4G30650	AT4G30650	AT4G30650_1	-3.568	0.0236	down	AT4G3065	-3.563	down	cold, salt induced Pmp3 domain Proteolipid membrane potential modulator	down
RCI2A	AT3G05880	RCI2A_1	-3.798	7.25E-05	down	RCI2A	-3.814	down	cold, ABA, salt, drought induced Pmp3 domain Proteolipid membrane potential modulator	down
PME41	AT4G02330	PME41_1	2.8314	1.21E-03	up	PME41	2.8198	up	cold, BR regulated	up
RCI2B	AT3G05890	RCI2B_1	-2.327	4.72E-03	down	RCI2B	-2.362	down	cold, salt induced Pmp3 domain Proteolipid membrane potential modulator	down
COR15B	AT2G42530	COR15B_1	-4.307	2.22E-03	down	COR15B	-4.32	down	cold-induced protein providing chloroplast membrane protection to freezing	down
LOG5	AT4G35190	-				LOG5	2.2212	up	cytokinin activating enzyme LONELY GUY 5	up
ARR5	AT3G48100					ARR5	-2.022	down	cytokinin response transcription repressor ARR5 response regulator 5	down
ABCG14	AT1G31770	ABCG14_1	2.0228	0.01579	up	ABCG14	2.0109	up	cytokinin root to shoot transporter	up
ALL1	AT4G24080	-				ALL1	-3.364	down	cytokinin signaling activator ALL 2-keto-3-deoxy-L-rhamnonate aldolase or 5-keto-4-deoxy-D-glu	down
CRF1	AT4G11140	-				CRF1	-2.574	down	cytokinin signaling cytokinin response factor 1 CRF1 AP2/ERF063	down
SOB5	AT5G08150	-				SOB5	-2.45	down	cytokinin synthesis stimulator SOB5 suppressor of phytochrome b 5	down
SHOC1	AT5G52290	-				SHOC1	4.296	up	DNA recombination meiosis XPF-like endonuclease SHOC1 shortage in chiasmata 1	up
ASY1	AT1G67370	-				ASY1	2.1501	up	DNA recombination meiotic chiasma ASYNAPTIC 1; ATASY1	up
MSH4	AT4G17380	-				MSH4	4.689	up	DNA recombination meiotic MSH4 MUTS-like protein 4	up
ATRMI1	AT5G63540	ATRMI1_1	94.993	0.02559	up	ATRMI1	2.6273	up	DNA recombination somatic crossover repressor RECQ MEDIATED INSTABILITY 1	up
HEI10	AT1G53490	HEI10_2	8.9653	6.01E-03	up	HEI10	5.3866	up	DNA recombination, meiotic crossover	up
MYH	At4g12740	MYH_2	93.08	0.02482	up	MYH	2.262	up	DNA repair base excision complex NUDIX_4 domain Adenine DNA glycosylase	up?
BRCA1	AT4G21070	-				BRCA1	2.2143	up	DNA repair BRCA1 homolog	up
AT4G22940	AT4G22940	AT4G22940_2	74.913	0.02849	up	AT4G2294	3.0802	up	DNA repair cell cycle, PK3A CDKF interacting kinase homolog	up
SYN3	AT3G59550					SYN3	2.5305	up	DNA repair cohesin cell division SISTER CHROMATID COHESION 1 PROTEIN 3 RAD21.2; ATSYN3	up
CYP82C4	AT4G31940	CYP82C4_1	4.8391	3.14E-04	up	CYP82C4	4.8061	up	DNA repair iron deficiency induced 8-methoxypsoralen inactivation	up
AT1G15940	AT1G15940	AT1G15940_1	2.1031	0.02219	up	AT1G1594	2.087	up	DNA repair meiosis Cohesin Cofactor PDS5 (SPO76)	up
PARP2	AT4G02390	PARP2_1	8.7311	0.04449	up	PARP2	2.2861	up	DNA repair Poly(ADP-Ribose) Polymerase PARP2	up
EME1A	AT2G21800	EME1A_2	133.45	0.01869	up	EME1A	2.6513	up	DNA repair recombination EME1-MUS81 endonuclease	up
GMI1	AT5G24280	GMI1_1	9.6438	2.89E-03	up	GMI1	4.6452	up	DNA repair recombination GMI1, a structural-maintenance-of-chromosomes-hinge domain-cont	up
PRD1	AT4G14180	PRD1_1	66.364	0.04436	up	PRD1	3.033	up	DNA repair recombination meiotic, yeast Spo11 homolog	up
CHR25	AT3G19210	-				CHR25	2.1602	up	DNA repair recombination SWI/SNF ATPase RAD54	up
AT5G43530	AT5G43530					AT5G4353	4.4996	up	DNA repair replicastione RAD5B SNF2 type DNA helicase homolog RING E3	up
TEB	At4g32700	-				TEB	2.0396	up	DNA repair replication TEBICHI	up
TAN	AT4G29860	-				TAN	2.3906	up	DNA repair TAN; TANMEI CUL4-DDB1 binding WD40 protein	up
DDB2	AT5G58760	DDB2_2	2.4259	0.04638	up	DDB2	2.5402	up	DNA repair UV base excision	up
XPB2	AT5G41360	XPB2_1	2.1399	0.04301	up	XPB2	2.0146	up	DNA repair XPB/Rad25 subunit of TFIIH	up
AT1G18090	AT1G18090	AT1G18090_1	359.69	2.73E-03	up	AT1G1809	2.6726	up	DNA repair XPG conserved site exonuclease	up
ABAP1	AT5G13060					ABAP1	2.1275	up	DNA replication cell division negative control ABAP1 ARMADILLO BTB protein 1	up
POLA2	AT1G67630					POLA2	2.039	up	DNA replication DNA polymerase alpha 2 subunit	up
MCM10	AT2G20980					MCM10	2.7633	up	DNA replication minichromosome maintenance 10	up
RPA3B	At4g18590	RPA3B_1	-2.111	0.03443	down	RPA3B	-2.133	down	DNA replication repair recombination replication protein A (RPA) complex subunit REPLICATION	down
AT4G19130	AT4G19130					AT4G1913	3.0714	up	DNA replication REPLICATION PROTEIN A 1E, RPA1E	up
AT5G07810	AT5G07810	-				AT5G0781	3.1101	up	DNA replication SWI/SNF SNF2 like Replication Stress Response Protein Zinc Finger Ran-binding	up
MCM2	AT1G44900	MCM2_1	4.3675	8.50E-03	up	MCM2	3.068	up	DNA replication, root meristem	up
DREB2D	AT1G75490	DREB2D_1	-3.342	0.04702	down	DREB2D	-3.384	down	drought DREB2D_1 AP2 TF	down
SAP5	AT3G12630	SAP5_1	-2.137	4.35E-03	down	SAP5	-2.164	down	drought osmotic stress heat, E3 of LOS2 with zf-A20 and ZnfAN1 domains	down
PUB46	At5g18320	-				PUB46	2.9721	up	drought tolerance ARM repeat RING E3	up
XERO1	AT3G50980	-				XERO1	-3.437	down	drought tolerance XERO1 dehydrin	down
EDA18	AT2G34920					EDA18	2.3069	up	embryo make meiosis EDA18 RING E3	up
EPFL5	AT3G22820	-				EPFL5	-3.526	down	epidermal cell patterning CHALLAH-LIKE 1, CLL1, EPFL5, EPIDERMAL PATTERNING FACTOR LIKE 5	down
NAI1	AT2G22770	NAI1_1	-2.688	5.79E-04	down	NAI1	-2.727	down	ER body formation bHLH TF	down
ERD2A	At1g29330	ERD2A_1	-2.82	1.20E-03	down	ERD2A	-2.874	down	ER lumen protein retaining receptor ERD2	down
OST4A	At3g12587	OST4A_1	-2.227	0.02791	down	OST4A	-2.256	down	ER oligosaccaryltansferase complex 37aa oligopeptide	down
OST4B	At5g02502	OST4B_1	-2.287	0.04214	down	OST4B	-2.317	down	ER oligosaccaryltansferase complex subunit 35aa oligopeptide	down
AT3G60540	AT3G60540					AT3G6054	-2.247	down	ER preprotein translocase subunit SecG Sec61beta	down
AT4G40042	AT4G40042					AT4G4004	-2.136	down	ER SCP12+microsomal signal peptidase 12 kDa subunit	down

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AT1G67650	AT1G67650					AT1G6765	3.1413	up	ER signal recognition particle RNA binding domain of the SRP72 subunit	up
anac103	AT5G64060	-				anac103	3.4282	up	ER stress induced bZIP60 induced NAC103 TF	up
TIN1	AT5G64510	TIN1_1	-2.632	0.04958	down	TIN1	-2.68	down	ER stress induced bZIP60 regulated ER protein	down
AT2G29020	AT2G29020	AT2G29020_1	-2.125	5.20E-03	down	AT2G2902	-2.15	down	ER vesicular transport cell death RAB5-interacting Rab5ip domain protein	down
AT1G01840	AT1G01840					AT1G0184	-2.597	down	ethylene, AP2-like ethylene-responsive transcription factor SNZ	down
LACS3	AT1G64400	LACS3_1	2.2532	0.01168	up	LACS3	2.2282	up	fatty acid and glycerolipid metabolism long-chain acyl-CoA synthetase 3	up
ECI1	AT1G65520	ECI1_1	-2.252	7.23E-03	down	ECI1	-2.279	down	fatty acid degradation peroxisomal delta3, delta2-enoyl CoA isomerase	down
A3G2XYLT	AT5G54060					A3G2XYLT	10.912	up	flavonoid anthocyanin UF3GT UDP-glucose:flavonoid 3-o-glucosyltransferase cytokinin induced	up
FLS1	AT5G08640	FLS1_1	3.4299	7.82E-04	up	FLS1	3.3816	up	flavonoid biosynthesis flavonol synthase 1 Co-expressed with CHI and CHS	up
AT1G23390	AT1G23390	AT1G23390_1	-2.756	7.54E-04	down	AT1G2339	-2.795	down	flavonoid UV, chalcone synthase degradation KFB F-box protein of CHS SCF E3	down
AT1G80440	AT1G80440	AT1G80440_1	-2.404	2.39E-03	down	AT1G8044	-2.431	down	flavonoid UV, phenylalanine ammonia-lyase degradation KFB20 KISS ME DEADLY 1; KMD1 F-box p	down
SKIP20	At3g59940	SKIP20_1	-2.485	6.40E-04	down	SKIP20	-2.511	down	flavonoid UV, phenylalanine ammonia-lyase degradation KFB50 KISS ME DEADLY 4; KMD4 F-box p	down
CHI1	AT3G55120	CHI1_1	2.2888	7.70E-03	up	CHI1	2.2601	up	flavonoid, UV pathogen	up
CHS	AT5G13930	CHS_1	2.3449	6.23E-03	up	CHS	2.3181	up	flavonoid, UV pathogen	up
PAL1	AT2G37040	PAL1_1	2.1754	0.01363	up	PAL1	2.1478	up	flavonoid, UV, pathogen	up
AT1G77520	AT1G77520	AT1G77520_1	-3.526	2.38E-03	down	AT1G7752	-3.567	down	flavonol lignin synthesis bispecific caffeic acid/5-hydroxyferulic acid O-methyltransferase	down
UGT76E12	AT3G46660	-				UGT76E12	-2.544	down	flavonol quercetin UDP-glucosyl transferase 76E12	down
HSL2	AT5G65710					HSL2	2.2639	up	flower abscission LRR receptor kinase HSL2 of INFLORESCENCE DEFICIENT IN ABSCISSION (IDA) pep	up
AHL21	AT2G35270					AHL21	-2.347	down	flower development, auxin AG controlled AT-hook TF of ETTIN	down
AGL17	AT2G22630	-				AGL17	-8.163	down	flowering time AGAMOUS-like 17 mutant is late	down
MIP1B	At3g21890	-				MIP1B	-3.288	down	flowering time B-BOX DOMAIN PROTEIN 31, BBX31, MICROPROTEIN 1A, MIP1A	down
COL9	AT3G07650	-				COL9	-2.443	down	flowering time B-box domain protein 7; BBX7; CONSTANS-like 9	down
AT1G69572	AT1G69572	-				AT1G6957	-2.514	down	flowering time CDF5 antisense RNA FLORE	down
ADO3	AT1G68050	-				ADO3	-2.456	down	flowering time circadian clock FKF SCF E3 F-box protein controlling CBF ubiquitination and CO exp	down
UBC2	AT2G02760	UBC2_2	-2.258	2.94E-03	down	UBC2	-2.156	down	flowering time FLC activation DNA repair N-end rule RAD6 homolog	down
CEN	AT2G27550	-				CEN	2.4128	up	flowering time flower development inhibitor	up
FLP2	At5g10625	FLP2_1	-2.168	0.0239	down	FLP2	-2.2	down	flowering time FPF1 homolog	down
DREB1F	AT1G12610	-				DREB1F	-3.037	down	flowering time GA DREB1F TF DWARF AND DELAYED FLOWERING 1	down
MLP328	AT2G01520	MLP328_1	-4.547	7.15E-10	down	MLP328	-4.595	down	flowering time inhibitor growth promoting cinnamate-induced major latex protein ZCN1 ((ZUSAM	down
FLC	AT5G10140	FLC_4	-7.636	5.92E-03	down	FLC	-6.211	down	flowering time repressor	down
BFT	AT5G62040	-				BFT	-2.693	down	flowering time repressor brother of FT BFT PEBP (phosphatidylethanolamine-binding protein)	down
TEM1	AT1G25560	TEM1_1	-3.784	4.37E-08	down	TEM1	-3.822	down	flowering time, circadian clock FT repressor EIN3 regulated activator of ethylene responsive ger	down
MLP329	AT2G01530	MLP329_1	-4.261	2.48E-08	down	MLP329	-4.318	down	flowering time, cytokinin regulated homolog of growth promoting cinnamate-induced major lat	down
AT5G27220	AT5G27220	AT5G27220_2	67.557	0.03695	up	AT5G2722	2.258	up	flowering time, FRIGIDA-domain protein	up
FRL5	At5g27230	-				FRL5	2.637	up	flowering time, FRIGIDA-domain protein	up
FOLB2	AT5G62980	FOLB2_1	-2.315	0.02083	down	FOLB2	-2.356	down	folate vitamin B9 synthesis FOLB2 Dihydroneopterin aldolase	down
GASA6	AT1G74670	GASA6_1	-2.105	0.01094	down	GASA6	-2.131	down	GA glucose signaling flowering time GASA6 Gibberellin-regulated protein with signal peptide	down
GASA3	AT4G09600	-				GASA3	-2.234	down	GA induced cysteine rich GASA3 protein with signal peptide	down
GASA1	AT1G75750	GASA1_1	-3.115	6.59E-05	down	GASA1	-3.155	down	GA induced GASA domain with signal peptide	down
GASA4	AT5G15230	GASA4_1	-2.337	2.01E-03	down	GASA4	-2.336	down	GA response redox GASA gibberellin regulated cysteine rich protein with signal peptide	down
ZFP5	AT1G10480	-				ZFP5	-2.017	down	GA signaling root hair trichome development ZFP5 zinc finger TF	down
AT3G44326	AT3G44326	AT3G44326_1	-3.346	0.01981	down	AT3G4432	-3.384	down	GA signalling proteolysis transmembrane SLEEPY interacting cytokinin induced SCF E3 F-box prot	down
ERF039	At4g16750					ERF039	-2.72	down	GA transcription DELLA partner DREB subfamily A-4 of ERF/AP2	down
NPF3.1	AT1G68570	NPF3.1_2	2.4841	1.58E-03	up	NPF3.1	2.0388	up	GA transporter root epidermis	up
AT4G26390	AT4G26390					AT4G2639	2.0012	up	glycolysis Pyruvate kinase	up
AT5G42420	AT5G42420	AT5G42420_1	-4.329	0.01833	down	AT5G4242	-2.35	down	Golgi localized bifunctional UDP-rhamnose/UDP-galactose transporter URG3	down
HSP17.4A	At3g46230	HSP17.4A_1	-3.372	1.40E-03	down	HSP17.4A	-3.421	down	heat protein folding HSP17.4 heat shock protein 17.4 accumulating during late seed maturation	down
HSP17.7	At5g12030	-				HSP17.7	-2.76	down	heat schock osmotic stress induced HSP17.6A heat shock protein 17.6A	down
HSP17.6B	At2g29500	HSP17.6B_1	-2.711	4.92E-03	down	HSP17.6B	-2.751	down	heat schock protein folding 17.6 kDa class I heat shock protein 2	down
HSP1	AT4G14830	-				HSP1	-2.055	down	heat shock drought CPK10 interacting HSP1 17.6 kDa class II heat shock protein	down
HSP22.0	At4g10250	-				HSP22.0	-2.703	down	heat shock HSP212 endomembrane chaperon with signal peptide	down
HSP17.6C	At1g53540					HSP17.6C	-2.638	down	heat shock protein HSP20 chaperonin	down
HSFB2A	AT5G62020	-				HSFB2A	-2.024	down	heat shock transcription factor B2A HSFB2A	down
HSA32	AT4G21320	HSA32_1	-3.241	0.01328	down	HSA32	-3.292	down	heat tolerance Coenzyme M (CoM; 2-mercaptoethanesulphonic acid) biosynthesis, COMA doma	down
PLC9	AT3G47220	-				PLC9	2.0748	up	heat tolerance plasma membrane-localized phosphoinositide-specific phospholipase C9	up
BBX18	AT2G21320	BBX18_1	2.6668	0.02944	up	BBX18	2.6294	up	heat tolerance, negative regulator induced by blue light and heat	up
MT2A	AT3G09390	MT2A_2	-2.795	1.40E-03	down	MT2A	-2.273	down	heavy metal removal oxidative stress METALLOTHIONEIN-K; ATMT-1; ATMT-K	down
HIPP43	At3g05920	HIPP43_2	95.086	0.02464	up	HIPP43	-2.128	down	heavy metal transport removal	down
AT1G62310	AT1G62310					AT1G6231	2.0243	up	histine demethylase JmjC domain RING E3	up
HAC2	AT1G67220					HAC2	7.0458	up	histone acetyltransferase of the CBP family 2	up
AT3G09480	AT3G09480					AT3G0948	-2.355	down	Histone H2B.5	down
ATXR1	AT1G26760	-				ATXR1	2.4861	up	histone H3 K3/K9 methylase SET and tetratricopeptide domain ATXR1; SET domain protein 35	up
HTA4	AT4G13570					HTA4	3.1177	up	histone HTA4 histone H2A 4	up
AT3G10040	AT3G10040	-				AT3G1004	2.1224	up	hypoxia HRA1, HYPOXIA RESPONSE ATTENUATOR1 MYB TF	up
AT5G57510	AT5G57510					AT5G5751	-2.501	down	hypoxia induced unknown DUF761 domain protein	down
AT2G23270	AT2G23270					AT2G2327	-6.518	down	hypoxia induced unknown protein with signal peptide	down
ATFRO5	AT5G23990	ATFRO5_2	-3.209	0.02899	down	ATFRO5	-3.185	down	iron chelate reductase Cu2+ uptake FRO5 ferric reduction oxidase 5	down
BTS	AT3G18290	BTS_1	2.3345	7.14E-04	up	BTS	2.3174	up	iron deficiency induced TF	up
ORG2	AT3G56970	ORG2_1	6.3067	7.68E-05	up	ORG2	6.257	up	iron deficiency induced TF	up
BHLH101	AT5G04150	-				BHLH101	2.6073	up	iron deficiency response key regulator of FIT nHLH101	up
ORG3	AT3G56980	ORG3_1	2.3092	0.0471	up	ORG3	2.288	up	iron deficiency, E3 Ubiquitin ligase of bHLH TFs	up
BHLH100	AT2G41240	BHLH100_1	4.1976	7.73E-04	up	BHLH100	4.232	up	iron deficiency, homeostasis	up
COPT1	AT5G59030	COPT1_1	-2.283	6.59E-04	down	COPT1	-2.309	down	iron homeostasis cell elongation COPT1 copper transporter 1	down
AT3G12900	AT3G12900	-				AT3G1290	2.3631	up	iron starvation induced coumarin synthesis Scopoletin 8-hydroxylase	up
ATMYB2	AT2G47190	-				ATMYB2	-2.021	down	iron transport cytokinin regulated shoot branching inhibitor	down
NAS2	AT5G56080	NAS2_1	9.6497	1.06E-03	up	NAS2	9.5952	up	iron transport, response to ethylene and zinc	up
ATOPT3	AT4G16370	ATOPT3_1	2.4756	5.74E-04	up	ATOPT3	2.4546	up	iron transporter, systemic iron signaling	up
FRO2	AT1G01580	FRO2_1	3.1471	2.79E-04	up	FRO2	3.1209	up	iron uptake root	up?
IRT3	AT1G60960	IRT3_3	-2.763	4.63E-03	down	IRT3	-2.012	down	iron zinc transporter plasma membrane IRT3	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT3G20160	AT3G20160	-				AT3G2016	-2.856	down	isoprenoid biosynthesis unknown polyprenyl synthetase	down
AT3G29430	AT3G29430	-				AT3G2943	-2.744	down	isoprenoid synthesis unknown polyprenyl synthetase	down
GGPP6	At1g49530	-				GGPP6	2.0301	up	isoprenoid terpenoid biosynthesis mitochondrial geranylgeranyl pyrophosphate synthase 6	up
CYP71A16	AT5G42590	CYP71A16_1	-3.078	0.03895	down	CYP71A16	-3.124	down	isoprenoid triterpenoid marneral oxidase CYP71A16	down
MRN1	AT5G42600	MRN1_1	-12.6	0.04455	down	MRN1	-12.33	down	isoprenoid, triterpenoid sterol biosynthesis	down
ANS	AT2G38240	-				ANS	-5.6	down	JA inactivation JAO4, JASMONATE-INDUCED OXYGENASE4, JASMONIC ACID OXIDASE 4, JOX4	down
NAC055	AT3G15500	NAC055_1	-2.628	0.02445	down	NAC055	-2.657	down	JA induced chlorophyll degradation NAC055/NAC3	down
VSP1	AT5G24780	VSP1_2	-3.036	3.71E-03	down	VSP1	-2.736	down	JA induced class B acid phosphatase VSP1 vegetative storage protein 1	down
PLA2-ALPHA	AT2G06925	PLA2-ALPHA_1	-2.643	0.01661	down	PLA2-ALPH	-2.645	down	JA negative regulation of oxylipin synthesis PLA2-ALPHA Phospholipase A2	down?
CYP74B2	AT4G15440	-				CYP74B2	-2.348	down	JA oxylipin 12-oxo phytodienoic acid galactolipid HPL1 hydroperoxide lyase 1	down
SDP1L	At3g57140					SDP1L	2.9611	up	JA patatin/phospholipase A2	up
AT5G38100	AT5G38100	AT5G38100_2	-67.52	4.81E-03	down	AT5G3810	-3.041	down	JA SA Methyltransf_7 domain protein	down
AT5G36670	AT5G36670	AT5G36670_2	-70.06	0.03063	down	AT5G3667	-13.1	down	JA signaling AT-hook TF with PHD and TPL-binding domain in jasmonate signalling	down
TIFY 5B	AT2G34600	-				TIFY 5B	-3.906	down	JA signaling repressor JAZ7 jasmonate-zim-domain protein 7	down
JAZ13	At3g22275	JAZ13_1	-19.33	0.01469	down	JAZ13	-19.08	down	JA signalling repressor MYC2/TOPLESS interactor	down
AT5G62210	AT5G62210					AT5G6221	2.3722	up	karrikin induced Embryo-specific protein 3, (ATS3)	up
AT1G11500	AT1G11500	-				AT1G1150	-2.203	down	leaf development unknown DUF1218 domain with signal peptide	down
ZPR1	AT2G45450	A feedback re	-			ZPR1	-2.017	down	leaf polarity REV HD-ZIPIII interacting factor ZPR1	down
ERF8	AT1G53170	ERF8_1	-2.054	0.03677	down	ERF8	-2.079	down	leaf senescence ABA ERF8 AP2 TF	down
AT3G15040	AT3G15040	AT3G15040_1	-2.189	5.42E-03	down	AT3G1504	-2.21	down	leaf senescence regulation Senescence_reg domain protein	down
AT5G03230	AT5G03230	AT5G03230_1	-2.257	7.14E-03	down	AT5G0323	-2.292	down	leaf senescence regulation Senescence_reg domain protein	down
AT4G21970	AT4G21970					AT4G2197	-3.163	down	leaf senescence regulation Senescence_reg domain protein	down
AT5G45630	AT5G45630					AT5G4563	-2.495	down	leaf senescence regulation Senescence_reg domain protein	down
AT4G04630	AT4G04630	AT4G04630_1	-2.429	0.01021	down	AT4G0463	-2.463	down	leaf senescence regulation, ABA dark SA and pathogen induced Senescence_reg domain protein	down
AT5G60680	AT5G60680	AT5G60680_1	-3.116	3.48E-06	down	AT5G6068	-3.153	down	leaf senescence regulation, ABA dark SA and pathogen induced Senescence_reg domain protein	down
AT2G28400	AT2G28400	-				AT2G2840	-2.179	down	leaf senescence regulation, ABA dark SA and pathogen induced Senescence_reg domain protein	down
PRE6	AT1G26945	PRE6_1	-2.162	0.01713	down	PRE6	-2.184	down	light signaling bHLH KIDARI inhibitor of HFR1	down
AT1G28590	AT1G28590	AT1G28590_1	50.737	0.046	up	AT1G2859	50.452	up	lipid degradation SGNH_hydrolase, or GDSL_hydrolase	up
AT5G09395	AT5G09395					AT5G0939	5.7117	up	lncRNA	up
AT4G20362	AT4G20362	AT4G20362_1	-2.945	0.04187	down	AT4G2036	-2.977	down	lncRNA	down
AT5G09125	AT5G09125	AT5G09125_1	-21.5	0.04905	down	AT5G0912	-21.32	down	lncRNA	down
AT5G09295	AT5G09295	AT5G09295_1	-22.96	3.82E-03	down	AT5G0929	-23.04	down	lncRNA	down
AT4G06810	AT4G06810					AT4G0681	-2.729	down	lncRNA	down
AT1G77992	AT1G77992					AT1G7799	-2.247	down	lncRNA	down
AT5G24205	AT5G24205	AT5G24205_1	18.095	0.04985	up	AT5G2420	18.052	up	Long noncoding RNA	up
PV42A	At1g15330	-				PV42A	-6.337	down	male meiosis Cystathionine beta-synthase (CBS) protein	down
MAPKKK21	AT4G36950	MAPKKK21_1	-12.87	0.04242	down	MAPKKK21	-12.83	down	MAPK signaling, unknown mitogen-activated protein kinase kinase kinase 21	down
MAPKKK14	AT2G30040					MAPKKK14	-2.444	down	MAPK signalling MAPKKK14 mitogen-activated protein kinase kinase kinase 14	down
RAX3	AT3G49690	-				RAX3	3.3527	up	meristem axillary meristem formation MYB84; myb domain protein 84 RAX3; REGULATOR OF AXIL	up
CLE14	AT1G63245					CLE14	-2.422	down	meristem CLAVATA signaling CLAVATA3/ESR-RELATED 14	down
CLE13	AT1G73965					CLE13	-2.436	down	meristem Clavata13 homolog CLE12 CLAVATA3/ESR-related13	down
CLE1	AT1G73165					CLE1	-8.082	down	meristem Clavata3 homolog CLE1 CLAVATA3/ESR-related 1	down
CLE2	AT4G18510	CLE2_1	-3.579	0.04794	down	CLE2	-3.628	down	meristem Clavata3 homolog CLE2 CLAVATA3/ESR-related 2	down
CLE6	AT2G31085					CLE6	-3.732	down	meristem Clavata6 homolog CLE6 CLAVATA3/ESR-RELATED 6	down
PLL1	AT2G35350					PLL1	2.0528	up	meristem size PLL1 POLTERGEIST-like	up
CLE44	AT4G13195					CLE44	-2.44	down	meristem vascular axillary bud formation Clavata3 homolog CLE44 CLAVATA3/ESR-related 44	down
WVD2	AT5G28646	WVD2_1				WVD2	-4.133	down	microtubule associated TPX2 domain protein WAVE-DAMPENED 2	down?
FPP2	At1g21810	FPP2_1	104.56	0.02128	up	FPP2	2.7733	up	microtubule binding, interactor of oligomeric golgi complex subunit-like protein	up
AT3G16120	AT3G16120					AT3G1612	-3.028	down	microtubule Dynein light chain type 1	down
KIN12E	At3g44050					KIN12E	2.8309	up	microtubule kinesin motor	up
KIN10A	At4g14330					KIN10A	2.4012	up	microtubule kinesin motor	up
KIN14S	At5g27550					KIN14S	2.1911	up	microtubule kinesin motor	up
KIN14P	At1g73860					KIN14P	2.8801	up	microtubule kinesin motor	up
KIN14C	At4g21270					KIN14C	2.283	up	microtubule kinesin motor ATK1, KATA, KATAP, KINESIN 1	up
KIN7N	At1g59540					KIN7N	2.281	up	microtubule kinesin motor ZCF125	up
AT5G23910	AT5G23910	AT5G23910_2	3.5251	0.0433	up	AT5G2391	2.7165	up	microtubule motor, Golgi	up?
SP1L2	AT1G69230	-				SP1L2	-2.101	down	microtubule organization SPIRAL1-like2	down
SP1L5	AT4G23496					SP1L5	-2.244	down	microtubule organization SPIRAL1-like5	down
PCAP2	AT5G44610	PCAP2_1	-3.082	7.16E-03	down	PCAP2	-2.399	down	microtubule polymerization inhibitor Ca2+/PA regulated plasmamembrane protein	down
ANP2	AT1G54960	-				ANP2	2.5046	up	microtubule redox signaling cell division MAPKKK2; MITOGEN-ACTIVATED PROTEIN KINASE KINASE	up
TOR1L2	At2g07170	TOR1L2_1	2.9051	0.04955	up	TOR1L2	2.902	up	microtubule unknown ARM/Heat-like repeat	up
KIN5B	At2g37420					KIN5B	2.4392	up	microtubules kinesin motor	up
CCB452	ATMG00180					CCB452	-3.169	down	mitochondrion cytochrome c biogenesis protein CCB452, CYTOCHROME C BIOGENESIS 452	down
ORF240A	ATMG00690	ORF240A_1	-4.534	0.02389	down	ORF240A	-4.6	down	mitochondrion FO-ATPase subunit	down
NDB3	AT4G21490	NDB3_1	66.364	0.04444	up	NDB3	31.396	up	mitochondrion NAD(P)H dehydrogenase B3	up
AT1G74350	AT1G74350	-				AT1G7435	2.1002	up	mitochondrion nad1 pre-mRNA maturase NMAT4, NUCLEAR-ENCODED MATURASE-RELATED 4	up
AT2G28815	AT2G28815					AT2G2881	6.1559	up	mitochondrion 50S ribosomal protein L16	up
AT2G07777	AT2G07777					AT2G0777	-3.855	down	mitochondrion ATP synthase 9 subunit	down
ORF262	ATMG01090					ORF262	-2.96	down	mitochondrion ATP synthase subunit 9	down
ORF315	ATMG00040					ORF315	-2.056	down	mitochondrion ATP synthase subunit C	down
AT2G07671	AT2G07671	AT2G07671_1	-3.541	4.01E-04	down	AT2G0767	-3.584	down	mitochondrion atp9 ATP synthase subunit C	down
ATP6-2	ATMG01170					ATP6-2	-3.06	down	mitochondrion ATPase subunit 6	down
ORF294	ATMG01200					ORF294	-4.107	down	mitochondrion ATPase, F1 complex, alpha subunit	down
ORF25	ATMG00640					ORF25	-2.092	down	mitochondrion b subunit of mitochondrial ATP synthase	down
HSR4	At3g50930	HSR4_1	4.8065	3.04E-03	up	HSR4	4.7751	up	mitochondrion cell death, pathogen SA, mitochondrial outer membrane AAA ATPase AtOM66 mi	up
CML1	AT2G15680	-				CML1	-2.427	down	mitochondrion CML30 calmodulin-like 30	down
AT2G07695	AT2G07695	AT2G07695_1	-4.459	0.02918	down	AT2G0769	-4.509	down	mitochondrion COII subunit of Cytochrome c oxidase	down
ORF313	ATMG00590					ORF313	-7.402	down	mitochondrion Cytochrome b/b6 protein	down
AT2G07718	AT2G07718	AT2G07718_1	-2.366	9.85E-03	down	AT2G0771	-2.393	down	mitochondrion Cytochrome b/b6, unknown transmembrane protein	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
CCB206	ATMG00110					CCB206	-4.794	down	mitochondrion cytochrome c biogenesis protein ABCI2, ATP-BINDING CASSETTE I2, CCB206, CYTOC	down
COX2	ATMG00160					COX2	-2.248	down	mitochondrion cytochrome c oxidase subunit 2 COX2, CYTOCHROME OXIDASE 2	down
ORF291	ATMG01280					ORF291	-4.134	down	mitochondrion cytochrome c oxidase subunit II	down
ATKP1	AT3G44730	-				ATKP1	2.0699	up	mitochondrion low temperature respiration VDAC3 interacting actin binding kinesin motor	up
AT5G66650	AT5G66650	-				AT5G6665	-2.403	down	mitochondrion MCU calcium uniporter	down
PCMP-E90	At3g02330	-				PCMP-E90	3.5758	up	mitochondrion MEF13, MITOCHONDRIAL EDITING FACTOR 13 PRR repeat protein	up
DYW9	AT4G30700					DYW9	2.1732	up	mitochondrion MEF29, MITOCHONDRIAL RNA EDITING FACTOR 29	up
AT3G29970	AT3G29970	AT3G29970_3				AT3G2997	-2.999	down	mitochondrion MLRQ subunit of mitochondrial NADH-ubiquinone reductase complex I	down
NAD4	ATMG00580					NAD4	-2.394	down	mitochondrion NAD4, NADH DEHYDROGENASE SUBUNIT 4	down
AT2G07751	AT2G07751					AT2G0775	-2.892	down	mitochondrion NADH:ubiquinone/plastoquinone oxidoreductase, chain 3	down
AT1G76065	AT1G76065					AT1G7606	-2.147	down	mitochondrion NADH-ubiquinone oxidoreductase complex I subunit	down
AT5G27660	AT5G27660	AT5G27660_1	-2.108	0.01023	down	AT5G2766	-2.128	down	mitochondrion protein folding DEG14 protease homolog of human PARK13, a mitochondrial prot	down
PCMP-H44	At2g03880					PCMP-H44	3.0708	up	mitochondrion PRR protein required for efficiency of mitochondrial editing 1	up
AT2G07734	AT2G07734					AT2G0773	-4.475	down	mitochondrion Ribosomal protein S4	down
AT1G12300	AT1G12300	-				AT1G1230	2.132	up	mitochondrion RNA editing RESTORER-OF-FERTILITY-LIKE 2, RFL2 pentatricopeptide repeat protei	up
AT1G05670	AT1G05670	AT1G05670_1	105.24	0.02252	up	AT1G0567	2.3044	up	mitochondrion RNA processing	up
SDH1-2	AT2G18450	-				SDH1-2	2.549	up	mitochondrion SDH1-2 succinate dehydrogenase 1-2	up
AT5G64710	AT5G64710					AT5G6471	2.4878	up	mitochondrion transcript processing MITOCHONDRIAL NUCLEASE 1, MNU1	up
TOM40-2	At1g50400					TOM40-2	2.5711	up	mitochondrion translocase of outer mitochondrial membrane 40 homolog	up
ORF275	ATMG00670					ORF275	-3.26	down	mitochondrion transmembrane protein	down
AT2G03690	AT2G03690					AT2G0369	-2.023	down	mitochondrion Ubiquinone biosynthesis protein COQ4 homolog	down
ORF114	ATMG01000					ORF114	-2.069	down	mitochondrion unknown ORF114	down
AT1G66890	AT1G66890					AT1G6689	-2.014	down	mitochondrion unknown protein	down
ORF101B	ATMG01210					ORF101B	-12.24	down	mitochondrion unknown protein ORF101B	down
ORF113	ATMG01220					ORF113	-3.708	down	mitochondrion unknown protein ORF113	down
ORF111D	ATMG01370					ORF111D	-3.136	down	mitochondrion unknown transmembrane protein ORF111D	down
AT1G22800	AT1G22800	AT1G22800_1	268.4	3.18E-03	up	AT1G2280	266.27	up	mitochondrion, homolog of NDUFAF5 NADH dehydrogenase (ubiquinone) complex I, assembly f	up
AT1G30170	AT1G30170	AT1G30170_1	243.59	3.86E-03	up	AT1G3017	242.36	up	mitochondrion, unknown	up
AT3G05932	AT3G05932	AT3G05932_1	4.4068	0.04221	up	AT3G0593	2.3416	up	nat-siRNA for the germin-like protein 8 gene	up
AT2G01422	AT2G01422	AT2G01422_1	55.424	1.65E-08	up	AT2G0142	54.911	up	ncRNA	up
AT1G78865	AT1G78865					AT1G7886	2.4408	up	ncRNA	up
AT4G13918	AT4G13918	-				AT4G1391	2.4133	up	ncRNA	up
AT1G17232	AT1G17232					AT1G1723	2.4276	up	ncRNA	up
AT3G54625	AT3G54625					AT3G5462	5.8147	up	ncRNA	up
AT4G27852	AT4G27852					AT4G2785	2.8727	up	ncRNA	up
AT1G04103	AT1G04103	AT1G04103_1	-70.4	0.03439	down	AT1G0410	-70.68	down	ncRNA	down
AT1G34418	AT1G34418	AT1G34418_1	-2.053	0.01535	down	AT1G3441	-2.079	down	ncRNA	down
AT1G52347	AT1G52347	AT1G52347_1	-2.227	0.01595	down	AT1G5234	-2.261	down	ncRNA	down
AT1G69252	AT1G69252	AT1G69252_1	-2.224	0.01849	down	AT1G6925	-2.26	down	ncRNA	down
AT1G79075	AT1G79075	AT1G79075_1	-2.087	0.04112	down	AT1G7907	-2.11	down	ncRNA	down
AT2G31585	AT2G31585	AT2G31585_1	-2.001	0.04851	down	AT2G3158	-2.028	down	ncRNA	down
AT3G48115	AT3G48115	AT3G48115_1	-2.214	0.01507	down	AT3G4811	-2.239	down	ncRNA	down
AT3G06125	AT3G06125	AT3G06125_1	-2.345	0.02963	down	AT3G0612	-2.307	down	ncRNA	down
AT2G45245	AT2G45245	AT2G45245_3	-16.83	0.02927	down	AT2G4524	-2.405	down	ncRNA	down
AT4G04223	AT4G04223	AT4G04223_1	-2.716	0.01529	down	AT4G0422	-2.295	down	ncRNA	down
AT1G29785	AT1G29785	AT1G29785_2	-2.893	1.14E-03	down	AT1G2978	-2.935	down	ncRNA	down
AT2G13665	AT2G13665					AT2G1366	-2.087	down	ncRNA	down
AT2G32795	AT2G32795					AT2G3279	-2.033	down	ncRNA	down
AT3G61198	AT3G61198					AT3G6119	-3.311	down	ncRNA	down
AT4G12917	AT4G12917					AT4G1291	-2.274	down	ncRNA	down
AT5G34871	AT5G34871					AT5G3487	-2.7	down	ncRNA	down
AT5G38005	AT5G38005					AT5G3800	-2.934	down	ncRNA	down
AT5G43725	AT5G43725					AT5G4372	-2.405	down	ncRNA	down
AT3G15536	AT3G15536					AT3G1553	-3.078	down	ncRNA	down
AT4G37225	AT4G37225	-				AT4G3722	-2.851	down	ncRNA	down
AT5G05435	AT5G05435					AT5G0543	-2.15	down	ncRNA	down
AT2G46572	AT2G46572	-				AT2G4657	2.2438	up	ncRNA, cell wall laccase 6 down	up
NPF7.2	AT4G21680	NPF7.2_1	2.9843	0.02016	up	NPF7.2	2.9801	up	nitrate transporter xylem, cadmium tolerance	up
PLDALPHA4	AT1G55180	-				PLDALPHA	2.3258	up	nitrogen signaling PLDEPSILON phospholipase D alpha 4	up
UREF	AT1G21840	-				UREF	-2.121	down	N-metabolism NH3 production urease activating UREF protein	down
AT1G62580	AT1G62580	-				AT1G6258	2.0185	up	NO signaling NITRIC OXIDE-DEPENDENT GUANYLATE CYCLASE 1, NOGC1	up
FPP7	At2g23360					FPP7	2.1366	up	nuclear envelop interacting Filament-like plant protein, long coiled-coil	up
FPP5	At4g36120					FPP5	2.6907	up	nuclear envelop interacting Filament-like plant protein, long coiled-coil	up
AT4G10370	AT4G10370					AT4G1037	8.16	up	nuclear import RanGDP binding PHD finger repeat protein	up
AT1G03710	AT1G03710	AT1G03710_1	53.065	0.04401	up	AT1G0371	2.2093	up	nuclear Proteinase inhibitor I25, cystatin, conserved region	up
BZIP1	AT5G49450	BZIP1_1	-2.654	1.34E-03	down	BZIP1	-2.697	down	nutrient starvation, N/C-response,osmotic dorught stress SnRK1 signaling, heterodimerization	down
AT1G73600	AT1G73600	AT1G73600_2	2.5227	4.94E-04	up	AT1G7360	2.462	up	osmotic stress NMT3, PHOSPHOETHANOLAMINE METHYLTRANSFERASE3	up
AHK1	AT2G17820	AHK1_1	3.0208	1.28E-04	up	AHK1	3.0018	up	osmotic stress, putative osmosensor	up
ROF1	AT3G25230	ROF1_1	2.4177	5.92E-03	up	ROF1	2.0089	up	osmotic stress, thermotolerance, Cd-induced	up?
AT3G20340	AT3G20340	-				AT3G2034	-2.26	down	oxidative stress repressed unknown protein	down
AT2G21640	AT2G21640	AT2G21640_1	2.6179	8.23E-03	up	AT2G2164	2.591	up	oxidative stress response marker protein	up
NDB4	AT2G20800	NDB4_1	16.728	2.90E-04	up	NDB4	16.71	up	oxidative stress, mitochondrion NAD(P)H dehydrogenase B4	up
AT5G27730	AT5G27730	AT5G27730_1	-2.214	7.89E-03	down	AT5G2773	-2.301	down	pathogen glycosaminoglycan degradation HGSNAT Heparan-α-glucosaminide N-acetyltransfera	down
AT2G42900	AT2G42900	AT2G42900_1	-2.934	7.82E-03	down	AT2G4290	-2.973	down	pathogen ABA-induced BSP basic secretory domain protein	down
HS1	AT3G17210	-				HS1	-2.011	down	pathogen antimicrobial HS1 heat stable protein 1	down
HOL2	AT2G43920	HOL2_1	-3.29	1.09E-04	down	HOL2	-2.135	down	pathogen auxin IAA glucosinolate methylase	down
AT1G70860	AT1G70860					AT1G7086	-2.792	down	pathogen Bet_v_1 domain PR10 protein	down
CYP71A13	AT2G30770	CYP71A13_1	-9.022	6.34E-03	down	CYP71A13	-8.866	down	pathogen camalexin synthesis CYP71A13	down
AT5G46960	AT5G46960	AT5G46960_1	-57.42	0.0437	down	AT5G4696	-56.47	down	pathogen cell wall AtPMEI12 Pectin Methylesterase Inhibitor	down

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WAK3	AT1G21240	WAK3_2	-9.864	0.04017	down	WAK3	-7.544	down	pathogen cell wall associated WAK3 kinase	down
ATL9	AT2G35000	-				ATL9	-2.28	down	pathogen chitin induced RING E3	down
PCC1	AT3G22231	PCC1_1	-32.56	0.02638	down	PCC1	-32.41	down	pathogen circadian clock, flowering time COP9 signalosome subunit 5 interaction	down
AT4G22390	AT4G22390	AT4G22390_1	67.833	0.04309	up	AT4G2239	4.1225	up	pathogen CPR30 homolog SCF E3 ligase F-box protein	up
AT4G33925	AT4G33925	-				AT4G3392	-2.186	down	pathogen DNA repair SSN2 (suppressor of sni1 2), a suppressor of SNI1 (AT4G18470)	down
PEP7	AT5G09978					PEP7	-2.875	down	pathogen elicitor PROPEP7 peptide 7 85aa oligopeptide	down
PEP2	At5g64890					PEP2	-4.92	down	pathogen elicitor peptide PROPEP2	down
PEP4	At5g09980					PEP4	-3.506	down	pathogen elicitor PROPEP4 peptide 4 81aa oligopeptide	down
AT4G11170	AT4G11170	-				AT4G1117	2.5599	up	pathogen flg22 induced RMG1 (Resistance Methylated Gene 1), a NB-LRR disease resistance pro	up
SIRK	At2g19190	-				SIRK	3.2836	up	pathogen FRK1 FLG22-induced receptor-like kinase 1	up
HR3	AT3G50470	-				HR3	-3.47	down	pathogen homolog of RPW8 3; INTRACELLULAR MILDEW A 10; MLA10	down
AT3G15395	AT3G15395	AT3G15395_5	-4.797	0.04957	down	AT3G1539	-2.197	down	pathogen HrpN-hairpin interacting transmembrane protein	down
DIR13	AT4G11190	DIR13_1	-4.5	1.31E-03	down	DIR13	-4.557	down	pathogen induced cell wall lignin, Dirigent domain protein with signal peptide	down
DIR14	AT4G11210					DIR14	-3.133	down	pathogen induced cell wall lignin, Dirigent domain protein with signal peptide	down
DIR23	AT2G21100	-				DIR23	-2.021	down	pathogen induced cell wall lignin, Dirigent domain protein with signal peptide	down
AT3G23170	AT3G23170	AT3G23170_1	-2.282	0.01847	down	AT3G2317	-2.304	down	pathogen induced MPK6 interacting protein	down
ATLP-3	AT1G75030					ATLP-3	-2.502	down	pathogen induced PR10 thaumatin domain protein	down
AT5G23820	AT5G23820	AT5G23820_1	-2.275	1.10E-03	down	AT5G2382	-2.298	down	pathogen JA ethylene induced MD-2-related lipid-recognition (ML) domain	down
AT1G53870	AT1G53870	AT1G53870_3	-2.882	0.01477	down	AT1G5387	-2.122	down	pathogen LURP-one-related protein	down
AT5G23840	AT5G23840	AT5G23840_2	-24.67	0.03945	down	AT5G2384	-9.506	down	pathogen ML lipid recognition domain protein	down
BHLH25	AT4G37850	-				BHLH25	-14.15	down	pathogen nematode susceptibility BHLH25 TF	down
atnudt8	AT5G47240	atnudt8_2	-2.37	1.29E-03	down	atnudt8	-2.299	down	pathogen NUDT8 nudix hydrolase homolog 8 mutant has enhanced sensitivity	down
AT5G05300	AT5G05300	-				AT5G0530	-5.927	down	pathogen PAMP induced 102aa oligopeptide with signal peptide	down
AT1G14960	AT1G14960					AT1G1496	-2.988	down	pathogen Pathogenesis-related protein Bet v I PR-10 domain protein	down
EGC2	AT2G18660	-				EGC2	-4.859	down	pathogen PLANT NATRIURETIC PEPTIDE A, PNP-A	down
ERF5	AT5G47230	-				ERF5	-2.152	down	pathogen positive regulator of JA ET responses ERF5 AP2 TF	down
PDF1.4	AT1G19610	PDF1.4_1	-2.656	0.02383	down	PDF1.4	-2.702	down	pathogen PR peptide KNOT1 domain defensin Knottin antimicrobial peptide	down
AT2G27385	AT2G27385	AT2G27385_1	-3.078	4.37E-05	down	AT2G2738	-3.115	down	pathogen PR protein with Pollen_Ole_e_I domain	down
AT4G33720	AT4G33720	-				AT4G3372	2.0329	up	pathogen PR1 cysteine-rich secretory protein with signal peptide	up
AT4G25780	AT4G25780					AT4G2578	-2.4	down	pathogen PR1 cysteine-rich secretory protein with signal peptide	down
MORC7	At4g24970	-				MORC7	2.0134	up	pathogen repressor MORC7 nuclear GHKL ATPases	up
NIMIN-1	AT1G02450	-				NIMIN-1	-5.459	down	pathogen repressor of NPR1-TGA activated PR gene expression	down
NATA1	AT2G39030					NATA1	-2.165	down	pathogen response JA ABA induced ornithine N-delta-acetyltransferase, NATA1	down
ALD1	AT2G13810	ALD1_1	-16.77	0.02819	down	ALD1	-16.46	down	pathogen response, cell death, amino acid, lysine synthesis, Diaminopimelate aminotransferas	down
AT5G63270	AT5G63270					AT5G6327	-2.392	down	pathogen RPM1-interacting protein 4 (RIN4) homolog	down
AT3G48450	AT3G48450					AT3G4845	-2.127	down	pathogen RPM1-interacting protein 4 (RIN4) homolog	down
BAD1	AT5G54610					BAD1	-4.527	down	pathogen SA induced BDA1; bian da 2 (becoming big in Chinese) ankyrin repeat protein acting do	down
CML43	AT5G44460	-				CML43	-3.185	down	pathogen SA-induced calmodulin Ca2+ CML43 calmodulin like 43	down
PR1	AT2G14610	PR1_1	-26.11	0.03527	down	PR1	-25.69	down	pathogen SA-induced marker	down
AT4G01895	AT4G01895					AT4G0189	-3.066	down	pathogen SAR NPR1 interacting NIMIN1 homolog	down
NIMIN-2	AT3G25882	-				NIMIN-2	-2.239	down	pathogen SAR positive regulator NPR1 interactor	down
HSPRO2	AT2G40000	HSPRO2_1	-2.407	5.96E-03	down	HSPRO2	-2.439	down	pathogen SnRK1 interacting SA induced JA/ethylene repressed Hs1pro-1 resistance protein	down
AT1G10300	AT1G10300	-				AT1G1030	2.1753	up	pathogen stomatal defense response Nucleolar GTP-binding protein 1 (NOG1)	up
AT5G23830	AT5G23830	AT5G23830_1	-3.021	1.82E-03	down	AT5G2383	-3.008	down	pathogen unknown ML (MD-2-related lipid-recognition) protein	down
AT4G19920	AT4G19920					AT4G1992	-4.028	down	pathogen unknown Toll-Interleukin-Resistance (TIR) domain prtein	down
AED1	AT5G10760					AED1	-2.599	down	pathogen Xylanase inhibitor with signal peptide AED1, APOPLASTIC, EDS1-DEPENDENT 1	down
AT1G51800	AT1G51800	AT1G51800_1	2.7994	2.17E-03	up	AT1G5180	2.7903	up	pathogen, ABA response IMPAIRED OOMYCETE SUSCEPTIBILITY1	up
DIR18	AT4G13580	DIR18_1	-2.649	0.01431	down	DIR18	-2.682	down	pathogen, auxin/BR induced unknown Disease resistance-responsive dirigent domain protein w	down
AT5G46890	AT5G46890	AT5G46890_1	-9.218	7.14E-03	down	AT5G4689	-9.24	down	pathogen, AZI1 class of unknown lipid transfer protein	down
AT5G46900	AT5G46900	AT5G46900_1	-8.593	2.73E-03	down	AT5G4690	-8.479	down	pathogen, AZI1 class of unknown lipid transfer protein	down
AIR1	AT4G12550	AIR1_1	-6.979	0.03642	down	AIR1	-6.933	down	pathogen, AZI1 class SAR azelaic acid (AZA) lipid transport protein	down
PLP2	AT2G26560	PLP2_1	2.4615	0.02806	up	PLP2	2.4598	up	pathogen, cell death, oxylipin	up
AtRLP52	AT5G25910					AtRLP52	3.3841	up	pathogen, chitin induced transmembrane LRR receptor	up
WRKY48	AT5G49520	WRKY48_1	3.0623	0.02986	up	WRKY48	3.0361	up	pathogen, chitin induced WRKY repressor of plant basal defense	up
DJA6	AT2G22360	DJA6_1	2.1472	3.83E-03	up	DJA6	2.1265	up	pathogen, chloroplast DJA6, DNA J PROTEIN A6 interactor of SR1 repressor of SA responses	up
DIR25	AT1G07730	DIR25_1	-153.9	0.01626	down	DIR25	-153.9	down	pathogen, Dirigent domain protein with signal peptide	down
DIR2	AT5G42500	-				DIR2	-3.427	down	pathogen, Dirigent domain protein with signal peptide	down
AT1G50060	AT1G50060					AT1G5006	-2.701	down	pathogen, extracellular PR1 homolog	down
ATTI3	AT2G43530	ATTI3_1	-2.074	0.03224	down	ATTI3	-2.102	down	pathogen, Knottin domain antibacterial defensin	down
ATTI4	AT2G43535	ATTI4_1	-2.064	7.04E-03	down	ATTI4	-2.087	down	pathogen, Knottin domain antibacterial defensin	down
ATTI6	AT2G43550	ATTI6_1	-3.281	3.36E-04	down	ATTI6	-3.313	down	pathogen, Knottin domain antibacterial defensin	down
ATTI2	AT2G43520					ATTI2	-2.218	down	pathogen, Knottin domain antibacterial defensin	down
AT4G22212	AT4G22212	AT4G22212_1	-2.181	0.0409	down	AT4G2221	-2.208	down	pathogen, Knottin domain antibacterial defensine	down
PDF1.3	AT2G26010	-				PDF1.3	2.8071	up	pathogen, PDF1.3 Knottin domain antibacterial defensine	up
PDF1.2C	AT5G44430	-				PDF1.2C	-3.65	down	pathogen, ROS induced Knottin domain antibacterial defensin 1.2C	down
PDF2.2	AT2G02100	PDF2.2_1	-2.388	0.01392	down	PDF2.2	-2.395	down	pathogen, ROS induced Knottin domain antibacterial defensine	down
ADR1	AT1G33560	ADR1_1	2.7313	1.65E-03	up	ADR1	2.7147	up	pathogen, SA, ROS	up
AT4G12510	AT4G12510	AT4G12510_1	-7.495	1.60E-03	down	AT4G1251	-7.606	down	pathogen, SAR AZI1 class SAR azelaic acid (AZA) lipid transport protein AZI5	down
AT4G12520	AT4G12520	AT4G12520_1	-4.132	6.11E-07	down	AT4G1252	-4.191	down	pathogen, SAR AZI1 class SAR azelaic acid (AZA) lipid transport protein AZI5	down
LLP	At5g03350	LLP_1	-3.219	6.38E-03	down	LLP	-3.254	down	pathogen, SAR induction, Lectin_legB domain protein with signal peptide	down
AT1G32928	AT1G32928	AT1G32928_1	-3.215	4.02E-03	down	AT1G3292	-3.253	down	pathogen, unknown Avr9/Cf-9 elicitor induced protein	down
NHL10	AT2G35980	NHL10_1	-4.31	0.03661	down	NHL10	-4.349	down	pathogen,nonerace induced disease resistance HR, virus induced homolog of tobacco hairpin-i	down
AT1G60590	AT1G60590	AT1G60590_1	3.3315	3.16E-03	up	AT1G6059	3.2979	up	pectin, polygalacturonase, extracellular	up
RHM1	AT1G78570	RHM1_1	2.2813	2.96E-03	up	RHM1	2.2581	up	pectin, sugar biosynthesis	up
PGL5	AT5G24420	PGL5_1	-2.524	0.02759	down	PGL5	-2.558	down	pentose phosphate pathway oxidative cytosolic 6-phosphogluconolactonase	down
PGL4	AT5G24410	-				PGL4	-2.752	down	pentose phosphate pathway oxidative PGL4 6-phosphogluconolactonase 4	down
DVL10	AT4G13395	-				DVL10	-3.319	down	peptide ligand growth factor DEVIL 10; DVL10; ROTUNDIFOLIA like 12	down
RTFL2	AT2G29125	-				RTFL2	-2.258	down	peptide ligand growth factor DEVIL 13; DVL13; ROTUNDIFOLIA like 2	down
RTFL14	AT3G63088					RTFL14	-3.977	down	peptide ligand growth factor DEVIL 14; DVL14; ROTUNDIFOLIA like 14	down

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RTFL6	AT4G35783					RTFL6	-2.422	down	peptide ligand growth factor DEVIL 17; DVL17; ROTUNDIFOLIA like 6	down
RTFL5	AT5G59510					RTFL5	-2.354	down	peptide ligand growth factor DEVIL 18; ROTUNDIFOLIA like 5	down
RTFL1	AT3G53232	-				RTFL1	-2.452	down	peptide ligand growth factor DEVIL 20; DVL20; ROTUNDIFOLIA like 1	down
RTFL17	AT1G13245	RTFL17_1	-2.704	1.86E-04	down	RTFL17	-2.742	down	peptide ligand growth factor DEVIL 4; DVL4; ROTUNDIFOLIA like 17	down
AT4G29905	AT4G29905	AT4G29905_1	-2.691	3.11E-03	down	AT4G2990	-2.735	down	peptide ligand growth factor DEVIL 4; DVL4; ROTUNDIFOLIA like 17	down
RTFL3	AT1G07490					RTFL3	-2.296	down	peptide ligand growth factor DEVIL 9; DVL9; ROTUNDIFOLIA like 3	down
FLP1	AT4G31380					FLP1	-4.968	down	peptide ligand growth factor FLP1 flowering-promoting factor-like	down
RALFL33	AT4G15800					RALFL33	-2.02	down	peptide ligand Rapid Alkalinization Factor (RALF) RALFL33 ralf-like 33	down
RALFL24	AT3G23805	RALFL24_1	-2.085	0.02465	down	RALFL24	-2.116	down	peptide ligand Rapid Alkalinization Factor (RALF) ralf-like 24	down
RALFL27	AT3G29780	-				RALFL27	-2.497	down	peptide ligand Rapid Alkalinization Factor (RALF) ralf-like 27	down
RALFL32	AT4G14010	RALFL32_1	-2.722	2.32E-03	down	RALFL32	-2.766	down	peptide ligand Rapid Alkalinization Factor (RALF) ralf-like 32	down
AT2G32885	AT2G32885					AT2G3288	-2.158	down	peptide ligand Rapid Alkalinization Factor (RALF) RALF-like 36	down
ICL	AT3G21720	ICL_1	2.4743	0.04596	up	ICL	2.46	up	peroxisome, citrate cycle isocitrate lyase	up
ATPP2-A9	AT1G31200					ATPP2-A9	-4.035	down	phloem transport protein AN4, ARATHNICTABA 4, ATPP2-A9, PHLOEM PROTEIN 2-A9	down
AT2G45900	AT2G45900	AT2G45900_1	170.95	0.01217	up	AT2G4590	2.1211	up	Phosphatidylinositol metabolism GA regulated	up
PTEN2B	AT3G50110	-				PTEN2B	2.0273	up	phosphoinositol, phosphatidic acid binding PTEN 3; PTEN2B phosphatase	up
ALA8	AT3G27870					ALA8	2.27	up	phospholipid membrane transport ATPase	up
AT1G19020	AT1G19020					AT1G1902	-2.238	down	phospholipid synthesis CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	down
ALA6	AT1G54280	ALA6_1	51.82	0.04689	up	ALA6	51.581	up	phospholipid-transporting membrane ATPase	up
GATA2	AT2G45050	GATA2_1	-2.253	0.01663	down	GATA2	-2.268	down	photomorphogenesis positive regulator GATA2TF	down
PAR1	AT2G42870	PAR1_1	-3.373	1.04E-05	down	PAR1	-3.414	down	photomorphogenesis, auxin bHLH1 TF repressor of SAUR15/68	down
PAR2	AT3G58850	PAR2_1	-2.578	6.16E-03	down	PAR2	-2.618	down	photomorphogenesis, auxin bHLH2 TF repressor of SAUR15/68	down
PKS4	AT5G04190	-				PKS4	-2.076	down	phototropis PHOT1 phosphorylated PKS4	down
LSH8	AT1G16910	-				LSH8	-3.037	down	Phy light signaling ALOG (Arabidopsis LSH1 and oryza G1) domain TF	down
APY5	AT1G14250	APY5_1	-3.145	0.01294	down	APY5	-3.172	down	plasmamembrane extracellular ATP hydrolysis ectonucleoside triphosphate diphosphohydrola	down
ROPGAP2	At4g03100	-				ROPGAP2	2.0431	up	polar cell growth Cdc42/Rac interacting Rho GTPase activating protein	up
CHX17	AT4G23700	CHX17_1	2.9825	1.63E-03	up	CHX17	2.0735	up	potassium transporter CHX17 cation/H+ exchanger 17	up
AT4G32950	AT4G32950					AT4G3295	2.1501	up	PP2C protein phosphatase 2C 61	up
AT2G05230	AT2G05230	AT2G05230_1	2.8298	0.03365	up	AT2G0523	2.8252	up	protein folding cytoplasmic DNAJ chaperon	up
HSP18.5	At2g19310	HSP18.5_1	-2.512	7.02E-03	down	HSP18.5	-2.555	down	protein folding heat shock protein HSP18.5	down
AT1G64065	AT1G64065					AT1G6406	-2.037	down	protein folding Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein	down
M10	AT2G41280					M10	-2.843	down	protein folding LATE EMBRYOGENESIS ABUNDANT M10	down
AT2G23110	AT2G23110					AT2G2311	-3.647	down	protein folding Late embryogenesis abundant protein, group 6	down
AT3G05975	AT3G05975	-				AT3G0597	-2.026	down	protein folding membrane bound LATE EMBRYOGENESIS ABUNDANT	down
AT2G01080	AT2G01080					AT2G0108	-2.003	down	protein folding membrane bound Late embryogenesis abundant (LEA)	down
AT1G26800	AT1G26800	AT1G26800_1	-2.289	8.26E-03	down	AT1G2680	-2.315	down	Protein folding protein quality control PQC E3 Misfolded Protein Sensing RING E3 ligase 1 (MPSR1	down
AT4G33120	AT4G33120					AT4G3312	-2.289	down	protein repair Protein-L-isoaspartate(D-aspartate) O-methyltransferase	down
AT3G04330	AT3G04330					AT3G0433	-2.926	down	proteolysis Kunitz-type trypsin inhibitor with signal peptide	down
AT4G24340	AT4G24340	-				AT4G2434	-3.559	down	purine metabolism Purine nucleoside phosphorylase	down
CDA8	AT4G29570					CDA8	8.8281	up	pyrimidine salvaging Cytidine deaminase	up
AT2G19810	AT2G19810	AT2G19810_1	-3.312	6.31E-06	down	AT2G1981	-3.353	down	redox Oxidation-related Zinc Finger 1 (OZF1) required for oxidative stress response	down
MIOX4	AT4G26260	-				MIOX4	-2.265	down	redox ascorbate synthesis MIOX4 myo-inositol oxygenase 4	down
CBSX3	AT5G10860	CBSX3_1	-2.219	4.46E-03	down	CBSX3	-2.239	down	redox CBX3 regulator of mitochondrial thioredoxins	down
FTRA2	AT5G08410	FTRA2_2	-2.486	3.78E-04	down	FTRA2	-2.51	down	redox chloroplast FTRA2 ferredoxin/thioredoxin reductase subunit A	down
PQL3	AT2G01918	-				PQL3	-2.588	down	redox chloroplast NDH PQL subunit	down
sks15	AT4G37160					sks15	-2.566	down	redox cupredoxin copper oxidase	down
SKS2	AT5G51480					SKS2	2.1301	up	redox cupredoxin copper oxidase SKS2 SKU5 similar 2	up
GRXS11	At1g06830	GRXS11_1	-4.91	1.49E-04	down	GRXS11	-4.952	down	redox glutaredoxin CEPD1 induced by N-starvation	down
GRXC13	At2g47880	GRXC13_1	-5.008	0.01299	down	GRXC13	-5.031	down	redox glutaredoxin CEPD2 induced by N-starvation	down
GRXC9	At1g28480					GRXC9	-4.156	down	redox glutaredoxin GRX480 TGA interactor PDF1.2 suppressor	down
GRXC8	At5g14070	GRXC8_1	-4.53	0.03932	down	GRXC8	-4.585	down	redox glutaredoxin ROXY2 TGA9/10 control of anther development	down
AT1G19900	AT1G19900					AT1G1990	-2.21	down	redox glyoxal oxidase with signal peptide	down
GSTU3	AT2G29470					GSTU3	-3.273	down	redox GSTU3 glutathione S-transferase tau 3	down
ALDH5F1	AT1G79440	-				ALDH5F1	-2.033	down	redox mitochondrion ALDH5F1 aldehyde dehydrogenase 5F1	down
AOX1C	AT3G27620	-				AOX1C	3.6914	up	redox mitochondrion AOX1C alternative oxidase 1C	up
GRXS10	At3g21460	-				GRXS10	-5.463	down	redox monothiol glutaredoxin-S10	down
GRXS6	At3g62930					GRXS6	-2.138	down	redox Monothiol glutaredoxin-S6 GRXS6 ROXY17	down
GRXC11	At3g62950	GRXC11_1	-4.939	7.29E-03	down	GRXC11	-4.994	down	redox nitrate induced ROXY4 Glutaredoxin-C11 controlling root growth	down
TRX5	AT1G45145	TRX5_1	-2.488	4.00E-03	down	TRX5	-2.53	down	redox oxidative stress pathogen induced cytoplasmic Thioredoxin H-type 5	down
GRXS9	At2g30540	-				GRXS9	-3.068	down	redox pathogen TGA interacting glutaredoxin 9	down
PER4	AT1G14540					PER4	-2.955	down	redox peroxidase 4	down
PER61	At5g24070					PER61	-3.205	down	redox peroxidase 61 with signal peptide	down
NUDT1	At1g68760	-				NUDT1	-2.001	down	redox protection nudix hydrolase 1	down
MSRB9	AT4G21850	MSRB9_1	-2.611	1.92E-04	down	MSRB9	-2.513	down	redox protein repair MSRB9 methionine sulfoxide reductase selenoprotein SELR homolog	down
LPR1	AT1G23010					LPR1	2.3392	up	redox root cupredoxin controlling cell division by phosphate starvation	up
GRXS5	At4g15690	GRXS5_1	-3.113	8.72E-03	down	GRXS5	-3.157	down	redox root growth glutaredoxin ROXY12	down
GRXS3	At4g15700	GRXS3_1	-2.685	0.04615	down	GRXS3	-2.718	down	redox root growth Monothiol glutaredoxin-S3 ROXY11	down
GRXS4	At4g15680	GRXS4_1	-3.602	0.04574	down	GRXS4	-3.643	down	redox root growth Monothiol glutaredoxin-S4 ROXY13	down
GRXS7	At4g15670	-				GRXS7	-3.331	down	redox root growth Monothiol glutaredoxin-S7 GRXS7 ROXY14	down
GRXS8	At4g15660	GRXS8_1	-5.262	0.02854	down	GRXS8	-5.304	down	redox root growth Monothiolglutaredoxin-S8, ROXY15	down
MSRB7	AT4G21830	-				MSRB7	-2.389	down	redox root oxidative stress tolerance MSRB7 methionine sulfoxide reductase B7	down
MSRB8	AT4G21840	-				MSRB8	-5.204	down	redox root oxidative stress tolerance MSRB8 methionine sulfoxide reductase B8 selenoprotein	down
ERF109	At4g34410	-				ERF109	-12.78	down	redox ROS inducing JA induced activator of auxin synthesis RRTF1 redox responsive transcription	down
MSRB6	AT4G04840	MSRB6_1	-2.521	8.44E-04	down	MSRB6	-2.557	down	redox selenoprotein R MSRB6 methionine sulfoxide reductase B6	down
CXXS1	AT1G11530	-	-2.211	7.92E-03	down	CXXS1	-2.231	down	redox thioredoxin h family with single Cys redox residue	down
GRXS14	At3g54900	GRXS14_1	-2.054	0.01335	down	GRXS14	-2.083	down	redox, chloroplast glutaredoxin	down
GSTU19	AT1G78380	GSTU19_1	-2.037	0.0106	down	GSTU19	-2.063	down	redox, drought oxidative stress indued GSTU19 glutathione S-transferase TAU 19	down
PIP2-4	At5g60660	PIP2-4_1	-2.981	4.66E-04	down	PIP2-4	-3.018	down	redox, H2O2 membrane transport water channel, plasma membrane intrinsic protein 2;4	down
OXS3	AT5G56550	OXS3_1	-3.789	1.31E-04	down	OXS3	-3.855	down	redox, oxidative stress, heavy metal tolerance, nuclear protein interacting with ribosome bioge	down

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PRXIIC	At1g65970	PRXIIC_1	-3.025	1.14E-03	down	PRXIIC	-3.075	down	redox, peroxisome, peroxiredoxin 5 homolog	down
AT5G07475	AT5G07475					AT5G0747	-2.192	down	redox, plastocyanin family Cu_bind_like domain	down
ENODL10	AT5G57920	ENODL10_2	-86.46	0.03243	down	ENODL10	-4.825	down	redox, plastocyanin family with cupredoxin domain	down
AT3G60270	AT3G60270					AT3G6027	-2.674	down	redox, plastocyanin family with cupredoxin domain	down
PER24	At2g39040	PER24_1	-11.12	0.01961	down	PER24	-11.13	down	redox, unknown peroxidase 24 with signal peptide	down
RPS16C	At5g18380	RPS16C_3	-4.342	2.37E-06	down	RPS16C	-2.231	down	ribosome 40S ribosomal protein S16-3	down?
AT2G16360	AT2G16360					AT2G1636	-2.026	down	ribosome 40S ribosomal protein S25-1	down
AT3G49725	AT3G49725					AT3G4972	2.2324	up	ribosome 50S GTPase GTP-binding HflX-like protein	up
RPP2C	At3g28500					RPP2C	2.8265	up	ribosome 60S acidic ribosomal protein P2-3	up
RPL34	AT1G69620	RPL34_1	-2.148	5.75E-03	down	RPL34	-2.171	down	ribosome 60S ribosomal protein L34-2	down
RPL26B	At5g67510	RPL26B_1	-2.139	4.28E-03	down	RPL26B	-2.165	down	ribosome 60S ribosomal protein L34-2	down
AT1G22270	AT1G22270	AT1G22270_1	-2.237	3.37E-03	down	AT1G2227	-2.263	down	ribosome biogenesis 18S RNA processing WBSCR22-TRMT112 complex subunit tRNA methyltrans	down
RH55	At1g71280	RH55_1	55.668	0.04526	up	RH55	12.549	up	ribosome biogenesis 60S assembly	up
AT2G45100	AT2G45100	AT2G45100_2	73.985	0.0325	up	AT2G4510	2.2477	up	ribosome biogenesis BRF1 homolog, subunit of RNA polymerase III transcription initiation factor	up
AT3G27550	AT3G27550	-				AT3G2755	2.1295	up	ribosome biogenesis CRS1_YhbY domain RNA binding coiled coil protein	up
AT3G01160	AT3G01160	AT3G01160_1	2.4416	4.91E-03	up	AT3G0116	2.4225	up	ribosome biogenesis ESF1, nucleolar pre-rRNA processing protein, homolog	up
TCP19	At5g51910	TCP19_2	-6.853	0.01493	down	TCP19	-2.017	down	ribosome biogenesis leaf development TCP19	down
AT3G12860	AT3G12860	AT3G12860_1	3.5274	0.02379	up	AT3G1286	3.5158	up	ribosome biogenesis NOP56-like pre RNA processing ribonucleoprotein	up
AT2G39240	AT2G39240					AT2G3924	4.3133	up	ribosome biogenesis RNA polymerase I specific transcription initiation factor RRN3	up
TCTP1	At3g16640	TCTP1_1	-2.182	6.86E-03	down	TCTP1	-2.209	down	ribosome biogenesis TOR signaling TCTP translationally controlled tumor protein homolog	down
EMB2777	AT2G43650	EMB2777_1	2.296	2.30E-03	up	EMB2777	2.2778	up	ribosome biogenesis Utp3/Sas19 U3 snRNP protein exosome-associated protein required for th	up
RH51	At3g18600	RH51_1	2.0521	7.37E-03	up	RH51	2.0401	up	ribosome biogenesis yeast HAS1 homolog	up
LSG1-2	At1g08410	LSG1-2_1	2.086	0.01609	up	LSG1-2	2.0732	up	ribosome biogenesis, auxin, root and leaf development	up
OLI2	AT5G55920	OLI2_1	2.0369	9.31E-03	up	OLI2	2.0243	up	ribosome biogenesis, cell cyle, NOP2, role on organ size control by promoting cell proliferation	up
AT1G13160	AT1G13160	AT1G13160_1	2.0536	0.01521	up	AT1G1316	2.0395	up	ribosome biogenesis, cell cyle, NUC130 domain	up
AT3G10530	AT3G10530	AT3G10530_1	2.1692	0.03236	up	AT3G1053	2.1551	up	ribosome biogenesis, cell division Utp7 homolog CUL4 E3 ligase subunit	up
NSN1	AT3G07050	NSN1_1	2.0521	6.54E-03	up	NSN1	2.0389	up	ribosome biogenesis, meristem, floral organ, leaf etc. development nucleolar GTPase nucleost	up
RPL27A	AT1G23290	RPL27A_1	-2.468	0.01339	down	RPL27A	-2.496	down	ribosome growth leaf development RIBOSOMAL PROTEIN L27A; RPL27A	down
AT1G79150	AT1G79150	AT1G79150_1	2.694	1.50E-03	up	AT1G7915	2.676	up	ribosome maturation and transport NOC3 nucleolar complex associated 3 homolog	up
AT1G24240	AT1G24240					AT1G2424	-2.013	down	ribosome Ribosomal protein L19	down
AT1G27350	AT1G27350					AT1G2735	-2.022	down	ribosome, Ribosome associated membrane protein RAMP4	down
AT3G19090	AT3G19090	-				AT3G1909	2.2902	up	RNA polIII LA TF homolog RNA binding protein	up
ATCTH	AT2G25900	ATCTH_1	-2.08	9.39E-03	down	ATCTH	-2.105	down	RNA decay ABA GA salt stress DNA/RNA binding ATCTH Zinc finger C-x8-C-x5-C-x3-H protein	down
NRPA1	AT3G57660	NRPA1_1	2.0571	8.71E-03	up	NRPA1	2.0477	up	RNA pol I largest sbunit ribosome RNA transcription	up
AT4G20340	AT4G20340					AT4G2034	2.0238	up	RNA pol II Transcription factor TFIIE, alpha subunit	up
NRPB5L1	At5g57980					NRPB5L1	2.5164	up	RNA polII RPB5C RNA polymerase II fifth largest subunit, C	up
APUM24	AT3G16810	APUM24_1	2.0352	0.01568	up	APUM24	2.0215	up	RNA stability nucleolar, RNA 3' UTR binding protein	up
AT2G16005	AT2G16005	AT2G16005_1	-4.426	2.68E-04	down	AT2G1600	-4.481	down	root auxin transport gravitropism synaptotagmin-1 interacting ML-domain protein ROSY1	down
BOR2	AT3G62270	BOR2_1	2.1661	7.35E-03	up	BOR2	2.1517	up	root boron exporter BOR2	up
AT5G54370	AT5G54370	AT5G54370_1	-4.161	2.76E-03	down	AT5G5437	-4.199	down	root cap, cell death, Root_cap domain protein with signal peptide	down
NPF2.4	At3g45700	-				NPF2.4	-2.78	down	root chloride NITRATE EXCRETION TRANSPORTER, NPF2.4	down
OCT1	AT1G73220	OCT1_1	4.8597	0.01751	up	OCT1	4.8026	up	root development carnitine transporter	up
RCH2	AT3G24240	RCH2_1	2.7825	0.04711	up	RCH2	2.7626	up	root development RGI1 (RGF1 Insensitive 1) LRRK	up
ATHB-52	AT5G53980	-				ATHB-52	-3.016	down	root elongation ethylene controlled HB52 homeobox protein 52 TF	down
RALF1	AT1G02900	RALF1_1	-2.198	9.18E-03	down	RALF1	-2.228	down	root elongation lateral root development, negative regulator BR antagonist peptide	down
ANR1	AT2G14210	-				ANR1	-2.254	down	root elongation nitrate dependent MADS TF AGL44 AGAMOUS-like 44	down
ERF071	At2g47520	ERF071_1	5.5269	0.01524	up	ERF071	5.4789	up	root elongation, DER/CRT-binding TF induced by hypoxia and osmotic stress	up
POT5	At4g13420	-				POT5	2.4256	up	root growth salt HAK5 high affinity K+ transporter 5	up
BLOS2	AT5G49550	-				BLOS2	-2.09	down	root growth vesicular transprot BLOS2 interactor of SNX1 on sorting endosomes	down
IRE	AT5G62310	-				IRE	3.314	up	root hair elongation INCOMPLETE ROOT HAIR ELONGATION IRE protein kinase	up
AT1G66800	AT1G66800	-				AT1G6680	-3.652	down	root hair UDP-sugar epimerase	down
RGF2	AT1G13620	-				RGF2	-4.633	down	root merisetm growth factor	down
RCH1	At5g48940	-				RCH1	2.1835	up	root meristem growth factor RGF1 receptor RGF1 INSENSITIVE 2, RGFR2, RGI2	up
WOX5	AT3G11260					WOX5	3.5327	up	root meristem stem cell niche WOX5 WUSCHEL related homeobox 5	up
AT2G28620	AT2G28620	-				AT2G2862	2.358	up	root microtubule kinesin motor with coiled coil	up
NPF5.3	At5g46040					NPF5.3	-4.11	down	root specific proton-dependent oligopeptide transporter (POT)	down
ERF035	At3g60490	ERF035_1	-3.457	0.04383	down	ERF035	-3.502	down	root stele DREB subfamily A-4 of ERF/AP2 TF ERF35, predicted regulator of TOM6 (TARGET OF MON	down
SWEET2	AT3G14770	SWEET2_1	-2.19	0.04437	down	SWEET2	-2.228	down	root vacuolar sugar transproter SWEET2	down
NHX6	AT1G79610	-				NHX6	2.0569	up	salt pH endosomal Na(+)/H(+) antiporter	up
CIPK11	AT2G30360	CIPK11_1	-2.305	4.10E-03	down	CIPK11	-2.339	down	salt pH Plasmamembrane proton transporter ATPase kinase SOS2 interacting protein SIP4	down
CNGC19	AT3G17690					CNGC19	4.6745	up	salt regulated unknown CNGC19 cyclic nucleotide gated channel 19	up
CHX4	AT3G44900					CHX4	2.8199	up	salt sodium-proton exchanger CHX4	up
AT5G44260	AT5G44260	AT5G44260_1	-3.112	8.55E-06	down	AT5G4426	-3.131	down	seed germination inhibitor andem CCCH Zinc Finger protein 5; TZF5 Zinc finger C-x8-C-x5-C-x3-H t	down
GER3	AT5G20630	GER3_1	-3.099	7.44E-03	down	GER3	-3.108	down	seed storage CUPIN domain protein with signal eptide cold, cytokinin induced	down
GLP9	AT4G14630	GLP9_1	-2.57	0.01578	down	GLP9	-2.597	down	seed storage CUPIN domain protein with signal peptide salt induced in roots	down
ATG8E	AT2G45170	ATG8E_1	-2.308	3.23E-03	down	ATG8E	-2.186	down	senescence leaf autophagy phosphatidylethanolamine binding AUTOPHAGY 8E protein	down
SRG1	AT1G17020	SRG1_1	2.1578	0.04695	up	SRG1	2.1349	up	senescence-induced	up
AT5G22390	AT5G22390	AT5G22390_1	-3.753	5.10E-03	down	AT5G2239	-3.815	down	shoot meristem growth WUS repressor FAF domain Fantastic Four meristem regulator homolog	down
HEN1	AT4G20910	HEN1_1	2.6234	0.02487	up	HEN1	2.258	up	silencing miRNA and siRNA methylase	up
AT3G48790	AT3G48790	-				AT3G4879	-2.289	down	sphingolipid biosynthesis SPT1 serine palmitoyltransferase 1	down
AT5G28390	AT5G28390					AT5G2839	2.2421	up	spliceosome associated hnRNP R, RRM domain protein	up
UBA1C	At2g19380	-				UBA1C	2.4454	up	spliceosome associated UBP1 interacting protein 1c	up
BRR2B	AT2G42270	BRR2B_1	2.4368	8.90E-03	up	BRR2B	2.4222	up	spliceosome BRR1 U5 small nuclear ribonucleoprotein 200kDa	up
STIPL2	At2g42330	STIPL2_2	105.82	0.02563	up	STIPL2	2.3169	up	spliceosome disassembly protein Ntr1 GC-rich DNA-binding factor-like with Tuftelin interacting	up
GFL	At5g25230	GFL_2	10.847	0.04483	up	GFL	8.481	up	spliceosome MEE5 homolog gametophyte factor 2 U5 snRNP GTPase SNU114	up
CYP19-2	AT2G21130	CYP19-2_1	-3.053	0.02128	down	CYP19-2	-3.055	down	spliceosome NTC associated atCypE1a/CYP2 Peptidyl-prolyl cis-trans isomerase CYP19-2	down
AT5G45990	AT5G45990					AT5G4599	3.8566	up	spliceosome NTC subunit atCRN1a putative crooked neck protein / cell cycle protein	up
PRL1	AT4G15900	PRL1_1	-2.294	1.39E-03	down	PRL1	-2.312	down	spliceosome NTC subunit PRL1	down
AT1G14640	AT1G14640	-				AT1G1464	2.4888	up	spliceosome U2snRNP subunit atSAP114-1b SWAP (Suppressor-of-White-APricot) domain	up

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AT4G38780	AT4G38780	-				AT4G3878	2.0679	up	spliceosome U5snRNP atU5-220/Prp8b Pre-mRNA-processing-splicing factor	up
MED37D	AT5G02490	MED37D_1	2.1851	8.12E-03	up	MED37D	2.1663	up	spliceosome, pathogen, NTC- associated HSC70-2 protein folding	up
ATO	AT5G06160	ATO_1	2.0419	8.96E-03	up	ATO	2.0265	up	spliceosome, U2 snRNP, gametophyte	up
ABCB14	AT1G28010	ABCB14_1	2.5407	7.05E-03	up	ABCB14	2.523	up	stomata, malate importer controlling stomatal response to CO2	up
AT1G80180	AT1G80180	AT1G80180_1	-2.005	0.03516	down	AT1G8018	-2.039	down	stommatal division MAPK3/6 substrate	down
AT2G32210	AT2G32210					AT2G3221	-2.566	down	stress induced CYSTM domain short cysteine-rich membrane protein	down
NUDT13	At3g26690	NUDT13_2	-2.882	0.04535	down	NUDT13	-2.163	down	stress signalling mitochondrion plant pyrophosphatase catalyzing the hydrolysis of long-chain d	down
AT3G22235	AT3G22235	AT3G22235_2	15.402	0.02654	up	AT3G2223	4.1337	up	stress tolerance THCYSTM8, CYSTEINE-RICH TRANSMEMBRANE MODULE 8 protein	up
SUS4	AT3G43190	-				SUS4	2.4108	up	sucrose uptake sucrose synthase 4	up
ATL31	AT5G27420	ATL31_1	-2.442	0.01848	down	ATL31	-2.464	down	sugar sensing HighC/N ratio membrane-bound RING E3 with signal peptide	down
SWEET16	AT3G16690	SWEET16_3	-2.244	0.01026	down	SWEET16	-2.22	down	sugar transport growth under stress conditions vacuolar sugar carrier AtSWEET16	down
SUC7	AT1G66570					SUC7	-9.074	down	sugar transport sucrose-proton symporter 7	down
SWEET4	AT3G28007					SWEET4	-3.178	down	sugar transport to sink SWEET4 facilitator	down
STP12	AT4G21480					STP12	-2.009	down	sugar transporter 12	down
ULP1B	AT4G00690					ULP1B	2.3453	up	SUMO desumoylation enzyme ULP1B UB-like protease 1B	up
AT5G45570	AT5G45570					AT5G4557	5.3865	up	SUMO protease C48 (Ulp1 endopeptidase family, clan CE)	up
REM2	At4g31615	-				REM2	3.1498	up	transcription B3 domain repeat TF	up
ERF054	At4g28140					ERF054	-2.836	down	transcription DREB subfamily A-6 of ERF/AP2 ERF54	down
AGL46	AT2G28700					AGL46	6.132	up	transcription AGL46 AGAMOUS-like 46 MADS TF	up
AT2G46040	AT2G46040	AT2G46040_1				AT2G4604	2.1259	up	transcription ARID adn ELM2 domain TF	up?
WRKY43	AT2G46130	-				WRKY43	-5.536	down	transcription ARID-ELM2 domain TF	down?
AT4G38062	AT4G38062					AT4G3806	2.0161	up	transcription bHLH131 TF	up
AtbZIP5	AT3G49760					AtbZIP5	-3.11	down	transcription bZIP5 basic leucine-zipper 5	down
AtbZIP6	AT2G22850	AtbZIP6_2	-2.338	0.04628	down	AtbZIP6	-2.381	down	transcription bZIP6	down
HAP2C	AT1G72830					HAP2C	2.2311	up	transcription CCAATbox TF complex subunit HAP2C; NF-YA3	up
NFYA5	AT1G54160	-				NFYA5	2.2857	up	transcription CCAATbox TF complex subunit NF-YA5	up
RAP2-10	At4g36900					RAP2-10	-2.007	down	transcription DEAR4; DREB AND EAR MOTIF PROTEIN 4 RAP2-10 ERF009 TF	down
ERF023	At1g01250	-				ERF023	-2.091	down	transcription ERF023 AP2 TF	down
ERF13	AT2G44840					ERF13	-2.53	down	transcription ERF13, ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13 subfamily B-3 of ERF/AP	down
AT4G25400	AT4G25400	-				AT4G2540	-2.319	down	Transcription factor bHLH118	down
AT5G51790	AT5G51790	AT5G51790_1	-5.463	3.60E-04	down	AT5G5179	-4.909	down	Transcription factor bHLH120	down
ZHD14	AT1G14687	-				ZHD14	-2.188	down	transcription flower development homeobox 32 ZF-HD_dimer domain protein	down
HDG4	AT4G17710					HDG4	13.726	up	transcription HDG4 homeodomain GLABROUS 4 TF	up
AT1G77570	AT1G77570					AT1G7757	-2.067	down	transcription Heat shock factor (HSF) is a transcriptional activator of heat shock genes	down
HDG8	AT3G03260					HDG8	5.4518	up	transcription HOMEODOMAIN GLABROUS 8 TF	up
IQM5	At5g57010					IQM5	-3.514	down	transcription microtubule associated IQ domain protein	down
IQD16	AT4G10640	-				IQD16	2.9681	up	transcription microtubule associated IQD16 IQ and calmodulin binding DUF4005 domain protei	up
iqd33	AT5G35670					iqd33	2.2366	up	transcription microtubule associated iqd33 IQ-domain 33 protein	up
TRFL10	AT5G03780					TRFL10	2.5614	up	transcription MYB TF with PHD domain	up
MYB49	AT5G54230					MYB49	-2.147	down	transcription MYB49 myb domain protein 49 TF	down
anac044	AT3G01600	anac044_1	9.3268	3.54E-08	up	anac044	9.2726	up	transcription NAC TF unknown	up
AGL94	AT1G69540	AGL94_2	58.515	0.0434	up	AGL94	4.0388	up	transcription pollen specific AGAMOUS-like 94 MADS TF	up
AT5G06250	AT5G06250	AT5G06250_4	51.97	5.96E-03	up	AT5G0625	5.0636	up	transcription polycomb/topless interacting TF seed size	up?
MEE14	AT2G15890	MEE14_2	-2.052	0.03964	down	MEE14	-2.065	down	transcription proposed TBP1 Mediator binding protein CCG BINDING PROTEIN1 (CBP1) specifying	down
RL5	AT1G19510	-				RL5	-3.076	down	transcription RADIALIS-LIKE SANT/MYB 4; RSM4	down
OFP17	AT2G30395	-				OFP17	-2.67	down	transcription repressor OFP17 ovate family protein 17	down
SPEAR1	At2g20080					SPEAR1	-4.255	down	transcription repressor TCP Interactor containing EAR motif protein 2	down
AT5G36740	AT5G36740	AT5G36740_5	9.0285	0.01744	up	AT5G3674	2.0998	up	transcription TF with RING/FYVE/PHD-type zinc finger and Acyl-CoA N-acyltransferase domains	up
AHL24	AT4G22810					AHL24	-2.152	down	transcription unknown AT-hook motif protein	down
AT4G30130	AT4G30130					AT4G3013	2.0972	up	transcription unknown bZIP TF	up
AT2G23530	AT2G23530					AT2G2353	2.3156	up	transcription zf-4CXXC_R1 repressor domain protein	up
AT2G01818	AT2G01818					AT2G0181	-2.36	down	transcription, B-Box-type zinc finger amd PLATZ TF	down
NFYA10	At5g06510	NFYA10_1	182.03	9.54E-03	up	NFYA10	2.5918	up	transcription, CCAAT-binding complex subunit NFYA10	up
NFYA6	At3g14020	NFYA6_2	2.2763	0.02011	up	NFYA6	2.334	up	transcription, CCAAT-binding complex subunit NFYA6	up
AT2G46670	AT2G46670					AT2G4667	-2.263	down	transcription, CCT (CONSTANS, CO-like, and TOC1) domain protein	down
ERF060	At4g39780	ERF060_1	-2.211	8.22E-03	down	ERF060	-2.243	down	transcription, DREB subfamily A-6 ERF/AP2 TF ERF060	down
GATA4	AT3G60530	GATA4_1	-2.061	3.03E-03	down	GATA4	-2.076	down	transcription, GATA4 ZnF_GATA domain TF	down
AT5G38690	AT5G38690	-				AT5G3869	2.3214	up	transcription, homolog of R1 transcription factor repressor of monoamine oxidase A	up
anac074	AT4G28530	anac074_1	48.521	4.12E-03	up	anac074	5.4533	up	transcription, TOPLESS interacting NAC074 TF	up
AT2G02060	AT2G02060					AT2G0206	-2.038	down	transcription, unknown MYB TF	down
DOF1.6	AT1G47655	-				DOF1.6	-2.721	down	transcription, unknown zf-Dof domain TF Dof1.6	down
REM10	At2g24700					REM10	2.3375	up	transcriptionunknown B3 domain repeat TF	up
AT4G27130	AT4G27130	AT4G27130_1	-2.176	4.54E-03	down	AT4G2713	-2.191	down	translation EIF1B eukaryotic translation initiation factor 1B	down
AT5G39900	AT5G39900					AT5G3990	2.1235	up	translation GTP-binding Elongation factor EF2 (EF-G)	up
TIF3C2	AT3G22860	TIF3C2_1	16.787	7.27E-04	up	TIF3C2	16.628	up	translation initiation factor 3 subunit C2	up
AT1G53880	AT1G53880	AT1G53880_1	2.0126	0.03411	up	AT1G5388	2.0043	up	translation initiation factor IF-2B, subunit 1 alpha, 26kDa	up
PAB7	AT2G36660					PAB7	3.7247	up	translation PAB7 poly(A) binding protein 7	up
AT3G26130	AT3G26130	AT3G26130_3				AT3G2613	5.722	up	transmembrane cellulase	up?
AT3G21000	AT3G21000					AT3G2100	11.363	up	transposon gag-polypeptide of LTR copia-type	up
ATHB-X	AT1G70920	-				ATHB-X	-2.927	down	trasncription HB18 homeobox-leucine zipper protein 18	down
TPPD	AT1G35910	TPPD_1	5.2794	0.04496	up	TPPD	5.2106	up	trehalose, salt stress	up
AT4G40000	AT4G40000					AT4G4000	2.0471	up	tRNA and ribosomal RNA (cytosine-5-)-methyltransferase TRM4A	up
AT1G78190	AT1G78190	-				AT1G7819	-2.173	down	tRNA methyltranferase Trm112p-like	down
AT5G40630	AT5G40630					AT5G4063	-2.695	down	ubiquitin	down
AT1G52450	AT1G52450					AT1G5245	2.3157	up	Ubiquitin carboxyl-terminal hydrolase	up
AT5G51530	AT5G51530					AT5G5153	5.7303	up	Ubiquitin carboxyl-terminal hydrolase with DUF627 and DUF629 domains	up
ARI3	AT3G27710					ARI3	5.5777	up	ubiquitin ligase RING E3 with IBR domains ARI3, ARIADNE 3	up
AT3G20710	AT3G20710	AT3G20710_1	14.548	0.0374	up	AT3G2071	14.405	up	ubiquitin SCF E3 ligase F-box with jancalin like lectin domain	up
AT2G24255	AT2G24255	AT2G24255_1	50.447	0.04967	up	AT2G2425	50.347	up	ubiquitin SCF E3 ligase F-box/kelch-repeat protein	up?

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AT4G00893	AT4G00893	AT4G00893_1	55.727	0.04021	up	AT4G0089	55.308	up	ubiquitin SCF E3 ligase F-box/kelch-repeat protein	up
AT1G77710	AT1G77710	AT1G77710_1	-2.047	0.01037	down	AT1G7771	-2.076	down	ubiquitin, CPP2 UMF1 ubiquitin-like protein	down
AT3G56230	AT3G56230					AT3G5623	-2.178	down	ubiquitination CUL3 E3 ligase BTB/POZ subunit	down
FBL11	At2g36370					FBL11	2.0741	up	ubiquitination CUL3 E3 ligase LRR repeat BTB/POZ subunit	up
AT1G53790	AT1G53790					AT1G5379	2.4598	up	ubiquitination N-terminal nucleophile aminohydrolase SCF E3 F-box protein	up
ARI13	AT5G63750	ARI13_1	165.5	8.34E-03	up	ARI13	164.25	up	ubiquitination RING (cl17238) domain ubiquitin ligase	up
AT1G24800	AT1G24800					AT1G2480	6.6584	up	ubiquitination SCF E3 F-box protein	up
AT1G30920	AT1G30920					AT1G3092	8.7579	up	ubiquitination SCF E3 F-box protein	up
AT1G48400	AT1G48400					AT1G4840	3.9945	up	ubiquitination SCF E3 F-box protein	up
AT1G24881	AT1G24881					AT1G2488	-2.378	down	ubiquitination SCF E3 F-box protein	down
AT1G10110	AT1G10110					AT1G1011	2.2471	up	ubiquitination SCF E3 F-box protein with C-type lectin (CTL) or carbohydrate-recognition domain	up
AT2G17036	AT2G17036					AT2G1703	2.214	up	ubiquitination SCF E3 F-box protein with DUF295 domain	up
AT5G60060	AT5G60060					AT5G6006	-5.095	down	ubiquitination SCF E3 F-box protein with DUF295 domain	down
AT5G50450	AT5G50450	AT5G50450_1	-2.277	0.02469	down	AT5G5045	-2.282	down	ubiquitination SCF E3 F-box protein with TPR and zf-MYND zinc finger domains	down
AT3G23880	AT3G23880	AT3G23880_1	-3.696	2.05E-04	down	AT3G2388	-3.742	down	ubiquitination SCF E3 F-box subunit CPR1 (Constitutive Expresser of PR Genes 1) homolog	down
AT5G07610	AT5G07610	-				AT5G0761	6.4502	up	ubiquitination SCF E3 Galactose oxidase domain F-box protein	up
JAL38	At3g59610					JAL38	3.1177	up	ubiquitination SCF E3 Jacalin domain F-box protein	up
AT5G26960	AT5G26960	AT5G26960_1	-2.078	0.01026	down	AT5G2696	-2.098	down	ubiquitination SCF E3 Kelch repeat F-box protein	down
AT3G14710	AT3G14710					AT3G1471	6.3147	up	ubiquitination SCF E3 LRR F-box protein	up
AT5G60610	AT5G60610					AT5G6061	2.1594	up	ubiquitination SCF E3 LRR repeat F-box protein	up
AT2G24240	AT2G24240	AT2G24240_1	-2.041	0.03121	down	AT2G2424	-2.069	down	ubiquitination unknown CUL3 E3 BTB domain protein	down
AT5G02350	AT5G02350					AT5G0235	3.7405	up	ubiquitination unknown PHD zinc finger and RING repeat E3	up
AT1G14200	AT1G14200	AT1G14200_1	-2.101	0.02796	down	AT1G1420	-2.122	down	ubiquitination unknown RING E3	down
AT3G10815	AT3G10815					AT3G1081	-2.064	down	ubiquitination unknown RING E3	down
ATL66	AT3G11110					ATL66	-2.156	down	ubiquitination unknown RING E3	down
AT3G51325	AT3G51325					AT3G5132	-3.187	down	ubiquitination unknown RING E3	down
AT4G00305	AT4G00305					AT4G0030	-3.7	down	ubiquitination unknown RING E3	down
AT3G47160	AT3G47160	AT3G47160_1	-2.496	2.48E-03	down	AT3G4716	-2.246	down	ubiquitination unknown RING E3	down?
AT2G45135	AT2G45135					AT2G4513	6.8681	up	ubiquitination unknown RING E3	up
AT5G64880	AT5G64880	AT5G64880_1	-2.104	0.01469	down	AT5G6488	-2.124	down	uknown membrane protein	down
AT4G05380	AT4G05380	AT4G05380_1	26.159	0.02057	up	AT4G0538	25.988	up	unknow DnaC (COG1484) domain ATPase protein	up
AT4G30250	AT4G30250	AT4G30250_1	2.5654	0.04657	up	AT4G3025	2.462	up	unknow DnaC (COG1484) domain ATPase protein	up
PCMP-E66	At1g69350					PCMP-E66	2.1363	up	unknown Pentatricopeptide repeat protein	up
PCMP-E74	At2g04860					PCMP-E74	3.1945	up	unknown Pentatricopeptide repeat protein	up
PCMP-H77	At3g49142					PCMP-H77	2.0457	up	unknown Pentatricopeptide repeat protein	up
PCMP-H89	At5g13230					PCMP-H89	2.7397	up	unknown Pentatricopeptide repeat protein	up
PCMP-H70	At1g71420					PCMP-H70	2.3249	up	unknown Pentatricopeptide repeat protein	up
AT1G74630	AT1G74630					AT1G7463	2.4283	up	unknown Pentatricopeptide repeat protein	up
AT2G19530	AT2G19530					AT2G1953	2.2088	up	unknown transmembrane protein	up
AT2G01580	AT2G01580					AT2G0158	-2.111	down	unknown transmembrane protein	down
RDL4	At4g11310					RDL4	-3.237	down	unknown CP1, CYSTEINE PROTEASE 1	down
AT5G02830	AT5G02830	AT5G02830_1	2.1452	0.01414	up	AT5G0283	2.1214	up	unknown Pentatricopeptide repeat protein	up
AT1G61550	AT1G61550					AT1G6155	3.5485	up	unknown S-locus lectin protein kinase	up
AT1G53620	AT1G53620					AT1G5362	-2.14	down	unknown 101aa oligopeptide with transmembrane domain	down
AT3G26395	AT3G26395	AT3G26395_1	-2.354	0.03356	down	AT3G2639	-2.381	down	unknown 24aa oligopeptide	down
AT1G53887	AT1G53887					AT1G5388	-2.283	down	unknown 31aa peptide	down
AT1G30757	AT1G30757					AT1G3075	-3.818	down	unknown 34aa peptide with transmembrane domain	down
AT5G03204	AT5G03204					AT5G0320	-7.7	down	unknown 36aa oligopeptide	down
AT1G29465	AT1G29465	AT1G29465_1	-3.325	3.40E-03	down	AT1G2946	-3.374	down	unknown 36aa transmembrane peptide	down
AT1G15625	AT1G15625					AT1G1562	-7.043	down	unknown 4 transmembrane domain protein	down
AT2G14460	AT2G14460	AT2G14460_1	-2.401	0.01532	down	AT2G1446	-2.43	down	unknown 41aa oligopeptide	down
AT3G13857	AT3G13857					AT3G1385	-2.578	down	unknown 42aa oligopeptide	down
AT5G21020	AT5G21020	AT5G21020_1	-2.574	1.63E-03	down	AT5G2102	-2.609	down	unknown 42aa transmembrane oligopeptide	down
AT1G43605	AT1G43605					AT1G4360	3.5106	up	unknown 43aa oligopeptide	up
AT3G24100	AT3G24100	AT3G24100_1	-2.216	5.46E-03	down	AT3G2410	-2.244	down	unknown 4F5domain protein	down
AT1G47395	AT1G47395					AT1G4739	3.0511	up	unknown 50aa oligopeptide	up
AT1G47400	AT1G47400					AT1G4740	2.3812	up	unknown 50aa oligopeptide	up
AT4G34881	AT4G34881					AT4G3488	-2	down	unknown 50aa oligopeptide with transmembrane domain	down
AT3G26742	AT3G26742					AT3G2674	-2.44	down	unknown 51aa oligopeptide	down
AT3G17626	AT3G17626					AT3G1762	-2.032	down	unknown 51aa oligopeptide with domain homology to 50S ribosomal protein L1	down
AT5G27889	AT5G27889					AT5G2788	3.1175	up	unknown 53aa oligopeptide	up
AT3G05937	AT3G05937	AT3G05937_1	-2.066	0.03287	down	AT3G0593	-2.096	down	unknown 53aa oligopeptide	down
AT1G32570	AT1G32570					AT1G3257	3.1295	up	unknown 55aa oligopeptide	up
AT5G10946	AT5G10946					AT5G1094	-2.766	down	unknown 55aa oligopeptide	down
AT1G04778	AT1G04778					AT1G0477	-2.265	down	unknown 56aa oligopeptide	down
AT1G49032	AT1G49032	AT1G49032_1	-2.618	3.73E-04	down	AT1G4903	-2.65	down	unknown 57aa oligopeptide with signal peptide	down
AT4G17085	AT4G17085					AT4G1708	-2.151	down	unknown 57aa transmembrane oligopeptide	down
AT5G22796	AT5G22796					AT5G2279	3.3504	up	unknown 58aa oligopeptide	up
AT1G55152	AT1G55152	AT1G55152_1	-2.225	3.68E-03	down	AT1G5515	-2.248	down	unknown 59aa oligopeptide	down
AT4G12735	AT4G12735					AT4G1273	5.2586	up	unknown 60aa oligopeptide with signal peptide	up
AT5G42110	AT5G42110	AT5G42110_1	-2.108	0.02591	down	AT5G4211	-2.134	down	unknown 62aa oligopeptide	down
AT5G54145	AT5G54145	AT5G54145_1	-2.223	0.01432	down	AT5G5414	-2.256	down	unknown 63 oligopeptide with signal peptide	down
AT1G49500	AT1G49500	AT1G49500_1	-3.171	1.80E-04	down	AT1G4950	-3.21	down	unknown 63aa oligopeptide	down
AT3G47836	AT3G47836	AT3G47836_2	-2.089	0.01284	down	AT3G4783	-2.114	down	unknown 64aa membrane oligopeptide	down
AT1G19960	AT1G19960					AT1G1996	-3.024	down	unknown 64aa oligopeptide	down
AT3G09162	AT3G09162					AT3G0916	-2.298	down	unknown 65 aa oligopeptide	down
AT1G03106	AT1G03106	-				AT1G0310	-3.193	down	unknown 65aa oligopeptide	down
AT1G68238	AT1G68238	AT1G68238_1	-2.356	0.03796	down	AT1G6823	-2.381	down	unknown 65aa transmembrane oligopeptide	down
AT1G21520	AT1G21520					AT1G2152	-2.429	down	unknown 66aa oligopeptide	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT5G50560	AT5G50560	-				AT5G5056	-2.767	down	unknown 67aa DUF3339 domain membrane protein	down
AT5G50660	AT5G50660					AT5G5066	-2.172	down	unknown 67aa DUF3339 domain protein	down
AT5G66052	AT5G66052	AT5G66052_1	-2.657	1.17E-04	down	AT5G6605	-2.682	down	unknown 67aa membrane oligopeptide	down
AT3G03020	AT3G03020	AT3G03020_1	-12.03	0.03689	down	AT3G0302	-2.016	down	unknown 67aa oligopeptide	down
AT5G10695	AT5G10695					AT5G1069	-2.178	down	unknown 67aa oligopeptide	down
AT2G20835	AT2G20835					AT2G2083	-3.457	down	unknown 68aa oligopeptide	down
AT5G40960	AT5G40960					AT5G4096	-2.022	down	unknown 68aa oligopeptide with DUF3339 domain	down
AT5G09225	AT5G09225	AT5G09225_1	-2.009	0.0169	down	AT5G0922	-2.035	down	unknown 68aa transmembrane oligopeptide	down
AT5G63500	AT5G63500	AT5G63500_1	-2.472	0.01186	down	AT5G6350	-2.511	down	unknown 69aa DUF3339 domain membrane anchored oligopeptide	down
AT2G24692	AT2G24692					AT2G2469	3.1177	up	unknown 69aa oligopeptide	up
AT2G13547	AT2G13547					AT2G1354	2.8019	up	unknown 70aa oligopeptide	up
AT3G07273	AT3G07273					AT3G0727	3.6581	up	unknown 70aa oligopeptide	up
AT3G52105	AT3G52105	AT3G52105_2	-2.533	6.05E-03	down	AT3G5210	-2.614	down	unknown 70aa oligopeptide with signal peptide	down
AT3G13432	AT3G13432					AT3G1343	-3.692	down	unknown 71aa oligopeptide with signal peptide	down
AT5G15537	AT5G15537					AT5G1553	2.3977	up	unknown 71aa oligopeptide with transmembrane domain	up
AT3G45730	AT3G45730	AT3G45730_1	-2.447	4.21E-03	down	AT3G4573	-2.482	down	unknown 72aa oligopeptide	down
AT1G24600	AT1G24600					AT1G2460	-2.146	down	unknown 72aa oligopeptide	down
AT5G65207	AT5G65207	AT5G65207_1	-2.235	0.01101	down	AT5G6520	-2.268	down	unknown 73aa oligopeptide	down
AT1G36622	AT1G36622					AT1G3662	-2.082	down	unknown 74aa oligopeptide with signal peptide	down
AT1G12805	AT1G12805					AT1G1280	2.3432	up	unknown 75aa oligopeptide	up
AT1G48330	AT1G48330					AT1G4833	-2.504	down	unknown 75aa oligopeptide	down
AT5G02550	AT5G02550					AT5G0255	-2.311	down	unknown 76aa oligopeptide	down
AT5G61412	AT5G61412					AT5G6141	2.0929	up	unknown 77aa oligopeptide	up
AT1G77885	AT1G77885					AT1G7788	-2.023	down	unknown 77aa oligopeptide	down
AT4G35905	AT4G35905					AT4G3590	-2.069	down	unknown 77aa oligopeptide with Trm112p domain	down
AT2G21820	AT2G21820					AT2G2182	-2.72	down	unknown 78aa oligopeptide	down
AT5G46871	AT5G46871					AT5G4687	-2.682	down	unknown 78aa oligopeptide with signal peptide	down
AT1G06010	AT1G06010	AT1G06010_1	-2.137	0.03671	down	AT1G0601	-2.16	down	unknown 78aa transmembrane oligopeptide	down
AT2G42885	AT2G42885					AT2G4288	-5.617	down	unknown 79aa oligopeptide with signal peptide	down
AT1G65510	AT1G65510					AT1G6551	-2.361	down	unknown 80aa oligopeptide with signal peptide	down
AT1G30250	AT1G30250					AT1G3025	-5.146	down	unknown 82aa oligopeptide	down
AT5G57887	AT5G57887	AT5G57887_1	-2.258	1.91E-03	down	AT5G5788	-2.283	down	unknown 82aa oligopeptide with signal peptide	down
AT5G15265	AT5G15265					AT5G1526	-2.49	down	unknown 83aa oligopeptide with signal peptide	down
AT5G28442	AT5G28442					AT5G2844	-2.151	down	unknown 84aa oligopeptide	down
AT5G02090	AT5G02090	AT5G02090_1	-2.487	6.81E-03	down	AT5G0209	-2.527	down	unknown 85aa oligopeptide	down
AT4G37295	AT4G37295					AT4G3729	-4.222	down	unknown 86aa oligopeptide	down
AT4G13860	AT4G13860	-				AT4G1386	-2.954	down	unknown 87aa oligopeptide with RNA binding RRM domain	down
AT2G05185	AT2G05185					AT2G0518	-2.659	down	unknown 88aa oligopeptide	down
AT4G16000	AT4G16000					AT4G1600	-2.976	down	unknown 89aa oligopeptide	down
AT5G44582	AT5G44582					AT5G4458	-2.423	down	unknown 92aa oligopeptide with signal peptide	down
AT1G53610	AT1G53610					AT1G5361	-3.113	down	unknown 94aa oligopeptide with transmembrane domain	down
AT2G31945	AT2G31945					AT2G3194	-2.076	down	unknown 95aa oligopeptide with transmembrane domain	down
AT4G36580	AT4G36580					AT4G3658	2.0153	up	unknown AAA-type ATPase with DUF3523 domain	up
EDA4	AT2G48140	EDA4_1	-2.235	0.01614	down	EDA4	-2.064	down	unknown AAI Plant lipid transfer protein / seed storage protein / trypsin-alpha amylase inhibitor	down
CAR10	AT2G01540	CAR10_1	-2.037	0.01523	down	CAR10	-2.061	down	unknown ABA regulated C2 Ca2+-dependent membrane-targeting module protein	down
SDR4	AT3G29250	SDR4_2	-2.907	2.29E-04	down	SDR4	-2.877	down	unknown ABA2 homolog polyketide and fatty acid synthase/short-chain dehydrogenase reducta	down?
PDR5	AT2G37280	PDR5_1	366.48	2.57E-03	up	PDR5	2.2893	up	unknown ABC membrane transporter	up
ABCA10	AT5G61740	ABCA10_1	187.54	6.46E-03	up	ABCA10	4.8608	up	unknown ABC transporter	up
ABCB11	AT1G02520	ABC11_2				ABCB11	2.131	up	unknown ABC transporter	up
ABCE1	AT3G13640	ABCE1_1	7.9983	0.04276	up	ABCE1	7.9439	up	unknown ABC transporter, interactor of DPB TRANSCRIPTION FACTOR	up
AT5G22460	AT5G22460					AT5G2246	2.7188	up	unknown Abhydrolase_1 domain protein with signal peptide	up
CXE9	AT2G45610	-				CXE9	-3.202	down	unknown Abhydrolase_3 domain protein Probable carboxylesterase 9	down
AT4G15730	AT4G15730	AT4G15730_2	617.09	3.61E-04	up	AT4G1573	2.7147	up	unknown AKIN11 and DDB1A interacting Zinc finger protein	up
SESA5	AT5G54740	SESA5_1	23.36	0.01537	up	SESA5	23.144	up	unknown albumin	up
AT4G00910	AT4G00910	-				AT4G0091	3.6569	up	unknown Alu tolerance malate transporter with Fusaric acid resistance protein domain	up
AT3G18670	AT3G18670	AT3G18670_1	59.274	0.043	up	AT3G1867	2.0472	up	unknown ankyrin repeat protein	up
AT5G54720	AT5G54720					AT5G5472	2.5956	up	unknown ankyrin repeat protein	up
AT1G11740	AT1G11740					AT1G1174	-2.215	down	unknown ankyrin repeat protein with GPCR_chapero_1 domain	down
AT3G45090	AT3G45090					AT3G4509	2.1238	up	unknown ATPase	up
AT3G28570	AT3G28570					AT3G2857	2.8132	up	unknown ATPase	up
AT2G18190	AT2G18190	AT2G18190_1	12.604	0.0126	up	AT2G1819	12.52	up	unknown ATPase DNA replication DnaC domain	up
AT5G40190	AT5G40190	AT5G40190_1	-2.073	7.51E-03	down	AT5G4019	-2.095	down	unknown auxin induced calmodulin binding 2'-5' RNA ligase domain protein	down
AT3G48620	AT3G48620					AT3G4862	7.8418	up	unknown Bac_surface_Ag domain protein	up
BGLU40	AT1G26560					BGLU40	2.0482	up	unknown BETA GLUCOSIDASE 40, BGLU40	up
AT1G06550	AT1G06550	AT1G06550_1	2.0639	7.64E-03	up	AT1G0655	2.0466	up	unknown blue light induced Enoyl-CoA hydratase/isomerase	up
DTX4	AT2G04070					DTX4	3.928	up	unknown boron induced membrane transporter	up
ARID2	AT4G11400					ARID2	3.2772	up	unknown BRIGHT, ARID (A/T-rich interaction domain) domain TF	up
AT4G11547	AT4G11547					AT4G1154	-2.026	down	unknown C1_3 domain containing 78aa oligopeptide	down
AT4G01200	AT4G01200					AT4G0120	-2.314	down	unknown C2 domain Ca2+-dependent membrane-targeting module protein	down
AT5G60250	AT5G60250	AT5G60250_1	6.9135	1.28E-07	up	AT5G6025	6.8687	up	unknown C3HC4-type RING finger TF	up
AT4G13440	AT4G13440					AT4G1344	-3.529	down	unknown Ca2+ binding EF hand protein with ZnF_ZZ domain	down
CML44	AT1G21550					CML44	-2.101	down	unknown Ca2+ binding EFh domain protein	down
AT1G64320	AT1G64320	AT1G64320_2	63.28	0.03913	up	AT1G6432	3.7317	up	unknown cadmium-induced coiled coil protein	up
AT2G43660	AT2G43660	-				AT2G4366	6.5712	up	unknown carbohydrate binding X8 domain protein with signal peptide	up
AT1G62630	AT1G62630					AT1G6263	2.2548	up	unknown CC-NBS-LRR protein	up
CCR4	AT5G47850					CCR4	-2.975	down	unknown CCR4 CRINKLY4 related 4 transmembrane receptor kinase	down
FAP3	AT1G53520	FAP3_1	-2.036	7.00E-03	down	FAP3	-2.056	down	unknown Chalcone isomerase domain protein	down
RHA1B	AT4G11360	RHA1B_1	-3.863	2.74E-06	down	RHA1B	-3.894	down	unknown chitin and cadmium induced RING E3	down
AT5G54710	AT5G54710	AT5G54710_1	3.0723	4.76E-03	up	AT5G5471	2.6135	up	unknown chloroplast kinesine-like	up

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT1G49940	AT1G49940	AT1G49940_3	50.447	0.04967	up	AT1G4994	8.5253	up	unknown chloroplast protein	up
AT1G52720	AT1G52720	AT1G52720_1	-2.022	0.0109	down	AT1G5272	-2.042	down	unknown chloroplast protein	down
AT2G18100	AT2G18100	AT2G18100_4	156.16	0.01175	up	AT2G1810	2.1226	up	unknown chloroplast transmembrane/coiled-coil protein (DUF726)	up
AT2G41040	AT2G41040	AT2G41040_1	2.0973	0.02553	up	AT2G4104	2.073	up	unknown chloroplast, methylase	up
DUF2	AT1G11420	-				DUF2	2.2925	up	unknown chromatin associated Aganet repeat and DUF724 domain protein	up
AT2G38600	AT2G38600	AT2G38600_2	-64.78	0.04528	down	AT2G3860	-2.146	down	unknown class B acid phosphatase of vegetative storage protein class (VPS25)	down
AT4G29270	AT4G29270	AT4G29270_1	-3.256	9.89E-05	down	AT4G2927	-3.296	down	unknown class B acid phosphatase with signal peptide	down
AT5G17160	AT5G17160	AT5G17160_1	3.7997	1.75E-03	up	AT5G1716	3.7902	up	unknown coiled coil protein	up
AT3G15550	AT3G15550					AT3G1555	2.5114	up	unknown coiled coil protein	up
AT5G61865	AT5G61865					AT5G6186	3.8412	up	unknown coiled coil protein	up
AT4G14840	AT4G14840					AT4G1484	2.609	up	unknown coiled coil protein	up
AT1G07985	AT1G07985					AT1G0798	-3.104	down	unknown coiled coil protein	down
AT1G10800	AT1G10800					AT1G1080	-3.06	down	unknown coiled coil protein	down
AT5G17460	AT5G17460					AT5G1746	-2.152	down	unknown coiled coil protein	down
AT3G57320	AT3G57320	AT3G57320_2	-2.442	8.00E-03	down	AT3G5732	-2.477	down	unknown coiled coil protein	down?
AT1G04030	AT1G04030	-				AT1G0403	2.3943	up	unknown coiled coil protein	up
AT5G21940	AT5G21940	AT5G21940_1	-3.406	5.87E-06	down	AT5G2194	-3.451	down	unknown CPK4 interacting protein	down
AT4G36700	AT4G36700					AT4G3670	4.0043	up	unknown Cupin_1 domain protein with signal peptide	up
AT4G28703	AT4G28703					AT4G2870	-2.812	down	unknown Cupin_3 domain protein	down
AT5G39150	AT5G39150	AT5G39150_1	-88.31	0.0324	down	AT5G3915	-88.91	down	unknown Cupin1 domain storage protein	down
CYP702A5	AT4G15393					CYP702A5	2.1744	up	unknown CYP702A5 cytochrome P450	up
CYP705A1	AT4G15330					CYP705A1	-3.42	down	unknown CYP705A1 cytochrome P450	down
CYP706A3	AT5G44620					CYP706A3	2.025	up	unknown CYP706A3 cytochrome P450	up
CP1	AT4G36880					CP1	2.2651	up	unknown cysteine proteinase1; RD21A-LIKE PROTEASE1; RDL1	up
AT2G12190	AT2G12190					AT2G1219	-3.523	down	unknown cytochrome P450	down
AT1G30260	AT1G30260	AT1G30260_1	-2.553	0.02687	down	AT1G3026	-2.595	down	unknown cytokinin induced protein	down
AT1G55390	AT1G55390					AT1G5539	2.6223	up	unknown DAG receptor C1 and metalloprotease domain PHD finger repeat protein	up
AT4G15070	AT4G15070	-				AT4G1507	2.4146	up	unknown Diacylglycerol (DAG) binding C1 domain repeat protein	up
AT4G19570	AT4G19570					AT4G1957	9.7349	up	unknown DnaJ domain chaperon with coiled coil domain	up
AT1G56300	AT1G56300					AT1G5630	-2.328	down	unknown DnaJ domain protein	down
AT2G42065	AT2G42065					AT2G4206	8.819	up	unknown DnaJ domain protein with coiled coil domain	up
AT3G02800	AT3G02800					AT3G0280	-2.174	down	unknown dual-specificity protein phosphatase with predicted MAP kinase phosphatase activity	down
AT4G01140	AT4G01140					AT4G0114	-2.537	down	unknown DUF1191 domain with signal peptide	down
AT3G15480	AT3G15480	AT3G15480_1	-2.444	3.12E-04	down	AT3G1548	-2.473	down	unknown DUF1218 domain protein with signal peptide	down
AT1G61065	AT1G61065					AT1G6106	-2.06	down	unknown DUF1218 domain protein with signal peptide	down
OBAP2A	At5g45690					OBAP2A	-3.19	down	unknown DUF1264 domain lipoprotein	down
AT5G25020	AT5G25020					AT5G2502	-2.623	down	unknown DUF1336 domain protein	down
AT5G67490	AT5G67490	AT5G67490_1	-2.104	6.40E-03	down	AT5G6749	-2.128	down	unknown DUF1674 domain protein	down
AT1G54095	AT1G54095					AT1G5409	-2.865	down	unknown DUF1677 domain protein	down
AT4G14819	AT4G14819					AT4G1481	-3.117	down	unknown DUF1677 domain protein	down
AT4G35720	AT4G35720					AT4G3572	-2.954	down	unknown DUF241 domain	down
AT3G51400	AT3G51400					AT3G5140	-2.084	down	unknown DUF241 domain protein	down
AT5G56060	AT5G56060					AT5G5606	3.1175	up	unknown DUF2431 domain protein	up
AT5G22550	AT5G22550					AT5G2255	2.1298	up	unknown DUF247 domain protein	up
AT2G32380	AT2G32380	AT2G32380_1	-2.095	0.03431	down	AT2G3238	-2.112	down	unknown DUF2781 domain protein	down
AT1G27580	AT1G27580					AT1G2758	2.1889	up	unknown DUF295 domain protein	up
AT5G52960	AT5G52960	AT5G52960_1	-2.017	7.39E-03	down	AT5G5296	-2.041	down	unknown DUF3143 domain protein	down
AT3G27027	AT3G27027					AT3G2702	-2.011	down	unknown DUF3339 domain 68aa oligopeptide	down
AT3G27030	AT3G27030					AT3G2703	-2.395	down	unknown DUF3339 domain protein	down
AT5G14110	AT5G14110					AT5G1411	-3.052	down	unknown DUF3339 domain protein	down
AT3G01940	AT3G01940					AT3G0194	-2.021	down	unknown DUF3339 domain transmembrane oligopeptide	down
AT2G19460	AT2G19460	AT2G19460_1	-2.141	0.03447	down	AT2G1946	-2.166	down	unknown DUF3511 domain protein	down?
AT1G63520	AT1G63520					AT1G6352	3.973	up	unknown DUF3527 domain protein	up
AT1G04490	AT1G04490					AT1G0449	4.1906	up	unknown DUF3527 domain protein	up
AT4G10265	AT4G10265					AT4G1026	2.6181	up	unknown DUF3774 domain protein	up
AT4G05070	AT4G05070	AT4G05070_1	-2.879	2.65E-05	down	AT4G0507	-2.908	down	unknown DUF3774 domain protein	down
AT2G14070	AT2G14070					AT2G1407	-2.237	down	unknown DUF3774 domain protein	down
AT5G45530	AT5G45530					AT5G4553	4.9371	up	unknown DUF4220 and DUF594 domain transmembrane protein	up
AT1G76600	AT1G76600	AT1G76600_1	-2.51	5.55E-03	down	AT1G7660	-2.547	down	unknown DUF4228 domain protein	down
AT3G03280	AT3G03280					AT3G0328	-3.295	down	unknown DUF4228 domain protein	down
AT3G50800	AT3G50800					AT3G5080	-2.28	down	unknown DUF4228 domain protein	down
AT5G17350	AT5G17350					AT5G1735	-2.25	down	unknown DUF4228 domain protein	down
AT5G67620	AT5G67620					AT5G6762	-2.446	down	unknown DUF4228 domain protein	down
AT4G23390	AT4G23390					AT4G2339	3.1177	up	unknown DUF4409 and DUF239 domain protein with signal peptide	up
AT1G50910	AT1G50910					AT1G5091	2.0391	up	unknown DUF4477 domain protein	up
AT5G16380	AT5G16380	AT5G16380_1	-2.412	0.02274	down	AT5G1638	-2.424	down	unknown DUF538 domain protein with signal peptide	down
AT4G22960	AT4G22960					AT4G2296	6.0412	up	unknown DUF544 domain protein	up
AT4G00390	AT4G00390					AT4G0039	4.4235	up	unknown DUF573 domain protein	up
AT5G44550	AT5G44550	AT5G44550_1	-2.448	1.80E-03	down	AT5G4455	-2.477	down	unknown DUF588 domain protein	down
AT4G37235	AT4G37235					AT4G3723	-5.031	down	unknown DUF588 domain protein	down
AT1G14160	AT1G14160					AT1G1416	-2.316	down	unknown DUF588 domain protein	down
AT3G50810	AT3G50810					AT3G5081	-2.247	down	unknown DUF588 domain protein	down
AT4G11655	AT4G11655					AT4G1165	-7.454	down	unknown DUF588 domain protein	down
AT4G19080	AT4G19080					AT4G1908	3.2746	up	unknown DUF594 domain protein	up
AT5G06990	AT5G06990					AT5G0699	-2.926	down	unknown DUF617 domain protein	down
AT1G02770	AT1G02770					AT1G0277	3.8954	up	unknown DUF626 domain protein	up
AT4G10200	AT4G10200	-				AT4G1020	16.945	up	unknown DUF659 domain with ZnF_TTF finger and Activator transposondimerization Dimer_Tnp	up
AT4G24310	AT4G24310	-				AT4G2431	-2.718	down	unknown DUF679 domain trasnmembrane protein DMP3, DUF679 DOMAIN MEMBRANE PROTEIN	down
AT5G45850	AT5G45850					AT5G4585	4.7947	up	unknown DUF688 domain protein	up

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT3G27475	AT3G27475					AT3G2747	7.0597	up	unknown DUF707 domain transmembrane protein	up
AT3G04860	AT3G04860	AT3G04860_1	-2.593	0.01646	down	AT3G0486	-2.62	down	unknown DUF868 domain protein	down
AT1G23790	AT1G23790					AT1G2379	2.9257	up	unknown DUF936 domain protein	up
EFL4	AT1G17455	-				EFL4	-2.395	down	unknown ELF4-like ELF4-L4 protein	down
AT4G16146	AT4G16146	AT4G16146_1	-5.024	0.03974	down	AT4G1614	-4.993	down	unknown Endosulfine domain protein	down
AT2G18193	AT2G18193	AT2G18193_1	9.4701	6.66E-16	up	AT2G1819	9.3987	up	unknown ER metal ion transporter ATPase	up
AT4G07820	AT4G07820	AT4G07820_1	-8.198	0.0479	down	AT4G0782	-8.215	down	unknown extracellular SCP / Tpx-1 / Ag5 / PR-1 / Sc7 family protein with signal peptide	down
AT3G03460	AT3G03460					AT3G0346	2.5087	up	unknown GLTSCR1 domain protein	up
AT1G01310	AT1G01310					AT1G0131	3.1175	up	unknown GLTSCR1 domain protein	up
AT2G05510	AT2G05510	AT2G05510_2	-5.2	0.04442	down	AT2G0551	-5.181	down	unknown glycine-rich protein	down
AT3G60990	AT3G60990					AT3G6099	-4.876	down	unknown Glyco_transf_92 domain protein	down
AT4G39670	AT4G39670					AT4G3967	-2.141	down	unknown Glycolipid transfer protein (GLTP)	down
AT4G31875	AT4G31875					AT4G3187	-2.004	down	unknown glycosidase	down
GAUT2	AT2G46480	GAUT2_2				GAUT2	21.609	up	unknown glycosyltransferase Glyco_transf_8 domain protein	up?
AT2G32090	AT2G32090	AT2G32090_2	-2.372	4.57E-03	down	AT2G3209	-2.279	down	unknown Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily protein	down
AT1G38065	AT1G38065	AT1G38065_2	10.314	0.04622	up	AT1G3806	9.5187	up	unknown Golgi GDP-fucose protein O-fucosyltransferase	up?
AT4G32290	AT4G32290	AT4G32290_1	-2.057	0.04252	down	AT4G3229	-2.068	down	unknown Golgi glycosyltransferase family 14 protein with signal peptide	down
AT5G23350	AT5G23350	AT5G23350_1	-4.177	0.04202	down	AT5G2335	-4.236	down	unknown GRAM domain protein	down
AT5G23360	AT5G23360					AT5G2336	-2.1	down	unknown GRAM domain protein	down
DGP2	AT4G10650					DGP2	2.2458	up	unknown GTP binding MMR_HSR1 domain protein	up
AT1G29100	AT1G29100					AT1G2910	-2.026	down	unknown heavy metal transporter with HMA domain	down?
AT3G48770	AT3G48770					AT3G4877	2.8908	up	unknown Histidine kinase-like ATPase with DNA binding BED zinc finger	up
AT5G62720	AT5G62720	AT5G62720_1	-2.402	0.03613	down	AT5G6272	-2.325	down	unknown HPP domain transmembrane protein	down
AT1G76780	AT1G76780					AT1G7678	2.3433	up	unknown HSP20-like chaperone with coiled coil domains	up
AT2G41730	AT2G41730	AT2G41730_1	2.2624	0.02773	up	AT2G4173	2.2368	up	unknown hypoxia peroxide induced calcium-binding site protein	up
AT5G64910	AT5G64910	AT5G64910_4	184.79	9.04E-03	up	AT5G6491	2.3956	up	unknown kinase	up
AT4G26660	AT4G26660					AT4G2666	2.1998	up	unknown Kinesin-related domain protein	up
AT2G29310	AT2G29310	AT2G29310_2	-2.533	4.33E-03	down	AT2G2931	-2.105	down	unknown KR domain protein	down
AT2G29170	AT2G29170					AT2G2917	-2.083	down	unknown KR domain protein	down
UNE15	AT4G13560	UNE15_2	-3.952	7.62E-03	down	UNE15	-3.983	down	unknown Late embryogenesis abundant protein UNE15, UNFERTILIZED EMBRYO SAC 15	down
AT1G20530	AT1G20530					AT1G2053	3.038	up	unknown leucine zipper DUF630 and DUF32 domain protein girdin	up
AT1G67720	AT1G67720					AT1G6772	2.0162	up	unknown Leucine-rich repeat receptor kinase	up
AT2G31540	AT2G31540					AT2G3154	-2.316	down	unknown Lipase_GDSL domain protein with signal peptide	down
AT1G74460	AT1G74460	AT1G74460_1	-2.228	7.50E-03	down	AT1G7446	-2.254	down	unknown lipid hydrolase with Lipase_GDSL domain and signal peptide	down
AT4G22666	AT4G22666	AT4G22666_1	-3.085	0.03017	down	AT4G2266	-3.107	down	unknown lipid transfer membrane protein with AAI domain	down
AT1G12100	AT1G12100	-				AT1G1210	-3.352	down	unknown lipid transfer membrane protein with AAI domain	down
AT2G37870	AT2G37870					AT2G3787	-2.183	down	unknown lipid transfer membrane protein with AAI domain	down
AT5G55460	AT5G55460					AT5G5546	-2.856	down	unknown lipid transfer membrane protein with AAI domain	down
AT3G22600	AT3G22600	-				AT3G2260	-2.03	down	unknown lipid transfer membrane protein with AAI domain GLYCOSYLPHOSPHATIDYLINOSITOL-AN	down
AT1G18280	AT1G18280	-				AT1G1828	-2.953	down	unknown lipid transfer membrane protein with AAI domain, GLYCOSYLPHOSPHATIDYLINOSITOL-A	down
LBD26	AT3G27940	LBD26_2	62.307	0.04021	up	LBD26	2.3119	up	unknown LOB domain protein	up
LBD21	AT3G11090	LBD21_1	-2.103	0.03208	down	LBD21	-2.136	down	unknown LOB DUF260 domain protein	down
LBD38	AT3G49940	LBD38_1	-2.314	9.83E-04	down	LBD38	-2.341	down	unknown LOB DUF260 domain protein	down
AT3G02700	AT3G02700	AT3G02700_1	-2.046	7.65E-03	down	AT3G0270	-2.068	down	unknown LRAT domain protein	down
AT5G37450	AT5G37450	AT5G37450_3	85.939	0.02896	up	AT5G3745	3.9478	up	unknown LRR kinase plasmamembrane	up?
AtRLP19	AT2G15080	AtRLP19_1	5.0918	0.02133	up	AtRLP19	2.2305	up	unknown LRR protein	up
AtRLP21	AT2G25470	AtRLP21_3	50.442	5.55E-03	up	AtRLP21	2.7826	up	unknown LRR protein	up
AT1G73066	AT1G73066					AT1G7306	2.6753	up	unknown LRR protein with signal peptide	up
AT1G52820	AT1G52820					AT1G5282	-4.365	down	unknown LRR protein with signal peptide	down
AtRLP37	AT3G23110	AtRLP37_1	4.3821	0.03194	up	AtRLP37	4.3487	up	unknown LRR receptor	up
AT1G05700	AT1G05700	-				AT1G0570	2.2009	up	unknown LRR receptor kinase with signal pepide and Malectin domain	up
AT1G29740	AT1G29740					AT1G2974	-4.344	down	unknown LRR receptor kinase with signal pepide and Malectin domain	down
RFK1	At1g29720	RFK1_1	2.6342	0.01978	up	RFK1	2.6113	up	unknown LRRK receptor kinase	up
LECRK15	At3g45430					LECRK15	-3.317	down	unknown L-TYPE LECTIN RECEPTOR KINASE I.5, LECRK-I.5	down
AT3G44800	AT3G44800					AT3G4480	3.6979	up	unknown MATH domain coiled coil protein	up
AT3G20360	AT3G20360					AT3G2036	2.8041	up	unknown MATH domain TRAF-like protein CUL4 interactor	up
AT1G11210	AT1G11210					AT1G1121	-2.629	down	unknown mebrane bound DUF4408 domain protein	down
AT1G06120	AT1G06120	-				AT1G0612	-3.776	down	unknown mebrane bound Fatty acid desaturase	down
PP2A10	At1g10150	PP2A10_1	-2.182	0.0135	down	PP2A10	-2.212	down	unknown mebrane-bound ATPase HATPase_c domain protein	down
AT1G70020	AT1G70020					AT1G7002	-2.314	down	unknown membrane bound DUF1163 domain protein	down
AT1G55240	AT1G55240					AT1G5524	-3.026	down	unknown membrane bound DUF716 domain protein	down
AT2G03360	AT2G03360	AT2G03360_2	-158.9	0.01585	down	AT2G0336	-2.182	down	unknown membrane bound glycosyltransferase family 61 protein	down?
ATL76	AT1G49210					ATL76	-5.521	down	unknown membrane bound RING E3	down
AT2G20142	AT2G20142					AT2G2014	2.0772	up	unknown membrane bound TIR domain protein	up
AT2G32340	AT2G32340					AT2G3234	2.0978	up	unknown membrane bound TraB domain protein	up
AT3G01345	AT3G01345					AT3G0134	4.5711	up	unknown membrane protein	up
AT2G29620	AT2G29620					AT2G2962	2.2423	up	unknown membrane protein	up
AT2G25510	AT2G25510	AT2G25510_1	-2.388	1.39E-03	down	AT2G2551	-2.421	down	unknown membrane protein	down
AT2G07719	AT2G07719					AT2G0771	-2.947	down	unknown membrane protein	down
AT1G17665	AT1G17665					AT1G1766	-2.557	down	unknown membrane protein	down
AT5G07570	AT5G07570	AT5G07570_2	-16.77	0.04793	down	AT5G0757	-16.74	down	unknown membrane protein with 10 transmembrane and Phage fibre protein domains	down?
AT5G56100	AT5G56100	AT5G56100_1	-2.686	1.60E-03	down	AT5G5610	-2.725	down	unknown membrane protein with 3 transmembrane domains	down
AT4G30670	AT4G30670	AT4G30670_1	-2.114	0.04642	down	AT4G3067	-2.125	down	unknown membrane protein with signal peptide	down
AT1G15010	AT1G15010					AT1G1501	-2.683	down	unknown membrane rprotein	down
DTX3	AT2G04050	DTX3_1	6.7172	4.23E-09	up	DTX3	6.6681	up	unknown membrane transporter Transport of bile salts and organic acids	up
AT4G03450	AT4G03450					AT4G0345	-5.33	down	unknown membrane-bound Ankyrin repeat protein	down
ATL8	AT1G76410	ATL8_1	-2.202	0.03735	down	ATL8	-2.221	down	unknown membrane-bound RING E3	down
AT3G43430	AT3G43430	AT3G43430_1	-2.178	0.03946	down	AT3G4343	-2.209	down	unknown membrane-bound RING E3	down
ATL23	AT5G42200	ATL23_1	-2.101	0.03948	down	ATL23	-2.127	down	unknown membrane-bound RING E3	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
ATL44	AT2G17450	ATL44_1	-3.465	1.10E-06	down	ATL44	-3.503	down	unknown membrane-bound RING E3, RING-H2 FINGER PROTEIN RHA3A	down
AT5G65520	AT5G65520	AT5G65520_1	-2.658	1.60E-03	down	AT5G6552	-2.691	down	unknown membrane-bound Tetratricopeptide protein	down
SBT5.6	At5g45650	SBT5.6_1	75.595	0.03872	up	SBT5.6	2.0076	up	unknown MEROPS family S8A, subtilisins with vacuolar receptor PA domain and signal peptide	up
AT5G44170	AT5G44170	AT5G44170_1	-2.019	0.01999	down	AT5G4417	-2.043	down	unknown Methyltransf_16 domain protein	down
AT2G18330	AT2G18330	AT2G18330_1	2.0647	0.02529	up	AT2G1833	2.0535	up	unknown mitochondrial membrane ATPase	up
AT3G28899	AT3G28899	AT3G28899_1	30.408	0	up	AT3G2889	30.171	up	unknown mitochondrial protein	up
AT4G36500	AT4G36500	AT4G36500_1	-2.254	5.00E-03	down	AT4G3650	-2.272	down	unknown mitochondrial protein	down
AT4G03292	AT4G03292	AT4G03292_1	22.799	0.0146	up	AT4G0329	22.808	up	unknown mitochondrial ribonuclease H-like protein	up
MAPKKK13	AT1G07150	-				MAPKKK13	-2.364	down	unknown mitogen-activated protein kinase kinase kinase MAPKKK13	down
AT2G26370	AT2G26370					AT2G2637	-2.77	down	unknown ML (MD-2-related lipid-recognition) domain protein	down
AT1G49920	AT1G49920					AT1G4992	3.4093	up	unknown MuDR transposase with ARM repeat	up
AT1G64253	AT1G64253	AT1G64253_3	79.276	0.03031	up	AT1G6425	5.9584	up	unknown MULE mutator transposase Zn-finger, DEK domain protein	up
AT1G55050	AT1G55050					AT1G5505	5.2605	up	unknown MYB TF	up
AT1G23880	AT1G23880					AT1G2388	2.1418	up	unknown NHL repeat transmembrane protein	up
AT5G49560	AT5G49560					AT5G4956	-2.405	down	unknown nicotinamide N-methyltransferase that may be involved in rDNA silencing	down
AT3G01630	AT3G01630	AT3G01630_2				AT3G0163	-2.183	down	unknown Nodulin-like domain transmembrane protein	down?
AT2G41450	AT2G41450	AT2G41450_1	20.011	0.04935	up	AT2G4145	3.8255	up	unknown nuclear N-acetyltransferase with Breast Cancer Suppressor Protein (BRCA1) domain	up
AT1G48580	AT1G48580	AT1G48580_3	251.05	3.57E-03	up	AT1G4858	2.3322	up	unknown nuclear protein	up
AT2G24550	AT2G24550	AT2G24550_1	-2.211	5.92E-03	down	AT2G2455	-2.246	down	unknown nuclear protein	down
AT3G27500	AT3G27500	AT3G27500_2	198.31	5.96E-03	up	AT3G2750	2.3136	up	unknown nuclear protein with C1 and PHD zinc finger domains	up
AT4G30760	AT4G30760	AT4G30760_2	-2.594	5.43E-04	down	AT4G3076	-2.17	down	unknown NYN domain protein	down?
BAHD1	AT5G47980					BAHD1	-2.191	down	unknown O-acetyltransferase	down
AT3G47010	AT3G47010					AT3G4701	-2.042	down	unknown O-Glycosyl hydrolase	down
AT3G58150	AT3G58150					AT3G5815	3.6183	up	unknown OPA3 domain protein	up
AT2G20670	AT2G20670	AT2G20670_1	-2.104	0.02358	down	AT2G2067	-2.133	down	unknown PDDEXK_6 domain protein	down
AT2G38820	AT2G38820	AT2G38820_1	-2.28	5.14E-03	down	AT2G3882	-2.07	down	unknown PDDEXK_6 domain protein	down
AT3G07350	AT3G07350	AT3G07350_1	-2.387	4.74E-03	down	AT3G0735	-2.416	down	unknown PDDEXK-like domain protein	down
AT1G23350	AT1G23350	-				AT1G2335	-3.232	down	unknown pectin methylesterase inhibitor	down
PCMP-H65	At4g01030					PCMP-H65	2.4209	up	unknown pentatricopeptide (PPR) repeat protein	up
PCMP-E33	At2g39620					PCMP-E33	2.9336	up	unknown Pentatricopeptide repeat (PPR) protein	up
PCMP-E51	At3g15930					PCMP-E51	4.6214	up	unknown Pentatricopeptide repeat (PPR) protein	up
PCMP-H42	At4g13650					PCMP-H42	2.8276	up	unknown Pentatricopeptide repeat (PPR) protein	up
AT4G14200	AT4G14200					AT4G1420	2.3231	up	unknown Pentatricopeptide repeat (PPR) protein	up
PCMP-H5	At4g37170					PCMP-H5	2.0168	up	unknown Pentatricopeptide repeat (PPR) protein	up
PCMP-H49	At5g46460					PCMP-H49	5.6711	up	unknown Pentatricopeptide repeat (PPR) protein	up
PCMP-E100	At4g08210					PCMP-E10	2.8165	up	unknown Pentatricopeptide repeat (PPR-like) protein	up
PCMP-H47	At5g65570					PCMP-H47	2.2341	up	unknown Pentatricopeptide repeat protein	up
SCPL41	AT5G42230					SCPL41	4.0676	up	unknown Peptidase_S10 scpl41 serine carboxypeptidase-like 41	up
PER69	At5g64100	PER69_1	-2.269	7.76E-04	down	PER69	-2.288	down	unknown peroxidase with signal peptide	down
AT1G05340	AT1G05340	AT1G05340_1	-3.319	3.41E-04	down	AT1G0534	-3.372	down	unknown peroxide induced cysteine-rich membrane protein	down
AT3G45530	AT3G45530					AT3G4553	3.2148	up	unknown PHD finger and C1 domain protein	up
AT5G54040	AT5G54040					AT5G5404	2.1931	up	unknown PHD finger and C1 domain protein	up
AT2G44380	AT2G44380	AT2G44380_1	-2.393	7.32E-03	down	AT2G4438	-2.431	down	unknown PHD finger and C1 domain protein	down
AT5G43520	AT5G43520	AT5G43520_1	-3.262	0.02111	down	AT5G4352	-3.293	down	unknown PHD finger and C1 domain protein	down
AT5G16480	AT5G16480	AT5G16480_1	-2.384	7.84E-03	down	AT5G1648	-2.167	down	unknown Phosphotyrosine protein phosphatase PFA-DSP5, putative MAP kinase phosphatase	down
PCR9	At1g58320	PCR9_1	-6.488	0.01272	down	PCR9	-6.546	down	unknown PLAC8 domain homolog of Plant Cadmium Resistance 1 Zinc/cadmium transporter	down
AT3G22570	AT3G22570	AT3G22570_1	-95.04	0.02986	down	AT3G2257	-5.734	down	unknown Plant lipid transfer protein / seed storage protein / trypsin-alpha amylase inhibitor do	down
AT1G51538	AT1G51538					AT1G5153	2.2375	up	unknown PMD domain protein	up
AT2G25770	AT2G25770					AT2G2577	-2.521	down	unknown polyketide cylcases/dehydrase	down
AT3G26760	AT3G26760					AT3G2676	-2.167	down	unknown polyketide or fatty acid synthase	down
AT1G49245	AT1G49245	-				AT1G4924	-2.168	down	unknown prefoldin co-chaperonin	down
AT3G24929	AT3G24929	AT3G24929_1	51.156	0.04365	up	AT3G2492	2.1227	up	unknown protein	up?
AT1G17360	AT1G17360	AT1G17360_1	2.252	0.01473	up	AT1G1736	2.2326	up	unknown protein	up
AT1G17820	AT1G17820	AT1G17820_1	244.98	5.52E-06	up	AT1G1782	243	up	unknown protein	up
AT2G38823	AT2G38823	AT2G38823_1	14.192	0.01305	up	AT2G3882	14.084	up	unknown protein	up
AT3G03130	AT3G03130	AT3G03130_1	2.7328	0.04171	up	AT3G0313	2.7188	up	unknown protein	up
AT4G12540	AT4G12540	AT4G12540_5	101	0.01991	up	AT4G1254	2.3171	up	unknown protein	up
AT2G33847	AT2G33847	AT2G33847_1	2.9639	0.04205	up	AT2G3384	2.8775	up	unknown protein	up
AT1G25141	AT1G25141					AT1G2514	3.361	up	unknown protein	up
AT1G29179	AT1G29179					AT1G2917	2.3881	up	unknown protein	up
AT1G61090	AT1G61090					AT1G6109	3.1175	up	unknown protein	up
AT2G16575	AT2G16575					AT2G1657	3.1175	up	unknown protein	up
AT2G40955	AT2G40955					AT2G4095	11.449	up	unknown protein	up
AT3G58770	AT3G58770					AT3G5877	6.6187	up	unknown protein	up
AT5G21080	AT5G21080					AT5G2108	9.3906	up	unknown protein	up
AT5G24640	AT5G24640					AT5G2464	3.2223	up	unknown protein	up
AT3G33528	AT3G33528					AT3G3352	12.159	up	unknown protein	up
AT3G56870	AT3G56870					AT3G5687	2.4378	up	unknown protein	up
AT1G32920	AT1G32920	AT1G32920_1	-2.339	2.03E-03	down	AT1G3292	-2.368	down	unknown protein	down
AT1G52342	AT1G52342	AT1G52342_1	-2.56	0.02526	down	AT1G5234	-2.608	down	unknown protein	down
AT1G73120	AT1G73120	AT1G73120_1	-2.398	0.01754	down	AT1G7312	-2.438	down	unknown protein	down
AT2G22122	AT2G22122	AT2G22122_1	-3.96	1.21E-04	down	AT2G2212	-3.988	down	unknown protein	down
AT2G25735	AT2G25735	AT2G25735_1	-2.686	0.01555	down	AT2G2573	-2.714	down	unknown protein	down
AT2G27830	AT2G27830	AT2G27830_1	-3.413	1.54E-05	down	AT2G2783	-3.461	down	unknown protein	down
AT2G37750	AT2G37750	AT2G37750_1	-3.366	4.41E-04	down	AT2G3775	-3.419	down	unknown protein	down
AT2G46490	AT2G46490	AT2G46490_1	-2.195	3.95E-03	down	AT2G4649	-2.213	down	unknown protein	down
AT3G11690	AT3G11690	AT3G11690_1	-2.032	0.01469	down	AT3G1169	-2.062	down	unknown protein	down
AT3G14560	AT3G14560	AT3G14560_1	-2.679	0.01302	down	AT3G1456	-2.725	down	unknown protein	down
AT3G15630	AT3G15630	AT3G15630_1	-4.185	2.97E-08	down	AT3G1563	-4.219	down	unknown protein	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT3G29370	AT3G29370	AT3G29370_1	-4.979	1.53E-04	down	AT3G2937	-4.993	down	unknown protein	down
AT3G48020	AT3G48020	AT3G48020_1	-3.244	0.03874	down	AT3G4802	-3.298	down	unknown protein	down
AT3G62070	AT3G62070	AT3G62070_1	-2.987	0.02572	down	AT3G6207	-3.022	down	unknown protein	down
AT4G07408	AT4G07408	AT4G07408_1	-21.48	9.51E-05	down	AT4G0740	-21.11	down	unknown protein	down
AT4G10910	AT4G10910	AT4G10910_1	-4.312	0.02415	down	AT4G1091	-4.371	down	unknown protein	down
AT4G15990	AT4G15990	AT4G15990_1	-3.317	0.01929	down	AT4G1599	-3.379	down	unknown protein	down
AT4G23870	AT4G23870	AT4G23870_1	-2.677	2.24E-03	down	AT4G2387	-2.71	down	unknown protein	down
AT4G26288	AT4G26288	AT4G26288_1	-3.287	4.78E-03	down	AT4G2628	-3.346	down	unknown protein	down
AT4G33960	AT4G33960	AT4G33960_1	-3.048	6.33E-04	down	AT4G3396	-3.08	down	unknown protein	down
AT4G37700	AT4G37700	AT4G37700_1	-4.177	0.04991	down	AT4G3770	-4.247	down	unknown protein	down
AT4G39675	AT4G39675	AT4G39675_1	-3.234	0.02218	down	AT4G3967	-3.29	down	unknown protein	down
AT5G11070	AT5G11070	AT5G11070_1	-2.796	2.08E-04	down	AT5G1107	-2.838	down	unknown protein	down
AT5G24610	AT5G24610	AT5G24610_1	-2.033	7.25E-03	down	AT5G2461	-2.051	down	unknown protein	down
AT5G42825	AT5G42825	AT5G42825_1	-2.533	9.10E-04	down	AT5G4282	-2.564	down	unknown protein	down
AT5G44005	AT5G44005	AT5G44005_1	-2.645	0.01022	down	AT5G4400	-2.682	down	unknown protein	down
AT5G49170	AT5G49170	AT5G49170_1	-3.252	0.03004	down	AT5G4917	-3.288	down	unknown protein	down
AT5G50335	AT5G50335	AT5G50335_1	-3.924	0.01007	down	AT5G5033	-3.97	down	unknown protein	down
AT5G51390	AT5G51390	AT5G51390_1	-2.956	0.03852	down	AT5G5139	-2.994	down	unknown protein	down
AT5G54585	AT5G54585	AT5G54585_1	-2.911	0.01068	down	AT5G5458	-2.962	down	unknown protein	down
AT5G49015	AT5G49015	AT5G49015_1	-3.474	0.03825	down	AT5G4901	-3.027	down	unknown protein	down
AT5G59080	AT5G59080	AT5G59080_2	-2.794	5.43E-03	down	AT5G5908	-2.683	down	unknown protein	down
AT5G25280	AT5G25280	AT5G25280_1	-2.106	4.99E-03	down	AT5G2528	-2.041	down	unknown protein	down
AT2G28570	AT2G28570	AT2G28570_2	-179	0.01344	down	AT2G2857	-2.22	down	unknown protein	down
AT1G19530	AT1G19530	AT1G19530_2	-2.071	0.02178	down	AT1G1953	-2.194	down	unknown protein	down
AT4G08330	AT4G08330	AT4G08330_2	-2.454	5.95E-03	down	AT4G0833	-2.367	down	unknown protein	down
AT2G01755	AT2G01755	AT2G01755_2	-2.815	0.01232	down	AT2G0175	-2.107	down	unknown protein	down
AT1G02350	AT1G02350					AT1G0235	-2.952	down	unknown protein	down
AT1G06923	AT1G06923					AT1G0692	-4.816	down	unknown protein	down
AT1G28070	AT1G28070					AT1G2807	-2.11	down	unknown protein	down
AT1G32690	AT1G32690					AT1G3269	-2.114	down	unknown protein	down
AT1G52855	AT1G52855					AT1G5285	-2.126	down	unknown protein	down
AT1G53633	AT1G53633					AT1G5363	-3.285	down	unknown protein	down
AT1G58420	AT1G58420					AT1G5842	-3.827	down	unknown protein	down
AT2G07774	AT2G07774					AT2G0777	-3.835	down	unknown protein	down
AT2G07775	AT2G07775					AT2G0777	-9.562	down	unknown protein	down
AT2G07798	AT2G07798					AT2G0779	-5.725	down	unknown protein	down
AT2G18210	AT2G18210					AT2G1821	-3.533	down	unknown protein	down
AT2G27180	AT2G27180					AT2G2718	-2.208	down	unknown protein	down
SMR11	At2g28330					SMR11	-2.252	down	unknown protein	down
AT2G35345	AT2G35345					AT2G3534	-2.57	down	unknown protein	down
AT2G44010	AT2G44010					AT2G4401	-2.112	down	unknown protein	down
AT3G15250	AT3G15250					AT3G1525	-7.379	down	unknown protein	down
AT3G22090	AT3G22090					AT3G2209	-6.67	down	unknown protein	down
AT3G27355	AT3G27355					AT3G2735	-2.04	down	unknown protein	down
AT3G46300	AT3G46300					AT3G4630	-5.941	down	unknown protein	down
AT3G50640	AT3G50640					AT3G5064	-2.034	down	unknown protein	down
AT3G54363	AT3G54363					AT3G5436	-2.273	down	unknown protein	down
AT3G59880	AT3G59880					AT3G5988	-2.108	down	unknown protein	down
AT3G62920	AT3G62920					AT3G6292	-2.007	down	unknown protein	down
AT3G62990	AT3G62990					AT3G6299	-12.58	down	unknown protein	down
AT4G08360	AT4G08360					AT4G0836	-3.327	down	unknown protein	down
AT4G13577	AT4G13577					AT4G1357	-12.6	down	unknown protein	down
AT5G02000	AT5G02000					AT5G0200	-6.237	down	unknown protein	down
AT5G02640	AT5G02640					AT5G0264	-2.383	down	unknown protein	down
AT5G05965	AT5G05965					AT5G0596	-5.011	down	unknown protein	down
AT5G15190	AT5G15190					AT5G1519	-2.493	down	unknown protein	down
AT5G19340	AT5G19340					AT5G1934	-2.008	down	unknown protein	down
AT5G23460	AT5G23460					AT5G2346	-2.069	down	unknown protein	down
AT5G35110	AT5G35110					AT5G3511	-3.522	down	unknown protein	down
AT5G40800	AT5G40800					AT5G4080	-7.035	down	unknown protein	down
AT5G40970	AT5G40970					AT5G4097	-2.107	down	unknown protein	down
AT5G54148	AT5G54148					AT5G5414	-3.49	down	unknown protein	down
AT5G56520	AT5G56520					AT5G5652	-2.041	down	unknown protein	down
AT5G56880	AT5G56880					AT5G5688	-3.79	down	unknown protein	down
AT5G62865	AT5G62865					AT5G6286	-2.026	down	unknown protein	down
AT5G63350	AT5G63350					AT5G6335	-2.398	down	unknown protein	down
AT1G15885	AT1G15885					AT1G1588	-2.396	down	unknown protein	down
AT1G31835	AT1G31835					AT1G3183	-2.381	down	unknown protein	down
AT1G54120	AT1G54120					AT1G5412	-2.954	down	unknown protein	down
AT1G71910	AT1G71910					AT1G7191	-2.029	down	unknown protein	down
AT2G04800	AT2G04800					AT2G0480	-2.874	down	unknown protein	down
AT2G07629	AT2G07629					AT2G0762	-3.533	down	unknown protein	down
AT2G39855	AT2G39855					AT2G3985	-5.693	down	unknown protein	down
AT3G61660	AT3G61660					AT3G6166	-6.079	down	unknown protein	down
AT5G16200	AT5G16200					AT5G1620	-2.116	down	unknown protein	down
AT5G66780	AT5G66780					AT5G6678	-4.189	down	unknown protein	down
AT3G05935	AT3G05935	AT3G05935_3	-17.37	0.01699	down	AT3G0593	-2.128	down	unknown protein	down?
AT5G40500	AT5G40500	AT5G40500_2	-2.288	0.01358	down	AT5G4050	-2.07	down	unknown protein	down?
AT5G53230	AT5G53230	AT5G53230_1	25.121	8.36E-03	up	AT5G5323	24.936	up	unknown protein (DUF295)	up

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT5G54450	AT5G54450	AT5G54450_1	30.695	0.01359	up	AT5G5445	30.407	up	unknown protein (DUF295)	up
AT5G54560	AT5G54560	AT5G54560_1	133.48	0.01237	up	AT5G5456	132.47	up	unknown protein (DUF295)	up
AT1G30160	AT1G30160	AT1G30160_2	12.927	2.80E-03	up	AT1G3016	4.7475	up	unknown protein (DUF295)	up
AT3G14900	AT3G14900					AT3G1490	2.1472	up	unknown protein EMBRYO DEFECTIVE 3120	up
AT1G33055	AT1G33055	AT1G33055_1	-2.716	4.24E-03	down	AT1G3305	-2.758	down	unknown protein hypoxia regulated	down
AT4G14780	AT4G14780					AT4G1478	5.3178	up	unknown protein kinase	up
PBL20	At4g17660					PBL20	7.6786	up	unknown protein kinase	up
AT5G03640	AT5G03640					AT5G0364	3.0795	up	unknown protein kinase	up
KIN2	AT2G02800	KIN2_1	-2.768	1.38E-03	down	KIN2	-2.803	down	unknown protein kinase	down
AT1G53625	AT1G53625	AT1G53625_1	-4.561	0.01022	down	AT1G5362	-4.621	down	unknown protein NUP1 2H interactor	down
AT1G80130	AT1G80130					AT1G8013	2.0006	up	unknown Protein prenylyltransferase	up
AT4G32340	AT4G32340	AT4G32340_1	-2.407	7.76E-03	down	AT4G3234	-2.415	down	unknown Protein prenylyltransferase domain protein	down
AT3G43850	AT3G43850	AT3G43850_1	-5.86	0.02317	down	AT3G4385	-5.886	down	unknown protein ribosome RNA processing	down?
AT2G15960	AT2G15960	AT2G15960_1	-3.647	4.78E-06	down	AT2G1596	-3.679	down	unknown protein TRANSCURVATA1 nucleoporin NUP58 2H interactor	down
AT3G06780	AT3G06780	AT3G06780_1	-2.488	9.18E-04	down	AT3G0678	-2.521	down	unknown protein with (Trans)glycosidase domain, interacting partner of RBP1 RNA binding prote	down
AT1G09645	AT1G09645	AT1G09645_1	-2.08	0.01485	down	AT1G0964	-2.105	down	unknown protein with 2 transmembrane domains	down
AT5G14330	AT5G14330	AT5G14330_1	-3.172	3.59E-04	down	AT5G1433	-3.209	down	unknown protein with 2 transmembrane domains	down
AT3G50685	AT3G50685	AT3G50685_1	-2.111	4.98E-03	down	AT3G5068	-2.137	down	unknown protein with 3 transmembrane domains	down
MEE60	AT5G05950	MEE60_1	-2.533	1.10E-03	down	MEE60	-2.561	down	unknown protein with 4 transmembrane domains	down
AT2G17705	AT2G17705	AT2G17705_1	-2.762	2.65E-03	down	AT2G1770	-2.789	down	unknown protein with Mss4-like domain	down
AT3G28750	AT3G28750					AT3G2875	2.9622	up	unknown protein with signal peptide	up
AT1G34047	AT1G34047					AT1G3404	2.0101	up	unknown protein with signal peptide	up
AT1G05835	AT1G05835	AT1G05835_1	-2.294	0.01833	down	AT1G0583	-2.327	down	unknown protein with signal peptide	down
AT3G13435	AT3G13435	AT3G13435_1	-5.526	0.02093	down	AT3G1343	-5.587	down	unknown protein with signal peptide	down
AT3G59930	AT3G59930	AT3G59930_1	-3.859	7.03E-03	down	AT3G5993	-3.915	down	unknown protein with signal peptide	down
AT5G42530	AT5G42530	AT5G42530_1	-3.618	1.10E-05	down	AT5G4253	-3.663	down	unknown protein with signal peptide	down
AT5G44585	AT5G44585	AT5G44585_1	-4.167	2.92E-03	down	AT5G4458	-4.189	down	unknown protein with signal peptide	down
AT1G77525	AT1G77525	AT1G77525_1	-104.1	0.02656	down	AT1G7752	-103	down	unknown protein with signal peptide	down
AT5G01015	AT5G01015	AT5G01015_2	-2.235	0.02233	down	AT5G0101	-2.263	down	unknown protein with signal peptide	down
AT1G24147	AT1G24147					AT1G2414	-2.99	down	unknown protein with signal peptide	down
AT1G56320	AT1G56320					AT1G5632	-2.036	down	unknown protein with signal peptide	down
AT5G09520	AT5G09520					AT5G0952	-2.297	down	unknown protein with signal peptide	down
AT3G04640	AT3G04640					AT3G0464	-2.226	down	unknown protein with signal peptide	down
AT5G48690	AT5G48690	AT5G48690_3	55.734	0.04038	up	AT5G4869	3.3975	up	unknown PUG domain protein	up
AT3G50850	AT3G50850	-				AT3G5085	-2.512	down	unknown putative nicotinamide N-methyltransferases involved in rRNA silencing	down
AT5G28237	AT5G28237	-				AT5G2823	-6.027	down	unknown Pyridoxal-phosphate dependent enzyme	down
SRO3	AT1G70440	-				SRO3	7.9101	up	unknown RCD1-like ADP ribosylation factor	up
AT1G10000	AT1G10000					AT1G1000	-4.981	down	unknown reverse transcriptase	down
AT4G24420	AT4G24420					AT4G2442	8.9609	up	unknown RNA-binding domain, RBD protein	up
AT4G36945	AT4G36945	AT4G36945_1	-2.394	0.03183	down	AT4G3694	-2.413	down	unknown SCOP domain d2plc protein with signal peptide	down
AT5G66590	AT5G66590	AT5G66590_1	-2.682	1.43E-03	down	AT5G6659	-2.718	down	unknown secreted SCP / Tpx-1 / Ag5 / PR-1 / Sc7 family of extracellular domain protein with signa	down
SCPL15	AT3G12240					SCPL15	-6.38	down	unknown serine carboxypeptidase-like 15	down
SCPL16	AT3G12220					SCPL16	-2.915	down	unknown serine carboxypeptidase-like 16	down
SCPL2	AT1G73300					SCPL2	-2.862	down	unknown serine carboxypeptidase-like 2	down
AT3G28880	AT3G28880	AT3G28880_1	9.7025	0.03429	up	AT3G2888	9.6474	up	unknown serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit	up
PHO1-H7	At1g26730					PHO1-H7	2.6266	up	unknown signaling G-protein inhibitor yeast SYG1 homolog	up
AT3G44690	AT3G44690	AT3G44690_1	407.03	1.32E-03	up	AT3G4469	5.2895	up	unknown SnRK2.6 Ost1 interacting protein	up
AT1G76740	AT1G76740					AT1G7674	2.7618	up	unknown Terpenoid cyclases/Protein prenyltransferase	up
AT5G33300	AT5G33300					AT5G3330	2.52	up	unknown Tesmin/TSO1-like CXC domain containing coiled coil protein	up
AT3G51280	AT3G51280					AT3G5128	2.4516	up	unknown tetratrico peptide repeat (TPR) protein	up
AT1G57630	AT1G57630					AT1G5763	-7.199	down	unknown TIR domain protein	down
AT4G09430	AT4G09430	AT4G09430_1	11.75	0.03126	up	AT4G0943	11.657	up	unknown TIR-NBS-LRR protein	up
AT5G41750	AT5G41750	AT5G41750_2	25.041	3.30E-04	up	AT5G4175	2.8332	up	unknown TIR-NBS-LRR protein	up
AT5G45200	AT5G45200	AT5G45200_3	57.034	0.03955	up	AT5G4520	6.6913	up	unknown TIR-NBS-LRR protein	up
AT4G16940	AT4G16940	AT4G16940_3	35.892	2.37E-03	up	AT4G1694	2.1322	up	unknown TIR-NBS-LRR protein	up
AT1G63730	AT1G63730					AT1G6373	2.9775	up	unknown TIR-NBS-LRR protein	up
AT5G40100	AT5G40100					AT5G4010	2.3442	up	unknown TIR-NBS-LRR protein	up
AT5G46260	AT5G46260					AT5G4626	2.469	up	unknown TIR-NBS-LRR protein	up
AT2G17050	AT2G17050					AT2G1705	2.3774	up	unknown TIR-NBS-LRR protein	up
AT4G09435	AT4G09435					AT4G0943	7.1751	up	unknown TIR-NBS-LRR protein	up
AT5G40000	AT5G40000					AT5G4000	8.5519	up	unknown transmembrane AAA - ATPases	up
AT1G17430	AT1G17430					AT1G1743	-2.056	down	unknown transmembrane Abhydrolase_6 domain protein	down
AT4G15820	AT4G15820					AT4G1582	2.2765	up	unknown transmembrane coiled coil protein	up
AT5G39330	AT5G39330					AT5G3933	3.389	up	unknown transmembrane DUF1163 domain protein	up
AT4G04990	AT4G04990					AT4G0499	-2.627	down	unknown transmembrane DUF761 domain protein	down
AT3G53950	AT3G53950	AT3G53950_1	-2.068	0.02045	down	AT3G5395	-2.089	down	unknown transmembrane glyoxylase oxidase domain protein	down
AT4G01410	AT4G01410	AT4G01410_1	-2.01	0.01138	down	AT4G0141	-2.031	down	unknown transmembrane late embryogenesis abundant LEA_2 domain protein	down
AtRLP32	AT3G05650	AtRLP32_1	3.3467	0.02901	up	AtRLP32	3.3222	up	unknown transmembrane LRR receptor	up
AtRLP31	AT3G05370					AtRLP31	2.4196	up	unknown transmembrane LRR receptor	up
AtRLP33	AT3G05660					AtRLP33	2.1378	up	unknown transmembrane LRR receptor	up
AT5G53320	AT5G53320					AT5G5332	2.0611	up	unknown transmembrane LRR receptor kinase	up
AT1G14390	AT1G14390					AT1G1439	3.5336	up	unknown transmembrane LRR receptor kinase with signal peptide	up
AT5G64790	AT5G64790					AT5G6479	-2.011	down	unknown transmembrane O-Glycosyl hydrolase	down
AT3G13950	AT3G13950					AT3G1395	-2.477	down	unknown transmembrane PGG domain protein	down
AT1G16630	AT1G16630					AT1G1663	2.1488	up	unknown transmembrane protein	up
AT5G22555	AT5G22555					AT5G2255	2.0927	up	unknown transmembrane protein	up
AT2G34530	AT2G34530					AT2G3453	2.4349	up	unknown transmembrane protein	up
AT1G45163	AT1G45163	AT1G45163_1	-3.27	3.53E-03	down	AT1G4516	-3.294	down	unknown transmembrane protein	down
AT1G50732	AT1G50732	AT1G50732_1	-2.025	0.03341	down	AT1G5073	-2.057	down	unknown transmembrane protein	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_ Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
AT1G55675	AT1G55675	AT1G55675_1	-2.117	0.01534	down	AT1G5567	-2.144	down	unknown transmembrane protein	down
AT3G12650	AT3G12650	AT3G12650_1	-2.309	5.94E-03	down	AT3G1265	-2.337	down	unknown transmembrane protein	down
AT3G14430	AT3G14430	AT3G14430_1	-2.248	9.91E-03	down	AT3G1443	-2.276	down	unknown transmembrane protein	down
AT4G04925	AT4G04925	AT4G04925_1	-2.645	3.31E-03	down	AT4G0492	-2.67	down	unknown transmembrane protein	down
AT5G02160	AT5G02160	AT5G02160_1	-2.626	4.93E-04	down	AT5G0216	-2.647	down	unknown transmembrane protein	down
AT5G18850	AT5G18850	AT5G18850_1	-2.144	0.01162	down	AT5G1885	-2.176	down	unknown transmembrane protein	down
AT3G52070	AT3G52070	AT3G52070_1	-2.867	3.45E-03	down	AT3G5207	-2.832	down	unknown transmembrane protein	down
AT1G10225	AT1G10225					AT1G1022	-4.257	down	unknown transmembrane protein	down
AT1G23530	AT1G23530					AT1G2353	-2.063	down	unknown transmembrane protein	down
AT1G27670	AT1G27670					AT1G2767	-3.024	down	unknown transmembrane protein	down
AT1G30515	AT1G30515					AT1G3051	-2.28	down	unknown transmembrane protein	down
AT1G35430	AT1G35430					AT1G3543	-2.056	down	unknown transmembrane protein	down
AT1G56555	AT1G56555					AT1G5655	-11.06	down	unknown transmembrane protein	down
AT1G75810	AT1G75810					AT1G7581	-2.046	down	unknown transmembrane protein	down
AT2G07815	AT2G07815					AT2G0781	-4.649	down	unknown transmembrane protein	down
AT2G41200	AT2G41200					AT2G4120	-2.133	down	unknown transmembrane protein	down
AT2G41610	AT2G41610					AT2G4161	-4.372	down	unknown transmembrane protein	down
AT3G03160	AT3G03160					AT3G0316	-2.018	down	unknown transmembrane protein	down
AT3G06890	AT3G06890					AT3G0689	-2.397	down	unknown transmembrane protein	down
AT3G15358	AT3G15358					AT3G1535	-2.358	down	unknown transmembrane protein	down
AT4G01110	AT4G01110					AT4G0111	-2.541	down	unknown transmembrane protein	down
AT5G07330	AT5G07330					AT5G0733	-2.867	down	unknown transmembrane protein	down
AT5G08240	AT5G08240					AT5G0824	-2.004	down	unknown transmembrane protein	down
AT5G20045	AT5G20045					AT5G2004	-3.366	down	unknown transmembrane protein	down
AT5G42785	AT5G42785					AT5G4278	-2.178	down	unknown transmembrane protein	down
AT2G07674	AT2G07674					AT2G0767	-3.628	down	unknown transmembrane protein	down
AT2G37530	AT2G37530					AT2G3753	-3.154	down	unknown transmembrane protein	down
AT4G05030	AT4G05030					AT4G0503	-17.37	down	unknown transmembrane protein	down
AT5G14690	AT5G14690					AT5G1469	-2.317	down	unknown transmembrane protein	down
AT1G79660	AT1G79660	AT1G79660_1	-2.071	8.19E-03	down	AT1G7966	-2.097	down	unknown transmembrane protein 93aa	down
AT4G34950	AT4G34950					AT4G3495	-2.636	down	unknown transmembrane protein with Nodulin-like domain	down
AT2G40530	AT2G40530	AT2G40530_1	-3.74	0.01225	down	AT2G4053	-3.797	down	unknown transmembrane protein with Phosphoenolpyruvate/pyruvate domain, ABA, BR and SA	down
AT1G12845	AT1G12845	AT1G12845_1	-2.719	8.76E-03	down	AT1G1284	-2.732	down	unknown transmembrane protein with signal peptide	down
AT1G54950	AT1G54950					AT1G5495	-2.405	down	unknown transmembrane protein with signal peptide	down
AT3G55790	AT3G55790					AT3G5579	-12.67	down	unknown transmembrane protein with signal peptide	down
AT1G10220	AT1G10220					AT1G1022	-2.44	down	unknown transmembrane protein ZCF37	down
ATL77	AT3G18773	ATL77_1	-2.838	9.59E-03	down	ATL77	-2.884	down	unknown transmembrane RING E3	down
AT3G60966	AT3G60966					AT3G6096	-2.288	down	unknown transmembrane RING E3	down
ATL7	AT4G10150					ATL7	-2.9	down	unknown transmembrane RING E3	down
TET9	AT4G30430					TET9	-3.275	down	unknown transmembrane TET9 tetraspanin9	down
UCC2	AT2G44790	UCC2_1	-2.112	4.59E-03	down	UCC2	-2.128	down	unknown transmembrane uclacyanin with Cu2+-binding domain and signal peptide	down
PCR3	At5g35525					PCR3	-4.999	down	unknown transporter PCR (PLANT CADMIUM RESISTANCE) homolog PCR3	down
AT1G64260	AT1G64260	AT1G64260_2	125.27	0.01683	up	AT1G6426	2.6339	up	unknown transposase	up
AT2G19960	AT2G19960					AT2G1996	7.27	up	unknown transposase Dimer_Tnp_hAT dimerization domain protein	up
AT4G10695	AT4G10695	AT4G10695_1	131.17	0.01304	up	AT4G1069	145.01	up	unknown ubiquitin SCF E3 ligase F-box protein	up
PUB56	At1g01670					PUB56	3.5234	up	unknown U-box E3 with coiled coil domain	up
AT1G01660	AT1G01660					AT1G0166	5.0234	up	unknown U-box E3 with coiled coil domains	up
UGT91B1	At5g65550					UGT91B1	3.1177	up	unknown UDP glycosyltransferase	up
UGT72C1	At4g36770					UGT72C1	4.0277	up	unknown UDP glycosyltransferase sugar metabolism	up
UGT74E1	At1g05675	UGT74E2_1				UGT74E1	4.5377	up	unknown UDP-Glycosyltransferase	up
ABCC10	AT3G59140	ABCC10_1	2.8978	1.15E-03	up	ABCC10	2.8669	up	unknown vacuolar ABC transpoter	up
AT3G62550	AT3G62550	AT3G62550_1	-2.206	2.12E-03	down	AT3G6255	-2.229	down	unknown vacuolar Usp universal stress domain protein	down
AT4G02370	AT4G02370	AT4G02370_1	-2.254	9.42E-03	down	AT4G0237	-2.266	down	unknown vacuole membrane DUF538 domain protein with signal peptide	down
AT5G13210	AT5G13210	AT5G13210_1	6.101	5.37E-04	up	AT5G1321	6.0597	up	unknown Von Willebrand factor type A (vWA) domain protein	up
VQ1	At1g17147					VQ1	-2.621	down	unknown VQ domain protein	down
AT4G20000	AT4G20000					AT4G2000	-3.744	down	unknown VQ domain protein	down
AT3G24780	AT3G24780					AT3G2478	4.7685	up	unknown VWA domain von Willebrand factor (vWF) type A domain protein	up
AT1G67760	AT1G67760	-				AT1G6776	3.6587	up	unknown VWA metal ion-dependent adhesion domain protein	up
AT3G26480	AT3G26480	AT3G26480_2	67.459	0.04368	up	AT3G2648	2.317	up	unknown WD40 protein	up
AT2G37670	AT2G37670					AT2G3767	5.3078	up	unknown WD40 protein	up
AT3G49400	AT3G49400	AT3G49400_4	7.1717	0.01224	up	AT3G4940	2.0024	up	unknown WD40 protein with zf-TFIIIC (pfam12660) domain	up
AT3G09080	AT3G09080					AT3G0908	2.0831	up	unknown WD40 repeat protein	up
AT2G42040	AT2G42040	AT2G42040_1	-2.061	0.01766	down	AT2G4204	-2.075	down	unknown WRC domain TF of Plant growth regulatory factor family	down
SAP2	At1g51200	SAP2_1	-2.239	6.58E-03	down	SAP2	-2.152	down	unknown zf-A20 and ZnF_AN1 domain TF	down
AtIDD12	AT4G02670	AtIDD12_1	75.99	0.03301	up	AtIDD12	2.3736	up	unknown Zinc finger, C2H2 TF ATM interactor	up
AT1G44414	AT1G44414					AT1G4441	-4.513	down	unknown zinc_ribbon_15 domain protein	down
AT1G53885	AT1G53885	AT1G53885_1	-4.494	3.75E-04	down	AT1G5388	-4.563	down	unknown zinc-finger of the FCS-type, C2-C2 domain protein	down
AT1G53903	AT1G53903	AT1G53903_1	-4.136	7.66E-04	down	AT1G5390	-4.194	down	unknown zinc-finger of the FCS-type, C2-C2 domain protein, AT1G53885 homolog	down
AT5G49120	AT5G49120					AT5G4912	-2.473	down	unknown zinc-finger of the FCS-type, C2-C2 protein	down
AT5G43540	AT5G43540					AT5G4354	-2.823	down	unknown ZnF_C2H2 domain TF	down
AT1G29560	AT1G29560					AT1G2956	2.3146	up	unknown ZnF_C3H1 domain protein	up
ZFWD4	At5g49200					ZFWD4	6.1552	up	unknown ZnF_C3H1 domain WD40 protein zfd4	up
AT1G52110	AT1G52110	AT1G52110_1	58.003	0.03805	up	AT1G5211	57.566	up	unknown, Kelch and jancalin lectin domains	up
AT1G14460	AT1G14460	AT1G14460_1	2.0778	0.04364	up	AT1G1446	2.059	up	unknown, STICHEL homolog	up
AT1G67920	AT1G67920					AT1G6792	-2.043	down	unknown67aa oligopeptide	down
AT1G18010	AT1G18010					AT1G1801	-2.057	down	unknowns UNC-93 ion channel regulatory protein homolog	down
AT1G03700	AT1G03700					AT1G0370	-3.037	down	unknwon DUF588 domain protein	down
AT3G52790	AT3G52790					AT3G5279	-2.732	down	unkonw LysM domain transmembrane protein	down
AT3G46150	AT3G46150	AT3G46150_1	-88	1.44E-03	down	AT3G4615	-87.59	down	unkown protein	down

CLC Bio	locus_name	DAS	Fold change _DAS	P-value	DAS_Change	DE	Fold change _DE	DE_Change	Pathway	Predicted effect on gene function
KIN1	AT1G14370					KIN1	-2.035	down	unkown PROTEIN KINASE 2A	down
AT2G44130	AT2G44130	AT2G44130_1	-2.806	6.54E-04	down	AT2G4413	-2.845	down	UV tolerance, cytokinin signaling, degradation cytokinin type B response regulators, KISS ME DE	down
RUP1	AT5G52250	RUP1_1	-2.839	5.36E-03	down	RUP1	-2.874	down	UV_B signaling repressor EFO1 CUL1-DDB1 interacting WD40 protein	down
VHA-C2	At1g19910	VHA-C2_2	-2.074	0.01113	down	VHA-C2	-2.093	down	vacuolar proton pubp ATPase F0/V0 complex, subunit C	down
VHA-E3	AT1G64200	VHA-E3_1	-2.429	3.65E-03	down	VHA-E3	-2.391	down	vacuole proton transporting ATPase	down
TIP2-3	At5g47450	TIP2-3_1	-7.17	0.04875	down	TIP2-3	-7.224	down	vacuole tonoplast ammonium transporter	down
DRP5A	AT1G53140	-				DRP5A	2.4215	up	vesicular transport cel division Dynamin, GTPase	up
PRA1F2	At1g55190	PRA1F2_1	-2.054	0.01479	down	PRA1F2	-2.081	down	vesicular transport cell death ACD11-interacting ER Golgi Prenylated Rab acceptor protein 1	down
ARFA1E	AT3G62290	ARFA1E_1	-2.063	8.27E-03	down	ARFA1E	-2.086	down	vesicular transport cell plate cell division ARFA1E ADP-ribosylation factor GTPase	down
AT1G33340	AT1G33340					AT1G3334	-3.079	down	vesicular transport clathrin coat nucleating phosphatidylinositol 4,5-bisphosphate binding ANT	down
PER23	At2g38390	PER23_1	-2.026	0.01701	down	PER23	-2.044	down	vesicular transport ER Golgi Prenylated Rab acceptor protein 1	down
SEC3B	AT1G47560					SEC3B	2.3123	up	vesicular transport exocytosis exocyst subunit SEC3B	up
VAMP725	AT2G32670	-				VAMP725	3.6291	up	vesicular transport exocytosis vesicle-associated membrane protein 725 VAMP725	up
PRA1F4	At3g13710	PRA1F4_1	-276.2	4.68E-03	down	PRA1F4	-280.2	down	vesicular transport GOLGI Rab GTPase Receptor PRA1.F4	down
VTI12	AT1G26670					VTI12	-2.015	down	vesicular transport Golgi SYN interacting v-SNARE VTI	down
ATVAMP713	AT5G11150	ATVAMP713_2	-2.796	0.02933	down	ATVAMP71	-2.592	down	vesicular transport LOGIN Synaptobrevin-like AtVAMP7C	down
PHYL1.1	At4g10170	-				PHYL1.1	-2.018	down	vesicular transport membrane bound Longin domain R-SNARE protein	down
ARAC11	AT3G51300					ARAC11	-2.028	down	vesicular transport polar cell elongation pollen-specific Rop GTPase ARABIDOPSIS RAC-LIKE 11, A	down
AT2G25350	AT2G25350	AT2G25350_1	109.77	0.02416	up	AT2G2535	2.0212	up	vesicular transport spectrin with phosphatidylinositol binding PX domain	up
ZIP2	AT1G08190	ZIP2_1	-2.439	9.49E-04	down	ZIP2	-2.464	down	vesicular transport to vacuole VPS41 (vacuolar protein sorting 41) homolog	down
PRA1F3	At3g13720	PRA1F3_1	-2.335	1.48E-03	down	PRA1F3	-2.362	down	vesicular transprot ER Golgi Prenylated Rab acceptor protein 1	down
AT5G02540	AT5G02540	AT5G02540_1	-2.185	0.04492	down	AT5G0254	-2.201	down	vitamin A1 synthesis DUF588 domain NADPH-dependent retinal reductase and a short-chain de	down
AT5G60730	AT5G60730					AT5G6073	3.4724	up	vitamin B12 cobalamin synthesis from uroporphyrinogen III, cobyrinic acid a,c-diamide synthase	up
AT1G06980	AT1G06980					AT1G0698	-2.495	down	vitamin B2 synthesis ribE - 6,7-dimethyl-8-ribityllumazine synthase	down
COAE	AT2G27490	-				COAE	-2.014	down	vitamin B5 pantothenate and coA synthesis dephospho-CoA kinase	down
PDX1L4	AT2G38210					PDX1L4	-2.105	down	vitamine B6 pyridoxal phosphate biosynthesis pyridoxal 5'-phosphate synthase subunit pdxS/S	down
AT1G72230	AT1G72230	AT1G72230_1	-2.239	0.01003	down	AT1G7223	-2.275	down		down

Table 9: DAS_alone list of differential alternatively spliced transcripts in the *prl1-1* mutant.

The list was filtered for prl1 TE/GE values > 0.2. TE: reads mapped to a specific transcript isoform; GE: reads mapped to all transcripts in a gene.

TAIR name	TAIR Uniprot Annotation	Splicing alteration	Altered ORF	ORF change	Predicted effect on gene function	prl1 TE total	wt TE total	prl1 GE total	wt GE total	prl1 /wt TE	prl1 /wt GE	prl1 TE/GE	wt TE/GE	Pathway	CLC Bio DAS prl1_wt	Fold change	P-value	CLC Bio Change
AT2G47900	tubby like protein 3	intron corresponding to retained intron, alternative 5' and 3' ends	no	wt	up	942	162	2996	2752	5.8	1.1	0.3	0.06	ABA osmotic stress signaling TLP3 tubby like F-box protein 3 PRK1, a receptor-like kinase interacting NET3C Kinase interacting (KIP1-like)	AtTLP3_1	4.911	5.55E-03	up
AT3G54810	GATA TRANSCRIPTION FACTOR 8	alternative 5' and 3' ends	no	wt	up	2387	863	6457	3375	2.8	1.9	0.4	0.26	ABA seed germination GATA TRANSCRIPTION FACTOR 8 BLUE MICROPYLAR END 3; BLUE MICROPYLAR END 3-ZINC FINGER; BME3-ZF	GATA8_1	2.296	0.0287113	up
AT5G10940	transducin family protein / WD-40 repeat family protein	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	up	607	212	1762	1160	2.9	1.5	0.3	0.18	ABA signaling negative regulator CUL4-DDB1 binding WD40 protein	AT5G10940_1	2.52	0.0450811	up
AT1G16540	SIRTINOL RESISTANT 3	retained intron	yes	wt	up	157	0	435	254	####	1.7	0.4	0	ABA synthesis drought tolerance ABA3/LOS5	SIR3_1	334.4	2.90E-03	up
AT2G34660	Multidrug resistance-associated protein 2	alternative 5' end	yes	302aa N-term deletion removing 5 transmembrane domains and part of the ABC_membrane domain	down	2283	704	6433	3378	3.2	1.9	0.4	0.21	ABA, chlorophyll degradation ABCC-type phytochelatin and vacuolar ABA transporter, arsenite tolerance	ABCC2_2_3	2.778	5.54E-04	up
AT3G11720	Polyketide cyclase/dehydrase and lipid transport superfamily protein	retained intron, alternative 5' end	yes	54aa N-term deletion	down ?	273	41	553	323	6.7	1.7	0.5	0.13	actin filaments, myosin motor MYSc domain protein	AT3G11720_3	5.419	0.0392022	up
AT1G03470	Networked 3A	alternative 5' end	no	wt	up	66	0	327	193	####	1.7	0.2	0	actin membrane achor	NET3A_1	165.9	0.01119	up
At3g58160	Myosin-16 (AtMYA3) (AtMYOS3) (Myosin XI J) (AtXIJ)	alternative 3' splice site, alternative 5' end	yes	C-term truncation pos 1139	down ?	91	0	226	100	####	2.3	0.4	0	actin Myosin XIJ	XI-J_3	185.9	8.44E-03	up
AT5G65940	beta-hydroxyisobutyryl-CoA hydrolase 1	alternative 3' end	no	wt	up	837	9	1928	1963	93	1	0.4	0	amino acid Branched-chain amino acid degradation CHY1 beta-hydroxyisobutyryl-CoA hydrolase 1	CHY1_4	70.44	1.56E-08	up
AT2G01170	At2g01170 (Bidirectional amino acid transporter 1)	intron corresponding to retained intron, alternative 5' and 3' ends	yes	wt	down	864	1615	1133	1792	0.5	0.6	0.8	0.9	amino acid GABA bidirectional phloem to sink transporter	BAT1_1_1	-2.129	0.0450645	down
AT4G32520	serine hydroxymethyltransferase 3	alternative 5' and 3' ends	no	wt	up	1490	579	4006	2811	2.6	1.4	0.4	0.21	amino acid one carbon pathway Ser to Gly SHM3 serine hydroxymethyltransferase 3	SHM3_2	2.197	0.0176192	up
AT2G39890	proline transporter 1	intron corresponding to retained intron	no	wt	down	786	1575	2351	2460	0.5	1	0.3	0.64	amino acid proline transporter 1	PROT1_2	-2.212	0.0177921	down
AT4G38090	Ribosomal protein S5 domain 2-like superfamily protein	intron corresponding to retained intron, alternative 5' end	yes	wt	down	410	791	510	853	0.5	0.6	0.8	0.93	amino acid starvation translation regulator Impact protein homolog	AT4G38090_1	-2.227	0.0365023	down
AT1G08630	threonine aldolase 1	none	no	wt	down	521	1431	1197	1909	0.4	0.6	0.4	0.75	amino acid Thr degradation to Gly threonine aldolase 1	THA1_6	-3.338	7.97E-03	down
AT1G69040	ACT domain repeat 4	alternative 5' and 3' ends	yes	4aa N-term deletion	down ?	521	17	2235	1454	31	1.5	0.2	0.01	amino acid, amino acid sensor/binding ACT domain protein	ACR4_1_1	24.3	8.55E-05	up
AT4G37670	N-acetyl-l-glutamate synthase 2	retained intron	yes	C-term truncation pos 541 removing the Acetyltransf_1 domain	down	129	6	329	171	22	1.9	0.4	0.04	amino acid, ornithine/Arg synthesis	NAGS2_2	16.16	9.60E-03	up
AT5G04770	cationic amino acid transporter 6	alternative 3' splice site, intron, corresponding to retained intron	yes	wt	down	322	749	959	1142	0.4	0.8	0.3	0.66	amino acid, sink cationic amino acid transporter 6	CAT6_1	-2.658	0.0426941	down
AT4G04620	autophagy 8b	alternative 3' splice site	no	wt	down	434	882	1480	2312	0.5	0.6	0.3	0.38	autophagy APG12 domain protein ATG8B Ubiquitin-like	ATG8B_3	-2.291	0.0270685	down
AT4G16520	autophagy 8f	alternative 5' and 3' ends	no	wt	down	2310	4342	5969	7872	0.5	0.8	0.4	0.55	autophagy ATG8F Ubiquitin-like superfamily protein	ATG8F_3	-2.137	5.16E-03	down
AT1G52030	myrosinase-binding protein 2	retained intron, alternative 5' and 3' ends	no	wt	up	46	3	217	258	15	0.8	0.2	0.01	auxin glucosinolate MBP2 myrosinase-binding protein 2	F-ATMBP_2	11.67	0.0479358	up
AT5G01240	like AUXIN RESISTANT 1	alternative 5' end	yes	wt	down	2408	4462	4298	6162	0.5	0.7	0.6	0.72	auxin influx transporter LAX1 lateral root vascular tissue differentiation	LAX1_2	-2.138	2.03E-03	down
AT1G01550	BYPASS 1	retained intron2, alternative 5' end	no	wt	up	2867	966	#####	9831	3	1.2	0.2	0.1	auxin shoot development inactivation of auxin signaling inhibitor	BPS1_2	2.444	2.10E-03	up
AT3G61830	auxin response factor 18	alternative 5' splice site, alternative 5' end	yes	51aa N-term deletion	down	366	0	1276	838	####	1.5	0.3	0	auxin signaling	ARF18_1	837.1	1.39E-04	up
AT1G19850	AUXIN RESPONSE FACTOR 5	alternative 5' end	yes	wt	up	856	286	1343	579	3	2.3	0.6	0.49	auxin signaling MONOPTEROUS/ARF5 shoot formation	ARF5_1	2.544	0.0154116	up
AT3G17185		none	no	wt	down	781	1684	781	1684	0.5	0.5	1	1	auxin TAS3 siRNA of auxin response factor genes ARF2, ARF4, ETT	TASIR-ARF_1_1	-2.461	0.0113663	down
AT1G06390	AT1G06390 protein	intron corresponding to retained intron, alternative 5' end	no	wt	up	965	340	4648	3314	2.8	1.4	0.2	0.1	BR signaling osmotic tolerance ABA induced GSK1 Shaggy BRZ1 kinase	ASK9_1_1	2.375	0.0226206	up
AT3G54930	Serine/threonine protein phosphatase 2A regulatory subunit	retained intron, alternative 5' end	yes	C-term truncation pos 396 removing part of the B56 domain	down	69	0	234	143	####	1.6	0.3	0	BR signalling PP2A B56 subunit	B'EPSILON_2	161.7	9.09E-03	up
At2g27580	Zinc finger A20 and AN1 domain-containing stress-associated protein 3 (AtSAP3)	retained intron,alternative 5' end	no	wt	down	866	1861	1876	2969	0.5	0.6	0.5	0.63	cell death A20- (an inhibitor of cell death)-like zinc finger ubiquitin-line STRESS ASSOCIATED PROTEIN3	SAP3_2	-2.425	3.65E-03	down
AT5G12080	mechanosensitive channel of small conductance-like 10	retained intron, alternative 5'-end	no	wt	up	447	0	1734	759	####	2.3	0.3	0	cell death JA accumulation MSL10 mechanosensitive channel of small conductance-like 10	MSL10_3	1025	8.11E-05	up

TAIR name	TAIR Uniprot Annotation	Splicing alteration	Altered ORF	ORF change	Predicted effect on gene function	prl1 TE total	wt TE total	prl1 GE total	wt GE total	prl1 /wt TE	prl1 /wt GE	prl1 TE/GE	wt TE/GE	Pathway	CLC Bio DAS prl1_wt	Fold change	P-value	CLC Bio Change
AT1G59560	E3 Ubiquitin ligase family protein	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 305 removing the RING domain	down	64	3	303	226	21	1.3	0.2	0.01	cell death, chloroplast RING E3 ligase with Mitochondrial ubiquitin ligase activator of NFKB 1 (MULAN, also known as GIDE) domain	SPL1_1_1	15.26	0.0301147	up
AT4G33260	Ankyrin repeat family protein	intron corresponding to retained intron, alternative 5' and 3' ends	yes	C-term aa replacement from pos 416	up?	99	4	483	205	25	2.4	0.2	0.02	cell division APC CDC20.2 WD40 subunit	CDC20-2_2	19.49	9.08E-03	up
AT3G16320	Tetratricopeptide repeat (TPR)-like superfamily protein	retained intron, alternative 5' and 3' ends	yes	11aa deletion pos 344-355 and C-term truncation pos 543 deleting 5 TRP repeats	down	49	0	208	98	####	2.1	0.2	0	cell division APC E3 G2/M	CDC27a_2	104.6	0.0212701	up
AT1G64690	BRANCHLESS TRICHOMES	retained intron, alternative 5' end	yes	50aa N-term deletion	down ?	52	0	237	117	####	2	0.2	0	cell division endoreduplication BLT1 coiled-coil domain protein	BLT_1	117.4	0.0162074	up
AT4G28760	Protein of unknown function (DUF3741)	exon, corresponding to exon skip	no	wt	up	1587	619	3397	1798	2.6	1.9	0.5	0.34	cell division G2/M DUF4378 TON1 RECRUITING MOTIF 20, TRM20	AT4G28760_1	2.153	0.0397769	up
AT4G35620	Cyclin B22	retained intron	yes	C-term truncation pos 381 removing the 2nd CYCLIN domain	down	88	0	294	143	####	2.1	0.3	0	cell division G2-M, CDKB interaction	CYCB2-2_2	178.8	9.26E-03	up
AT3G09370	myb domain protein 3r-3	alternative 3' splice site	yes	7aa deletion pos 13-20	down ?	283	38	521	299	7.4	1.7	0.5	0.13	cell division inhibitor of G2/M transition	MYB3R-3_1	6.353	0.0405146	up
AT1G56440	tetratricopeptide repeat 5	alternative 3' splice site	yes	10aa deletion pos 13-23	up?	656	169	804	544	3.9	1.5	0.8	0.31	cell division polarity root meristem, homolog of RNA-polymerase II-associated protein 3 (RPAP3), which binds to Monad and is involved in regulating apoptosis [(PUBMED:18538670)].	TPR5_1	3.505	0.0484918	up
AT3G27010	TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20	alternative 3' splice site	no	wt	up	123	6	364	431	21	0.8	0.3	0.01	cell division ribosome biogenesis TCP20 PCF (TCP)-DOMAIN FAMILY PROTEIN 20; PCF1; TEOSINTE BRANCHED 1	TCP20_2	17.54	0.0200469	up
AT1G06230	global transcription factor group E4	alternative 3' splice site	no	wt	up	2564	1036	3932	2481	2.5	1.6	0.7	0.42	cell division, cell number control BET bromodomain factor	GTE4_1	2.2	9.25E-03	up
AT3G01780	ARM repeat superfamily protein	alternative 5' splice site, alternative 5' end	yes	C-term truncation pos 840	down ?	1728	613	3498	2732	2.8	1.3	0.5	0.22	cell division, cell plate vesicular transport	TPLATE_1	2.437	0.0131257	up
AT5G55820	Inner centromere protein, ARK-binding region protein	exon skip	yes	31aa N-term deletion, 65aa deletion pos 1005-1070, C-term truncation removing part of the Aurora kinase binding INCENP_ARK-bind domain	up?	141	4	504	229	35	2.2	0.3	0.02	cell division, chromosome inner centromer protein (INCENP)	AT5G55820_1	23.19	0.0144888	up
AT5G25380	Cyclin a21	alternative 3' splice site, intron corresponding to retained intron, alternative 5' and 3' ends	yes	wt	up	31	0	61	55	####	1.1	0.5	0	cell division, cyclin CYCA2;1	CYCA2-1_1	65	0.0403523	up
AT5G05970	NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-REGULATED GENE 1	alternative 3' splice site	yes	wt	up	291	46	665	616	6.3	1.1	0.4	0.07	cell division, microtubule organization gamma-tubulin interacting NEDD1/GCP-WD protein	NEDD1_2	5.439	0.0314817	up
AT5G66610	DA1-related protein 7	retained intron, alternative 5' and 3' ends	yes	wt	up	42	0	73	51	####	1.4	0.6	0	cell division, organ size, ubiquitin interacting/receptor with LIM and DUF3633 domains	DAR7_3	93.71	0.0213125	up
AT5G60210	ROP interactive partner 5	alternative 5' and 3' ends	no	wt	up	770	264	1434	751	2.9	1.9	0.5	0.35	cell elongation polar growth RIP5 ROP interactive partner 5	RIP5_4	2.461	0.0475022	up
AT1G31650	ROP (rho of plants) guanine nucleotide exchange factor 14	alternative 5' end	yes	wt	up	1420	582	1586	761	2.4	2.1	0.9	0.76	cell elongation polarized growth ROPGEF14 RHO guanyl-nucleotide exchange factor 14	ROPGEF14_2	2.116	0.0258018	up
AT1G20190	expansin 11	alternative 5' and 3' ends	yes	wt	down	1060	2019	1333	2093	0.5	0.6	0.8	0.96	cell elongation secreted DPBB_1 domain containing expansin 11	EXPA11_1	-2.211	5.10E-03	down
AT2G46330	arabinogalactan protein 16	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 39 removing the DUF1070 domain	down	1671	531	8111	#####	3.1	0.7	0.2	0.05	cell wall arabinogalactan protein 16	AGP16_1	2.64	1.28E-03	up
AT2G28470	beta-galactosidase 8	retained introns	no	wt	up	2989	1260	5873	3328	2.4	1.8	0.5	0.38	cell wall BETA-GALACTOSIDASE 8, BGAL8 with signal peptide and D-galactoside binding lectin domain	BGAL8_5	2.058	9.36E-03	up
AT1G68200	Zinc finger C-x8-C-x5-C-x3-H type family protein	alternative 3' splice site, alternative 5' end	yes	wt	up	32	0	49	36	####	1.36	0.65	0	cell wall callose synthesis regulator ZnF_C3H1 domain TF	AT1G68200_1	73.645	0.02927639	up
AT5G15310	myb domain protein 16	retained intron, alternative 3' end	yes	C-term truncation pos 204	down ?	981	159	2290	1298	6.17	1.76	0.43	0.12	cell wall cuticule formatiion positive regulator MYB16 TF	ATMYB16_2	5.3229	1.98E-05	up
AT2G38650	galacturonosyltransferase 7	retained intron, alternative 5' end	no	wt	up	2420	962	2987	1587	2.52	1.88	0.81	0.61	cell wall homogalacturonan:galacturonosyltransferase	GAUT7_1	2.1578	9.00E-03	up
AT3G16340	ATP-binding cassette G29	alternative 5' and 3' ends	no	wt	up	969	338	1373	642	2.87	2.14	0.71	0.53	cell wall lignin biosynthesis p-coumaryl alcohol exporter involved in lignin biosynthesis	ABCG29_1	2.4666	0.02597947	up
AT1G25054	Probable UDP-3-O-acyl-N-acetylglucosamine deacetylase 3, mitochondrial (UDP-3-O-acyl-GlcNAc deacetylase 3) (EC 3.5.1.108) (Protein LIPID X C3) (AtLpxC3) (UDP-3-O-[R-3-hydroxymyristoyl]-N-acetylglucosamine deacetylase 3)	none	no	wt	up	1010	126	1010	126	8.02	8.02	1	1	cell wall lipidA biosynthesis UDP-3-O-acyl N-acetylglycosamine deacetylase	LPXC3_2_1	6.897	1.48E-04	up
AT1G25145	Probable UDP-3-O-acyl-N-acetylglucosamine deacetylase 4, mitochondrial (UDP-3-O-acyl-GlcNAc deacetylase 4) (EC 3.5.1.108) (Protein LIPID X C4) (AtLpxC4) (UDP-3-O-[R-3-hydroxymyristoyl]-N-acetylglucosamine deacetylase 4)	none	no	wt	down	442	1327	442	1327	0.33	0.33	1	1	cell wall lipidA biosynthesis UDP-3-O-acyl N-acetylglycosamine deacetylase	LPXC3_3_1	-3.4089	1.72E-03	down
AT4G29540	bacterial transferase hexapeptide repeat-containing protein	retained intron	yes	95aa N-term deletion of Hexapep domain	down	34	0	140	118	####	1.19	0.24	0	cell wall lipopolysaccharide UDP-N-acetylglucosamine acyltransferase	LPXA_1	75.228	0.03210778	up
AT3G15720	Pectin lyase-like superfamily protein	intron corresponding to retained intron	no	wt	up	181	11	264	133	16.5	1.98	0.69	0.08	cell wall pectate lyases or rhamnogalacturonase A	AT3G15720_2	13.212	7.60E-03	up
AT2G22620	Rhamnogalacturonate lyase family protein	none	no	wt	up	82	1	122	119	82	1.03	0.67	0.01	cell wall pectin Rhamnogalacturonate lyase	AT2G22620_1	48.309	6.01E-03	up

TAIR name	TAIR Uniprot Annotation	Splicing alteration	Altered ORF	ORF change	Predicted effect on gene function	prl1 TE total	wt TE total	prl1 GE total	wt GE total	prl1 /wt TE	prl1 /wt GE	prl1 TE/GE	wt TE/GE	Pathway	CLC Bio DAS prl1_wt	Fold change	P-value	CLC Bio Change
ATCG00330	30S ribosomal protein S14, chloroplastic	none	no	wt	down	574	1232	574	1232	0.47	0.47	1	1	chloroplast 30S ribosomal protein S14	RPS14_2_1	-2.5062	5.71E-03	down
ATCG00820	30S ribosomal protein S19, chloroplastic	none	no	wt	up	1274	410	1274	410	3.11	3.11	1	1	chloroplast 30S RIBOSOMAL PROTEIN S19, RPS19	RPS19_2_1	2.5114	0.01664631	up
ATCG00790	50S ribosomal protein L16, chloroplastic	none	no	wt	up	11502	4700	11502	4700	2.45	2.45	1	1	chloroplast 50S RIBOSOMAL PROTEIN L16, RPL16	RPL16_2_1	2.002	0.01422529	up
AT4G31990	aspartate aminotransferase 5	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 451	down ?	2884	972	8697	5738	2.97	1.52	0.33	0.17	chloroplast amino acid aspartate aminotransferase 5	ASP5_1	2.5566	4.90E-03	up
AT1G29410	phosphoribosylanthranilate isomerase 3	retained intron, exon skip	yes	22aa N-term deletion pos 3-25	down	90	7	217	194	12.9	1.12	0.41	0.04	chloroplast amino acid, auxin, TRP synthesis 3rd step, phosphoribosylanthranilate	PAI3_5	10.552	0.0250779	up
At2g45290	Transketolase-2, chloroplastic (TK) (EC 2.2.1.1)	intron, corresponding to retained intron, alternative 5' and 3' ends	no	wt	up	1308	554	1718	1059	2.36	1.62	0.76	0.52	chloroplast Calvin cycle TKL2; transketolase 2	TKL-2_1	2.0252	0.03392129	up
AT4G23420	NAD(P)-binding Rossmann-fold superfamily protein	alternative 5' and 3' ends	yes	25aa N-term deletion	down	76	0	186	206	####	0.9	0.41	0	chloroplast carotenoid vitamin A synthesis homolog of RDH12 retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	AT4G23420_1	176.28	7.38E-03	up
AT5G56500	Chaperonin 60 subunit beta 3, chloroplastic (CPN-60 beta 3)	alternative 3' splice site	no	wt	up	2285	949	2444	1058	2.41	2.31	0.93	0.9	chloroplast chaperonin Cpn60beta3 TCP-1/cpn60	CPN60B3_1	2.0409	7.94E-03	up
AT4G39710	Photosynthetic NDH subcomplex L 4	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	down	1836	3567	3226	5462	0.51	0.59	0.57	0.65	chloroplast cytochrome b6f complex NDH subcomplex L 4 subunit	PNSL4_2	-2.2501	1.57E-03	down
AT2G36250	Tubulin/FtsZ family protein	retained intron	no	wt	up	729	135	3516	3168	5.4	1.11	0.21	0.04	chloroplast division FTSZ2-1 tubulin	FTSZ2-1_2	4.6194	1.11E-03	up
AT3G16000	MAR binding filament-like protein 1	none	no	wt	up	6104	2533	6104	2533	2.41	2.41	1	1	chloroplast DNA-binding protein MFP1 MAR binding filament-like protein 1	MFP1_1	2.0004	0.01047465	up
AT3G22690	LOW protein: PPR containing-like protein	retained intron	yes	C-term truncation pos 841 removing the DYW_deaminase asnd DUF1685 domains	down	85	0	129	85	####	1.52	0.66	0	chloroplast editing of rpoB beta subunit of the plastid-encoded RNA polymerase transcript	AT3G22690_2	177.69	8.97E-03	up
AT3G20320	trigalactosyldiacylglycerol2	alternative 3' splice site	yes	wt	down	1357	2761	1848	2932	0.49	0.63	0.73	0.94	chloroplast ER lipid transporter	TGD2_3	-2.3466	1.20E-03	down
AT2G26310	fatty-acid-binding protein 2	alternative 3' end	no	wt	up	38	0	85	40	####	2.13	0.45	0	chloroplast fatty acid binding protein with chalcone isomerase 2 domain	FAP2_1	87.355	0.02779084	up
At3g49160	Plastidial pyruvate kinase 4, chloroplastic (PKp4) (EC 2.7.1.40)	retained intron, intron corresponding to retained intron	yes	89aa N-term deletion	down	285	29	654	565	9.83	1.16	0.44	0.05	chloroplast glycolysis pyruvate kinase	PKP4_1	8.3764	6.84E-03	up
AT3G57680	Peptidase S41 family protein	alternative 5' and 3' ends	yes	150aa N-term deletion removing the ClpP/crotonase domain	down	71	1	233	119	71	1.96	0.3	0.01	chloroplast lumen ClpP protease with PDZ and TSPCc domains	CTPA3_1	44.191	5.31E-03	up
AT5G22800	EMBRYO DEFECTIVE 86	alternative 5' end	yes	wt	up	1742	14	5840	2695	124	2.17	0.3	0.01	chloroplast mitochondrion EMB1030 Alanyl-tRNA synthetase, class IIc	EMB86_2	92.148	0	up
AT2G30170	Protein phosphatase 2C family protein	alternative 3' splice site, intron, corresponding to retained intron	yes	wt	down	515	1217	972	1565	0.42	0.62	0.53	0.78	chloroplast PBCP PP2C PHOTOSYSTEM II CORE PHOSPHATASE	AT2G30170_1	-2.6775	3.17E-03	down
At3g04870	Zeta-carotene desaturase, chloroplastic/chromoplastic (EC 1.3.5.6) (9,9'-di-cis-zeta-carotene desaturase) (Carotene 7,8-desaturase)	alternative 3' splice site, alternative 5' and 3' ends	no	wt	up	2103	268	7955	4035	7.85	1.97	0.26	0.07	chloroplast photoprotection cell death SPC1; SPONTANEOUS CELL DEATH 1; zeta-carotene desaturase	ZDS1_4	6.869	1.32E-03	up
At1g05385	Photosystem II D1 precursor processing protein PSB27-H2, chloroplastic (Psb27-H2) (LOW PSII accumulation 19 protein) (LPA19) (Thylakoid lumenal protein PSB27-H2)	alternative 5' end	yes	wt	down	424	914	591	965	0.46	0.61	0.72	0.95	chloroplast Photosystem II D1 precursor processing protein PSB27-H2	PSB27-2_2	-2.491	0.01181183	down
AT1G30610	EMBRYO DEFECTIVE 2279	intron, corresponding to retained intron, alternative 5' and 3' ends	yes	29aa deletion pos 720-749	down	1343	551	1365	607	2.44	2.25	0.98	0.91	chloroplast PPR repeat protein	EMB2279_1	2.0129	0.03671622	up
AT1G45474	photosystem I light harvesting complex gene 5	alternative 5' and 3' ends	no	wt	down	2809	5413	6268	9030	0.52	0.69	0.45	0.6	chloroplast PSI light harvesting complex protein 5	LHCA5_2	-2.225	1.59E-03	down
AT1G29040	50S ribosomal protein L34	alternative 5' splice site	yes	9aa deletion pos 148-157 in the Lin0512_fam domain	up	493	1003	1167	1646	0.49	0.71	0.42	0.61	chloroplast ribosome 50S ribosomal protein L34	AT1G29040_4	-2.3338	0.01341337	down
AT4G02260	RELA/SPOT homolog 1	alternative 5' splice site, alternative 5' and 3' ends	no	wt	up	1738	659	4176	2643	2.64	1.58	0.42	0.25	chloroplast stress signaling RSH1 RELA/SPOT homolog 1	RSH1_1	2.3363	4.84E-03	up
AT1G56200	embryo defective 1303	alternative 5' and 3' ends	no	wt	down	4736	9116	8877	13191	0.52	0.67	0.53	0.69	chloroplast unknown essential protein	emb1303_1	-2.1791	3.41E-03	down
AT1G60990	Glycine cleavage T-protein family	alternative 5' end	no	wt	up	791	294	1783	1069	2.69	1.67	0.44	0.28	chloroplast-localized COG0354 protein that requires folate for its function in Fe/S cluster biogenesis.	AT1G60990_2	2.3403	0.04604725	up
AT1G61215	bromodomain 4	alternative 5' and 3' ends	yes	53aa N-term deletion removing the SANT domain	down	37	0	155	164	####	0.95	0.24	0	chromatin histone K-acetyl binding bromodomain Myb TF	BRD4_1	80.045	0.02998073	up
AT2G28290	SPLAYED	intron corresponding to retained intron	yes	32aa deletion pos 3338-3370	up?	2665	261	5839	3929	10.2	1.49	0.46	0.07	chromatin remodelling meristem maintenance flowering time SWI/SNF CHR3, CHROMATIN REMODELING COMPLEX SUBUNIT R 3, SPLAYED, SYD	SYD_3	8.0212	9.26E-04	up
AT3G15430	Regulator of chromosome condensation (RCC1) family protein	retained intron, alternative 5' end	no	wt	up	783	198	2154	1817	3.95	1.19	0.36	0.11	chromatin unknown regulator of chromosome condensation (RCC1) repeat family	AT3G15430_1	3.2636	0.02280786	up

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AT1G65470	FASCIATA 1	alternative 5' splice site, alternative 5' and 3' ends	yes	7aa deletion pos 269-276 in the coiled coil domain	down ?	133	5	523	239	26.6	2.19	0.25	0.02	chromatin, heterochromatin assembly recombination cell cycle	FAS1_1	21.114	0.01038059	up
AT5G42140	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	retained intron, alternative 5' end	no	wt	up	1054	423	1265	617	2.49	2.05	0.83	0.69	chromosome condensation RCC1 repeat protein phosphatidylinositol binding Pleckstrin homology, FYVE and Brevis radix-like domains	AT5G42140_2	2.0858	0.03328157	up
AT5G02520	Dentin sialophosphoprotein-like protein	alternative 3' ends	no	wt	up	31	0	98	58	####	1.69	0.32	0	chromosome kinetochore protein KINETOCHORE NULL 2, KNL2	AT5G02520_1	62.42	0.04771131	up
AT2G46790	Arabidopsis pseudo-response regulator 9	retained intron	yes	C-term truncation pos 438 removing part of the CCT domain	down	171	17	676	390	10.1	1.73	0.25	0.04	circadian clock CCA_LHY repressor	APRR9_2	8.5855	0.03210172	up
AT3G22420	with no lysine (K) kinase 2	retained intron, alternative 5' and 3' ends	yes	wt	up	419	48	1898	1602	8.73	1.18	0.22	0.03	circadian rythm flowering time ABA	WNK2_5	7.1211	0.02144038	up
AT3G14940	phosphoenolpyruvate carboxylase 3	alternative 5' and 3' ends	no	wt	up	1390	572	2179	1041	2.43	2.09	0.64	0.55	citrate cycle PHOSPHOENOLPYRUVATE CARBOXYLASE 3, PPC3	PPC3_1	2.0314	0.0317892	up
AT1G53310	phosphoenolpyruvate carboxylase 1	alternative 5' splice site	no	wt	up	3072	102	8835	4289	30.1	2.06	0.35	0.02	Citrate cycle PPC1 phosphoenolpyruvate carboxylase 1	PPC1_2	26.977	3.47E-12	up
AT3G07740	homolog of yeast ADA2 2A	alternative 5' splice site, alternative 5' end	yes	72aa N-term deletion removing part of ZnF_ZZ domain	down	298	0	677	406	####	1.67	0.44	0	cold, osmotic stress, transcription co-activator CBF1 and GCN5 interactor	ADA2A_2	677.15	2.81E-04	up
AT2G41510	CYTOKININ OXIDASE/DEHYDROGENASE 1	alternative 5' and 3' ends	yes	62aa N-term deletion	up?	73	0	255	126	####	2.02	0.29	0	cytokinin degradation root shoot meristem	ATCKX1_2	161.11	0.01110397	up
AT1G80050	adenine phosphoribosyl transferase 2	intron corresponding to retained intron, alternative 5' end	yes	wt	down	684	1294	859	1397	0.53	0.61	0.8	0.93	cytokinin purine salvage APT2 adenine phosphoribosyl transferase 2	APT2_1	-2.1509	0.01656274	down
AT2G01760	response regulator 14	retained intron, alternative 5' and 3' ends	yes	65aa N-term deletion removing part of the REC domain	down	112	6	505	618	18.7	0.82	0.22	0.01	cytokinin response regulator 14	ARR14_1	14.136	0.01602503	up
At3g05740	ATP-dependent DNA helicase Q-like 1 (EC 3.6.4.12) (RecQ-like protein 1) (AtRecQ1) (AtRecQl1)	retained intron, alternative 5' end	yes	85aa N-term deletion	up?	109	6	138	79	18.2	1.75	0.79	0.08	DNA recombination	RECQL1_1	14.589	0.01501246	up
AT1G62740	Hsp70-Hsp90 organizing protein 2 (AtHop2)	none	no	wt	up	3317	1334	3317	1334	2.49	2.49	1	1	DNA recombination HOP2-MND1 heterodimer is essential for meiotic homologous recombination	HOP2_2_1	2.1131	6.29E-03	up
AT3G22880	DISRUPTION OF MEIOTIC CONTROL 1	alternative 5' and 3' ends	yes	C-term truncation pos 330	down ?	450	114	778	412	3.95	1.89	0.58	0.28	DNA recombination meiosis gametophyte	DMC1_1	3.1804	0.03837438	up
AT4G24710	P-loop containing nucleoside triphosphate hydrolases superfamily protein	alternative 5' and 3' ends	yes	C-term truncation pos 347 removing part of the ATPase domain	down	58	0	226	141	####	1.6	0.26	0	DNA recombination meiosis PCH2 homolog	AT4G24710_4	144.03	0.01388063	up
AT3G20475	MUTS-homologue 5	retained intron	yes	C-term truncation pos 735 removing part of the ATPase domain of DNA mismatch repair MUTS	down	38	0	73	55	####	1.33	0.52	0	DNA recombination, meiosis	MSH5_3	86.589	0.02791322	up
AT2G31865	poly(ADP-ribose) glycohydrolase 2	retained intron	yes	C-term truncation pos 400 removing the PARG_cat domain	down	64	0	200	219	####	0.91	0.32	0	DNA repair cell death pathogen response poly(ADP-ribose) glycohydrolase 2	PARG2_1	135.32	0.01299252	up
AT5G40840	Rad21/Rec8-like family protein	alternative 3' splice site	yes	wt	up	62	0	212	118	####	1.8	0.29	0	DNA repair cohesin Rad21	SYN2_5	123.58	0.02068479	up
AT1G19025	DNA repair metallo-beta-lactamase family protein	retained intron	yes	106aa N-term deletion in the Lactamase_B domain	down	32	0	144	87	####	1.66	0.22	0	DNA repair Ku70/80 interacting metallo-beta-lactamase	AT1G19025_1	64.392	0.04619374	up
AT4G02485	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	alternative 5' end; missing intron	no	wt	up	65	0	192	96	####	2	0.34	0	DNA repair putaive AlkB DNA repair enzyme	AT4G02485_1	168.7	0.01409504	up
AT5G44750	DNA-directed DNA polymerases	alternative 5' splice site	yes	wt	up	508	8	1440	829	63.5	1.74	0.35	0.01	DNA repair UV tolerance Y-family DNA polymerase	REV1_2	51.571	1.06E-06	up
AT4G24900	Coiled coil protein	alternative 3' splice site	yes	3aa deletion pos 253-256 in the CCDC84 domain	down ?	171	9	414	205	19	2.02	0.41	0.04	endosperm development, coiled coil protein	TTL_1_1	15.286	6.97E-03	up
At1g35350	Phosphate transporter PHO1 homolog 8 (Protein PHO1 homolog 8) (AtPHO1;H8)	retained intron, alternative 5' and 3' ends	yes	184aa N-term deletion removing part of the SPX domain	down	1728	691	2203	1066	2.5	2.07	0.78	0.65	ER G-protein interacting transmembrane SPX-EXS domain protein	PHO1-H8_1	2.0876	0.01295398	up
AT1G06515	Protein of unknown function (DUF3317)	alternative 5' end	no	wt	down	814	1452	962	1631	0.56	0.59	0.85	0.89	ER palmitoyl transferase complex associated SMALL SUBUNIT OF SPT A, SSSPTA	AT1G06515_2	-2.0447	0.02207045	down
AT2G04350	long-chain acyl-CoA synthetase 8	alternative 5' end	no	wt	up	2616	863	3480	1693	3.03	2.06	0.75	0.51	fatty acid long chain oil synthesis long-chain acyl-CoA synthetase 8	LACS8_2	2.6147	4.54E-03	up
AT2G23000	serine carboxypeptidase-like 10	retained intron, alternative 3' end	no	wt	up	1096	355	2166	1093	3.09	1.98	0.51	0.32	flavonoid phenylpropanoid metabolism anthocyanine sinapoylglucose acyltransferases SNG1	SCPL10_2	2.6148	0.04028816	up
AT4G22880	leucoanthocyanidin dioxygenase	alternative 3' splice site, alternative 3' end	no	wt	up	89	0	128	55	####	2.33	0.7	0	flavonoid protoanthocyanine synthesis LDOX leucoanthocyanidin dioxygenase	LDOX_3	191.58	7.79E-03	up
At1g06000	UDP-glycosyltransferase 89C1 (EC 2.4.1.-) (Flavonol 7-O-rhamnosyltransferase) (UDP-rhamnose: flavonol 7-O-rhamnosyltransferase)	none	no	wt	up	1657	743	1657	743	2.23	2.23	1	1	flavonol biosynthesis flavonol-7-O-rhamnosyltransferase involved in the formation of rhamnosylated flavonols	UGT89C1_1	2.0153	0.03386423	up
At5g64667	Protein IDA-LIKE 2	intron corresponding to retained intron, alternative 5' end	no	wt	down	1407	2720	1753	2994	0.52	0.59	0.8	0.91	flower abscission 95aa transmembrane IDL2, INFLORESCENCE DEFICIENT IN ABSCISSION (IDA)-LIKE 2 peptide ligand of LRR receptor kinases HAE amd HSL2	MUB3_1	-2.2088	3.30E-03	down

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AT5G44180	RINGLET 2	alternative 5' and 3' ends	no	wt	up	868	280	2961	1821	3.1	1.63	0.29	0.15	flowering time represor, ISWI CHROMATIN REMODELING11 (CHR11) and CHR17 interacting RINGLET 2 TF	RLT2_3	2.6594	0.01631314	up
AT5G25040	Major facilitator superfamily protein	intron corresponding to retained intron, alternative 5' and 3' ends	yes	26 aa deletion pos 294-320 removing part of the BT1 domain	down	90	0	440	431	####	1.02	0.2	0	folate C1 transport metabolism	AT5G25040_2	213.94	6.73E-03	up
AT1G04570	Major facilitator superfamily protein	alternative 3' splice site	yes	wt	up	32	0	50	34	####	1.47	0.64	0	folate-biopterin transporter	AT1G04570_1	70.879	0.03496505	up
AT4G26520	Aldolase superfamily protein	alternative 3' end	yes	wt	down	507	1143	1262	1965	0.44	0.64	0.4	0.58	glycolysis fructose-bisphosphate aldolase 7	AT4G26520_3	-2.5215	0.01324449	down
AT3G08590	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	retained intron, alternative 5' and 3' ends	no	wt	up	6501	2739	12650	5587	2.37	2.26	0.51	0.49	glycolysis iPGAM2 Phosphoglycerate mutase stomatal movement	AT3G08590_2	2.0671	3.15E-03	up
AT5G03860	malate synthase	alternative 5' end; missing intron	no	wt	up	68	0	238	169	####	1.41	0.29	0	glyoxalate cycle MLS malate synthase	MLS_2	166.09	0.01112201	up
AT3G56800	Calmodulin-3 (CaM-3)	none	no	wt	down	8839	16819	8839	16819	0.53	0.53	1	1	heat shock signaling CAM3 calmodulin 3	CAM2_2_1	-2.1799	5.92E-03	down
AT3G57980	DNA-binding bromodomain-containing protein	alternative 3' splice site, alternative 5' end	yes	wt	up	307	50	519	245	6.14	2.12	0.59	0.2	histone acetyl binding bromodomain MYB TF	AT3G57980_1	5.0795	0.03886495	up
AT1G73150	global transcription factor group E3	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 416	down	245	34	351	286	7.21	1.23	0.7	0.12	histone acetyl H3 binding bromodomain, ATX2 and SDG histone methylase interacting factor	GTE3_2	6.1319	0.0372639	up
AT1G75060	Uncharacterized protein	retained intron	yes	C-term truncation pos 189	down ?	32	0	125	114	####	1.1	0.26	0	histone deacetylase complex HD1/9 subunit	AT1G75060_3	74.987	0.03333159	up
AT2G02470	alfin-like 6	alternative 3' splice site	yes	wt	down	344	805	1344	1750	0.43	0.77	0.26	0.46	histone H3Kme3/me3 binding PHD TF phosphate starvation root hair growth	AL6_3	-2.7208	0.01018652	down
AT1G07820	Histone superfamily protein	intron corresponding to retained intron	no	wt	down	985	2433	2437	3978	0.4	0.61	0.4	0.61	Histone H4	AT1G07820_1	-2.8973	3.83E-05	down
AT1G77310	Wound-responsive family protein	exon skip	yes	170aa N-term deletion removing the HPC2 HUN domain	down	64	0	260	179	####	1.45	0.25	0	histone nucleosome assembly silencing HPC2 (Histone promoter control 2) domain protein	AT1G77310_2	127.53	0.02020028	up
AT4G26630	DEK domain-containing chromatin associated protein	alternative 5' and 3' ends	no	wt	up	4006	890	6955	4679	4.5	1.49	0.58	0.19	histones H3 and H4 binding chromatin DEK-DOMAIN CONTAINING PROTEIN 3, DEK3	AT4G26630_2	4.0337	5.81E-03	up
AT3G61750	Cytochrome b561/ferric reductase transmembrane with DOMON related domain	retained intron	yes	26aa N-term deletion removing the signal peptide	down	231	26	1030	540	8.88	1.91	0.22	0.05	iron reduction, Cytochrome b-561 / ferric reductase with DOMON domain	AT3G61750_1	7.4342	0.02033883	up
AT1G23020	ferric reduction oxidase 3	alternative 5' and 3' ends	no	wt	up	2594	896	4513	2047	2.9	2.2	0.57	0.44	iron uptake FRO3 ferric reduction oxidase 3	FRO3_4	2.4948	5.63E-04	up
AT3G45130	lanosterol synthase 1	alternative 3' end	yes	C-term truncation of the last 8aa	up?	26	0	66	39	####	1.69	0.39	0	isoprenoid sterol biosynthesis lanosterol synthase	LAS1_4	62.976	0.04041284	up
AT1G78955	camelliol C synthase 1	retained introns	yes	67aa N-term deletion, C-term truncation pos 669 removing the 2nd Prenyltrans domain	down	21	0	50	37	####	1.35	0.42	0	isoprenoid, triterpene synthesis	CAMS1_5	53.481	0.04805473	up
AT5G05600	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	intron corresponding to retained intron, alternative 5' and 3' ends	yes	wt	down	1714	3039	1876	3097	0.56	0.61	0.91	0.98	JA pathogen JASMONIC ACID OXIDASE 2, JOX2	AT5G05600_2	-2.0505	0.01278193	down
AT3G44530	homolog of histone chaperone HIRA	exon skip	yes	35aa deletion pos 745-780 in the Hira domain	down	338	39	812	684	8.67	1.19	0.42	0.06	leaf development histone chaperone HIRA	HIRA_2	8.0911	0.0412459	up
AT1G30210	TEOSINTE BRANCHED 1, cycloidea, and PCF family 24	alternative 5' end	no	wt	down	630	1196	1829	2152	0.53	0.85	0.34	0.56	leaf development, ribosome biogenesis TCP24 TEOSINTE BRANCHED 1, cycloidea	TCP24_1	-2.2662	0.0277496	down
AT5G13390	NO EXINE FORMATION 1	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	up	1726	717	4014	3671	2.41	1.09	0.43	0.2	lipid biosynthesis or transport transmembrane protein	NEF1_2	2.0798	0.02302372	up
AT5G08030	PLC-like phosphodiesterases superfamily protein	alternative 5' end	yes	15aa N-term deletion of signal peptide	down	71	0	165	149	####	1.11	0.43	0	lipid degradation GDPD6, GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE 6	AT5G08030_1	169.82	0.01340767	up
AT1G67360	Rubber elongation factor protein (REF)	alternative 5' and 3' ends	no	wt	up	438	49	1516	1327	8.94	1.14	0.29	0.04	lipid droplet associated protein LDAP1, SMALL RUBBER PARTICLE PROTEIN, SRP1 drought stress organ development	AT1G67360_1	8.2425	3.18E-03	up
AT1G80900	magnesium transporter 1	alternative 5' and 3' ends	no	wt	up	82	0	341	223	####	1.53	0.24	0	magnesium transporter 1 MGT1	MRS2-10_2	187.3	6.41E-03	up
AT2G42890	MEI2-like 2	alternative 5' end	yes	13aa N-term deletion	up?	562	79	1808	1465	7.11	1.23	0.31	0.05	meiosis RAPTOR interacting RNA binding protein	ML2_1	6.0947	0.03182631	up
AT3G50100	small RNA degrading nuclease 1	alternative 5' and 3' ends	yes	97aa N-term deletion	down ?	87	3	215	163	29	1.32	0.4	0.02	microRNA degradation	SDN1_2	24.788	0.01116457	up
AT1G14690	microtubule-associated protein 65-7	retained intron	no	wt	up	1545	504	2330	1420	3.07	1.64	0.66	0.35	microtubule associated protein 65-7	MAP65-7_1	2.5884	2.52E-03	up
AT1G11160	Transducin/WD40 repeat-like superfamily protein	intron corresponding to retained intron, alternative 5' end	yes	wt	up	39	0	86	51	####	1.69	0.45	0	microtubule katanin p80 subunit	AT1G11160_3	89.528	0.02670004	up

TAIR name	TAIR Uniprot Annotation	Splicing alteration	Altered ORF	ORF change	Predicted effect on gene function	prl1 TE total	wt TE total	prl1 GE total	wt GE total	prl1 /wt TE	prl1 /wt GE	prl1 TE/GE	wt TE/GE	Pathway	CLC Bio DAS prl1_wt	Fold change	P-value	CLC Bio Change
At5g27950	Kinesin-like protein KIN-14U	intron corresponding to retained intron, alternative 3' end	yes	wt	up	606	186	2364	1013	3.26	2.33	0.26	0.18	microtubule kinesin motor	KIN14U_1	2.6999	0.0408128	up
AT3G53760	GAMMA-TUBULIN COMPLEX PROTEIN 4	exon skip	yes	28aa deletion pos 393-421 in the spindle body Spc97_Spc98 domain	down	119	0	447	322	####	1.39	0.27	0	microtubule nucleation chromosome segregation stability	GCP4_1	262.99	3.32E-03	up
AT2G47920	Networked 3C	retained intron	no	wt	up	37	0	125	96	####	1.3	0.3	0	microtubule PM interaction	NET3C_1	88.886	0.03195332	up
AT5G37510	embryo defective 1467	intron corresponding to retained intron, alternative 5' and 3' ends	yes	wt	up	2684	1145	9954	6666	2.34	1.49	0.27	0.17	mitochondrion subunit of the 400 kDa subcomplex of the mitochondrial NADH dehydrogenase (complex I)	EMB1467_1	2.1042	0.01918874	up
AT4G26180	Mitochondrial substrate carrier family protein	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 291 removing part of the 3rd Mito_carr domain	down	88	7	330	281	12.6	1.17	0.27	0.02	mitochondrion Co-A transporter	AT4G26180_2	10.25	0.03996061	up
AT5G18800	Cox19-like CHCH family protein	alternative 3' splice site, alternative 5' end	no	wt	down	1578	2785	2673	4187	0.57	0.64	0.59	0.67	mitochondrion COX19-like CHCH domain protein	AT5G18800_1	-2.061	8.20E-03	down
AT4G21090	MITOCHONDRIAL FERREDOXIN 2	alternative 3' splice site	no	wt	up	174	22	628	508	7.91	1.24	0.28	0.04	mitochondrion FERREDOXIN 2	MFDX2_3	6.8395	0.03524958	up
AT3G59650	mitochondrial ribosomal protein L51/S25/CI-B8 family protein	intron corresponding to retained intron, alternative 3' end	no	wt	down	644	1134	681	1153	0.57	0.59	0.95	0.98	mitochondrion L51_S25_CI-B8 domain protein	AT3G59650_2	-2.0148	0.03305029	down
AT4G37190	AT4G37190 protein (Plasma membrane, autoregulation-binding site, misato segment II, myosin-like, tubulin/FtsZ protein)	alternative 5' end	yes	46aa N-term deletion removing part of the Misat_Tub_SegII domain	down	282	13	1214	787	21.7	1.54	0.23	0.02	mitochondrion misato 1, mitochondrial distribution and morphology regulator	AT4G37190_2	18.781	8.48E-04	up
AT1G67350	Uncharacterized protein	alternative 5' end	no	wt	down	1910	3720	2936	4374	0.51	0.67	0.65	0.85	mitochondrion NADH-ubiquinone oxidoreductase	AT1G67350_1	-2.2232	4.16E-03	down
AT2G07707		none	no	wt	down	28	183	28	183	0.15	0.15	1	1	mitochondrion Plant mitochondrial ATPase, F0 complex, subunit 8	YMF19_1_1	-7.4895	8.55E-11	down
AT3G22370	alternative oxidase 1A	none	no	wt	up	6460	2775	6460	2775	2.33	2.33	1	1	mitochondrion redox cold tolerance AOX1A alternative oxidase 1A	AOX1A_1	2.0129	3.41E-03	up
At5g08490	Putative pentatricopeptide repeat-containing protein At5g08490	retained intron	yes	wt	up	29	0	57	42	####	1.36	0.51	0	mitochondrion RNA editing PPR repeat protein	PCMP-E32_5	64.539	0.03813318	up
At3g23330	Putative pentatricopeptide repeat-containing protein At3g23330	retained intron, alternative 5' and 3' ends	yes	wt	up	98	0	112	67	####	1.67	0.88	0	mitochondrion RNA processing PPR repeat protein	PCMP-H32_2	205.78	6.68E-03	up
ATMG00290	Ribosomal protein S4, mitochondrial	none	no	wt	down	46	0	46	0	####	####	1	####	mitochondrion SSU RIBOSOMAL PROTEIN S4, RPS4	RPS4_2_1	99.47	0.02003135	up
AT2G30920	coenzyme Q 3	alternative 3' splice site, alternative 5' and 3' ends	no	wt	up	438	39	1133	711	11.2	1.59	0.39	0.05	mitochondrion ubiquinone synthesis hexaprenyldihydroxybenzoate methyltransferase COQ3 coenzyme Q 3	COQ3_1	9.7693	1.55E-03	up
AT4G04790	Tetratricopeptide repeat (TPR)-like superfamily protein	retained intron	yes	138aa N-term deletion	down	44	0	166	122	####	1.36	0.27	0	mitochondrion unknown PPR domain protein	AT4G04790_3	94.284	0.02429211	up
At4g14170	Pentatricopeptide repeat-containing protein At4g14170	intron, corresponding to retained intron	yes	99aa deletion pos 106-205 removing the 1st and 2nd PPR domains	down	59	3	125	128	19.7	0.98	0.47	0.02	mitochondrion, RNA editing MITOCHONDRIAL EDITING FACTOR 32	PCMP-E17_2	15.129	0.02714083	up
AT3G61620	3'-5'-exoribonuclease family protein	alternative 5' end	no	wt	up	216	19	905	744	11.4	1.22	0.24	0.03	mRNA processing ribosome biogenesis exosome subunit SKI6, ECM20; RRP41	RRP41_2	9.6559	0.01039685	up
AT3G12640	RNA binding (RRM/RBD/RNP motifs) family protein	alternative 5' and 3' ends	no	wt	up	693	182	1801	924	3.81	1.95	0.38	0.2	mRNA processing SR-related PWI-RRM domain protein	AT3G12640_3	3.3889	0.04438897	up
AT2G29200	pumilio 1	alternative 5' end	no	wt	up	856	142	1341	905	6.03	1.48	0.64	0.16	mRNA stability translation PUM1 pumilio 1	APUM1_2	5.0286	6.49E-04	up
At3g13050	Organic cation/carnitine transporter 7 (AtOCT7)	alternative 5' end	no	wt	up	371	35	823	646	10.6	1.27	0.45	0.05	NAD biosynthesis nicotinate transporter NiaP	OCT7_1	8.8371	0.01765366	up
AT3G52072	other RNA	retained introns	no	wt	up	24	0	86	85	####	1.01	0.28	0	ncRNA	AT3G52072_6	58.761	0.03926674	up
AT1G26208	other RNA	retained intron	no	wt	up	151	0	544	345	####	1.58	0.28	0	ncRNA	AT1G26208_3	325.98	2.26E-03	up
AT5G45472		retained intron, alternative 5' and 3' splice sites	no	wt	up	103	0	385	236	####	1.63	0.27	0	ncRNA	AT5G45472_2	256.74	4.81E-03	up
AT1G72855	other RNA	retained intron	no	wt	up	78	0	335	271	####	1.24	0.23	0	ncRNA	AT1G72855_3	197.35	8.21E-03	up
AT4G26795	other RNA	retained intron, alternative 3' splice site	no	wt	up	36	0	164	130	####	1.26	0.22	0	ncRNA	AT4G26795_4	79.202	0.03080023	up
AT4G24020	NIN like protein 7	intron corresponding to retained intron	yes	280aa N-term deletion removing part of the GAF domain	down	1172	419	4824	3664	2.8	1.32	0.24	0.11	nitrate sensing NLP7 NIN like protein 7 TF	NLP7_1	2.352	0.01316847	up
AT3G03970	ARM repeat superfamily protein	intron, corresponding to retained intron, alternative 5' splice site	no	wt	up	139	5	371	178	27.8	2.08	0.37	0.03	nuclear envelop SUN1/2 interacting actin colocalized SINE2 ARM repeat membrane protein	AT3G03970_3	19.27	8.28E-03	up

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AT1G68910	WPP domain-interacting protein 2	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	up	314	44	1059	667	7.14	1.59	0.3	0.07	nuclear export/import RAN_GAP anchor protein	WIT2_3	5.9237	0.02787159	up
AT1G33410	Nuclear pore complex protein NUP160 (AtNUP160) (Nucleoporin 160) (Protein SUPPRESSOR OF AUXIN RESISTANCE 1)	alternative 3' splice site	yes	wt	up	704	114	2344	1407	6.18	1.67	0.3	0.08	nuclear pore component NUP160, repression of auxin signaling, cold, pathogen	SAR1_1_1	5.4025	7.00E-03	up
AT4G05110	equilibrative nucleoside transporter 6	alternative 3' end, retained intron	yes	C-term truncation pos 412	up?	56	0	262	171	####	1.53	0.21	0	nucleoside transporter ATEN6 equilibrative nucleoside transporter 6	ATENT6_3	134.12	0.01903193	up
AT3G23610	dual specificity protein phosphatase 1	alternative 3' splice site	yes	wt	up	42	0	143	157	####	0.91	0.29	0	osmotic stress negative regulation of MAP kinase signaling	DSPTP1_3	91.484	0.02573675	up
AT5G43730	Disease resistance protein (CC-NBS-LRR class) family	alternative 5' and 3' ends	no	wt	up	179	12	329	151	14.9	2.18	0.54	0.08	pathogen CC-NBS-LRR RESISTANCE SILENCED GENE 2, RSG2	AT5G43730_5	11.786	0.02795752	up
AT5G20480	EF-TU receptor	retained intron	no	wt	up	347	0	590	382	####	1.54	0.59	0	pathogen EFR LRR receptor kinase for EF-Tu	EFR_1	714.56	4.12E-04	up
AT5G55390	ENHANCED DOWNY MILDEW 2	alternative 3' splice site	no	wt	up	619	77	1636	946	8.04	1.73	0.38	0.08	pathogen ENHANCED DOWNY MILDEW 2 TF activator of RPP7	EDM2_3	6.4628	5.57E-03	up
AT5G46330	Leucine-rich repeat receptor-like protein kinase (Fragment)	retained intron	no	wt	up	650	73	2381	1100	8.9	2.16	0.27	0.07	pathogen FLAGELLIN-SENSITIVE 2 Leucine-rich receptor-like protein kinase	FLS2_1_2	7.1965	0.01888469	up
AT2G03440	Nodulin-related protein 1 (AtNRP1) (RPS2-interacting protein 11)	none	no	wt	down	11508	20893	11508	20893	0.55	0.55	1	1	pathogen induced NODULIN-RELATED PROTEIN 1, NRP1	NRP1_2_1	-2.106	9.77E-03	down
AT1G20030	Pathogenesis-related thaumatin superfamily protein	alternative 5' end	yes	wt	down	611	1336	1088	1593	0.46	0.68	0.56	0.84	pathogen induced PR5 Thaumatin with signal peptide	AT1G20030_2	-2.5153	0.02028106	down
AT1G10170	NF-X-like 1	retained intron, alternative 5' and 3' ends	yes	wt	up	3039	1230	5163	3791	2.47	1.36	0.59	0.32	pathogen negative regulator of defence response homologue of the putative human transcription repressor NF-X1	ATNFXL1_1	2.1498	0.01544897	up
AT3G09830	Protein kinase superfamily protein	alternative 3' splice site	no	wt	up	224	27	721	526	8.3	1.37	0.31	0.05	pathogen PATTERN-TRIGGERED IMMUNITY (PTI) COMPROMISED RECEPTOR-LIKE CYTOPLASMIC KINASE 1, PCRK1	AT3G09830_2	7.0165	0.02937419	up
AT2G18750	Calmodulin-binding protein 60 C	retained intron	no	wt	up	764	165	3509	2548	4.63	1.38	0.22	0.06	pathogen SA CALMODULIN-BINDING PROTEIN60	CBP60C_2	3.9723	7.80E-04	up
At3g50950	Disease resistance RPP13-like protein 4 (Disease resistance protein ZAR1) (Protein HOPZ-ACTIVATED RESISTANCE 1)	alternative 5' and 3' ends	no	wt	up	2293	733	3986	2339	3.13	1.7	0.58	0.31	pathogen ZAR1 HOPZ-ACTIVATED RESISTANCE 1	RPP13L4_2	2.5713	2.01E-03	up
AT5G45050	Disease resistance protein (TIR-NBS-LRR class)	alternative 5' end	yes	140aa N-term deletion of TIR PDB domain 3JRN|A	down	844	124	1601	696	6.81	2.3	0.53	0.18	pathogen, AvrRPS4 recognition	WRKY16_3	5.722	4.55E-05	up
AT5G45100	BOI-related gene 1	retained intron, alternative 5' and 3' ends	yes	28aa N-term deletion	down ?	354	31	1766	1292	11.4	1.37	0.2	0.02	pathogen, flowering time inhibitor RING E3	BRG1_2	9.9202	2.71E-03	up
AT1G79110	BOI-related gene 2	retained intron	yes	22aa N-term. deletion	down ?	327	0	1120	879	####	1.27	0.29	0	pathogen, flowering time repressor ubiquitin RING E3	BRG2_3	731.38	2.16E-04	up
AT5G38210	Protein kinase family protein	alternative 5' end	yes	270aa N-term amino acid exchange	down	485	43	845	497	11.3	1.7	0.57	0.09	pathogen, rust resistance homolog transmembrane kinase with signal peptide and Wall-associated receptor kinase C-terminal	AT5G38210_2	9.8243	3.60E-03	up
AT2G01490	phytanoyl-CoA 2-hydroxylase	retained intron	no	wt	down	2576	4741	4932	7281	0.54	0.68	0.52	0.65	peroxisome branch chain fatty acid oxidation PAHX phytanoyl-CoA dioxygenase	PAHX_1	-2.1047	3.32E-03	down
AT3G52880	monodehydroascorbate reductase 1	exon, corresponding to exon skip, alternative 5' and 3' ends	yes	wt	up	7828	3133	16806	11834	2.5	1.42	0.47	0.26	peroxisome, ROS removal	ATMDAR1_1	2.1501	6.42E-03	up
AT5G19430	RING/U-box superfamily protein	retained intron	yes	60aa N-term deletion removing part of the RING domain	down	328	35	1590	1287	9.37	1.24	0.21	0.03	phosphate starvation regulated RING E3	AT5G19430_2	7.3631	0.01470878	up
AT4G04450	WRKY family transcription factor	retained intron	yes	95aa N-term deletion	down ?	23	0	55	25	####	2.2	0.42	0	phosphate uptake negative regulator WRKY TF	WRKY42_1	53.439	0.04185982	up
AT2G31830	endonuclease/exonuclease/phosphatase family protein	retained introns	yes	C-term truncation pos 905 removing part of the IPPc Inositol polyphosphate phosphatase catalytic domain	down	29	0	117	62	####	1.89	0.25	0	phosphatidylinositol dephosphorylation	AT2G31830_1	70.997	0.03099436	up
At1g49340	Phosphatidylinositol 4-kinase alpha 1 (PI4-kinase alpha 1) (PtdIns-4-kinase alpha 1) (EC 2.7.1.67) (Phosphatidylinositol 4-OH kinase alpha1) (AtPI4Kalpha1) (PI-4Kalpha1)	alternative 5' splice site, intron corresponding to retained intron, alternative 3' end	yes	7aa deletion pos 440-447	up?	1745	733	3956	3220	2.38	1.23	0.44	0.23	phosphatidylinositol synthesis 1st step	PI4KA1_4	2.046	0.01916741	up
AT2G43900	Endonuclease/exonuclease/phosphatase family protein	retained intron	yes	wt	up	410	50	1174	861	8.2	1.36	0.35	0.06	phosphoinositol, 5-inositol-phosphate phosphatase	AT2G43900_1	7.0761	0.01904179	up
At1g71710	Type IV inositol polyphosphate 5-phosphatase 3 (At5PTase3) (EC 3.1.3.36) (EC 3.1.3.86)	alternative 5' end	yes	wt	up	888	246	1591	804	3.61	1.98	0.56	0.31	phosphoinositol, ROS salt signaling	IP5P3_1	3.1968	0.01160664	up
AT3G09560	PHOSPHATIDIC ACID PHOSPHOHYDROLASE 1	retained intron	no	wt	up	366	52	1552	732	7.04	2.12	0.24	0.07	phospholipid synthesis PAH1; PHOSPHATIDIC ACID PHOSPHOHYDROLASE 1	PAH1_1	6.1311	0.01482846	up
AT3G59060	PHYTOCHROME-INTERACTING FACTOR 5	alternative 3' splice site, retained intron, alternative 5' end	no	wt	up	5637	1778	13837	8310	3.17	1.67	0.41	0.21	phytochrome B signaling negative regulator APRR1/TOC1 associated PHYTOCHROME-INTERACTING FACTOR 5; PIF5 BHLH65	PIF5_1	2.6453	1.02E-03	up
AT3G15340	proton pump interactor 2	alternative 5' end	no	wt	up	39	0	123	54	####	2.28	0.32	0	plasma membrane H+ ATPase AHA1 interacting PPI2 (proton pump interactor 2)	PPI2_2	96.14	0.02471601	up

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AT2G02170	Remorin family protein	alternative 5' and 3' ends	yes	125aa N-term deletion	down ?	255	33	1050	734	7.73	1.43	0.24	0.04	plasma-membrane lipid draft associated remorin domain protein	AT2G02170_1	6.6369	0.03950883	up
AT5G49960	Ion channel protein	retained intron	yes	C-terminal truncation pos 631	down	145	0	364	297	####	1.23	0.4	0	potassium transport Castor and Pollux ion channel transmembrane protein	AT5G49960_2	305.94	2.62E-03	up
AT1G30450	cation-chloride co-transporter 1	alternative 5' and 3' ends	yes	131aa N-term deletion	down ?	485	102	2391	1686	4.75	1.42	0.2	0.06	potassium transport cation-chloride co-transporter 1	CCC1_3	3.9494	0.04483588	up
AT1G53850	Proteasome subunit alpha type-5-A (EC 3.4.25.1) (20S proteasome alpha subunit E-1)	alternative 5' end	no	wt	down	1021	1896	2663	3079	0.54	0.86	0.38	0.62	proteasome alpha subunit E1, alpha 5	PAE1_2_1	-2.1338	0.01349494	down
AT1G37150	holocarboxylase synthetase 2	alternative 3' splice site, alternativ 5' and 3' ends	no	C-term truncation pos 291 removing part of the BPL_C domain	down	38	0	77	42	####	1.83	0.49	0	protein biotinylation biotin protein ligase / holocarboxylase synthetase HCS2	HCS2_8	87.043	0.02327346	up
At1g11660	Heat shock 70 kDa protein 16 (Heat shock protein 70-16) (AtHsp70-16)	retained intron, alternative 5' end	yes	wt	up	1893	768	1980	1063	2.46	1.86	0.96	0.72	protein folding heat shock HSP70-16	HSP70-16_1	2.0429	0.04628413	up
AT4G16660	heat shock protein 70 (Hsp 70) family protein	retained intron	yes	wt	up	1012	218	4677	2294	4.64	2.04	0.22	0.1	protein folding HSP70 with signal peptide	AT4G16660_1	3.9572	1.49E-03	up
AT3G21650	Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' zeta isoform (AtB' zeta) (PP2A, B' subunit, zeta isoform)	retained intron	no	wt	up	399	82	1097	1230	4.87	0.89	0.36	0.07	Protein phosphatase 2A regulatory B' zeta	B'ZETA_2	4.3886	0.0439201	up
AT2G25740	ATP-dependent protease La (LON) domain protein	retained intron	yes	65aa N-term deletion	down	325	68	962	621	4.78	1.55	0.34	0.11	proteolysis human CRBN-like ATP-dependent nuclear LON protease	AT2G25740_1	3.9864	0.03829269	up
AT2G23890	HAD-superfamily hydrolase, subfamily IG, 5'-nucleotidase	retained intron	no	wt	up	280	0	966	633	####	1.53	0.29	0	purine nucleotide metabolism purine specific 5'-nucleotidase	AT2G23890_2	614.97	6.08E-04	up
AT4G31290	Gamma-glutamylcyclotransferase 2-2 (AtGGCT2;2) (EC 4.3.2.9) (Gamma-glutamyl cyclotransferase 2;2)	none	no	wt	down	3940	8120	3940	8120	0.49	0.49	1	1	redox heavy metal tolerance gamma-glutamyl cyclotransferase 2;2; GGCT2;2	GGCT2_2_1	-2.3986	1.78E-04	down
AT1G08830	copper/zinc superoxide dismutase 1	alternative 3' splice site, alternative 5' end	no	wt	down	1922	4285	2892	4757	0.45	0.61	0.66	0.9	redox sucrose/miR398 repressed copper/zinc superoxide dismutase 1	CSD1_2	-2.4811	1.98E-03	down
At5g09510	40S ribosomal protein S15-4	alternative 5' and 3' ends	yes	wt	down	1341	2816	6668	8846	0.48	0.75	0.2	0.32	ribosome 40S ribosomal protein S15-4	RPS15D_1	-2.4239	8.72E-04	down
AT3G04400		alternative 5' and 3' ends	yes	wt	down	6314	11816	26583	40495	0.53	0.66	0.24	0.29	ribosome 60S ribosomal protein L23	RPL23B_3_1	-2.1543	3.09E-03	down
AT5G06110	DnaJ domain ;Myb-like DNA-binding domain	alternative 5' splice site	no	wt	up	1012	160	4874	2394	6.33	2.04	0.21	0.07	ribosome associated RF1B, ZUOTIN-RELATED FACTOR 1B, DNAJC2 DnaJ heat shock protein family (Hsp40) member C2 homolog	AT5G06110_1	5.6209	1.95E-03	up
AT1G67120	ATPases;nucleotide binding;ATP binding;nucleoside-triphosphatases;transcription factor binding	alternative 3' splice site, alternative 5' end	yes	7aa deletion pos 3196-3203	up?	1176	104	1626	845	11.3	1.92	0.72	0.12	ribosome biogenesis 60S rRNA maturation ATPase	AT1G67120_1	9.8982	9.59E-04	up
AT1G43860	sequence-specific DNA binding transcription factors	retained intron, alternative 3' end	yes	45aa N-term deletion removing part of the SBDS domain	down	969	384	1142	558	2.52	2.05	0.85	0.69	ribosome biogenesis factor	AT1G43860_1	2.1345	0.04001026	up
AT1G69070	Nucleolar-like protein	alternative 3' splice site, alternative 5' and 3' ends	yes	3aa deletion pos 640-643 in the Nop14 domain	down	556	89	2095	921	6.25	2.27	0.27	0.1	ribosome biogenesis NOP14 nucleolar protein homolog	AT1G69070_1	5.352	1.18E-03	up
AT2G40430	AT2G40430 protein (Fragment)	retained intron, alternative 5' and 3' ends	yes	wt	up	1442	342	3021	1520	4.22	1.99	0.48	0.23	ribosome biogenesis NOP53, cell division, small organ	AT2G40430_2	3.5457	0.02579395	up
AT1G30240	Proline-, glutamic acid/leucine-rich protein	alternative 3' splice site, alternative 5' and 3' ends	no	2aa deletion pos 436	up?	407	79	673	381	5.15	1.77	0.6	0.21	ribosome biogenesis RIX1 homolog	AT1G30240_1	4.5865	0.03231787	up
AT3G57940	Domain of unknown function (DUF1726) ;Putative ATPase (DUF699)	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	up	789	294	828	414	2.68	2	0.95	0.71	ribosome biogenesis tRNA/histone acetylase NAT10 homolog	AT3G57940_1	2.2839	0.04629643	up
AT4G04940	transducin family protein / WD-40 repeat family protein	alternative 5' end	yes	wt	up	805	290	816	371	2.78	2.2	0.99	0.78	ribosome biogenesis UTP21 homolog	AT4G04940_2	2.3914	0.02811752	up
AT3G16840	P-loop containing nucleoside triphosphate hydrolases superfamily protein	alternative 5' end	no	wt	up	961	190	2125	911	5.06	2.33	0.45	0.21	ribosome biogenesis yeast MAK5 DEAD-box helicase homolog	AT3G16840_2	4.268	2.49E-04	up
AT1G29970	60S ribosomal protein L18A-1	alternative 5' and 3' ends	yes	C-term truncation pos 139 removing the Ribosomal_L18ae domain	up	1331	2636	2646	4153	0.5	0.64	0.5	0.63	ribosome transmembrane 60S ribosomal protein L18a-like protein	RPL18AA_2_3	-2.2628	5.23E-03	down
At3g60500	Exosome complex component RRP45B (Protein ECERIFERUM 7) (RNA-processing protein CER7) (RRP45 homolog B) (Ribosomal RNA-processing protein 45B)	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 356	down ?	292	30	929	581	9.73	1.6	0.31	0.05	RNA degradation exosome RRP45/EXOS9	RRP45B_4	7.9664	9.32E-03	up
AT1G09800	Pseudouridine synthase family protein	alternative 5' splice site, alternative 3' end	yes	wt	down	287	1011	771	1265	0.28	0.61	0.37	0.8	RNA modification Pseudouridine synthase	AT1G09800_2	-3.7036	0.01563041	down
AT4G04920	MEDIATOR 16	alternative 3' splice site, alternative 5' end	yes	wt	up	575	107	2230	1377	5.37	1.62	0.26	0.08	RNA pol II cold, pathogen SA signaling Mediator subunit 16	MED16_1	4.3849	8.94E-03	up
AT4G31200	SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein	alternative 5' splice site, alternative 5' end	no	wt	up	305	0	1345	1011	####	1.33	0.23	0	RNA polII CTD biding Suppressor-of-White-APricot splicing regulator	AT4G31200_2	711.21	3.50E-04	up
AT1G49540	elongator protein 2	alternative 3' splice site	yes	2aa deletion pos 115 in the 2nd WD40 repeat	down ?	398	0	1078	694	####	1.55	0.37	0	RNA polII elongator complex subunit 2 root development pathogen	ELP2_1	971.58	1.03E-04	up

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AT4G00450	mediator 12	alternative 5' and 3' ends	no	wt	up	830	240	4009	2784	3.46	1.44	0.21	0.09	RNA polII Mediator subunit 12 CENTER CITY; CRP; CRYPTIC PRECOCIOUS; GCT; GRAND CENTRAL;	MED12_3	2.7806	0.04252841	up
AT1G07480	Transcription factor IIA, alpha/beta subunit	retained intron, alternative 5'-end	no	wt	up	374	0	1787	1144	####	1.56	0.21	0	RNA polII Transcription factor IIA, alpha/beta subunit	AT1G07480_3	880.89	1.24E-04	up
AT3G49410	Transcription factor IIIC, subunit 5	alternative 3' end	no	wt	up	43	0	119	55	####	2.16	0.36	0	RNA polIII Transcription factor IIIC, subunit 5	AT3G49410_4	93.465	0.02471185	up
AT1G60850	DNA-directed RNA polymerase family protein	alternative 3' splice site	no	wt	up	492	131	943	581	3.76	1.62	0.52	0.23	RNA POLYMERASE I SUBUNIT 42	ATRPAC42_2	3.3642	0.03314163	up
AT4G12610	transcription activators;DNA binding;RNA polymerase II transcription factors;catalytics;transcription initiation factors	intron corresponding to retained intron, alternative 5' and 3' ends	yes	wt	up	1072	399	1840	850	2.69	2.16	0.58	0.47	RNA polymerase II transcription initiation factor IIF subunit alpha RAP74	RAP74_1	2.3087	0.02443599	up
At3g16430	PYK10-binding protein 2 (Jacalin-related lectin 31) (Jasmonate inducible protein isolog)	alternative 5' and 3' ends	no	wt	down	1308	2723	2208	3358	0.48	0.66	0.59	0.81	root cell wall scopolin glucosidase stimulating JAL31 jacalin-related lectin 31	PBP2_2	-2.3241	3.14E-03	down
AT2G28670	Disease resistance-responsive (dirigent-like protein) family protein	intron corresponding to retained intron, alternative 5' and 3' ends	yes	wt	down	581	1103	1111	1673	0.53	0.66	0.52	0.66	root ESB1 ENHANCED SUBERIN 1 Drigent protein with signal peptide required for Casparian strip formation	AT2G28670_2	-2.2234	0.0134896	down
AT2G24610	cyclic nucleotide-gated channel 14	retained intron	yes	24aa N-term deletion of Signal peptide	down	38	0	149	104	####	1.43	0.26	0	root gravitropism Cyclic Nucleotide-Gated Channel CNGC14	ATCNGC14_1	76.227	0.03775254	up
AT1G70630	Nucleotide-diphospho-sugar transferase family protein	alternative 5' splice site, retained intron	yes	216aa N-term deletion removing the transmembrane domains	down	126	9	209	115	14	1.82	0.6	0.08	root growth cell wall AGP glycosylation	AT1G70630_2	11.375	0.02375543	up
AT3G46200	nudix hydrolase homolog 9	retained intron, alternative 5' and 3' ends	yes	30aa N-term deletion and C-term truncation pos 372 in the NUDIX domain	down	76	0	296	254	####	1.17	0.26	0	root growth NH3 induced GDP-d-mannose pyrophosphohydrolase	NUDT9_6	179.59	9.37E-03	up
AT4G29180	root hair specific 16	alternative 5' splice site	yes	18aa alteration pos 400-418 in the LRR8 domain	down ?	47	0	81	54	####	1.5	0.58	0	root hair transmembrane receptor kinase with signal prptide and malectin-like and LRR domains	RHS16_3	117.78	0.01872935	up
AT2G35620	FEI 2	alternative 5' and 3' splice sites	no	wt	up	1441	387	2390	1735	3.72	1.38	0.6	0.22	root hypocotyl elongation LRR receptor kinase FEI1	FEI2_1	3.2174	4.33E-04	up
At3g63500	Protein OBERON 4	retained introns, alternative 5' and 3' ends	yes	wt	up	932	359	4561	3385	2.6	1.35	0.2	0.11	root meristem initiation PHD finger TF	OBE4_1	2.256	0.04201128	up
AT2G27230	LONESOME HIGHWAY	alternative 5' splice site, alternative 3' end	no	wt	up	1499	578	2645	1790	2.59	1.48	0.57	0.32	root meristem vascular stele differentiation LONESOME HIGHWAY bHLH TF with RRM domain	LHW_1	2.1462	0.0268185	up
AT3G45660	Major facilitator superfamily protein	alternative 5' and 3' ends	no	wt	up	25	0	31	17	####	1.82	0.81	0	root nitrate efflux nitrate excretion transporter1 NAXT1 homolog	AT3G45660_3	54.766	0.04647254	up
AT3G08800	SHORT-ROOT interacting embryonic lethal	alternative 5' and 3' splice sites	yes	C-term truncation pos 630	down ?	79	0	220	202	####	1.09	0.36	0	root patterning SH endosomal transport	SIEL_3	157.14	0.0142142	up
AT1G68130	indeterminate(ID)-domain 14	retained intron, alternative 5'-end	yes	87aa deletion removing the first N-term ZnF_C2H2 domain	down	215	0	989	548	####	1.8	0.22	0	root regulation of auxin biosynthesis transport lateral organ differentiation	IDD14_1	487.45	7.06E-04	up
At1g07880	Mitogen-activated protein kinase 13 (AtMPK13) (MAP kinase 13) (EC 2.7.11.24)	retained intron	yes	C-term truncation pos 249 removing part of the catalytic S_TKc domain	down	57	4	172	142	14.3	1.21	0.33	0.03	root, cell division lateral root MKK6 activated MPK13	MPK13_2	11.113	0.04659552	up
AT5G17860	Calcium exchanger 7	intron corresponding to retained intron, alternative 5' end	yes	36aa deletion pos 228-264 in the 1st Na_Ca_ex domain	down	508	112	2066	1844	4.54	1.12	0.25	0.06	ROS Ca2+ signaling induction of senescence transmembrane sodium/calcium exchanger	CCX1_1	3.9634	0.01109805	up
AT1G09090	respiratory burst oxidase homolog B	retained intron	yes	C-term truncation pos 617 removing part of the FAD_binding_8 domain and the NAD_binding_6 domain	down	34	0	108	120	####	0.9	0.31	0	ROS signaling, seed germination ABA induced	RBOHB_2	68.337	0.04288914	up
AT2G30340	LOB domain-containing protein 13	retained intron	yes	wt	up	38	0	80	91	####	0.88	0.48	0	shoot metistem , unknown LOB domain TF	LBD13_1	89.017	0.02296411	up
AT3G48670	INVOLVED IN DE NOVO 2	alternative 5' end	no	wt	up	964	328	1194	516	2.94	2.31	0.81	0.64	silencing RDM12; RNA-DIRECTED DNA METHYLATION 12	IDN2_2	2.4289	0.01795696	up
AT3G18090	nuclear RNA polymerase D2B	retained intron	yes	C-term truncation removing the RNA_pol_Rpb2_6 and _7 domains	down	94	0	317	219	####	1.45	0.3	0	silencing siRNA	NRPD2B_3	191.3	7.25E-03	up
AT3G04380	SET-domain containing protein lysine methyltransferase family protein	retained intron	yes	wt	up	41	0	194	106	####	1.83	0.21	0	silencing transposon H3K9me3 SUVR4, a nucleolar histone methyltransferase	SUVR4_6	82.145	0.03487488	up
AT3G23780	nuclear RNA polymerase D2A	alternative 5' splice site	no	wt	up	1346	494	1553	981	2.72	1.58	0.87	0.5	silencing transposon RNA polymerase IV	NRPD2_1	2.3593	0.02096132	up
AT1G17640	RNA-binding (RRM/RBD/RNP motifs) family protein	alternative 5' and 3' ends	no	wt	up	135	10	357	240	13.5	1.49	0.38	0.04	spliceosome associated hnRNP protein AtRNPA/B_8b, RNA recognition motif-containing protein	AT1G17640_2	10.698	0.04564749	up
AT5G59950	RNA-binding (RRM/RBD/RNP motifs) family protein	alternative 5' and 3' splice sites, alternative 3' end	yes	1aa deletion pos 188 in the heterochromatin directing FoP_duplication domain	down ?	2076	3808	3175	4602	0.55	0.69	0.65	0.83	spliceosome associated TREX/THO complex subunit 4 ALY homolog atALY-1b	AT5G59950_5	-2.0817	5.11E-03	down
AT2G43810	SM-like 6B	alternative 5' end	no	wt	down	647	1362	2016	2387	0.48	0.84	0.32	0.57	spliceosome atLSM6b U6 snRNA-associated Sm-like protein LSm6	LSM6B_2	-2.4793	4.55E-03	down
AT3G25840	Protein kinase superfamily protein	exon corresponding to exon skip, alternative 3' end	yes	262aa N-term deletion	down	945	337	2405	1616	2.8	1.49	0.39	0.21	spliceosome Bact complex PRP4 kinase	AT3G25840_2	2.3994	0.02452053	up

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AT4G21110	G10 family protein	alternative 5' and 3' ends	no	wt	down	1830	3295	3219	4754	0.56	0.68	0.57	0.69	spliceosome NTC subunit AtBud31 bud site selection protein 31 Cwc14	AT4G21110_2	-2.0734	7.31E-03	down
At4g36690	Splicing factor U2af large subunit A (U2 auxiliary factor 65 kDa subunit A) (U2 small nuclear ribonucleoprotein auxiliary factor large subunit A) (U2 snRNP auxiliary factor large subunit A)	retained intron	yes	C-term truncation pos 506 removing part of the 3rd RNA-binding RRM domain	down	1326	538	4575	3124	2.46	1.46	0.29	0.17	spliceosome splice site seletion U2 snRNP atU2AF65a/AULb Splicing factor U2af large subunit A	U2AF65A_3	2.0783	0.02626873	up
At1g20920	DEAD-box ATP-dependent RNA helicase 42 (EC 3.6.4.13) (DEAD-box RNA helicase RCF1) (REGULATOR OF CBF GENE EXPRESSION 1)	alternative 5' splice site	no	wt	up	830	146	2865	1693	5.68	1.69	0.29	0.09	spliceosome U2snRNP atPrp5-1b DEAD-box ATP-dependent RNA helicase 42	RH42_6	4.7941	5.73E-04	up
AT5G56900	CwfJ-like family protein / zinc finger (CCCH-type) family protein	alternative 5' and 3' ends	yes	93aa N-term deletion	down ?	973	139	1812	1409	7	1.29	0.54	0.1	spliceosome, NTC-associated NTR CWF19L1 protein	AT5G56900_1	5.9766	0.01665514	up
AT3G18660	glucuronic acid substitution of xylan 1	alternative 5' and 3' ends	no	wt	up	136	0	199	165	####	1.21	0.68	0	starch and cell wall xylan synthesis PGSIP1 plant glycogenin-like starch initiation protein 1	GUX1_1	310.11	2.31E-03	up
AT4G39210	Glucose-1-phosphate adenylyltransferase family protein	alternative 5' and 3' ends	no	wt	up	868	145	1135	511	5.99	2.22	0.76	0.28	starch synthesis APL3 large subunit of ADP-Glucose Pyrophosphorylase	APL3_2	5.2331	5.16E-03	up
AT5G50375	cyclopropyl isomerase	retained intron	yes	C-term truncation pos 246	up	431	837	679	911	0.51	0.75	0.63	0.92	sterol biosynthesis CYCLOEUCALENOL CYCLOISOMERASE	CPI1_2	-2.3567	0.03154018	down
AT1G69530	expansin A1	retained introns	yes	C-term truncation pos 245 removing part of the Pollen_allerg_1 domain	down	1806	9	7351	6874	201	1.07	0.25	0	stomata opening expansin	ATEXPA1_1	157.15	0	up
AT1G51850	Leucine-rich repeat protein kinase family protein	alternative 5' and 3' ends	no	wt	up	282	40	788	382	7.05	2.06	0.36	0.1	STRESS INDUCED FACTOR 1 SIF1 Glc2-N-glycan recognizing Malectin_like domain ER protein with signal peptide	AT1G51850_2	5.8928	0.04310191	up
AT1G08420	BRI1 suppressor 1 (BSU1)-like 2	alternative 3' splice site, alternative 5' end	yes	wt	down	1344	2613	4405	4963	0.51	0.89	0.31	0.53	sucrose synthase regulation PP2A protein phosphatase with Kelch repeats	BSL2_1	-2.1812	4.83E-03	down
AT1G73370	sucrose synthase 6	alternative 5' end	no	wt	up	62	0	240	118	####	2.03	0.26	0	sucrose uptake degradation sucrose synthase 6	SUS6_3	148.4	0.01696392	up
AT5G44160	NUCLEAR CAGE	retained intron	yes	47aa N-term deletion	down	97	0	284	138	####	2.06	0.34	0	sugar root flowering time, SHORT ROOT interaction, IDD8; INDETERMINATE DOMAIN 8; nutcracker transcription activator of SUS4, proposed AKIN10 substrate	NUC_1	209.12	5.15E-03	up
At5g61520	Sugar transport protein 3 (Hexose transporter 3)	retained intron, alternative 5' and 3' ends	yes	49aa N-term truncation removing part of the Sugar_tr domain	down	327	24	1593	1616	13.6	0.99	0.21	0.01	sugar transporter STP3	STP3_1	11.568	4.50E-03	up
AT3G12520	Sulfate transporter 42	retained intron, alternative 5'end	yes	wt	up	468	87	770	371	5.38	2.08	0.61	0.23	sulfate transport, sulfate limitation induced sulfate transporter 4;2	SULTR4_1_2	4.646	4.07E-03	up
AT1G22150	Sulfate transporter 13	alternative 5' end	no	wt	up	33	1	33	1	33	33	1	1	sulfate transporter 1;3	SULTR1_1_4	20.585	0.02940111	up
AT1G73730	ETHYLENE-INSENSITIVE3-like 3	alternative 5' end	yes	12aa N-term deletion	up?	186	17	914	590	10.9	1.55	0.2	0.03	sulfate uptake positive regulator	EIL3_2	8.8531	0.0499897	up
AT4G31790	Tetrapyrrole (Corrin/Porphyrin) Methylases	retained intron, alternative 5' and 3' ends	no	wt	up	345	7	1004	904	49.3	1.11	0.34	0.01	Tetrapyrrole protoporphyrine methylase	AT4G31790_1	40.129	2.98E-06	up
AT4G29530	Pyridoxal phosphate phosphatase-related protein	retained intron, alternative 5' end	yes	47aa N-term deletion removing part of the HAD domain	down	101	0	256	196	####	1.31	0.39	0	thiamine biosynthesis	AT4G29530_1	223.72	5.88E-03	up
AT3G17100	AT3G17100 protein	intron corresponding to retained intron, alternative 5' end	no	wt	down	2123	4626	3829	6225	0.46	0.62	0.55	0.74	transcription AIF3, ATBS1 INTERACTING FACTOR 3 bHLH147 TF	BHLH147_1	-2.5331	1.86E-04	down
AT1G18840	IQ-domain 30	retained intron, alternative 5'end	no	wt	up	407	80	1310	897	5.09	1.46	0.31	0.09	transcription calmodulin interacting IQ and DUF4005 domain protein	IQD30_1	4.4695	0.02006488	up
At1g56170	Nuclear transcription factor Y subunit C-2 (AtNF-YC-2) (Transcriptional activator HAP5B)	alternative 5' splice site, alternative 5' and 3' ends	no	wt	up	578	136	954	469	4.25	2.03	0.61	0.29	transcription CCAATbox TF complex subunit HAP5B, NF-YC2	NFYC2_2	3.7845	0.01169091	up
AT5G03960	IQ-domain 12	alternative 5' end	no	wt	up	24	0	69	47	####	1.47	0.35	0	transcription microtubule associated IQ12 IQ and calmodulin binding DUF4005 domain protein	IQD12_3	56.426	0.04222491	up
AT5G27030	TOPLESS-related 3	alternative 5' and 3' ends	no	wt	up	295	0	1409	1153	####	1.22	0.21	0	transcription repressor LEUNING-like TPR3 TOPLESS-related 3	TPR3_2_1	639.76	5.40E-04	up
AT1G35516	myb-like transcription factor family protein	alternative 5' splice site	yes	C-terminal truncation pos 47	down ?	772	1407	1482	2549	0.55	0.58	0.52	0.55	transcription unknown Myb TF	AT1G35516_1	-2.0824	0.01823246	down
AT2G24645	Transcriptional factor B3 family protein	alternative 3' splice site, retained intron	yes	8aa deletion pos 19-27 in the 1st B3 domain; C-term truncation pos 410 removing the 4th B3 domain	down	62	0	167	140	####	1.19	0.37	0	transcription, unknown B3 domain TF	AT2G24645_4	123.58	0.02071625	up
AT2G20100	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	retained intron	yes	C-term truncation pos 297	down ?	109	7	417	309	15.6	1.35	0.26	0.02	transcription, unknown bHLH TF	AT2G20100_2	11.64	0.04060753	up
AT5G27640	translation initiation factor 3B1	alternative 3' splice site	yes	wt	up	2393	839	7139	4205	2.85	1.7	0.34	0.2	translation COP9 signalosome spliceosome associated translation initiation factor 3 subunit B (TIF3B1)	TIF3B1_1	2.3867	4.03E-03	up
AT3G59630	diphthamide synthesis DPH2 family protein	alternative 5' and 3' ends	yes	61aa N-term deletion removing part of the Diphthamide_syn domain	down	400	69	965	482	5.8	2	0.41	0.14	translation EF2 modification	AT3G59630_2	5.0176	0.02677096	up
AT5G01940	eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	alternative 5' and 3' ends	yes	32aa N-term deletion	down ?	138	0	201	170	####	1.18	0.69	0	translation initiation beta subunit of eukaryotic translation initiation factor 2 (IF2beta)	AT5G01940_2	342.16	2.84E-03	up

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AT1G18070	Translation elongation factor EF1A/initiation factor IF2gamma family protein	alternative 3' splice site, alternative 5' end	yes	11aa deletion pos 331-342	down ?	2176	685	7527	4134	3.18	1.82	0.29	0.17	translation release factor sup35/GSPT1 homolog	AT1G18070_2	2.6995	4.97E-03	up
AT4G27340	Met-10+ like family protein	alternative 5' and 3' ends	no	wt	up	879	374	1115	584	2.35	1.91	0.79	0.64	tRNA methyltransferase 5B TRM5B	AT4G27340_1	2.0696	0.04835346	up
AT3G02370	tRNA-splicing endonuclease subunit	alternative 3' end	no	wt	up	28	0	139	114	####	1.22	0.2	0	tRNA-splicing endonuclease subunit	AT3G02370_3	72.054	0.03595928	up
AT1G14400	ubiquitin carrier protein 1	alternative 5' and 3' ends	no	wt	down	6522	12613	10515	17635	0.52	0.6	0.62	0.72	ubiquitin CONJUGATING ENZYME 1	UBC1_1	-2.2035	3.63E-03	down
AT5G53300	ubiquitin-conjugating enzyme 10	alternative 5' and 3' ends	yes	wt	down	14597	30946	41363	63695	0.47	0.65	0.35	0.49	ubiquitin conjugating enzyme 10	UBC10_4	-2.4475	1.16E-03	down
AT5G10250	DEFECTIVELY ORGANIZED TRIBUTARIES 3	alternative 3' splice site	yes	wt	up	76	0	89	61	####	1.46	0.85	0	ubiquitination CUL3 E3 ligase BTB/POZ subunit vein pattern root shoot development	DOT3_2	161.1	0.01085578	up
AT4G00755	F-box family protein	retained intron, alternative 5' end	no	wt	up	1056	350	1406	957	3.02	1.47	0.75	0.37	ubiquitination SCF E3 F-box protein	AT4G00755_1	2.5465	0.02511698	up
AT4G10400	F-box/RNI-like/FBD-like domains-containing protein	retained intron	no	wt	up	78	0	368	307	####	1.2	0.21	0	ubiquitination SCF E3 LRR F-box protein	AT4G10400_2	175.24	7.44E-03	up
AT1G13780	F-box/RNI-like/FBD-like domains-containing protein	retained intron	yes	C-term truncation pos 316 removing the FBD domain	down	87	6	389	308	14.5	1.26	0.22	0.02	ubiquitination SCF E3 LRR F-box protein	AT1G13780_1	11.396	0.03540039	up
AT2G26860	FBD, F-box and Leucine Rich Repeat domains containing protein	retained intron, alternative 5' and 3' ends	no	wt	up	102	0	374	395	####	0.95	0.27	0	ubiquitination SCF E3 LRR repeat F-box protein	AT2G26860_2	202.53	8.99E-03	up
AT3G52680	F-box/RNI-like/FBD-like domains-containing protein	retained intron, alternative 5' end	yes	C-term truncation pos 343 removing the F-box FBD domain	down	97	0	202	158	####	1.28	0.48	0	ubiquitination SCF E3 uniquitin ligase F-box protein	AT3G52680_2	222.59	4.36E-03	up
AT3G26922	F-box/RNI-like superfamily protein	retained intron	yes	30aa N-term deletion removing the FBOX domain	down	51	0	173	147	####	1.18	0.29	0	ubiquitination SCF E3 uniquitin ligase F-box protein with LRR domain	AT3G26922_1	101.88	0.02688273	up
At1g67530	U-box domain-containing protein 7 (EC 2.3.2.27) (Plant U-box protein 7) (RING-type E3 ubiquitin transferase PUB7)	alternative 5' and 3' ends	no	wt	up	386	9	1147	673	42.9	1.7	0.34	0.01	ubiquitination unknown RIN E3 with ARM repeats	PUB7_1	36.325	6.75E-06	up
AT2G01275	RING/FYVE/PHD zinc finger superfamily protein	alternative 5' and 3' ends	yes	27aa N-term deletion	up?	25	0	54	38	####	1.42	0.46	0	ubiquitination unknown RINGv domain E3 ligase	AT2G01275_2	65.246	0.04539471	up
AT3G47550	RING/FYVE/PHD zinc finger superfamily protein	retained intron, alternative 5' end	yes	C-term truncation pos 217 removing part of the DUF3675 domain	down	486	33	2199	2287	14.7	0.96	0.22	0.01	ubiquitination unknown RINGv domain E3 with DUF3675 domain	AT3G47550_2	11.643	3.28E-03	up
AT3G08690	ubiquitin-conjugating enzyme 11	alternative 5' splice site, alternative 5' and 3' ends	no	wt	down	917	1853	2756	3983	0.49	0.69	0.33	0.47	ubiquitin-conjugating enzyme 11	UBC11_1	-2.2955	0.01171474	down
AT3G24515	ubiquitin-conjugating enzyme 37	retained intron	yes	149aa N-term deletion removing part of the UBCc domain	down	36	0	176	91	####	1.93	0.2	0	ubiquitin-conjugating enzyme 37	UBC37_3	72.282	0.04028633	up
AT2G25910	3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein	alternative 5' and 3' ends	no	wt	up	662	209	2814	2084	3.17	1.35	0.24	0.1	ubknown 3' -5' exonuclease proofreading and KH RNA-binding domain protein, likely Rnase D	AT2G25910_2	2.8114	0.02924198	up
AT1G20380	Prolyl oligopeptidase family protein	retained intron	yes	162aa N-term deletion removing part of the Peptidase_S9_N domain	down	63	0	307	172	####	1.78	0.21	0	uknown prolyl oligopeptidase	AT1G20380_1	125.56	0.02064823	up
AT2G47860	Phototropic-responsive NPH3 family protein	retained intron, alternative 5' and 3'-ends	yes	wt	up	103	0	286	247	####	1.16	0.36	0	unknown non-phototropic hypocotyl 3 (NPH3) protein blue light	AT2G47860_5	233.15	4.02E-03	up
AT5G02860	Pentatricopeptide repeat (PPR) superfamily protein	alternative 3' splice site	no	wt	up	268	0	801	718	####	1.12	0.33	0	unknown Pentatricopeptide repeat protein	AT5G02860_2	530.96	1.25E-03	up
AT3G27640	Transducin/WD40 repeat-like superfamily protein	retained intron	yes	36aa N-term deletion removing part of the BTB domain	down	43	0	109	46	####	2.37	0.39	0	unknown phototropin NRL (for NPH3/RPT2-Like) family, CUL3 interacting	AT3G27640_2	86.091	0.03238058	up
AT4G21585	endonuclease 4	retained introns, alternative 5' and 3' ends	yes	C-term truncation pos 262 removing part of the S1-P1_nuclease domain	down	42	2	183	131	21	1.4	0.23	0.02	unknown S1 and P1 nuclease	ENDO4_5	14.036	0.04216585	up
AT2G25640	SPOC domain / Transcription elongation factor S-II protein	retained intron	yes	C-term truncation pos. 660 removing the SPOC domain	down	170	0	607	461	####	1.32	0.28	0	unknown Transcription elongation factor S-II domain protein	AT2G25640_1	381.95	1.52E-03	up
AT4G23510	Disease resistance protein (TIR-NBS-LRR class) family	retained intron, alternative 3' end	yes	25aa N-term deletion removing part of the 1st TIR domain	down	34	0	89	93	####	0.96	0.38	0	unknown (TIR-NBS-LRR protein	AT4G23510_2	73.515	0.03025373	up
AT5G43450	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	retained intron, alternative 5' end	yes	C-term truncation pos 279 removing the 2OG-FeII_Oxy domain	down	1891	463	5510	3137	4.08	1.76	0.34	0.15	unknown 2-oxoglutarate/Fe(II)-dependent dioxygenase	AT5G43450_1	3.5868	2.01E-05	up
AT3G27770	Uncharacterized protein	retained intron, alternative 5' end	yes	wt	down	3186	5772	5764	9596	0.55	0.6	0.55	0.6	unknown 7 transmembrane protein	AT3G27770_2	-2.1409	1.31E-03	down
AT1G67910	Uncharacterized protein	retained intron, alternative 5' end	no	wt	down	991	1735	1053	1749	0.57	0.6	0.94	0.99	unknown 91aa oligopeptide	AT1G67910_2	-2.0457	0.02913981	down
AT5G60400	Uncharacterized protein	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	down	622	1154	1272	1833	0.54	0.69	0.49	0.63	unknown 91aa oligopeptide	AT5G60400_1	-2.1158	0.02149011	down

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AT1G30420	ATP-binding cassette C11	intron corresponding to retained intron	yes	wt	up	190	25	266	139	7.6	1.91	0.71	0.18	unknown ABC transporter	ABCC11_2	6.302	0.03177158	up
AT5G01670	NAD(P)-linked oxidoreductase superfamily protein	retained intron	yes	wt	up	180	6	493	381	30	1.29	0.37	0.02	unknown aldo-keto reductase	AT5G01670_2	23.763	1.61E-03	up
AT4G14290	alpha/beta-Hydrolases superfamily protein	alternative 3' end	yes	54aa N-term deletion removing part of Hydrolase_4 domain	down	69	0	270	181	####	1.49	0.26	0	unknown alpha-beta hydrolase	AT4G14290_1	158.67	9.04E-03	up
AT3G04710	tetratricopeptide repeat 10	alternative 5' and 3' ends	yes	223aa N-term deletion of the DUF1685 domain	down	900	339	1051	455	2.65	2.31	0.86	0.75	unknown ankyrin and TRP repeat protein, chaperon SHEPERD interactor	TPR10_2	2.3336	0.04034381	up
AT3G24530	AAA-type ATPase family protein / ankyrin repeat family protein	alternative 5' end	yes	wt	up	362	0	1636	1051	####	1.56	0.22	0	unknown ankyrin domain ATPase	AT3G24530_3	748.5	3.70E-04	up
AT2G28840	XB3 ortholog 1 in Arabidopsis thaliana	retained intron, alternative 5' and 3' ends	yes	60aa N-term exchange removing the 1st ANK repeat	up?	8189	14042	9444	14312	0.58	0.66	0.87	0.98	unknown ankyrin repeat RING E3	XBAT31_2	-2.0286	0.04065782	down
AT2G11910	Expressed protein (Uncharacterized protein At2g11910)	retained intron	no	wt	down	3024	5612	5334	7289	0.54	0.73	0.57	0.77	unknown ARM repeat protein	AT2G11910_2	-2.0795	5.46E-03	down
AT5G23050	acyl-activating enzyme 17	retained intron	yes	C-term truncation pos 581 removing the AMP-binding_C domain	down	397	20	1787	1600	19.9	1.12	0.22	0.01	unknown ATP-binding acyl-activating enzyme	AAE17_2	16.52	4.08E-03	up
AT1G35340	ATP-dependent protease La (LON) domain protein	introns corresponding to retained introns, alternative 3' end	yes	wt	down	800	1617	1840	1930	0.49	0.95	0.43	0.84	unknown ATP-dependent LON protease	AT1G35340_1	-2.2859	5.36E-03	down
AT5G03830	CDK inhibitor P21 binding protein	retained intron	no	wt	up	50	0	200	166	####	1.2	0.25	0	unknown Bcp1 homolog	AT5G03830_3	110.43	0.01986312	up
AT4G26140	beta-galactosidase 12	retained intron	yes	C-term truncation pos 574	down ?	164	8	815	467	20.5	1.75	0.2	0.02	unknown beta galactosidase	BGAL12_4	18.29	0.01002662	up
AT4G28790	Basic helix-loop-helix (BHLH) DNA-binding superfamily protein	retained introns, alternative 5' and 3' ends	yes	C-term truncation pos 287 removing the HLH domain	down	64	0	279	130	####	2.15	0.23	0	unknown BHLH TF	BHLH23_8	133.17	0.01596197	up
AT4G05170	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	retained intron, alternative 5' and 3' ends	yes	wt	up	38	0	78	40	####	1.95	0.49	0	unknown BHLH TF B70 homolog	AT4G05170_5	92.782	0.02581615	up
AT1G58807	Probable disease resistance protein RF45	retained intron	yes	wt	up	1631	521	2806	1245	3.13	2.25	0.58	0.42	unknown CC-NBS-LRR protein	RF45_1_1	2.6088	0.01719144	up
AT5G43740	Disease resistance protein (CC-NBS-LRR class) family	alternative 3' splice site, alternative 5' and 3' ends	no	wt	up	103	0	485	312	####	1.55	0.21	0	unknown CC-NBS-LRR protein	AT5G43740_1	231.07	4.34E-03	up
AT1G59124	Probable disease resistance protein RDL5	intron corresponding to retained intron, alternative 3' end	yes	C-term truncation pos 850 removing part of the RNI-like LRR domain	down	1641	491	2833	1253	3.34	2.26	0.58	0.39	unknown CC-NBS-LRR protein	RF45_2_2	2.7972	0.0113475	up
At4g31110	Wall-associated receptor kinase-like 18 (EC 2.7.11.-)	alternative 5' splice site	yes	wt	up	37	0	113	85	####	1.33	0.33	0	unknown cell wall associated kinase	WAKL18_2	88.886	0.0319512	up
AT4G31570	Nucleoporin	alternative 3' splice site	yes	34aa deletion pos 2662-2697	up?	625	18	2193	978	34.7	2.24	0.28	0.02	unknown coiled coil domain repeat protein	AT4G31570_1	29.312	5.88E-04	up
AT3G05900	neurofilament protein-related	retained intron, alternative 5' and 3' ends	yes	27aa N-term deletion	up?	5398	2099	9559	5762	2.57	1.66	0.56	0.36	unknown coiled coil protein	AT3G05900_1	2.1672	5.64E-03	up
AT2G25670	Uncharacterized protein	retained intron	no	wt	up	3148	1309	5709	4196	2.4	1.36	0.55	0.31	unknown coiled coil protein	AT2G25670_2	2.0515	5.64E-03	up
AT3G10880	Uncharacterized protein	alternative 3' splice site	yes	wt	up	48	0	90	49	####	1.84	0.53	0	unknown coiled coil protein	AT3G10880_4	107.48	0.01727875	up
AT3G09730	POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND protein	retained intron	yes	C-term truncation pos 391	down ?	96	0	154	74	####	2.08	0.62	0	unknown coiled coil protein	AT3G09730_3	222.2	4.40E-03	up
AT4G32030	At4g32030 (Uncharacterized protein AT4g32030) (Uncharacterized protein F10N7.160)	retained introns, alternative 5' and 3' ends	yes	C-term truncation pos 168 removing the coiled coil domain	down ?	667	152	3046	2947	4.39	1.03	0.22	0.05	unknown coiled coil protein	AT4G32030_2	3.698	4.68E-03	up
AT4G25690	Uncharacterized protein	intron corresponding to retained intron	no	wt	down	1279	2189	1488	2385	0.58	0.62	0.86	0.92	unknown coiled coil protein	AT4G25690_1	-2.0113	9.64E-03	down
AT4G11100	Gelsolin protein (Uncharacterized protein At4g11100)	alternative 5' and 3' ends	no	wt	down	803	1359	1475	1543	0.59	0.96	0.54	0.88	unknown coiled coil protein	AT4G11100_1	-2.0064	0.03123432	down
AT3G20120	cytochrome P450, family 705, subfamily A, polypeptide 21	alternative 5' end	yes	136aa N-term deletion removing the transmembrane domain and part of the p450 domain	down	271	57	647	492	4.75	1.32	0.42	0.12	unknown CYP705A21 cytochrome P450	CYP705A21_4	4.2227	0.04474243	up
AT4G04570	cysteine-rich RLK (RECEPTOR-like protein kinase) 40	retained intron	yes	C-term truncation pos 560 removing part of the catalytic Pkinase domain	down	1572	571	3188	1577	2.75	2.02	0.49	0.36	unknown cysteine-rich RLK	CRK40_1	2.348	3.44E-03	up
AT4G23260	cysteine-rich RLK (RECEPTOR-like protein kinase) 18	alternative 5' and 3' splice sites, alternative5' and 3' ends	yes	44aa exchange pos 280-324 in the transmembrane domain	down	952	334	2134	1109	2.85	1.92	0.45	0.3	unknown cysteine-rich RLK	CRK18_1	2.3986	0.01430457	up
AT1G66450	Cysteine/Histidine-rich C1 domain family protein	alternative 5' and 3' ends	yes	wt	up	36	0	65	56	####	1.16	0.55	0	unknown Diacylglycerol receptor with C1, PHD and C1-2/2 domains	AT1G66450_2	81.923	0.02508376	up

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AT1G68340	Protein of unknown function (DUF1639)	retained intron	yes	1aa C-term exchange	up?	58	0	198	153	####	1.29	0.29	0	unknown DUF1639 domain protein	AT1G68340_1	123.14	0.0169878	up
AT5G39530	Protein of unknown function (DUF1997)	intron corresponding to retained intron, alternative 3' end	yes	wt	down	3663	6451	4239	6841	0.57	0.62	0.86	0.94	unknown DUF1997 domain protein	AT5G39530_2	-2.0703	5.81E-03	down
AT3G04890	Uncharacterized conserved protein (DUF2358)	alternative 3' splice site, intron, corresponding to retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 187	up?	440	1009	740	1138	0.44	0.65	0.59	0.89	unknown DUF2358 domain protein	AT3G04890_1	-2.5976	8.01E-03	down
AT1G65985	Plant protein of unknown function (DUF247)	alternative 5' end	no	wt	up	80	7	227	203	11.4	1.12	0.35	0.03	unknown DUF247 domain protein	AT1G65985_1	9.5658	0.04466609	up
AT1G05540	Protein of unknown function (DUF295)	retained intron	yes	C-term truncation pos 261 removing the DUF295 domain	down	38	0	174	85	####	2.05	0.22	0	unknown DUF295 domain protein	AT1G05540_2	87.726	0.02282312	up
AT1G64355	1-acyl-sn-glycerol-3-phosphate acyltransferase	retained intron, alternative 5' and 3' ends	yes	127aa N-term deletion removing part of the DUF3593 domain	down	503	103	2371	2760	4.88	0.86	0.21	0.04	unknown DUF3593 domain protein	AT1G64355_1	4.1253	6.61E-03	up
AT3G15770	AT3G15770 protein	alternative 5' end	no	wt	down	533	1106	869	1340	0.48	0.65	0.61	0.83	unknown DUF4050 domain protein	AT3G15770_1	-2.4356	0.01646274	down
AT2G22270	Uncharacterized protein	alternative 5' end	yes	40aa N-term deletion	down ?	356	43	786	495	8.28	1.59	0.45	0.09	unknown DUF4057 domain protein	AT2G22270_1	6.7798	0.01323347	up
AT1G15400	Uncharacterized protein At1g15400	alternative 3' splice site, alternative 5' end	yes	C-terminal truncation pos 140	up?	1654	2990	3521	5632	0.55	0.63	0.47	0.53	unknown DUF4666 domain protein	AT1G15400_2	-2.088	7.00E-03	down
AT3G19520	Protein of unknown function (DUF626)	alternative 3' splice site, alternative 3' end	yes	12aa deletion pos 212 223 in the DUF626 domain	up	709	1347	2438	3449	0.53	0.71	0.29	0.39	unknown DUF626 domain protein	AT3G19520_3	-2.2467	0.01156509	down
AT3G17450	hAT dimerisation domain-containing protein	retained intron, alternative 5' and 3' ends	no	wt	up	922	64	1509	734	14.4	2.06	0.61	0.09	unknown DUF659 domain with BED finger and Activator transposondimerization Dimer_Tnp_hAT domains	AT3G17450_1	12.085	3.00E-04	up
AT5G45370	nodulin MtN21 /EamA-like transporter family protein	retained intron	yes	102aa N-term deletion removing part of the 1st EamA domain	down	103	7	237	223	14.7	1.06	0.43	0.03	unknown EamA domain membrane transporter	AT5G45370_5	11.056	0.03018019	up
AT4G28040	nodulin MtN21 /EamA-like transporter family protein	alternative 3' splice site, alternative 5' and 3' ends	no	wt	down	1148	2307	3877	4835	0.5	0.8	0.3	0.48	unknown EamA domain membrane transporter	AT4G28040_1	-2.3343	0.01404948	down
AT1G11450	nodulin MtN21 /EamA-like transporter family protein	retained intron, alternative 5' and 3' ends	yes	C-term truncation pos 312 removing part of the 2nd EamA domain	down	54	0	228	267	####	0.85	0.24	0	unknown EamA domain membrane transporter	AT1G11450_2	127.72	0.01359745	up
AT1G06620	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	intron corresponding to retained intron	yes	wt	down	344	657	404	680	0.52	0.59	0.85	0.97	unknown Fe(2+) and 2-oxoglutarate (2OG)-dependent dioxygenase	AT1G06620_1	-2.2508	0.04240585	down
AT3G19370	Plant protein of unknown function (DUF869)	alternative 5' and 3' ends	no	wt	up	1035	423	1118	475	2.45	2.35	0.93	0.89	unknown Filament-like plant protein, long coiled-coil	AT3G19370_2	2.0828	0.03571419	up
AT5G51470	Auxin-responsive GH3 family protein	alternative 5' end	yes	wt	up	37	0	39	20	####	1.95	0.95	0	unknown GH3 domain protein	AT5G51470_2	85.434	0.02376649	up
AT5G17510	Uncharacterized protein	alternative 5' and 3' ends	no	wt	up	297	29	1316	766	10.2	1.72	0.23	0.04	unknown GLTSCR1 domain protein	AT5G17510_1	8.5352	0.03895122	up
AT3G59570	Ypt/Rab-GAP domain of gyp1p superfamily protein	retained intron	yes	C-term truncation pos 687	down ?	48	0	183	94	####	1.95	0.26	0	unknown GTP-activator of a Rab-like GTPase	AT3G59570_2	95.957	0.02917065	up
AT5G58370	P-loop containing nucleoside triphosphate hydrolases superfamily protein	alternative 3' splice site, alternative 5' and 3' ends	yes	C-term truncation pos 438 removing part of the MMR_HSR1 domain	down	363	56	976	487	6.48	2	0.37	0.11	unknown GTP-binding MMR_HSR1 domain protein	AT5G58370_1	5.7502	0.0172229	up
AT2G31510	ARIADNE 7	retained intron	yes	C-term truncation pos 498	up?	553	151	2637	1740	3.66	1.52	0.21	0.09	unknown imprinted IBR domain RING E3	ARI7_1	3.0357	0.03306069	up
AT2G47350	HIT zinc finger ;PAPA-1-like conserved region	alternative 5' splice site, alternative 5' and 3' ends	yes	wt	up	460	139	685	405	3.31	1.69	0.67	0.34	unknown INO80 interacting PAPA-1 domain zf-HIT domain zinc finger protein	AT2G47350_2	2.9694	0.04743342	up
AT3G28300	UPF0496 protein At3g28300 (Protein At14a)	none	no	wt	down	200	638	200	638	0.31	0.31	1	1	unknown integrin-like DUF677 domain protein	AT14A_2_1	-3.8245	0.01380549	down
AT3G28290	UPF0496 protein At3g28290 (Protein At14a)	none	no	wt	down	213	628	213	628	0.34	0.34	1	1	unknown integrin-like DUF677 domain protein	AT14A_1_1	-3.5162	0.02412155	down
AT4G32350	Regulator of Vps4 activity in the MVB pathway protein	alternative 5' and 3' ends	no	wt	up	781	252	1295	639	3.1	2.03	0.6	0.39	unknown Ist1 domain protein	AT4G32350_1	2.6257	0.03268135	up
AT4G35030	Protein kinase superfamily protein	retained introns	yes	C-term truncation pos 345 removing part of the Pkinase domain	down	63	0	291	144	####	2.02	0.22	0	unknown kinase	AT4G35030_3	144.6	0.01108212	up
AT1G48260	CBL-interacting protein kinase 17	alternative 5' end	yes	85aa N-term deletion removing part of the catalytic S_TKc domain	down	53	0	257	261	####	0.98	0.21	0	unknown kinase, calcineurin B-like activated CIPK	CIPK17_2	119.89	0.01449686	up
AT1G67520	lectin protein kinase family protein	retained introns	yes	23aa deletion of N-term signal peptide	down	51	0	249	125	####	1.99	0.2	0	unknown lectin receptor kinase	AT1G67520_1	118.89	0.01493572	up
AT2G02780	Leucine-rich repeat protein kinase family protein	retained intron, alternative 5'-end	yes	C-term truncation removing part of the catalytic kinase domain	down	209	0	793	639	####	1.24	0.26	0	unknown LRR kinase	AT2G02780_3	462.3	7.88E-04	up

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AT4G13810	receptor like protein 47	retained intron	yes	wt	up	182	14	681	456	13	1.49	0.27	0.03	unknown LRR membrane receptor	RLP47_1	11.014	0.01523826	up
AT2G33170	Leucine-rich repeat receptor-like protein kinase family protein	intron corresponding to retained intron, alternative 5' and 3' ends	no	wt	up	834	289	2014	879	2.89	2.29	0.41	0.33	unknown LRR receptor kinase	AT2G33170_2	2.5432	0.02868551	up
AT1G29730	Leucine-rich repeat transmembrane protein kinase	exon corresponding to exon skip	yes	wt	up	38	0	74	47	####	1.57	0.51	0	unknown LRR receptor kinase with signal pepide and Malectin domain	AT1G29730_1	76.227	0.03775529	up
AT3G18900	Ternary complex factor MIP1 leucine-zipper protein	alternative 5' and 3' ends	yes	81aa N-term deletion removing part of the Lzipper-MIP1 domain	down	40	1	94	64	40	1.47	0.43	0.02	unknown Lzipper-MIP1 and DUF547 domain, potential interaction with MADS TFs	AT3G18900_6	23.406	0.02564639	up
AT1G67060	Peptidase M50B-like protein	alternative 5' splice site	yes	wt	down	617	1083	781	1182	0.57	0.66	0.79	0.92	unknown M50B-like peptidase	AT1G67060_1	-2	0.03461184	down
AT1G60095	Mannose-binding lectin superfamily protein	alternative 5' end	yes	144aa N-term deletion removing the 1st Jacalin domain	down	32	0	71	35	####	2.03	0.45	0	unknown mannose binding Jancalin repeat protein	AT1G60095_1	76.983	0.0378549	up
AT2G37300	Transmembrane protein	retained intron, alternative 5' end	yes	57aa N-term deletion of transmembrane domain	down	40	0	188	195	####	0.96	0.21	0	unknown membrane bound coiled coil protein	AT2G37300_4	80.172	0.03623593	up
AT4G09630	Protein of unknown function (DUF616)	retained intron, alternative 5' end	yes	wt	up	1664	652	1864	893	2.55	2.09	0.89	0.73	unknown membrane bound DUF616 domain glucosyltransferase	AT4G09630_2	2.1538	0.01840797	up
AT1G52420	UDP-Glycosyltransferase superfamily protein	none	no	wt	up	2405	1001	2405	1001	2.4	2.4	1	1	unknown membrane bound Glycosyl-transferase family 4 protein	AT1G52420_1	2.0074	0.01172789	up
AT3G13437	Uncharacterized protein	retained intron	yes	15aa N-term deletion	down ?	48	0	127	93	####	1.37	0.38	0	unknown membrane protein	AT3G13437_2	95.957	0.02915206	up
AT2G41640	Glycosyltransferase family 61 protein	alternative 5' and 3' ends	yes	wt	up	672	90	865	506	7.47	1.71	0.78	0.18	unknown membrane-bound glycosyltransferase family 61 protein	AT2G41640_2	6.6516	1.81E-03	up
AT2G44280	Major facilitator superfamily protein	retained intron	no	wt	up	66	0	243	147	####	1.65	0.27	0	unknown MFS/sugar transporter	AT2G44280_1	131.48	0.01925603	up
AT5G41170	Pentatricopeptide repeat (PPR-like) superfamily protein	retained intron	yes	wt	up	53	0	82	46	####	1.78	0.65	0	unknown mitochondrial PPR protein	AT5G41170_1	124.2	0.01395577	up
AT1G35190	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	alternative 3' splice site	yes	24aa deletion pos 147-171 removing part of the 2OG-FeII_Oxy domain	down	401	1	1744	1456	401	1.2	0.23	0	unknown non-haem dioxygenase in morphine synthesis domain protein	AT1G35190_1	251.12	2.83E-07	up
AT5G41140	Myosin heavy chain-related protein	alternative 5' splice site, alternative 5' end	yes	wt	up	1633	492	1728	770	3.32	2.24	0.95	0.64	unknown NT-C2 and coiled coil domain protein	AT5G41140_2	2.7989	4.05E-03	up
AT5G04830	Nuclear transport factor 2 (NTF2) family protein	retained intron, alternative 5' and 3' ends	no	wt	up	1032	333	3474	2860	3.1	1.21	0.3	0.12	unknown NTF2-like domain protein	AT5G04830_1	2.7206	0.01910436	up
AT4G02540	Cysteine/Histidine-rich C1 domain family protein	retained intron, alternative 5' and 3' ends	yes	wt	up	2602	1068	3073	1425	2.44	2.16	0.85	0.75	unknown nuclear PHD zinc finger protein	AT4G02540_2	2.0319	9.51E-03	up
AT1G10590	Nucleic acid-binding, OB-fold-like protein	alternative 5' splice site, alternative 5' and 3' ends	no	wt	down	1259	2681	4984	6354	0.47	0.78	0.25	0.42	unknown OB-fold nucleic acid binding protein	AT1G10590_1	-2.4812	5.93E-04	down
AT5G04250	Cysteine proteinases superfamily protein	alternative 3' splice site, alternative 3' end	no	wt	up	49	2	210	206	24.5	1.02	0.23	0.01	unknown OTU domain cysteine peptidase	AT5G04250_1	16.583	0.04097847	up
AT4G17483	alpha/beta-Hydrolases superfamily protein	exon skip	yes	74aa N-term deletion removing part of the Palm_thioest domain	down	36	1	76	52	36	1.46	0.47	0.02	unknown palmitoyl-protein thioesterase	AT4G17483_4	22.858	0.04424052	up
AT1G04700	PB1 domain-containing protein tyrosine kinase	alternative 5' and 3' ends	no	wt	up	44	0	118	66	####	1.79	0.37	0	unknown PB1 dimerization domain containing protein kinase	AT1G04700_1	108.27	0.0211014	up
AT5G63130	Octicosapeptide/Phox/Bem1p family protein	retained intron	no	wt	up	74	0	140	107	####	1.31	0.53	0	unknown PB1 dimerization domain protein	AT5G63130_1	162.3	0.01067362	up
AT3G60960	Tetratricopeptide repeat (TPR)-like superfamily protein	alternative 3' end	no	wt	up	175	0	548	691	####	0.79	0.32	0	unknown Pentatricopeptide repeat protein	AT3G60960_1	353.3	2.29E-03	up
AT1G56130	Leucine-rich repeat transmembrane protein kinase	alternative 5' end; missing intron	yes	149aa deletion removing the N-term signal peptide	down	77	0	118	54	####	2.19	0.65	0	unknown PM LRR kinase	AT1G56130_3	158.84	0.01154602	up
AT5G20710	beta-galactosidase 7	alternative 5' end	yes	205aa N-term deletion removing the signal peptide and Glyco_hydro_42 domain	down	71	3	110	60	23.7	1.83	0.65	0.05	unknown pollen abundant beta-galactosidase	BGAL7_1	18.398	0.02475901	up
AT1G28090	Polynucleotide adenylyltransferase family protein	alternative 5' and 3' ends	yes	66aa N-term deletion	down	444	71	997	649	6.25	1.54	0.45	0.11	unknown polyA polymerase	AT1G28090_3	5.2695	0.04913267	up
AT5G15940	NAD(P)-binding Rossmann-fold superfamily protein	alternative 5' end	no	wt	up	27	0	52	38	####	1.37	0.52	0	unknown polyketide or fatty acid synthase	AT5G15940_2	67.639	0.03690191	up
AT1G62610	NAD(P)-binding Rossmann-fold superfamily protein	alternative 5' splice site	yes	7aa N-term deletion	down ?	124	0	591	545	####	1.08	0.21	0	unknown polyketide synthase KR domain	AT1G62610_4	295.97	5.09E-03	up
AT2G20710	Tetratricopeptide repeat (TPR)-like superfamily protein	retained intron	yes	95aa N-term deletion	down ?	96	0	198	141	####	1.4	0.48	0	unknown PPR repeat protein	AT2G20710_2	220.56	6.11E-03	up

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AT5G25630	Tetratricopeptide repeat (TPR)-like superfamily protein	retained intron	yes	51aa N-term deletion removing part of the1st PPR repeat, and 26aa deletion pos 317-343	down	1577	369	3662	2082	4.27	1.76	0.43	0.18	unknown PPR repeat protein likely chloroplast	AT5G25630_3	3.4645	1.07E-03	up
AT4G29920	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	alternative 3' splice site, alternative 5' and 3' ends	yes	3aa deletion pos 442-445	up?	167	14	237	123	11.9	1.93	0.7	0.11	unknown protease targeting Clp_N domain coiled coil protein	AT4G29920_1	9.7934	0.02631343	up
AT3G14172	GPI-anchored adhesin-like protein	alternative 5' splice site, alternative 5' and 3' ends	yes	8aa deletion pos 74-82	up?	277	33	1269	742	8.39	1.71	0.22	0.04	unknown protein	AT3G14172_2	6.7083	0.03570783	up
AT1G19860	Zinc finger C-x8-C-x5-C-x3-H type family protein	exon skip	yes	wt	up	1266	521	1490	807	2.43	1.85	0.85	0.65	unknown protein	AT1G19860_2	2.1221	0.0184756	up
AT5G07980	dentin sialophosphoprotein-related	alternative 3' splice site, alternative 5' and 3' ends	no	wt	up	941	351	1518	950	2.68	1.6	0.62	0.37	unknown protein	AT5G07980_1	2.3761	0.03607487	up
AT1G77270	Uncharacterized protein At1g77270	alternative 3' splice site	no	wt	up	181	0	324	132	####	2.45	0.56	0	unknown protein	AT1G77270_1	385.88	1.59E-03	up
AT5G58210	hydroxyproline-rich glycoprotein family protein	alternative 5' and 3' ends	no	wt	up	204	20	595	402	10.2	1.48	0.34	0.05	unknown protein	AT5G58210_2	8.9056	0.02336677	up
AT1G69280	Uncharacterized protein	intron corresponding to retained intron	yes	wt	up	28	0	97	134	####	0.72	0.29	0	unknown protein	AT1G69280_3	67.459	0.04378136	up
AT1G77350	Uncharacterized protein	alternative 3' splice site, alternative 5' end	no	wt	up	229	30	1015	1208	7.63	0.84	0.23	0.02	unknown protein	AT1G77350_2	6.8352	0.04556927	up
AT2G21195	Uncharacterized protein	introns corresponding to retained introns	yes	22aa deletion pos 60-82	down ?	252	599	512	851	0.42	0.6	0.49	0.7	unknown protein	AT2G21195_4	-2.7106	0.02718738	down
AT4G16380	Heavy metal transport/detoxification superfamily protein	alternative 5' splice site, alternative 5' end	yes	61aa N-term deletion	down ?	1813	443	7873	5731	4.09	1.37	0.23	0.08	unknown protein	AT4G16380_1	3.6246	1.69E-03	up
AT3G51620	PAP/OAS1 substrate-binding domain superfamily	exon skip, alternative 3' splice site	yes	60aa deletion pos 170-230 in the SCOP domain d1f5aa2	down ?	538	65	1436	1221	8.28	1.18	0.37	0.05	unknown protein	AT3G51620_2	6.8892	3.51E-03	up
AT1G05087	Dentin sialophosphoprotein	retained intron	yes	110aa N-term deletion	down	78	0	165	98	####	1.68	0.47	0	unknown protein	AT1G05087_1	163.86	0.01051437	up
AT4G24920	secE/sec61-gamma protein transport protein	alternative 5' and 3' ends	yes	wt	down	1284	2328	2924	4133	0.55	0.71	0.44	0.56	unknown protein	AT4G24920_2	-2.0063	0.04951881	down
AT1G22790	Uncharacterized protein	alternative 3' splice site, alternative 5' and 3' ends	no	wt	down	277	718	899	1378	0.39	0.65	0.31	0.52	unknown protein	AT1G22790_2	-2.9667	7.33E-03	down
AT3G45050	Uncharacterized protein	alternative 5' splice site	no	wt	down	460	1061	1560	2295	0.43	0.68	0.29	0.46	unknown protein	AT3G45050_2	-2.7362	2.67E-03	down
AT1G73460	Protein kinase superfamily protein	retained intron	no	wt	up	1987	764	2141	1040	2.6	2.06	0.93	0.73	unknown protein kinase	AT1G73460_1	2.1941	4.08E-03	up
AT1G55200	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	retained intron	no	wt	up	62	0	183	103	####	1.78	0.34	0	unknown protein kinase	AT1G55200_3	142.06	0.01437224	up
At5g02290	Probable serine/threonine-protein kinase PBL11 (EC 2.7.11.1) (PBS1-like protein 11)	alternative 5' end	no	wt	up	727	83	2962	2709	8.76	1.09	0.25	0.03	unknown protein kinase	PBL11_1	7.0396	0.02000465	up
AT3G63180	TICKLE	alternative 3' splice site, alternative 5' end	yes	wt	down	448	922	1565	1466	0.49	1.07	0.29	0.63	unknown protein TIC-LIKE TICKLE	ATTKL_1	-2.3261	0.01900493	down
AT3G17900	AT3g17900/MEB5_12 (Heat-inducible transcription repressor)	alternative 5' end	no	wt	up	669	106	2467	1931	6.31	1.28	0.27	0.05	unknown protein Topless interactor	AT3G17900_2	5.0339	0.03065386	up
AT5G56990	Proteinase inhibitor I25, cystatin, motif protein	retained intron, alternative 5' and 3' ends	yes	20aa N-term exchange	down ?	50	0	189	149	####	1.27	0.26	0	unknown protein with cystatine-like domain	AT5G56990_2	106.93	0.02075789	up
AT2G32150	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	retained intron, alternative 5' and 3' ends	yes	wt	down	1859	3135	6869	8936	0.59	0.77	0.27	0.35	unknown protein with Hydrolase_like domain	AT2G32150_3	-2.0055	0.02885888	down
At5g62730	Protein NRT1/ PTR FAMILY 4.7 (AtNPF4.7)	alternative 5' end	yes	wt	up	67	0	146	77	####	1.9	0.46	0	unknown proton dependent PM oligopeptide transporter	NPF4.7_1	151.58	0.01254391	up
At2g37900	Protein NRT1/ PTR FAMILY 5.6 (AtNPF5.6)	retained intron	yes	79aa N-term deletion	down	55	0	247	197	####	1.25	0.22	0	unknown proton-dependentoligopeptide transporter	NPF5.6_1	139.68	0.01490375	up
AT3G01410	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	intron corresponding to retained intron, alternative 5'and 3' ends	no	wt	up	105	0	455	312	####	1.46	0.23	0	unknown Reverse transcriptase-like protein	AT3G01410_2	237.04	5.37E-03	up
AT4G18375	RNA-binding KH domain-containing protein	retained intron	yes	C-term deletion pos 531 removing the last KH domain hnRNP domain	down	25	0	114	61	####	1.87	0.22	0	unknown RNA-binding KH domain repeat protein	AT4G18375_2	56.196	0.04538465	up
AT3G01210	RNA-binding (RRM/RBD/RNP motifs) family protein	alternative 5' and 3' ends	no	wt	down	380	1026	873	1462	0.37	0.6	0.44	0.7	unknown RRM domain RNA binding protein	AT3G01210_1	-3.0494	4.59E-03	down
AT3G12940	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	retained introns	yes	wt	up	276	9	607	417	30.7	1.46	0.45	0.02	unknown SCOP domain d1dcs protein	AT3G12940_1	24.003	1.29E-03	up

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AT5G36180	serine carboxypeptidase-like 1	intron corresponding to retained intron, alternative 5' end	yes	wt	up	63	0	187	206	####	0.91	0.34	0	unknown serine carboxypeptidase-like 1	SCPL1_4	155.96	0.01251661	up
AT1G73310	serine carboxypeptidase-like 4	alternative 5' end; missing intron	yes	103aa -N-term deletion removing the signal peptide and C-term truncation pos 401 in thePeptidase_S10 domain	down	74	0	299	220	####	1.36	0.25	0	unknown serine carboxypeptidase-like 4	SCPL4_3	161.06	8.97E-03	up
AT2G37290	Ypt/Rab-GAP domain of gyp1p superfamily protein	alternative 5' and 3' ends	yes	15aa N-term exchange	up?	48	0	79	33	####	2.39	0.61	0	unknown TBC GTPase-activator GAP of Rab-like GTPases	AT2G37290_2	102.59	0.02204677	up
AT4G39160	Homeodomain-like superfamily protein	alternative 5' and 3' ends	yes	C-term truncation pos 600	down ?	296	15	1023	598	19.7	1.71	0.29	0.03	unknown TBP interacting MYB TF	AT4G39160_2	17.314	9.33E-04	up
AT2G25290	Phox1	alternative 5' and 3' ends	no	wt	up	243	0	384	194	####	1.98	0.63	0	unknown Tetratricopeptide repeat protein with PB1 dimerization domain	Phox1_2	544.14	5.21E-04	up
AT5G22690	Disease resistance protein (TIR-NBS-LRR class) family	retained intron	yes	wt	up	615	157	738	333	3.92	2.22	0.83	0.47	unknown TIR-NBS-LRR protein	AT5G22690_1	3.2279	0.0486976	up
AT4G19510	Disease resistance protein (TIR-NBS-LRR class)	retained introns, alternative 3' splice site	yes	wt	up	344	33	1658	1042	10.4	1.59	0.21	0.03	unknown TIR-NBS-LRR protein	AT4G19510_2	8.3711	6.89E-03	up
AT5G46450	Disease resistance protein (TIR-NBS-LRR class) family	intron corresponding to retained intron, alternative 5' and 3' ends	yes	34aa deletion pos 877-911	down ?	475	36	2134	1066	13.2	2	0.22	0.03	unknown TIR-NBS-LRR protein	AT5G46450_3	11.441	2.52E-03	up
AT1G72860	Disease resistance protein (TIR-NBS-LRR class) family	retained introns	yes	33aa deletion pos 626-659 and C-term truncation pos 1132	down	29	0	43	22	####	1.95	0.67	0	unknown TIR-NBS-LRR protein	AT1G72860_1	61.922	0.04076551	up
AT1G72840	Disease resistance protein (TIR-NBS-LRR class)	alternative 5' and 3' ends	yes	167aa N-term deletion removing the TIR domain	down	122	5	333	232	24.4	1.44	0.37	0.02	unknown TIR-NBS-LRR protein	AT1G72840_1	20.225	5.38E-03	up
AT3G06920	Tetratricopeptide repeat (TPR)-like superfamily protein	retained intron	yes	wt	up	214	0	457	228	####	2	0.47	0	unknown TPR protein	AT3G06920_3	504.93	6.65E-04	up
AT5G04680	Ankyrin repeat family protein	intron corresponding to retained intron, alternative 5' and 3' ends	yes	30aa deletion pos 293-323	up?	31	0	100	44	####	2.27	0.31	0	unknown transmembrane ankyrin repeat protein with PGG domain	AT5G04680_3	76.835	0.03219529	up
AT2G45830	downstream target of AGL15 2	intron corresponding to retained intron, alternative 5' end	yes	wt	up	104	3	494	337	34.7	1.47	0.21	0.01	unknown transmembrane CAP10 domain protein for extracellular polysaccharide deposition	DTA2_4	27.509	3.78E-03	up
AT3G02900	Uncharacterized protein	alternative 3' splice site, alternative 5' and 3' ends	yes	24aa N-term exchange	down ?	382	1087	1286	1714	0.35	0.75	0.3	0.63	unknown transmembrane coiled coil protein	AT3G02900_1	-3.2102	1.65E-03	down
AT2G28310	Protein of unknown function (DUF707)	alternative 5' end	no	wt	up	927	290	1353	909	3.2	1.49	0.69	0.32	unknown transmembrane DUF707 domain protein siggested ribosome biogenesis 2,2,7-trimethylguanosine capping of sno and snRNAs	AT2G28310_3	2.6805	9.87E-03	up
AT2G41820	PXY/TDR-correlated 3	none	no	wt	up	1696	724	1696	724	2.34	2.34	1	1	unknown transmembrane LRR receptor	PXC3_1	2.0082	0.02002323	up
AT5G10290	leucine-rich repeat transmembrane protein kinase family protein	alternative 5' and 3' ends	no	wt	up	657	111	1354	1015	5.92	1.33	0.49	0.11	unknown transmembrane LRR receptor kinase	AT5G10290_2	4.4532	0.0283822	up
AT2G31740	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	retained intron, alternative 5' and 3' ends	yes	197aa deletion of N-term Methyltransf_18 domain	down	820	9	1815	1095	91.1	1.66	0.45	0.01	unknown transmembrane methylase	AT2G31740_2	75.394	1.44E-12	up
AT1G70280	NHL domain-containing protein	retained intron	yes	62aa N-term deletion removing the signal peptide	down	853	88	2569	1313	9.69	1.96	0.33	0.07	unknown transmembrane NHL domain protein	AT1G70280_1	7.2822	0.01528754	up
AT5G42280	Cysteine/Histidine-rich C1 domain family protein	retained intron, alternative 5' end	yes	164aa N-term deletion removing the 1st PHD domain	down	130	12	170	111	10.8	1.53	0.76	0.11	unknown transmembrane PHD C4HC3 zinc-finger-like and DAG C1_3 domain protein	AT5G42280_2	9.4249	0.03634005	up
AT5G20120	At5g20120 (Testis-and ovary-specific PAZ domain protein) (Uncharacterized protein At5g20120)	intron corresponding to retained intron, alternative 5' end	no	wt	down	920	1651	1135	1727	0.56	0.66	0.81	0.96	unknown transmembrane protein	AT5G20120_2	-2.0265	0.02023609	down
AT4G02725	Spindle pole body-associated protein	intron corresponding to retained intron	yes	wt	down	1209	2235	1598	2496	0.54	0.64	0.76	0.9	unknown transmembrane protein	AT4G02725_2	-2.1336	4.01E-03	down
At4g15080	Probable protein S-acyltransferase 19 (EC 2.3.1.225) (Probable palmitoyltransferase At4g15080) (Zinc finger DHHC domain-containing protein At4g15080)	retained intron, alternative 5' and 3' ends	no	wt	up	471	31	2065	1267	15.2	1.63	0.23	0.02	unknown transmembrane zf-DHHC domain protein	PAT19_1	13.139	1.15E-03	up
AT1G11360	Adenine nucleotide alpha hydrolases-like superfamily protein	alternative 5' and 3' splice sites	no	wt	down	933	1622	1690	2350	0.58	0.72	0.55	0.69	unknown universal stress protein UspA	AT1G11360_4	-2.0511	0.01277348	down
AT2G44850	Uncharacterized protein	alternative 5' and 3' splice sites, alternative 5' and 3' ends	yes	117aa N-term deletion	down ?	83	0	262	380	####	0.69	0.32	0	unknown UPF0565 domain protein	AT2G44850_1	175.52	9.41E-03	up
AT2G30933	Carbohydrate-binding X8 domain superfamily protein	alternative 5' end	yes	C-term truncation pos 159 removing part of the X8 carbohydrate binding domain and C-term transmembrane domain	down	39	0	95	74	####	1.28	0.41	0	unknown X8 domain protein	AT2G30933_3	93.011	0.02542064	up
AT4G12040	stress-associated protein 7	intron corresponding to retained intron, alternative 5' and 3' ends	no	wt	down	3177	6155	4097	6784	0.52	0.6	0.78	0.91	unknown zf-A20 and ZnF_AN1 domain TF	SAP7_2	-2.2236	2.51E-03	down
AT1G55915	zinc ion binding	alternative 5' and 3' ends	yes	54aa N-term deletion	down	112	1	263	213	112	1.23	0.43	0	unknown Zn-dependent peptidase WLM with RAN-GDP-binding ZnF_RBZ domains	AT1G55915_1	76.559	1.72E-03	up
AT3G02820	zinc knuckle (CCHC-type) family protein	alternative 5' and 3' ends	yes	wt	up	139	0	276	148	####	1.86	0.5	0	unknown ZnF_C2HC and SWI3 replication fork domain protein	AT3G02820_2	304.85	3.36E-03	up

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AT3G17609	HY5-homolog	retained intron	yes	30aa N-term deletion	down ?	235	15	1015	504	15.7	2.01	0.23	0.03	UV, blue light, HY5 bZIP homolog HYH, cold anthocyanine synthesis GA auxin	HYH_2	13.385	1.69E-03	up
AT4G26710	V-type proton ATPase subunit e2 (V-ATPase subunit e2) (Vacuolar H(+)-ATPase subunit e isoform 2) (Vacuolar proton pump subunit e2)	intron corresponding to retained intron, alternative 5' and 3' ends	no	wt	down	2890	5637	5673	8338	0.51	0.68	0.51	0.68	vacuole ATPase, V0 complex, subunit E	VHA-E2_2_1	-2.2113	2.23E-03	down
AT4G24490	RAB geranylgeranyl transferase alpha subunit 1	retained intron, alternative 5' and 3'-ends	no	wt	up	474	0	1832	1239	####	1.48	0.26	0	vesicular trafficking polar growth RGTA1 RAB geranylgeranyl transferase alpha subunit 1	RGTA1_1	1004.2	8.84E-05	up
AT4G23460	Beta-adaptin-like protein	alternative 5' end	yes	95aa N-term deletion removing part of the HEAT_2 domain	down	768	266	2757	2197	2.89	1.25	0.28	0.12	vesicular transport adaptor-related protein complex 1, beta 1 subunit	BETAC-AD_1	2.4767	0.03556855	up
AT3G46830	RAB GTPase homolog A2C	alternative 5' splice site, alternative 5' and 3' ends	no	wt	down	1396	2691	2373	3333	0.52	0.71	0.59	0.81	vesicular transport cell plate cell division RABA2c RAB GTPase homolog A2C	RABA2C_1	-2.206	3.08E-03	down
AT3G01810	Uncharacterized protein At3g01810	alternative 5' end	no	wt	up	1217	404	2393	1236	3.01	1.94	0.51	0.33	vesicular transport endocytosis NT-C2 domain protein	AT3G01810_2	2.5733	4.97E-03	up
AT3G54840	Ras-related small GTP-binding family protein	alternative 3' splice site	yes	C-term truncation pos 189 removin 9aa from the RAB domain	down	439	35	1946	2368	12.5	0.82	0.23	0.01	vesicular transport endosome membrane RAB GTPase carbon homeostasis	RABF1_3	11.194	2.90E-03	up
AT2G33470	glycolipid transfer protein 1	alternative 3' splice site	no	wt	down	1245	2507	3204	4290	0.5	0.75	0.39	0.58	vesicular transport GLTP1 glycolipid transfer protein 1	GLTP1_1	-2.2995	3.73E-03	down
AT4G02900	ERD (early-responsive to dehydration stress) family protein	retained introns	yes	C-term truncation pos 766	down ?	124	6	458	193	20.7	2.37	0.27	0.03	vesicular transport Golgi Ca2+ dependent phosphate channel	AT4G02900_4	16.968	7.65E-03	up
AT1G32410	Vacuolar protein sorting 55 (VPS55) family protein	alternative 3' splice site	no	wt	down	546	1139	1613	2369	0.48	0.68	0.34	0.48	vesicular transport Golgi to vacuole sorting Vps55 domain protein	AT1G32410_4	-2.4019	4.95E-03	down
AT4G09720	RAB GTPase homolog G3A	alternative 5' and 3' ends	yes	77aa deletion pos.115-122 in the RAB GTPase domain	down	273	0	1328	1205	####	1.1	0.21	0	vesicular transport small GTPase Golgi cell wall	ATRABG3A_1	620.73	4.94E-04	up
AT1G51160	SNARE-like superfamily protein	alternative 3' splice site, alternative 5' and 3' ends	no	wt	down	524	1117	2383	3780	0.47	0.63	0.22	0.3	vesicular transport TRAPP trafficking protein particle complex subunit 1	AT1G51160_2	-2.4146	0.02196209	down
AT3G50380	Protein of unknown function (DUF1162)	intron corresponding to retained intron	yes	678aa N-term deletion	down	710	246	1725	839	2.89	2.06	0.41	0.29	vesicular transport, Vacuolar-sorting-associated 13 protein	AT3G50380_4	2.4388	0.04796492	up
AT1G19400	Erythronate-4-phosphate dehydrogenase family protein	alternative 5' splice site	no	wt	down	2312	4085	3900	5760	0.57	0.68	0.59	0.71	vitamin B6 Pyridoxal-5'-phosphate synthesis Erythronate-4-phosphate dehydrogenase	AT1G19400_4	-2.0916	4.72E-03	down
AT4G30110	heavy metal atpase 2	alternative 5' end	no	wt	up	296	37	565	293	8	1.93	0.52	0.13	zinc transporter HMA2 heavy metal ATPase 2	HMA2_1	7.528	0.03150949	up
AT1G50840	polymerase gamma 2	alternative 5' end	no	wt	up	2629	1039	3441	1772	2.53	1.94	0.76	0.59		POLGAMMA2_2	2.1438	0.01547236	up
AT2G07690	MINICHROMOSOME MAINTENANCE 5	alternative 5' and 3' ends	no	wt	up	708	219	1122	480	3.23	2.34	0.63	0.46		MCM5_2	2.7798	0.02151207	up
AT3G54750	Downstream neighbor of Son	alternative 3' end	no	wt	up	427	0	1039	602	####	1.73	0.41	0		AT3G54750_2	906.07	1.23E-04	up
AT5G54650	formin homology5	retained intron, alternative 5' and 3' ends	no	wt	up	226	19	598	387	11.9	1.55	0.38	0.05		FH5_1	10.245	0.01163097	up
AT1G16340	Aldolase superfamily protein	retained intron, alternative 5' and 3' ends	no	wt	up	176	12	737	557	14.7	1.32	0.24	0.02		ATKDSA2_4	12.356	7.25E-03	up
At2g17500	Protein PIN-LIKES 5 (Auxin efflux carrier-like protein 5)	alternative 5' end	no	wt	down	2491	4970	4364	7066	0.5	0.62	0.57	0.7		PILS5_3	-2.2697	2.14E-03	down
AT1G18730	Photosynthetic NDH subcomplex B 4	alternative 5' and 3' ends	no	wt	down	1368	2722	3474	5736	0.5	0.61	0.39	0.47		PNSB4_1	-2.3243	1.17E-03	down
AT4G15010	Mitochondrial substrate carrier family protein	alternative 3' splice site	no	wt	down	353	669	921	997	0.53	0.92	0.38	0.67		AT4G15010_1	-2.3097	0.04822902	down
AT1G02930	glutathione S-transferase 6	retained intron, alternative 5' and 3' ends	no	wt	down	1438	2670	5163	6835	0.54	0.76	0.28	0.39		GSTF6_1	-2.2524	3.92E-03	down

Table 10: DE-DAS+DE-alone list of differentially regulated genes in the *prl2* mutant cells.

Entries corresponding to unknown gene functions were removed.

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
At3g07540	no	down	actin binding cell division transmembrane Formin Homology 2 Domain protein with signal peptide	FH10_1	-2.457	0.0189	down	FH10	-2.585	7E-04	down	
AT1G19520		down?	fertilization kayogamy female gametopyhe development pentatricopeptide (PPR) repeat protein					NFD5	-2.307	0.024	down	
At2g23030	no	up	ABA osmotic stress signaling SNRK2-9; SUCROSE NONFERMENTING 1-RELATED PROTEIN KINASE 2-9					SRK2J	8.2622	0.019	up	
AT1G07240	no	down	ABA UDP-glucosyl transferase 71C5 UGT71C5	UGT71C5_1	-4.399	0.0067	down	UGT71C5	-4.743	4E-04	down	
AT1G68790	no	down	ABA ABI5 degradation heterochromatin nuclear size control CROWDED NUCLEI 3; CRWN3;; LITTLE NUCLEI3	CRWN3_1	-2.349	6E-06	down	CRWN3	-2.484	2E-10	down	
AT1G18100	no	down	ABA ABI5/ABI3 induced regulator of seed germination FT/TFL1-line phosphatidylcholin binding protein					MFT	-4.025	0.007	down	
AT2G46400	no	up	ABA drought auxin BR signaling lateral root development WRKY 46 Transcription Factor; Group III					WRKY46	2.4454	0.015	up	
At2g20880	no	down	ABA drought induced AP2/ERF TF	ERF053_1	-7.558	9E-07	down	ERF053	-8.013	1E-12	down	down
AT4G27410	yes	up	ABA drought response senescence activator ANAC072/RD26 TF					RD26	-2.093	0.039	down	up
AT1G66600	no	up	ABA drought stress signaling ABA overly sensitive mutant 3; ATWRKY63	WRKY63_1	3.5603	0.0164	up	WRKY63	3.3852	0.002	up	
At3g01770		down?	ABA glucose signaling BT2 BTB-domain protein interacting bromodomain TF	GTE11_1	-3.03	0.0123	down	GTE11	-2.738	5E-04	down	
AT5G44120	yes	up	ABA induced 12S globulin CRA1, CRU1, CRUCIFERINA					CRA1	-40.9	0.042	down	up?
AT4G28520	no	down	ABA induced 12S seed storage protein	CRC_2_5	-205.7	0.0094	down	CRC_2	-11.05	0.025	down	
AT1G25480	no	up	ABA induced stomatal closure vacuolar anion channel aluminum activated malate transporter 4					ALMT4	4.0546	0.012	up	
AT1G67030	no	up	ABA light GA cytokinin signalling trichome development regulating ZFP6 zinc finger protein 6	ZFP6_1	18.851	0.0142	up	ZFP6	17.82	0.002	up	down
AT5G25160	no	up	ABA light signaling repressor ZFP3 zinc finger protein 3	ZFP3_1	60.462	0.0401	up	ZFP3	57.617	0.029	up	
AT1G08160	no	down	ABA osmotic stress Dehydrin					AT1G08160	-13.36	0.043	down	
AT3G28580	no	down	ABA oxidative stress induced unknown membrane ATPase	AT3G28580_2	-3.083	2E-07	down	AT3G28580	-3.231	5E-11	down	up
AT3G02860	no	up	ABA oxidative stress ROS ARS1 ABA AND ROS SENSITIVE 1 C2H2 zinc finger TF	AT3G02860_1	-3.112	0.0144	down	AT3G02860	-2.038	0.015	down	
AT1G66360	no	up	ABA receptor PM targeting C2-DOMAIN ABA-RELATED2, CAR2					CAR2	43.545	0.039	up	
AT4G01026	no	down	ABA receptor PYR1-like 7; RCAR2; regulatory components of ABA receptor 2					PYL7	-2.128	1E-03	down	
AT1G01360	no	down	ABA receptor RCAR1 regulatory component of ABA receptor 1	PYL9_1	-6.164	0.0084	down	PYL9	-6.59	4E-04	down	
AT5G17640	no	up	ABA salt induced DUF1005 domain ABIOTIC STRESS GENE 1, ASG1	AT5G17640_1	7.7553	0.0387	up	AT5G17640	7.4529	0.007	up	
AT1G09950	no	up	ABA salt stress induced DOG1 domain TF RAS1 RESPONSE TO ABA AND SALT 1	RAS1_1	16.638	0.0262	up	RAS1	15.717	0.007	up	
AT5G41790	no	down	ABA signaling COP1-interactive protein 1	CIP1_2	-2.595	2E-08	down	CIP1	-2.424	5E-11	down	
AT1G07430	no	down	ABA signaling negativeregulation of seed dormancy AIP1; AKT1 interacting protein phosphatase 1; AtAIP1; highly ABA-induced PP2C gene 2; HON; HONSU	AIP1_1	-3.957	0.0014	down	AIP1	-4.213	3E-05	down	
AT4G34220	no	down	ABA signaling positive regulator RECEPTOR DEAD KINASE1 transmembrane LRR receptor kinase					AT4G34220	-2.616	0.032	down	
AT1G50280	no	up	ABA signaling repressor BTB/POZ subunit of CUL3 E3	AT1G50280_2	52.13	0.0473	up	AT1G50280	49.365	0.035	up	
AT3G01220	no	up	ABA signaling seed endosperm homeodomain leucine zipper class I (HD-Zip I) HD20 TF					ATHB-20	6.2194	0.037	up	
AT5G63650	no	up	ABA signaling SNF1-RELATED PROTEIN KINASE 2H; SNRK2-5; SRK2H					SRK2H	37.161	0.047	up	
AT4G25700		up?	ABA synthesis chloroplast zeaxanthin oxidative stress BETA-OHASE 1 beta-hydroxylase 1	BETA-OHASE 1_1	9.4685	0.0381	up	BETA-OHASE 1	9.0965	0.005	up	down
AT3G17320	no	up	ABA ubiquitin SCF E3 ligase F-box protein F-box overexpressed/oppressed ABA signaling 1 FOA1					AT3G17320	10.348	0.023	up	
AT1G02130	no	up	ABA vesicular transport ER to Golgi RESPONSIVE TO ABSCISIC ACID 1B; ATRAB1B; ATRABD2A; RAB D2A; RABD2A; RAS 5 small GTPase					RABD2A	2.7712	0.043	up	
AT5G25110	no	up	abiotic stress signaling CBL-interacting protein kinase 25					CIPK25	4.208	0.035	up	
AT5G67470	no	down	actin binding formin homolog 6	FH6_1	-2.198	0.0353	down	FH6	-2.329	0.002	down	
AT4G17210	no	up	actin binding weak chloroplast movement under blue light protein (DUF827)	AT4G17210_1	80.206	0.0289	up	AT4G17210	76.529	0.02	up	
AT5G35700	no	down	actin bundlingFIM2; fimbrin-like protein 2; FIMBRIN5 pollen tube polar growth					FIM5	-2.082	0.046	down	
AT4G21820	no	up	actin Ca2+ signaling, actin binding calponin homology calmodulin binding IQ domain repeat protein	AT4G21820_3	121.08	0.0215	up	AT4G21820	6.1384	0.027	up	down
AT4G00680	yes	up	actin depolymerizing factor 8	ADF8_1	13.754	0.0248	up	ADF8	12.994	0.007	up	
At5g42880	no	down	actin interacting WEMBL EAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT-like protein (DUF827)					WEL3	-2.796	0.021	down	
AT2G40480	no	down	actin interacting WEMBL EAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT-like protein (DUF827)					AT2G40480	-2.249	0.009	down	
AT4G15200	no	up	actin nucleation cell polarity FH3 formin 3					AFH3	88.371	0.016	up	
At4g29340	no	up	actin polymerization pollen tube specific PRF4 profilin 4	PRO3_1	39.938	0.0069	up	PRO3	37.75	0.002	up	
At5g48360	no	down	actin profilin binding formin 2 domain protein	FH9_1	-9.442	0.0025	down	FH9	-9.98	3E-05	down	
AT5G01730	yes	up?	actin Wave complex SCAR activator of ARF2/3 actin nucleator	SCAR4_11	-523.1	0.0015	down	SCAR4	-2.865	0.034	down	down
AT1G29170	yes	up	actin WAVE complex, cell elongation SCAR complex subunit SCAR3; WASP (WISKOTT-ALDRICH SYNDROME PROTEIN)-FAMILY VERPROLIN HOMOLOGOUS PROTEIN 2	SCAR3_1	12.382	0.0345	up	SCAR3	8.3084	0.012	up	up
At3g05470	no	up	Actin-binding transmembrane FH2 (formin homology 2) protein with signal peptide	FH11_1	93.481	0.0243	up	FH11	88.301	0.016	up	
AT5G28020	yes	up	amino acid chloroplast CYSD2, CYSTEINE SYNTHASE D2	CYSD2_6	-34.02	0.0255	down	CYSD2	-37.32	0.009	down	
AT5G63850	no	up	amino acid AAP4, AMINO ACID PERMEASE 4 inhibited by dehydration					AAP4	9.4774	0.039	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G16880		up?	amino acid chloroplast Glutamine Synthetase GS2 activating ACR11 ACT domain-containing protein					ACR11	5.6138	0.029	up	
AT2G02000	no	up	amino acid GABA synthesis GAD3 glutamate decarboxylase 3					GAD3	10.566	0.032	up	
AT2G02010	yes	up?	amino acid GABA synthesis GAD4 glutamate decarboxylase 4	GAD4_1	202.49	0.0084	up	GAD4	192.47	0.005	up	
AT3G01760	no	up	amino acid LHT6, LYSINE-HISTIDINE-LIKE TRANSPORTER 6 Ala,Gluc and Phe transporter root specific					AT3G01760	9.2791	0.025	up	
AT1G62960	no	down	amino acid metabolism aminotransferase with broad specificity for aspartate and aromatic amino aids such as tyrosine and phenylalanine					ACS10	-3.141	0.045	down	
AT3G16150	no	down	amino acid metabolism ASPGB1 asparaginase					AT3G16150	-2.197	0.02	down	
AT1G77380	no	up	amino acid permease 3 AAP3 which transports basic amino acids.					AAP3	5.8683	0.037	up	
AT3G16700		up?	amino acid Phe catabolism Fumarylacetoacetate (FAA) hydrolase					AT3G16700	90.568	0.016	up	
AT4G01290	no	down	amino acid Phe Trp Tyr synthesis chorismate synthase	AT4G01290_2	-2.053	0.0328	down	AT4G01290	-2.153	0.001	down	
AT2G36590	yes	down	amino acid Pro, glycine-betaine transporter					PROT3	-7.671	0.028	down	
AT2G39890	no	up	amino acid proline transporter 1 vascular phloem specific					PROT1	3.8128	0.042	up	down
AT5G65010	no	up	amino acid synthesis ASN2 asparagine synthetase 2					ASN2	3.5882	0.017	up	
AT1G24909	no	up	amino acid transamination Glutamine amidotransferase type 1					AT1G24909	10.56	0.031	up	
AT2G42005	no	up	amino acid transmembrane vacuolar transporter ATAVT3B	AT2G42005_1	27.291	0.0162	up	AT2G42005	25.78	0.005	up	
AT3G05190	no	down	amino acid unknown pyridoxal-phosphate dependent Aminotransferase	AT3G05190_3	-56.14	0.0461	down	AT3G05190	-58.97	0.027	down	up
AT3G11900	no	up	amino acid, auxin IAA 2,4D transporter ANT1	ANT1_2	3.987	0.0445	up	ANT1	2.7777	0.044	up	
AT2G24850	no	up	amino acid, TYR metabolism tyrosine aminotransferase 3	TAT3_1	15.13	0.024	up	TAT3	14.293	0.006	up	down
At3g16240	no	down	ammonium and water transporter vacuolar					TIP2-1	-2.601	0.037	down	down
AT4G13510	no	down	ammonium transporter 1.1 AMT1.1					AMT1-1	-2.119	0.014	down	
AT3G59030	yes	up	anthocyanin proanthocyanidin vacuolar transporter TTT12; TRANSPARENT TESTA 12	DTX41_1	63.762	0.0377	up	DTX41	71.287	0.021	up	
At4g27570	no	up	anthocyanine accumulation UDP-glycosyltransferase 79B3	UGT79B3_1	100.22	0.0225	up	UGT79B3	94.722	0.015	up	
AT1G26100	no	up	ascorbate recycling Cytochrome b-561 / ferric reductase					CYB561D	7.9801	0.04	up	
AT5G50370		up?	ATP salvage energy balance Adenylate kinase 2					ADK2_2	6.3858	0.026	up	
AT1G73130	no	up	autophagy ATG8A/F interacting protein ATI3C	AT1G73130_3	84.259	0.0321	up	AT1G73130	4.0944	0.035	up	
AT3G13970	no	up	autophagy, APG12B Ubiquitin-like protein					ATG12B	52.216	0.037	up	
AT1G51780	no	down	auxin amino acid conjugate hydrolase ILL5	ILL5_1	-9.781	0.0132	down	ILL5	-10.64	0.001	down	
AT5G10510	yes	up	auxin cell differentiation organ growth flower root stem cell PIN1 auxin INTEGUMENTA-like 6, PLETHORA 3, PLT3 TF	AIL6_3	-3.379	0.0207	down	AIL6	-2.603	0.004	down	down
AT4G32280	no	up	auxin cell elongation phototropism PIF3/4 regulated IAA29 ARF7 pair	IAA29_2	9.7477	0.0447	up	IAA29	9.2758	0.01	up	up?
AT1G54070	no	up	auxin dormancy-associated auxin-repressed protein	AT1G54070_1	65.525	0.0363	up	AT1G54070	62.368	0.026	up	
AT1G23080	no	down	auxin ebryo apical-basal polarity auxin efflux carrier PINFORMED 7	PIN7_3	-4.541	0.0164	down	PIN7	-3.053	0.002	down	
AT1G70940	no	down	auxin efflux carrier PINFORMED 3	PIN3_1	-3.136	0.0119	down	PIN3	-3.343	3E-04	down	
AT5G57090	yes	down	auxin efflux carrier root geotropism ethylene ETHYLENE INSENSITIVE ROOT 1,PIN-FORMED 2, PIN2, WAV6, WAVY ROOTS 6	PIN2_1	78.977	0.0294	up	PIN2	10.794	0.014	up	
At1g71090	no	down	auxin ER efflux carrier	PILS2_1	-4.869	0.0036	down	PILS2	-5.248	2E-04	down	
AT1G12130	no	up	auxin flavin-containing monooxygenase FMOGS-OX6 involved in biosynthesis of aliphatic glucosinolates	AT1G12130_1	23.311	0.024	up	AT1G12130	22.082	0.008	up	
At1g62570	no	up	auxin glucosinolate glucosinolate S-oxygenase that catalyzes the conversion of methylthioalkyl glucosinolates to methylsulfinylalkyl glucosinolates	FMOGS-OX4_1	4.1333	0.0257	up	FMOGS-OX4	3.9067	0.003	up	
AT1G54010	no	up	auxin glucosinolate metabolism β-glucosidase myrosinase associated GLL23 GDSL-like Lipase					GLL23	6.2116	0.043	up	
AT5G57220	no	down	auxin glucosinolate synthesis pathogen CYP81F2 cytochrome P450, family 81	CYP81F2_1	-2.386	0.0317	down	CYP81F2	-2.544	0.002	down	
AT1G21120	no	down	auxin iindole glucosinolate O-methyltransferase 2	AT1G21120_1	-2.417	0.0085	down	AT1G21120	-2.564	1E-04	down	
AT4G00580	yes	down?	auxin indol glucosinolate synthesis CYP81F3 cytochrome P450					AT4G00580	-6.394	0.047	down	
AT4G17280	no	up	auxin induced ascorbate recycling transmembrane Cytochrome b-561 / ferric reductase					AT4G17280	8.4788	0.019	up	
AT3G59900	no	down	auxin induced cell elongation organ size controlling ARGOS transmembrane protein	ARGOS_1	-8.447	0.012	down	ARGOS	-9.131	6E-04	down	down
At5g12900	no	up	auxin induced cytoplasmic interactor for inflorescence and root apices receptor-like kinase (IRK)	IRKI_1	51.589	0.049	up	IRKI	48.849	0.037	up	
AT1G15050		up?	auxin induced IAA34 repressor TF					IAA34	6.9842	0.043	up	down
At5g01830	no	down	auxin induced SAUR21 U-box E3 ARM repeat protein					PUB16	-2.105	0.011	down	down
AT2G23610	no	down	auxin JA methyl IAA esterase, methyl jasmonate esterase					MES3	-5.251	0.032	down	
AT5G60450	yes	down?	auxin leaf polarity ARF4 TF	ARF4_2	-18.85	0.0217	down	ARF4	-6.374	0.002	down	
AT3G22810	no	up	auxin leaf vascular patterning PIN1 membtane targeting FKD1 FORKED 1 homolog Pleckstrin homology and Auxin canalisation domain protein					AT3G22810	37.143	0.048	up	
AT3G27490	yes	up	auxin mediated seed dormany and germination GERMOSTATIN RESISTANCE LOCUS 1, GSR1 PhD repeat transcription co-repressor	AT3G27490_1	-19.67	0.0359	down	AT3G27490	-10.11	0.035	down	
AT4G11260	no	down	auxin pathogen SCF-TIR1 E3 component SGT1b	SGT1B_1	-2.071	0.0278	down	SGT1B	-2.202	0.001	down	
AT5G47990	no	down	auxin root flavonoid triterpene thalianol synthesis, auxin transport gravitropism					CYP705A5	-19.46	0.026	down	down
AT2G24400	no	up	auxin SAUR38; SMALL AUXIN UPREGULATED RNA 38	AT2G24400_1	65.197	0.0369	up	AT2G24400	62.128	0.026	up	
AT1G19840	no	up	auxin SAUR53 SMALL AUXIN UPREGULATED RNA 53	AT1G19840_1	31.347	0.0118	up	AT1G19840	29.738	0.004	up	
AT5G20820	no	up	auxin SAUR76; SMALL AUXIN UPREGULATED RNA 76					AT5G20820	9.4692	0.039	up	
AT4G36110	no	up	auxin SAUR9 SMALL AUXIN UPREGULATED RNA 9					AT4G36110	8.5415	0.035	up	
AT1G01550	no	down	auxin shoot development inactivation of auxin signaling inhibitor	BPS1_2	-2.714	0.0371	down	BPS1	-2.288	0.001	down	up
AT1G04180	no	up	auxin synthesis ethylene lignification YUC9 YUCCA 9	YUC9_1	11.681	0.045	up	YUC9	11.034	0.014	up	
AT1G14120	no	down	auxin, root cap ATDAO2, AUXIN OXIDASE	AT1G14120_1	-14.4	0.0339	down	AT1G14120	-15.81	0.009	down	down
AT2G16580	no	up	auxin, SAUR8; SMALL AUXIN UPREGULATED RNA 8					AT2G16580	8.9025	0.019	up	
AT1G19220	no	down	auxinand ethylene signaling leaf and lateral root development ARF19 auxin response factor 19 TF					ARF19	-2.007	8E-04	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G23160	no	up	Auxin-induced GH3 family protein	AT1G23160_1	51.937	0.0473	up	AT1G23160	49.279	0.035	up	
AT3G49900	no	up	blue light Phototropic-responsive NPH3 protein	AT3G49900_2	11.047	0.036	up	AT3G49900	10.48	0.011	up	
AT1G51600	no	up	blue light signaling Cry1-activator GATA28 ZINC FINGER PROTEIN EXPRESSED IN INFLORESCENCE MERISTEM LIKE 2 TF	GATA28_1	22.993	0.0047	up	GATA28	3.1053	0.015	up	
AT5G47800	yes	down?	blue light signaling CUL3 interacting BTB domain Phototropic-responsive NPH3	AT5G47800_3	-648.9	0.0013	down	AT5G47800	-5.11	0.049	down	
AT2G34490	no	down	BR biosynthesis C22-sterol desaturase	CYP710A2_1	-19.33	0.0358	down	CYP710A2	-20.2	0.012	down	
AT4G39070	no	up	BR sigaling BZS1 B-box zinc finger inhibitor of hypocotyl elongation	BBX20_1	84.563	0.0273	up	BBX20	79.88	0.019	up	
AT5G42750	no	up	BR signaling BKI1 BRI1 kinase inhibitor 1	BKI1_1	66.629	0.0364	up	BKI1	63.003	0.026	up	
AT1G63500	no	up	BR signaling brassinosteroid-signaling kinase 7	AT1G63500_1	2.4381	0.0145	up	AT1G63500	2.3316	0.003	up	
AT4G03080	no	down	BR signaling BSL1 BRI1 suppressor 1 (BSU1)-like 1 Kelch repeat PP2A					BSL1	-2.181	0.011	down	
AT4G25820	no	up	BR signaling cell wall extencio root elongation XTH14 xyloglucan endotransglucosylase/hydrolase 14	XTH14_1	13.743	0.0393	up	XTH14	13.148	0.012	up	
AT3G26940	no	down	BR signaling CONSTITUTIVE DIFFERENTIAL GROWTH 1 cytoplasmic RLCKVII receptor-like kinase					CDG1	-12.35	0.049	down	
AT1G16900	no	down	BR signaling ER alpha1,6 mannosyltransferase	ALG9_1	-3.332	0.0221	down	ALG9	-3.527	0.002	down	
AT2G42080	no	up	BR signaling mitochondrion protein folding DnaJ/Hsp40 chaperon	AT2G42080_1	14.619	0.0085	up	AT2G42080	14.048	8E-04	up	
AT3G54930	no	down	BR signalling PP2A B56 subunit					B'EPSILON	-6.147	0.016	down	down
AT1G73650	no	up	BR sterol biosynthesis DET2 related 3-oxo-5-alpha-steroid 4-dehydrogenase	AT1G73650_4	123.46	0.0205	up	AT1G73650	6.0048	0.012	up	
AT4G33000		up?	Ca2+ sensor calcineurin B-like calcium sensor BR sensitivity negative regulationof osmotic stress tolerance					CBL10	9.1693	0.023	up	
AT4G36070	yes	up?	ca2+ signaling CPK18 calcium-dependent protein kinase 18	CPK18_1	53.114	0.0458	up	CPK18	12.908	0.022	up	
AT4G04710	yes	down	Ca2+ signaling CPK22 calcium-dependent kinase	CPK22_3	82.268	0.028	up	CPK22	92.578	0.015	up	up
AT4G26470	yes	down	Ca2+ signaling EF hand domain repea protein with signal peptide	AT4G26470_2	13.268	0.0347	up	AT4G26470	5.5912	0.035	up	
AT4G34070	no	up	Ca2+ signaling TLDc domain EF hand protein					AT4G34070	5.2696	0.018	up	
AT4G27790	no	up	Ca2+ signaling transmembrane Ca2+ binding EF hand repat protein	AT4G27790_1	76.64	0.0315	up	AT4G27790	20.294	0.008	up	
AT4G35920	no	up	Ca2+ uptake root mechanical sensing PLCA8 domain MCA1, MID1-COMPLEMENTING ACTIVITY 1					MCA1	25.514	0.001	up	
AT5G61260	no	up	Ca2+/CAM signaling CaM_binding protein					AT5G61260	40.434	0.044	up	
AT3G54570	no	up	Ca2+/CAM signaling Plant calmodulin-binding domain protein	AT3G54570_1	59.659	0.0403	up	AT3G54570	56.353	0.029	up	
AT5G62070	no	up	calmodulin binding IQ domain protein 23					IQD23	4.0678	0.041	up	
At3g58480	no	up	calmodulin binding IQM6					IQM6	9.923	0.025	up	
AT1G70510	no	up	carpel development cytokinin chromatin remodeling SWI/SNF KNAT2 homeobox TF	KNAT2_2	14.104	0.0365	up	KNAT2	9.4076	0.015	up	
AT5G01690	no	down	cation transport Na+/K+ exchanger CATION/HYDROGEN EXCHANGER 27; ATCHX27					CHX27	-8.067	0.02	down	
AT4G37630		up	cell cycle CYCD5;1 cyclin d5;1 quantitative trait gene for endoreduplication					CYCD5-1	44.01	0.04	up	
AT1G01300	no	down	cell death BAG6 cleavage Aspartyl protease family protein 2					APF2	-2.258	0.048	down	
AT1G12680	no	down	cell death DAPK2 death associated protein kinase 2					PEPKR2	-2.74	0.031	down	
AT5G61910	yes	down	cell death embryo development pathogen DCD (Development and Cell Death), C2 and VWA domain protein	AT5G61910_5	436.45	0.002	up	AT5G61910	2.1051	0.042	up	
AT4G33100	no	up	cell death human cell-survival mediator p53CSV UPF0203 domain homolog					AT4G33100	5.5338	0.017	up	
At1g69490	no	down	cell death leaf senescence floral meristem specific AP3/PI activated NAC029 TF					NAC029	-2.675	0.026	down	
AT1G32540	yes	down	cell death positive regulator					LOL1	17.479	0.012	up	down?
AT1G02170	no	down	cell death positive regulator MC1 metacaspase 1					AMC1	-2.064	0.012	down	
AT1G01010	no	up	cell death SnRK1 substrate ANAC001, NAC DOMAIN CONTAINING PROTEIN 1, NAC001, NTL10 TF	NAC001_1	37.366	0.0036	up	NAC001	35.446	4E-04	up	
At3g19260	no	up	cell death sphingolipid ceramid signaling LCFA-ceramide synthase LAG1 HOMOLOG 2; LAG1 homologue 2; LONGEVITY ASSURANCE GENE1 HOMOLOG 2					LAG2	2.486	0.043	up	
At3g25540	yes	down	cell death sphingolipid metabolism Very Long Chain Fatty acid VLCFA-Ceramide synthase LAG One Homologue 1; LAG1 HOMOLOG 1; LOH1; LONGEVITY ASSURANCE GENE 1	LAG1_2	107.52	0.0242	up	LAG1	5.4616	0.009	up	
AT5G52060	no	down	cell death ubiquitination proteasomal degradation BAG1; BCL-2-associated athanogene 1					BAG1_2	-3.137	0.045	down	
AT4G38360	yes	down?	cell death vacuolar BR signaling LAZARUS1 DUF300 protein					LAZ1	-2.202	0.049	down	
AT3G48150	yes	up	cell division anaphase-promoting complex subunit 8; CDC23	APC8_2	-7.492	0.0021	down	APC8	-4.614	1E-03	down	
AT3G23270	yes	down?	cell division BREVIS RADIX (BRX) RCC repeat TF with FYVE zinc finger and Pleckstrin homology domain					AT3G23270	44.624	0.04	up	
AT1G19880	no	down	cell division chromosome separation microtubule binding kinetochore protein RCC2 regulator of chromosome condensation 2					AT1G19880	-2.079	0.016	down	
AT2G01905	no	up	cell division CYCJ18, CYCLIN J18	CYCJ18_1	16.978	0.0368	up	CYCJ18	16.19	0.014	up	
At1g78080	no	up	cell division dedifferentiation ethylene signaling WIND1; wound induced dedifferentiation 1 DREB subfamily A-6 of ERF/AP2 transcription factor	RAP2-4_1	2.1765	2E-06	up	RAP2-4	2.0594	3E-08	up	
AT1G17930	no	down	cell division differentiation MERISTEM MAINTENANCE PMD domain protein	MAIN_1	-4.449	0.0466	down	MAIN	-3.879	0.015	down	up
AT5G27610	no	down	cell division DIRP (Domain in Rb-related Pathway) motive containing MYB TF					ALY1	-2.05	0.041	down	up
AT1G07500	no	up	cell division DNA damage checkpoint CDKA inhibitor SIAMESE-RELATED 5; SMR5					SMR5	41.396	0.043	up	down
AT1G47870	no	down	cell division DNA replication photomorphogenesis E2FC TF					E2FC	-2.641	7E-04	down	
AT5G14960	yes	down	cell division DP-E2F-like 2; E2FD; E2L1 TF activator of E2F genes					E2FD	7.0788	0.032	up	
AT5G08320	no	up	cell division EAPP E2F associated phosphoprotein	AT5G08320_1	8.2814	0.0467	up	AT5G08320	6.7062	0.021	up	
AT5G09210	no	down	cell division endoreduplication Increased level of polyploidy1 homolog GC-rich sequence DNA-binding factor	AT5G09210_1	-14.53	0.0256	down	AT5G09210	-15.78	0.006	down	
AT3G10525	no	up	cell division endoreduplication petal CDK inhibitor LOSS OF GIANT CELLS FROM ORGANS; SIAMESE RELATED 1; SMR1					SMR1	41.404	0.043	up	
AT1G47210		up?	cell division G0/S cyclin A3:2					CYCA3-2	3.4986	0.042	up	
AT1G07990	yes	down	cell division G1 SIT4 phosphatase associated SAPS domain protein	AT1G07990_2	-2.689	0.0076	down	AT1G07990	-2.512	2E-04	down	
AT5G65420	yes	down	cell division G1/S lateral root stomatal differentiation cyclin D4;1					CYCD4	2.5866	0.039	up	down
AT2G39435	yes	up?	cell division G2/M DUF4378 TON1 RECRUITING MOTIF 18, TRM18					AT2G39435	64.658	0.025	up	
AT3G63430	yes	up?	cell division G2/M DUF4378 TON1 RECRUITING MOTIF 5, TRM5	AT3G63430_2	191.48	0.0092	up	AT3G63430	192.44	0.005	up	

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AT5G62170		down?	cell division G2/M DUF4378 TON1 RECRUITING MOTIF25, TRM25					AT5G62170	18.395	0.013	up	down?
AT1G70210	no	up	cell division Go/S transition cyclin D1;1					CYCD1-1	7.5018	0.04	up	
AT1G22260	yes	down?	cell division meiotic synaptosomal filament protein	ZYP1A_1	-11.98	0.0225	down	ZYP1A	-3.725	0.047	down	up
AT5G08390	no	up	cell division microtubule centromer coupling KATNB1 katanin regulatory subunit B1					AT5G08390	3.5504	0.034	up	
AT5G62500	no	down	cell division microtubule END BINDING PROTEIN 1B					EB1B	-2.387	0.047	down	
AT1G69380	no	up	cell division mitochondrial protein RRG RETARDED ROOT GROWTH DUF155 domain					AT1G69380	4.8411	0.024	up	
AT1G47230	no	up	cell division mitosis specific CYCA3;4, CYCLIN A3;4					CYCA3-4	6.4522	0.013	up	
AT1G61000	no	down	cell division NUF2 component of Ndc80 kinetochore-spindle complex	AT1G61000_1	-3.317	0.0149	down	AT1G61000	-3.499	1E-03	down	
AT3G12280	no	down	cell division retinoblastoma tumor suppressor homolog	RBR1_1	-3.677	0.0468	down	RBR1	-2.366	0.015	down	
AT1G49040	yes	up	cell division stomata leaf negative regulator of basal pathogen resistance CUL4-DDB1-WD40 receptor, RAB GTPase interacting DENN domain MAPK signaling	SCD1_3	-2141	2E-05	down	SCD1	-2.646	0.001	down	down
AT3G46590	no	up	cell division telomer binding v-MYB TF	TRP2_5	88.598	0.0363	up	TRP2	7.0379	0.006	up	
AT3G12400	yes	up?	cell division trichome endoreduplication vacuolar sorting ESCRT-III subunit ATELC, ELC, VACUOLAR PROTEIN SORTING 23A, VPS23A	ELC_1	-2.577	0.0333	down	ELC	-2.254	0.006	down	
AT5G61480	no	down	cell division vascular polarity PHLOEM INTERCALATED WITH XYLEM; TDIF receptor; TDR	TDR_1	-3.29	0.0039	down	TDR	-3.487	2E-05	down	
AT1G02970	no	up	cell division WEE1 kinase inhibitor of mitosis	WEE1_1	29.625	0.0137	up	WEE1	27.985	0.004	up	
AT5G15920	no	down	cell division, DNA replication recombination sister chromatid separation Smc5 ATPase of the Smc5-Smc6 complex					SMC5	-2.477	0.011	down	
AT3G44200	no	down	cell division, epidermal cell patterning NEK6 IBO1; NIMA (never in mitosis; NIMA-RELATED KINASE6					NEK6	-2.069	0.001	down	
AT2G47980	no	down	cell division, meiosis kinetochore cohesin complex SCC3 subunit	SCC3_1	-2.04	0.0167	down	SCC3	-2.162	4E-04	down	
At4g19045	no	up	cell division, nuclear division Mob1_phocein domain protein					MOB1B	2.1761	0.031	up	
AT4G29730	yes	down	cell division,silencing FVE homolog HISTONE DEACETYLASE 6 (HDA6) RBR-binding MSI5; nucleosome/chromatin assembly factor group C5	MSI5_1	65.107	0.042	up	MSI5	6.4505	0.039	up	
AT4G32295		up?	cell divison, Leaf development, KIX9 Topless corepressor of PEAPOD2 CYCLIND activator	AT4G32295_3	16.018	0.0431	up	AT4G32295	20.533	0.009	up	down
AT2G35610	no	down	cell elonation extensine arabinosyltransferase					XEG113	-2.835	0.012	down	
AT2G43150	no	down	cell elongation cell wall extensin Extensin_2 domain	AT2G43150_1	-2.231	0.0049	down	AT2G43150	-2.354	8E-05	down	
AT1G71380	no	down	cell elongation cell wall root CEL3 cellulase 3	CEL3_1	-2.058	2E-06	down	CEL3	-2.181	5E-10	down	
AT1G19360	no	down	cell elongation extensin arabinosyltransferase root hair	RRA3_1	-6.612	0.016	down	RRA3	-4.281	0.006	down	
AT5G13870	no	up	cell expansion cell wall EXGT-A4, endoxyloglucan transferase, XTH5 xyloglucan endotransglucosylase/hydrolase 5	XTH5_2	72.15	0.0391	up	XTH5	5.8415	0.036	up	down
AT5G65730	no	up	cell expansion cell wall XTH6 xyloglucan endotransglucosylase/hydrolase 6	XTH6_1	67.927	0.0356	up	XTH6	64.395	0.025	up	
AT5G35190	no	up	cell expansion elongation hydroxyproline-rich glycoprotein extensine 13					AT5G35190	8.5485	0.028	up	
AT2G03090	no	up	cell expansion elongation Rare lipoprotein A (RlpA)-like double-psi beta-barrel expansin 15					EXPA15	8.9288	0.047	up	
AT4G08950	no	down	cell expansion leaf BR/Phosphate-responsive 1 EXORDIUM protein with signal peptide	EXO_1	-2.617	0.0143	down	EXO	-2.763	4E-04	down	
AT1G26770	yes	up?	cell expansion transmembrane expansin 10	ATEXPA10_1	7.6431	0.0134	up	ATEXPA10	3.7915	0.001	up	
AT3G48187	no	down	cell growth differentiation nuclear PWWP domain protein					AT3G48187	-10.36	0.025	down	
At1g03982	no	up	cell polarity elongation pollen tube CRIB (for Cdc42/Rac-interactive binding) motif protein partner of GTP-bound Rop1					RIC8	9.169	0.044	up	
AT4G29460	no	down	cell polarity ER/Golgi PLA2-GAMMA Phospholipase A2 pollen tube polar growth					PLA2-GAMMA	-11.61	0.036	down	
At5g12150	no	down	cell polarity Rho GTPase-activating protein 6	ROPGAP6_1	-5.585	0.0013	down	ROPGAP6	-2.912	0.002	down	down
AT5G49270	no	up	cell polarity root hair tip growth CONRA_LIKE 9 cell wall glycosyl-phosphatidyl inositol-anchored protein DEFORMED ROOT HAIRS 9, DER9, MRH4, MUTANT ROOT HAIR 4, SHAVEN 2, SHV2					COBL9	5.6304	0.049	up	
AT4G38190	no	down	cell polarity tip growth cell wall CSLD4 cellulose synthase like D4					CSLD4	-11.46	0.016	down	
AT2G44470		up?	cell wall beta glucosidase 29 BGLU29					BGLU29	45.679	0.038	up	
AT2G03210	no	up	cell wall fucosyltransferase 2 FUT2					FUT2	45.3	0.039	up	
AT4G20040	no	up	cell wall pectate lyase					AT4G20040	6.0489	0.045	up	
AT4G09030	no	down	cell wall AGP10 arabinogalactan protein 10					AGP10	-2.088	8E-04	down	
AT2G22470	no	down	cell wall AGP2 arabinogalactan protein 2	AGP2_1	-2.552	0.0002	down	AGP2	-2.715	1E-06	down	
AT1G68560	no	down	cell wall ALPHA-XYLOSIDASE 1; altered xyloglucan 3; ATXYL1; AXY3; thermoinhibition resistant germination 1; TRG1					XYL1	-2.5	0.015	down	
AT1G55120	yes	down	cell wall apoplastic 6-FRUCTAN EXOHYDROLASE levanase					CWINV3	10.69	0.048	up	up
At3g06440		down?	cell wall arabinogalactan protein hydroxyproline-O-galactosyltransferase					GALT3	7.4638	0.034	up	
AT2G46330	no	down	cell wall arabinogalactan protein 16	AGP16_2	-2.178	0.0254	down	AGP16	-2.136	0.001	down	down
AT5G09730	no	down	cell wall ATBXL3; beta-xylosidase 3	BXL3				BXL3	-4.017	0.03	down	
AT5G64570	yes	down	cell wall beta-d-xylosidase, stem					BXL4	7.1352	0.045	up	down
AT3G52840	yes	down	cell wall betagalactosidase	BGAL2_2	14.248	0.0193	up	BGAL2	13.544	0.003	up	up
AT4G36360	no	down	cell wall BETA-GALACTOSIDASE 3, BGAL3	BGAL3_2	-6.171	4E-06	down	BGAL3	-2.259	2E-04	down	
AT5G56870	no	down	cell wall BGAL4 beta-galactosidase 4					BGAL4	-2.079	0.002	down	
AT3G47540	yes	down?	cell wall chitinase O-Glycosyl hydrolase	AT3G47540_2	11.74	0.0083	up	AT3G47540	7.6426	1E-03	up	
AT3G25050	no	up	cell wall elongation XTH3 xyloglucan endotransglucosylase/hydrolase 3					XTH3	39.307	0.046	up	
AT3G06390	no	up	cell wall endodermis lignin Casparian Strip CASP-LIKE PROTEIN 1D2, CASPL1D2	AT3G06390_1	16.633	0.0262	up	AT3G06390	15.712	0.007	up	down
AT2G26250		down?	cell wall epidermis cuticle long chain lipid synthesis 3-ketoacyl-CoA synthase 10; FDH; FIDDLEHEAD					FDH	6.8149	0.03	up	
AT2G40190	no	up	cell wall ER alpha-1,2-mannosyltransferase in N-linked glycoprotein (homologous to yeast ALG11) LEAF WILTING 3, LEW3					ALG11	4.8513	0.05	up	
AT5G48070	no	up	cell wall expansion cell division stele root inflorescence XTH20 xyloglucan endotransglucosylase/hydrolase 20	XTH20_1	22.452	0.0243	up	XTH20	21.338	0.007	up	
AT5G15630	yes	down	cell wall expansion IRX6 COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein	COBL4_1	15.024	0.0257	up	COBL4	6.9024	0.022	up	
AT5G40940	no	up	cell wall FLA20, PUTATIVE FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 20	FLA20_1	11.141	0.0425	up	FLA20	10.587	0.01	up	
AT2G28100	no	up	cell wall FUC1 alpha-L-fucosidase 1	FUC1_1	13.465	0.0279	up	FUC1	12.721	0.006	up	

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AT1G19940	no	down	cell wall GH9B5, GLYCOSYL HYDROLASE 9B5	AtGH9B5_1	-10.23	0.0187	down	AtGH9B5	-9.879	0.003	down	
AT1G18310	no	up	cell wall glucan beta-1,3(4)-glucanase belonging to glycoside hydrolase family 81					AT1G18310	37.142	0.049	up	
AT1G80290		down?	cell wall glycosaminoglycan synthesis glycosyltransferase 64 with signal peptide					AT1G80290	-4.224	0.031	down	
At1g27600	no	down	cell wall IRX9-L Nucleotide-diphospho-sugar transferase involved in glucuronoxylan biosynthesis	IRX9H_1	-4.13	0.0417	down	IRX9H	-2.716	0.008	down	
AT1G28290		down	cell wall JA-repressed arabinogalactan protein 31	AGP31_2	-2.971	0.0014	down	AGP31	-2.199	8E-06	down	
AT2G40370	no	up	cell wall lignin mopdification, redox Multicopper oxidase LAC5 laccase 5	LAC5_1	58.82	0.0418	up	LAC5	55.64	0.031	up	
AT4G34230	no	down	cell wall lignin synthesis root vascular tissue CAD5 cinnamyl alcohol dehydrogenase 5	CAD5_2	-5.142	0.036	down	CAD5	-2.128	3E-07	down	
AT5G24230	no	up	cell wall lipid metabolism feruloyl esterase A					AT5G24230	16.537	0.012	up	
AT1G52100		down?	cell wall mannose-binding jancalin lectin domain repeat protein					AT1G52100	43.575	0.04	up	
AT3G19620	no	up	cell wall O-Glycosyl hydrolase					BXL5	5.6087	0.049	up	
AT1G57590	no	up	cell wall PAE2, PECTIN ACETYESTERASE 2					PAE2_1	85.836	0.018	up	
AT5G55720	no	up	cell wall Pectate lyase	AT5G55720_1	50.816	0.0496	up	AT5G55720	48.735	0.037	up	
AT5G14650		up?	cell wall pectate lyase PbH1 domain protein with signal peptide					AT5G14650	10.014	0.035	up	
AT1G04680	no	down	cell wall Pectate lyase pollen germination					AT1G04680	-2.022	0.004	down	
AT5G49215	no	up	cell wall pectate lyase withsignal peptide					AT5G49215	6.7563	0.028	up	
AT5G44670	no	down	cell wall pectin GALS2 galactan synthase 2					GALS2	-7.943	0.029	down	
At3g43270	no	up	cell wall pectin methylesterase	PME32_1	77.805	0.0297	up	PME32	73.498	0.021	up	
AT3G14300	no	up	cell wall PECTIN METHYLESTERASE 26; ATPME26	PME26_1	64.258	0.0372	up	PME26	60.701	0.027	up	
AT2G47670	no	up	cell wall PECTIN METHYLESTERASE INHIBITOR 6, PMEI6					AT2G47670	37.168	0.047	up	
AT2G40320	no	up	cell wall pectin PC-Esterase TBL33 TRICHOME BIREFRINGENCE-LIKE 33	TBL33_1	12.679	0.0435	up	TBL33	11.977	0.012	up	
AT5G01620		up?	cell wall pectin PC-Esterase TBL35 TRICHOME BIREFRINGENCE-LIKE 35	TBL35_2	134.09	0.0228	up	TBL35	5.9457	0.043	up	down
AT1G29050	no	up	cell wall pectin PC-Esterase TBL38 TRICHOME BIREFRINGENCE-LIKE 38	TBL38_1	60.73	0.0409	up	TBL38	57.56	0.03	up	
AT1G09890	yes	up	cell wall pectin rhamnogalacturonan I (RG-I) backbone hydrolase	AT1G09890_1	-184.4	0.0064	down	AT1G09890	-9.3	0.013	down	
AT2G22620		up?	cell wall pectin Rhamnogalacturonate lyase					AT2G22620	49.588	0.037	up	up
AT1G63930	no	down	cell wall pectin seed coat exocyst interactor ROH1 protein	ROH1_1	-26.01	0.0195	down	ROH1	-26.8	0.005	down	
AT5G15890	no	up	cell wall pectin synthesis TBL21 TRICHOME BIREFRINGENCE-LIKE 21					TBL21	11.044	0.043	up	
AT3G54260	no	down	cell wall pectin synthesis TBL36 TRICHOME BIREFRINGENCE-LIKE 36	TBL36_1	-2.056	0.0041	down	TBL36	-2.163	5E-05	down	
AT1G16160	no	up	cell wall pectin-binding transmembrane WAK-like kinase WAKL5					WAKL5	6.0529	0.036	up	
At3g60730	no	up	cell wall Pectinesterase/inhibitor					PME36	39.288	0.046	up	
AT4G25260	no	up	cell wall phytochorome/shade avoidance induced Plant invertase/pectin methylesterase inhibitor PMEI7 with signal peptide	AT4G25260_1	174.72	0.0105	up	AT4G25260	166.73	0.007	up	down
AT5G62350	no	down	cell wall Plant invertase/pectin methylesterase inhibitor with signal peptide					AT5G62350	-2.1	0.037	down	
AT2G39445		up?	cell wall PM glycan synthesis Phosphatidylinositol N-acetylglucosaminyltransferase, GPI19/PIG-P subunit	AT2G39445_2	121.04	0.0176	up	AT2G39445	38.316	0.002	up	
AT4G35530	no	up	cell wall polarity transmembrane PIG-H component of GPI-GnT (glycosylphosphatidylinositol anchor biosynthesis transferase) complex					AT4G35530	5.1797	0.047	up	
AT3G03210	no	up	cell wall polysaccharide O-acetylation ALTERED XYLOGLUCAN 9, AXY9 acyl-esterase					AT3G03210	5.998	0.027	up	
At4g13990	no	up	cell wall proteoglycan, transmembrane Exostosin glycosyltransferase required for the biosynthesis of heparan sulfate	GT14_1	73.325	0.0372	up	GT14	89.695	0.016	up	
AT1G09880	yes	down	cell wall pwctin degradation rhamnogalacturonan lyase (RG-lyase)					AT1G09880	37.172	0.048	up	
AT5G58860	no	up	cell wall root suberin synthesis fatty acid omega-hydroxylase CYP86A1 cytochrome P450					CYP86A1	6.3623	0.048	up	
AT5G63560	no	up	cell wall root wax synthesis FACT FATTY ALCOHOL:CAFFEOYL-CoA CAFFEOYL TRANSFERASE	AT5G63560_1	21.76	0.027	up	AT5G63560	20.627	0.009	up	
AT4G39350	no	down	cell wall secondary wall thickening cellulose synthase A2					CESA2	-2.156	0.045	down	
AT5G67210	no	up	cell wall secondary wall xylan deposition IRX15-L IRREGULAR XYLEM protein (DUF579)	IRX15-L_1	15.995	0.0246	up	IRX15-L	15.11	0.007	up	
AT4G18596	no	down	cell wall secreted Pollen_Ole_e_I domain protein with signal peptide	AT4G18596_1	-438.8	0.0029	down	AT4G18596	-17.07	0.008	down	
AT5G19120	no	down	cell wall secreted Xylanase inhibitor with signal peptide, 2h interacting partner of PXL1 LRR receptor kinase					AT5G19120	-2.055	0.032	down	down
AT3G59010	no	up	cell wall stem PME35, a pectin methylesterase					PME35	6.6508	0.044	up	
AT5G03170	no	up	cell wall stem sclerenchyma FLA11 FASCICLIN-like arabinogalactan-protein 11					FLA11	7.6147	0.037	up	
AT3G02940	no	up	cell wall suberin biosynthesis positive regulator MYB107 TF	MYB107_1	127.36	0.016	up	MYB107	120.3	0.011	up	
AT5G23190	no	up	cell wall suberin fatty acid very long chain hydroxylase					CYP86B1	48.566	0.04	up	
AT3G11430	no	up	cell wall suberin seed coat and root GPAT5 glycerol-3-phosphate acyltransferase 5	GPAT5_1	116.99	0.019	up	GPAT5	111.82	0.012	up	
AT2G37360	no	up	cell wall suberin synthesis ABCG2 ABC-2 type transporter					ABCG2	5.7771	0.044	up	
AT5G59070	no	down	cell wall subfamily 4 glycosyltransferase					AT5G59070	-41.07	0.042	down	
AT3G51710	no	up	cell wall transmembrane Bulb-type mannose-specific lectin					AT3G51710	13.292	0.025	up	
AT4G19370	no	up	cell wall transmembrane DUF1218 domain chitin synthase MODIFYING WALL LIGNIN-2, MWL-2	AT4G19370_1	17.213	0.0164	up	AT4G19370	16.26	0.003	up	
AT5G19670	no	up	cell wall transmembrane exostose heparan sulfate glycosyltransferase	AT5G19670_2	84.808	0.0378	up	AT5G19670	5.736	0.046	up	
At5g47500	no	up	cell wall transmembrane PECTIN METHYLESTERASE 5, PME5	PME68_1	15.478	0.0469	up	PME68	14.69	0.021	up	
At2g26450	no	up	cell wall transmembrane Pectinesterase/ihibitor					PME13	7.3052	0.032	up	
AT2G36670	no	up	cell wall transmembrane Xylanase inhibitor with signal peptide	AT2G36670_4	145.56	0.0164	up	AT2G36670	7.1261	0.027	up	
AT5G59290	no	down	cell wall UDP-xylose synthesis UXS3 UDP-glucuronic acid decarboxylase 3					UXS3	-2.046	0.035	down	down?
At3g05620	no	down	cell wall unknown pectin methylesterase with signal peptide	PME22_1	-169.5	0.0127	down	PME22	-185	0.006	down	
AT1G51500	no	up	cell wall wax synthesis lipid transporter ATWBC12; CER5; D3; ECERIFERUM 5;; WBC12; WHITE-BROWN COMPLEX 12	ABCG12_1	192.98	0.0091	up	ABCG12	182.3	0.005	up	
AT5G43760	no	down	cell wall wax very long chain fatty acid 3-ketoacyl-CoA synthase 20, KCS20	KCS20_1	-2.948	0.0096	down	KCS20	-3.122	7E-05	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT2G28760	yes	down?	cell wall xylan synthesis UXS6 UDP-XYL synthase 6	UXS6_3	78.867	0.0297	up	UXS6	28.402	0.004	up	
AT5G19110		down?	cell wall Xylanase inhibitor	AT5G19110_1	-3.044	4E-05	down	AT5G19110	-2.801	4E-08	down	down
AT2G03200	no	up	cell wall Xylanase inhibitor with signal peptide					AT2G03200	39.315	0.045	up	
AT1G64830	no	down	cell wall Xylanase inhibitor with signal peptide	AT1G64830_1	-36.66	0.0043	down	AT1G64830	-39.97	6E-04	down	
AT3G61820	no	down	cell wall Xylanase inhibitor with signal peptide	AT3G61820_1	-5.672	8E-05	down	AT3G61820	-6.038	4E-08	down	
AT5G19100	no	down	cell wall Xylanase inhibitor with signal peptide	AT5G19100_1	-5.446	0.0407	down	AT5G19100	-5.87	0.004	down	
AT3G23550	no	up	cell wall, liginin synthesis, Hydroxycinnamic Acid Amide transporter DTX18					DTX18	11.644	0.027	up	
AT1G30000	yes	down	cell wall, root development, Golgi alpha-mannosidase					MNS3	2.9544	0.036	up	down
AT4G17980	yes	down?	celldivision auxin inflorescence meristem NAC071 TF					anac071	-8.545	0.026	down	
AT3G14040	no	up	cellwall pectin lyase PbH1 domain protein with signal peptide					AT3G14040	9.4719	0.043	up	
AT1G05810		up?	chloroplast , thylakoid stress RABA5E Rab GTPase-like A5A protein	ARA_2	14.643	0.0451	up	ARA	19.832	0.009	up	up
ATCG00170	no	up	chloroplast ? RNA polymerase beta' subunit-2	RPOC2_1	2.127	0.0006	up	RPOC2	2.0135	2E-05	up	
AT5G12860	no	down	chloroplast 2-OXOGLUTARATE/MALATE TRANSLOCATOR; dicarboxylate transporter 1	DIT1_1	-3.069	0.0129	down	DIT1	-3.16	8E-04	down	
ATCG00770	no	up	chloroplast 30S RIBOSOMAL PROTEIN S11, RPS11					RPS8	3.8541	0.019	up	up
ATCG00050	no	up	chloroplast 30S ribosomal protein S16					RPS16	12.744	0.021	up	
ATCG00650	no	up	chloroplast 30S ribosomal protein S18	RPS18_1	5.8346	4E-05	up	RPS18	5.5309	2E-08	up	
ATCG00160	no	up	chloroplast 30S ribosomal protein S2	RPS2_3_1	2.801	5E-05	up	RPS2_3	2.6531	3E-07	up	
At2g38140	no	up	chloroplast 30S ribosomal protein S31					RPS31	5.2997	0.047	up	
ATCG00820	no	up	chloroplast 3ßS RIBOSOMAL PROTEIN S19, RPS19					RPS19_2	2.2975	3E-04	up	up
ATCG00780	no	up	chloroplast 50S RIBOSOMAL PROTEIN L14, RPL14					RPL14	2.508	0.013	up	up
ATCG00790	no	up	chloroplast 50S RIBOSOMAL PROTEIN L16, RPL16					RPL16_2	2.4369	1E-05	up	up
ATCG00660	no	up	chloroplast 50S ribosomal protein L20	RPL20_1	2.1674	0.0045	up	RPL20	2.052	4E-04	up	
ATCG00810	no	up	chloroplast 50S RIBOSOMAL PROTEIN L22, RPL22	RPL22_1	2.8684	0.0001	up	RPL22	2.7094	2E-06	up	up
AT3G23700	no	up	chloroplast ABA RNA processing RNA chapeone S1 RNA-BINDING RIBOSOMAL PROTEIN 1, SRRP1	AT3G23700_1	22.56	0.0107	up	AT3G23700	21.311	0.002	up	
AT3G29320	no	down	chloroplast alpha-glucan phosphorylase					PHS1_2	-2.475	0.022	down	
AT1G15410	no	down	chloroplast aspartate or glutamate racemase					AT1G15410	-2.232	0.037	down	
AT2G24060	no	up	chloroplast ATIF3-2, ATINFC-2, INITIATION FACTOR 3-2, SUPPRESSOR OF VARIEGATION9, SVR9	AT2G24060_1	24.179	0.0082	up	AT2G24060	22.844	9E-04	up	
AT4G09650	no	up	chloroplast ATPase delta-subunit PDE332; PIGMENT DEFECTIVE 332	ATPD_1	14.066	0.048	up	ATPD	13.287	0.021	up	
ATCG00130	no	up	chloroplast ATPase F subunit	ATPF_1	3.3398	0.0077	up	ATPF	3.1591	3E-04	up	
AT2G45980	no	up	chloroplast autophagy ATG8-interacting protein 1;	ATI1_1	3.078	0.0495	up	ATI1	2.9161	0.01	up	
AT1G63680	no	down	chloroplast biogenesis embryo ALBINO OR PALE-GREEN 13; APG13; ATMURE; PIGMENT DEFECTIVE EMBRYO 316	ATMURE_1	-16.36	0.0377	down	ATMURE	-2.876	0.007	down	
AT5G15530	no	up	chloroplast biotin carboxyl carrier protein isoform 2 (BCCP2)					BCCP2	3.2673	0.039	up	
AT4G15530	yes	up	chloroplast C4 cycle, cytosole glycolysis PPDK pyruvate orthophosphate dikinase	PPDK_7	-2.013	0.0273	down	PPDK	-2.072	0.003	down	
AT2G21330	no	up	chloroplast Calvin cycle fructose-bisphosphate aldolase 1					FBA1	5.7003	0.041	up	down
AT5G03940	no	down	chloroplast carotenoid CPSRP54 chloroplast signal recognition particle 54 kDa subunit					FFC	-2.184	0.007	down	
AT1G10830	yes	down	chloroplast carotenoid synthesis 15-cis-zeta-carotene isomerase	Z-ISO_2	134.21	0.0156	up	Z-ISO	4.682	0.042	up	
AT4G23420	yes	up?	chloroplast carotenoid vitamin A synthesis homolog of RDH12 retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	AT4G23420_2	21.085	0.0084	up	AT4G23420	4.6962	0.033	up	down
AT5G04900	no	up	chloroplast chlorophyll b degradation NOL NYC1-like chlorophyll b reducatase	NOL_1	11.324	0.006	up	NOL	10.731	3E-04	up	
AT3G51820	no	up	chloroplast chlorophyll synthase CHLG					CHLG	8.3317	0.012	up	
ATCG00670	no	up	chloroplast ClpP (caseinolytic protease)	CLPP1_1	2.2079	2E-05	up	CLPP1	2.0783	6E-07	up	
AT1G36390	no	up	chloroplast Co-chaperone GrpE					AT1G36390	5.4739	0.038	up	
ATCG00340	no	up	chloroplast D1 subunit of photosystem I reaction center	PSAB_1	2.3793	4E-08	up	PSAB	2.2546	4E-10	up	
AT5G35220	no	down	chloroplast development membrane ATP-independent metalloprotease EGY1					EGY1	-9.39	0.024	down	
AT1G69390	no	up	chloroplast division MinE topological specificity factor					MINE1	7.8904	0.015	up	
At3g02450	no	up	chloroplast division FtsH mettaloprotease AAA ATPase	FTSHI3_1	13.747	0.0074	up	FTSHI3	13.087	5E-04	up	
AT1G58200	no	down	chloroplast division mechanosensitive channel homolog MSL3 MSCS-like 3	MSL3				MSL3	-2.13	0.003	down	
AT5G04440	yes	up	chloroplast DUF1997 domain protein	AT5G04440_2	9.9443	0.0149	up	AT5G04440	4.0629	0.03	up	
AT4G13010	no	down	chloroplast ENVELOPE QUINONE OXIDOREDUCTASE HOMOLOG					AT4G13010	-2.132	0.006	down	
At5g14060		down?	chloroplast essential amino acid biosynthesis aspartokinase 2					AK2	-2.542	0.045	down	
At5g16230	yes	down?	chloroplast fatty acid desaturated AAD3 ACYL-ACYL CARRIER PROTEIN DESATURASE3					S-ACP-DES3	-3.176	0.049	down	up
AT4G11430	no	down	chloroplast fatty acid fatty acyl-CoA reductase FAR6	AT4G11430_1	-47.29	0.0054	down	AT4G11430	-50.75	9E-04	down	
ATCG00500	no	up	chloroplast fatty acid synthesis ACETYL-COA CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA	ACCD_1	3.6052	5E-15	up	ACCD	3.4015	0	up	
AT2G38040	no	down	chloroplast fatty acid synthesis CAC3 acetyl Co-enzyme a carboxylase carboxyltransferase alpha subunit	CAC3_2	-2.656	0.031	down	CAC3	-2.643	2E-04	down	
AT1G60950	no	down	chloroplast FD2; FERREDOXIN 2; FERRODOXIN A					FD2	-6.026	0.005	down	
AT1G54520	no	down	chloroplast FLAP1, FLUCTUATING-LIGHT- ACCLIMATION PROTEIN1	AT1G54520_1	-3.045	0.0166	down	AT1G54520	-3.283	0.002	down	
AT1G32900	no	down	chloroplast granule bound starch synthase 1	GBSS1_1	-17.46	0.0268	down	GBSS1	-18.21	0.006	down	up
AT5G08050	no	down	chloroplast grna core localized DUF1118 domain protein					AT5G08050	-7.33	0.042	down	
AT3G25770	no	down	chloroplast JA biosynthesis AOC2 allene oxide cyclase 2					AOC2	-9.821	0.041	down	down
At4g26555	no	down	chloroplast light stress lumenal immunophilin	FKBP16-1_2	-181	0.0084	down	FKBP16-1	-5.402	0.025	down	
AT5G16390	no	down	chloroplast lipid biosyynthesis biotin carboxyl-carrier subunit of the multi-enzyme plastidial acetyl-coenzyme A carboxylase complex	BCCP1_1	-3.094	0.0002	down	BCCP1	-3.284	9E-06	down	
AT4G28740	no	up	chloroplast LOW PSII ACCUMULATION-like DUF3493 domain protein					AT4G28740	41.469	0.042	up	
AT3G07480	no	up	chloroplast LSU1 interacting 2Fe-2S ferredoxin-like domain protein	AT3G07480_1	2.6612	0.0448	up	AT3G07480	2.5169	0.012	up	
At4g19830	no	up	chloroplast lumen protein folding FKBP-like peptidyl-prolyl cis-trans isomerase					FKBP17-1	9.4301	0.022	up	
AT1G06130	no	up	chloroplast methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione glyoxalase 2-4					GLX2-4	2.9722	0.045	up	
AT3G15000	no	down	chloroplast mitochondriumRNA editing MORF8; multiple organellar RNA editing factor 8; RNA-editing factor interacting protein 1	MORF8_1	-2.753	0.001	down	MORF8	-2.921	4E-06	down	
AT1G66840	no	down	chloroplast movement coiled coil protein ; WEAK CHLOROPLAST MOVEMENT UNDER BLUE LIGHT 2; WEB2					PMI2_1	-5.456	0.018	down	
AT5G52780	no	up	chloroplast NAD(P)H dehydrogenase complex assembly factor					AT5G52780	8.4573	0.014	up	
ATCG01090	no	up	chloroplast NAD(P)H dehydrogenase complex subunit NDHI					NDHI	4.0044	0.04	up	
ATCG01100	no	up	chloroplast NADH dehydrogenase ND1 NDHA1 subunit	NDHA_1	2.9481	0.0442	up	NDHA	2.7806	0.007	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
ATCG00420	no	up	chloroplast NADH DEHYDROGENASE SUBUNIT J, NDHJ					NDHJ	6.5318	0.048	up	
ATCG01050	no	up	chloroplast NDHD subunit of the NAD(P)H dehydrogenase complex	NDHD_1	2.4984	0.0356	up	NDHD	2.3683	0.004	up	
AT5G44820	no	down	chloroplast nucleotide-diphospho-sugar transferase					AT5G44820	-6.316	0.03	down	
AT3G09150		up?	chloroplast nucleus signaling phytochrome chromophore synthesis phytochromobilin:ferredoxin oxidoreductase GENOMES UNCOUPLED 3; GUN3	HY2_2	93.009	0.0249	up	HY2	8.1006	0.015	up	up
AT2G32290	no	up	chloroplast oligosaccharide degradation BAM6 beta-amylase 6					BAM6	9.7886	0.021	up	
AT1G61800		down?	chloroplast organ growth GPT2 glucose-6-phosphate/phosphate translocator 2					GPT2	-8.314	0.038	down	
AT4G02482	no	up	chloroplast outer membrane Translocase of chloroplast 159/132, membrane anchor domain					AT4G02482	7.3008	0.039	up	
AT4G32260	no	down	chloroplast PDE334 ATPase, F0 complex, subunit B/B'					AT4G32260	-2.309	0.033	down	
ATCG00720	no	up	chloroplast PETB, PHOTOSYNTHETIC ELECTRON TRANSFER B subunit of the cytochrome b6f complex	PETB_1	5.2468	4E-15	up	PETB	4.987	0	up	
AT4G30580	no	down	chloroplast phosphatidic acid biosynthesis EMB1995; EMBRYO DEFECTIVE 1995; LPAT1; lysophosphatidic acid acyltransferase 1; PHOSPHOLIPID/GLYCEROL ACYLTRANSFERASE					LPAT1	-4.159	0.01	down	
AT5G56610	no	up	chloroplast phospholipid synthesis phosphatidylglycerophosphate (PGP) phosphatase	AT5G56610_1	12.765	0.0349	up	AT5G56610	7.7266	0.013	up	
AT5G64280	no	down	chloroplast photorespiration DiT2.2 dicarboxylate transporter 2.2					DIT2-2	-2.092	0.04	down	
AT1G12550	no	up	chloroplast photorespiratory hydroxypyruvate/glyoxylate reductase	HPR3_1	11.049	0.0317	up	HPR3	10.51	0.007	up	
AT5G51545	no	up	chloroplast Photosystem II assembly factor LPA2 low psii accumulation2	LPA2_1	17.232	0.0199	up	LPA2	16.328	0.004	up	
AT4G01480	no	down	chloroplast PPa5 pyrophosphorylase 5	PPA5_1	-4.139	0.0228	down	PPA5	-4.444	0.002	down	down
AT1G21650	no	up	chloroplast protein importSACA2 subunits of thylakoid-localized Sec system					SECA2	2.6738	0.037	up	down
AT3G21055		down?	chloroplast PSBTN photosystem II subunit T					PSBTN	-8.211	0.011	down	down
AT1G52230	no	down	chloroplast PSI-H, photosystem I subunit H2	PSAH2_1	-77.21	0.0323	down	PSAH2	-80.42	0.019	down	
AT3G47060	no	down	chloroplast PSII repair protease FTSH7					FTSH7	-5.208	0.014	down	
AT5G52570		up?	chloroplast redox ABA synthesis BETA-OHASE 2 beta-carotene hydroxylase 2					BETA-OHASE 2	5.8824	0.03	up	
AT5G54290		up	chloroplast redox CcdA cytochrome c biogenesis protein					CcdA	3.0898	0.005	up	up
AT2G15780	no	down	chloroplast redox Cu-binding phytocyanin	AT2G15780_1	-4.21	0.0438	down	AT2G15780	-4.457	0.002	down	
AT4G36040	no	down	chloroplast redox DNAJ chaperone DJC23, DNA J PROTEIN C23, DNAJ11, J11					ATJ11	-2.523	0.018	down	down
AT4G31870	no	up	chloroplast redox GPX7 glutathione peroxidase 7	GPX7_1	73.181	0.0329	up	GPX7	69.126	0.023	up	
AT1G76560	no	down	chloroplast redox oxidative proteion of Calvin cycle enzymes CP12-3 CP12 domain-containing protein 3					CP12-3	-4.146	0.006	down	
AT2G03130	no	up	chloroplast ribosome 50S ribosomal protein L12	AT2G03130_1	68.676	0.0345	up	AT2G03130	64.87	0.025	up	
AT2G07732	no	up	chloroplast Ribulose bisphosphate carboxylase large chain, catalytic					AT2G07732	2.4942	0.036	up	
AT5G53080	no	up	chloroplast RNA editing tetratricopeptide WHITE TO GREEN 1, WTG1 protein	AT5G53080_1	50.201	0.0041	up	AT5G53080	47.916	8E-04	up	
ATCG00180	no	up	chloroplast RNA polymerase beta' subunit-1	RPOC1_1	2.2023	2E-06	up	RPOC1	2.0852	2E-08	up	up
AT4G08940	no	up	chloroplast RNA recognition (PORR) domain (DUF860) component of group II intron ribonucleoprotein particles					AT4G08940	8.621	0.023	up	
AT3G53460	yes	up	chloroplast RRM domain repeat RNA-BINDING PROTEIN 29	CP29_1	-74.1	0.0004	down	CP29	-2.219	0.01	down	
AT1G50000	yes	down	chloroplast rRNA methyltransferase	AT1G50000_5	15.503	0.022	up	AT1G50000	5.5757	0.013	up	down
AT3G63140	no	up	chloroplast rRNA processing STEM-LOOP BINDING PROTEIN OF 41 KDA, CSP41A	CSP41A_1	34.264	0.0099	up	CSP41A	32.711	0.003	up	
AT3G24430	no	up	chloroplast scaffold protein that specifically assembles [4Fe-4S] clusters HIGH-CHLOROPHYLL-FLUORESCENCE 101	HCF101_1	4.973	0.0021	up	HCF101	4.7675	8E-05	up	
AT4G01800	yes	down	chloroplast SEC translocon subunit AGY1, ALBINO OR GLASSY YELLOW 1, ARABIDOPSIS THALIANA CHLOROPLAST SECA, ATCPSECA, SECA1	AGY1_3	-719.7	0.0006	down	AGY1	-2.034	0.029	down	
AT3G10130	no	up	chloroplast SOUL domain hem binding protein	AT3G10130_1	145.07	0.0149	up	AT3G10130	137.51	0.01	up	
AT4G24620	no	down	chloroplast starch synthesis phosphoglucose isomerase 1	PGI1_2	-2.154	0.0494	down	PGI1	-2.274	0.004	down	
AT1G68830	no	up	chloroplast STN7 Serine/Threonine kinase	STN7_1	13.154	0.0198	up	STN7	12.551	0.003	up	
AT5G64380	no	up	chloroplast stroma Calvin cycle fructose-1,6-bisphosphatase (FBPase) class 1 family	AT5G64380_1	30.803	0.0122	up	AT5G64380	29.099	0.004	up	
AT5G61310	no	up	chloroplast stroma unknown protein EMBRYO DEFECTIVE 2799	AT5G61310_1	3.5688	1E-10	up	AT5G61310	3.3572	1E-15	up	
AT4G16060	no	up	chloroplast stroma unknown protein with signal peptide					AT4G16060	6.0773	0.034	up	
AT2G24020	no	up	chloroplast stromal protein interactor of ALB3/4 STIC2, SUPPRESSOR OF TIC40	AT2G24020_1	314.55	0.004	up	AT2G24020	7.1527	0.024	up	
ATCG00730	no	up	chloroplast subunit IV of the cytochrome b6/f complex PETD, PHOTOSYNTHETIC ELECTRON TRANSFER D	PETD_1	3.2482	0.0137	up	PETD	3.0673	0.002	up	
AT4G00690	no	up	chloroplast SUMO desumoylation enzyme ULP1B UB-like protease 1B					ULP1B	7.3051	0.034	up	up
AT1G68720	no	down	chloroplast TADA tRNA arginine adenosine deaminase					TADA	-2.169	0.012	down	
AT1G03475	no	down	chloroplast tetrapyrrole biosynthesis cell death pathogen response COPROPORPHYRINOGEN III OXIDASE; CPO; ; HEMF1; LESION INITIATION 2					CPX1	-2.649	0.028	down	
AT5G54770	no	down	chloroplast thiamine/vitamine B1 thiazol biosynthesis THI4; THIAMINE4; THIAZOLE REQUIRING; TZ	THI1_1	-3.01	0.0257	down	THI1	-3.215	0.002	down	
AT4G08280	no	up	chloroplast thioredoxin					AT4G08280	2.0866	0.025	up	
AT2G15570	no	down	chloroplast thioredoxin-M, iron homeostasis, vesicular transport	GAT1_4	-204.9	0.0098	down	GAT1	-2.607	0.036	down	
AT4G02530		up?	chloroplast thylakoid lumen protein					AT4G02530	76.303	0.02	up	
AT3G12345	no	up	chloroplast thylakoid protein folding FKBP-type peptidyl-prolyl cis-trans isomerase					AT3G12345	8.7264	0.018	up	
AT3G47070	no	up	chloroplast thylakoid unknown phosphorylated protein TSP9	AT3G47070_1	27.301	0.0161	up	AT3G47070	25.79	0.005	up	
AT2G31400	no	down	chloroplast to nucleus signaling GUN1 pentatricopeptide protein					GUN1	-2.03	0.002	down	
AT5G51080	no	up	chloroplast transcription R-loop RNase H	AT5G51080_2	61.964	0.0386	up	AT5G51080	9.2669	0.019	up	
AT2G28800	no	up	chloroplast translation membrane targetuing ALB3 63 kDa inner membrane family protein	ALB3_2	1174.1	0.0002	up	ALB3	2.1699	0.025	up	
AT1G71720	no	down	chloroplast translation RbcL mRNA S1 binding domain protein; RLSB					AT1G71720	-3.004	0.028	down	
AT5G16620	no	down	chloroplast translocon subunit Tic40					TIC40	-2.476	0.007	down	
AT1G06950	no	down	chloroplast translocon subunit TIC110					TIC110	-2.298	0.021	down	
ATCG00040	no	up	chloroplast tRNAK intron maturase	MATK_1	4.2193	0.0006	up	MATK	4.0078	3E-06	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
At1g15710	no	down	chloroplast tyrosine biosynthesis					TYRAAT2	-2.519	0.025	down	
AT2G33255	no	up	chloroplast unknown haloacid dehydrogenase (HAD)					AT2G33255	4.6536	0.035	up	
AT1G79790	yes	up	chloroplast vitamin G riboflavin synthesis from FMN FHY1 FMN hydrolase 1					FHY1	7.4601	0.025	up	
ATCG00530	no	up	chloroplast YCF10 CemA inner envelope membrane protein					CEMA	3.354	0.018	up	
ATCG00520	no	up	chloroplast YCF4 protein required for photosystem I assembly and stability					YCF4	5.294	0.026	up	
AT2G36390	no	down	chloroplast/amylopaslt starch synthesis SBE2.1 starch branching enzyme 2.1					SBE2.1	-2.218	0.023	down	
AT2G35410	no	up	chlroplast RNA binding tandem RRM domain protein					AT2G35410	5.1047	0.016	up	
AT1G50900	no	up	chlroroplast ankyrin repeat protein required for grana formation Grana Deficient Chloroplast 1; LHCP translocation defect; LTD	LTD_1	66.258	0.0367	up	LTD	63.29	0.026	up	
AT5G55660	no	down	chromatin nucleosome H3/4 binding DEK domain-containing chromatin associated protein	AT5G55660_1	-2.415	1E-07	down	AT5G55660	-2.553	6E-13	down	
AT5G08430	yes	down	chromatin remodelin SWIB, PLUS3 and GYF domain protein	AT5G08430_2	75.162	0.0366	up	AT5G08430	4.4539	0.027	up	
AT2G46020		down	chromatin remodeling SWI/SNF ATPase BRAHMA	BRM_5	-435.9	0.0029	down	BRM	-2.415	1E-04	down	up
AT1G73910	yes	down	chromatin remodeling SWI/SNF subunit ARP4A actin-related proteins 4A					ATARP4A	42.881	0.047	up	
AT3G03590	no	up	chromatin remodelling potential SWI/SNF component SWI3B domain protein SWI3B4	AT3G03590_1	23.272	0.0218	up	AT3G03590	21.983	0.007	up	
AT1G20220	no	down	chromatin structure repression mRNA stability ALBA RNA/DNA binding protein	AT1G20220_1	-2.428	0.007	down	AT1G20220	-2.579	6E-05	down	
AT5G55600	no	down	chromatin unknown BAH (bromo-adjacent homology) and Agenet domain protein	AT5G55600_3	-2.761	0.0096	down	AT5G55600	-2.38	9E-04	down	up
AT4G26630	no	down	chromatine nucleosome histones H3 and H4 bindin chromatin DEK-DOMAIN CONTAINING PROTEIN 3, DEK3	AT4G26630_1	-2.064	0.0217	down	AT4G26630	-2.546	6E-07	down	up
AT5G15510		down?	chromosome centromeric kinesin-like TPX2 domain protein					AT5G15510	-2.874	0.023	down	down
AT4G10890	no	down	chromosome segregation telomer maintenance DDE endonuclease	AT4G10890_1	-12.86	0.0367	down	AT4G10890	-3.843	0.001	down	
At5g08330	no	up	circadian clock CHE repressor of CCA1 ATTCP21, CCA1 HIKING EXPEDITION, CHE, TCP DOMAIN PROTEIN 21, TCP21 TF					TCP21	6.4339	0.038	up	
AT5G64813		down	circadian clock endoreduplication salt stress Light Insensitive Period1 small G-protein repressor of light entraining					LIP1_4	-2.212	0.001	down	
AT2G06255	no	up	circadian clock evening complex ELF4-L3 ELF4-like 3	EFL3_1	145.65	0.0134	up	EFL3	138.9	0.009	up	down
AT5G02080		up?	coenzyme A synthesis phosphopantothenoylcysteine synthetase	AT5G02080_4	68.713	0.035	up	AT5G02080	132.57	0.009	up	
AT2G15970	yes	down	cold acclimation WCOR413-like transmembrane protein ABA induced	COR413PM1_1	4.0815	0.0221	up	COR413PM1	3.0664	0.005	up	up
At5g51190	no	down	cold freezing tolerance ERF105 AP2 TF	ERF105_1	-227.5	0.0063	down	ERF105	-244.9	0.003	down	
AT2G38170	no	up	cold inducible vacuolar calcium antiporter ATCAX1, CATION EXCHANGER 1, CAX1, RARE COLD INDUCIBLE 4, RCI4	CAX1_3	52.935	0.0456	up	CAX1	50.003	0.034	up	
AT5G20270	no	up	cold osmotic stress signaling HlyIII domain 7 transmembrane receptor HHP1 heptahelical transmembrane protein1	HHP1_1	12.686	0.0452	up	HHP1	11.983	0.013	up	
AT2G02450	yes	down?	cold response flowering time PHOT1/2 interacting LONG VEGETATIVE PHASE 1 (LOV1) NAC035 TF					NAC035	-20.48	0.024	down	
AT4G30660	no	up	cold salt induced Pmp3 Proteolipid membrane potential modulator	AT4G30660_2	68.734	0.0345	up	AT4G30660	16.551	0.012	up	down
AT5G28300	no	down	cold salt stress Ca2+/calmodulin binding GT2-like MybTF with double SANT domain and coiled coil					AT5G28300	-6.887	0.009	down	
AT1G09350		up?	cold stress osmolyte GolS3 galactinol synthase 3					GOLS3	37.183	0.048	up	
AT4G25470	no	up	cold tolerance CBF2; C-repeat/DRE binding factor 2; DRE/CRT-BINDING PROTEIN; DRE/CRT-BINDING PROTEIN 1C; DREB1C; FREEZING TOLERANCE QTL 4; FTQ4					DREB1C	41.441	0.042	up	
At3g26420	no	up	cold tolerance spliceosome ATRZ-1A, at-hnRNP-G2 protein wih RNA recognition motif CCHC-type zinc finger	RZ1A_1	6.5474	2E-08	up	RZ1A	6.1994	1E-13	up	
AT3G49990	no	down	cold tolerance yeast low-temperature viability protein LTV1 homolog					AT3G49990	-2.399	0.006	down	
AT1G63440	no	down	copper detoxification root HMA5 heavy metal atpase 5	HMA5_1	-2.545	0.0001	down	HMA5	-2.697	4E-07	down	
AT5G22720	no	up	cotyledon vein patterning ubiquitination SCF E3 LRR repeat F-box protein					AT5G22720	45.294	0.04	up	
AT5G06300	no	up	cytokinin activating enzyme merisetm size LONELY GUY 7					LOG7	44.645	0.04	up	
AT1G68870	no	up	cytokinin positive control of cytokinin levels SOFL2 SOB five-like 2 ARM repeat protein	ATSOFL2_1	31.069	0.0125	up	ATSOFL2	29.754	0.004	up	
At4g18220	no	down	cytokinin purine transporting membrane permease PUP21					PUP21	-4.715	0.044	down	
AT1G31770	no	down	cytokinin root to shoot transporter	ABCG14_1	-2.81	0.0393	down	ABCG14	-2.976	0.003	down	up
AT2G23460	no	down	cytokinin signaling root development extra-large G-protein 1	XLG1_1	-2.429	0.0453	down	XLG1	-2.581	0.003	down	
AT1G68460	no	up	cytokinin synthesis IPT1 isopentenyltransferase 1					IPT1	5.8414	0.038	up	
At1g68550	no	up	cytokinin transcription CRF10, CYTOKININ RESPONSE FACTOR 10, ERF118 subfamily B-6 of ERF/AP2 transcription factors	ERF118_2	437.2	0.0041	up	ERF118	4.9506	0.02	up	
AT5G05870	no	up	cytokinin UGT76C1 UDP-glucosyl transferase 76C1	UGT76C1_1	99.752	0.0229	up	UGT76C1	94.529	0.015	up	
At4g08700	no	up	cytokinin, purine transporter PUP13	PUP13_1	28.456	0.0152	up	PUP13	26.97	0.005	up	
AT1G09860	no	up	cytokinin/purine transporter PUP16 purine permease 16					PUP16	39.071	0.049	up	
AT2G33750	yes	down	cytokinin/purine transporter PUP2 purine permease 2					PUP2	38.54	0.048	up	
At4g37710	no	up	deetiolation repressor of PIF1 VQ MOTIF-CONTAINING PROTEIN 29, VQ29	VQ29_2	62.751	0.044	up	VQ29	8.8266	0.017	up	
AT1G30360	no	down	dehydration induced Golgi 10TM putative phosphate transporter	ERD4_1	-2.831	0.0309	down	ERD4	-3.007	0.002	down	
AT4G23610	no	up	dehydration protein folding transmembrane Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein					AT4G23610	6.628	0.032	up	
AT4G35170	no	up	dehydration stress induced protein folding transmembrane LEA protein CC4, COMPANION OF CELLULOSE SYNTHASE 4					AT4G35170	46.022	0.039	up	
AT1G67280	no	down	detoxification redox glyoxalase 4 Glyoxalase/Bleomycin resistance protein/Dioxygenase					AT1G67280	-2.443	0.036	down	
At4g24750	no	up	detoxification Rhodanese, sulphurtransferase involved in cyanide detoxification					STR11	6.4899	0.046	up	
AT3G15160	no	up	DNA recombination AP5Z1 adaptor related protein complex 5 subunit zeta 1	AT3G15160_1	170.85	0.011	up	AT3G15160	3.7665	0.03	up	
AT5G63920	no	up	DNA recombination meiosis crossover suppressor TOP3A topoisomerase 3alpha					TOP3A	8.2199	0.013	up	
AT1G63990	no	up	DNA recombination meiosis SPO11-2 sporulation 11-2	SPO11-2_2	14.646	0.0455	up	SPO11-2	13.835	0.019	up	
AT5G52290	no	up	DNA recombination meiosis XPF-like endonuclease SHOC1 shortage in chiasmata 1					SHOC1	43.083	0.045	up	up
At1g01880	no	up	DNA recombination repair endoreduplication GEN1 Holliday junction 5' flap endonuclease Rad2/XPG nuclease	GEN1_1	105.21	0.0214	up	GEN1	6.2905	0.033	up	up
AT3G20475		up?	DNA recombination, meiosis	MSH5_1	116.59	0.0183	up	MSH5	130.17	0.01	up	down
AT1G11780	no	up	DNA repair AlkB is a DNA repair enzyme	AT1G11780_1	71.09	0.0017	up	AT1G11780	67.163	3E-04	up	

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AT3G12380	no	down	DNA repair ARP5 subunit of INO80 chromatin-remodeling complex	ARP5_2	-219.3	0.0064	down	ARP5	-3.22	0.03	down	
AT1G75090	no	up	DNA repair base excision DNA-3-methyladenine glycosylase I	AT1G75090_1	89.033	0.0259	up	AT1G75090	84.103	0.018	up	
AT3G50880	no	down	DNA repair base excision methylation ENDO3c domain endonuclease III (DNA-(apurinic or apyrimidinic site) lyase), alkylbase DNA glycosidase					AT3G50880	-2.903	0.008	down	
AT4G03130	yes	up?	DNA repair breast cancer DNA-repair protein BRCA1 tandem domain protein	AT4G03130_4	187.84	0.0119	up	AT4G03130	7.2716	0.019	up	
AT4G25290	no	up	DNA repair DNA photolyase					AT4G25290	9.1638	0.024	up	
AT3G15960	no	up	DNA repair MutS_II domain mismatch repair protein					AT3G15960	9.7934	0.02	up	
AT1G53250	no	up	DNA repair NUMOD3 (nuclease associated modular domain 3) homing nuclease					AT1G53250	6.9599	0.026	up	
AT4G02485	no	up	DNA repair putaive AlkB DNA repair enzyme	AT4G02485_1	95.877	0.0234	up	AT4G02485	107.62	0.012	up	up
AT5G06420	no	up	DNA repair RAD51C interacting ring finger protein 113A1 homolog	AT5G06420_1	48.841	0.0045	up	AT5G06420	17.481	0.002	up	
AT2G45280		down?	DNA repair RAD51C RAS associated with diabetes protein 51C					ATRAD51C	-6.051	0.013	down	
AT3G05480		down?	DNA repair RAD9 cell cycle checkpoint control protein homolog					ATRAD9	44.927	0.04	up	
AT2G26270	no	up	DNA repair tandem breast cancer carboxy-terminal domain protein					AT2G26270	6.7005	0.044	up	
AT3G47830	no	up	DNA repair unknown endonuclease III (DNA-(apurinic or apyrimidinic site) lyase) domain protein	AT3G47830_1	102.67	0.0218	up	AT3G47830	96.991	0.014	up	
AT1G07270	yes	down	DNA replication cell division CDC6	CDC6B_2	-105	0.0226	down	CDC6B	-9.062	0.023	down	down
AT2G16440	no	down	DNA replication complex MINICHROMOSOME MAINTENANCE 4	MCM4_1	-2.642	0.0149	down	MCM4	-2.82	5E-04	down	
At2g47210	no	up	DNA replication histone acetylation DNA methyltransferase 1 associated protein 1 EAF2; SWC4; MEAF2; DNMAP1; DNMTAP1	SWC4_3	61.958	0.0449	up	SWC4	3.7794	0.019	up	
At3g12530		up?	DNA replication initiation GINS complex Psf2 subunit					GINS2	16.42	0.007	up	up?
AT1G63160	no	up	DNA replication licencing factor C					RFC2	4.2433	0.011	up	
AT2G29680	no	up	DNA replication licencing factor CDC6 cell divison	CDC6_2	7.1968	0.0352	up	CDC6	4.2519	0.014	up	
AT5G46280	no	down	DNA replication MCM3 3' to 5' helicase	MCM3_2	-2.656	0.0069	down	MCM3	-2.703	5E-05	down	up
AT3G25100	no	down	DNA replication meiosis MCM7 and DNA pol alpha interacting CDC45	CDC45_1	-8.294	0.0363	down	CDC45	-8.675	0.011	down	
AT1G08130	no	down	DNA replication repair major DNA ligase 1	LIG1_1	-2.853	0.0348	down	LIG1	-3.028	0.002	down	
At1g07370	no	down	DNA replication repair PCNA proliferating cell nuclear antigen 1	PCNA_1	-2.055	0.015	down	PCNA	-2.186	6E-04	down	
AT3G50980	no	up	drought tolerance XERO1 dehydrin	XERO1_1	50.616	0.0481	up	XERO1	47.811	0.036	up	down
AT3G23110	no	up	EMB2800, EMBRYO DEFECTIVE 2800, transmembrane LRR RECEPTOR LIKE PROTEIN 37, RLP37	AtRLP37_1	86.713	0.0263	up	AtRLP37	81.908	0.018	up	up
At2g16505	no	up	embryo 77aa oligopeptide Maternally expressed gene (MEG)					ESFL9	6.6825	0.044	up	
AT5G24400	no	down	embryo chloroplast redox oxidative pentose phosphate pathway 6-PHOSPHOGLUCONOLACTONASE 3, EMBRYO DEFECTIVE 2024	PGL3_2	-5.192	0.004	down	PGL3	-5.28	2E-04	down	
AT1G41830	no	down	embryo cotyledon vacular patterning SKU5 SIMILAR 6; SKU5-similar 6					SKS6	-3.236	0.006	down	
AT4G33460	no	up	embryo defective 2751 unknown ABC transporter ATNAP13; ATP-binding cassette I10	ABCI10_1	9.9525	0.0452	up	ABCI10	9.5007	0.011	up	
AT1G34550		down?	EMBRYO DEFECTIVE 2756 unknown protential transmembrane DUF616 domain glycosyltransferase					EMB2756	-2.55	0.014	down	
AT2G02150	no	up	EMBRYO DEFECTIVE 2794 Pentatricopeptide repeat protein	AT2G02150_2	73.247	0.0321	up	AT2G02150	14.791	0.007	up	down
AT4G37140		up?	embryo development ATMES20; MATERNAL EFFECT EMBRYO ARREST 69; MES20; METHYL ESTERASE 20					MES20	37.168	0.048	up	
AT1G36160	no	down	embryo development cold tolerance acetyl-CoA carboxylase 1 is essential for very long chain fatty acid elongation and embryo development	ACC1_2	-3.366	0.0471	down	ACC1	-2.806	3E-05	down	
AT4G29860	no	down	embryo development DNA repair TAN; TANMEI CUL4-DDB1 binding WD40 protein					TAN	-4.349	0.01	down	up
AT4G04890	no	up	embryo development meristemL1 specific homeobox TF PDF2 protodermal factor 2 with START (StAR-related lipid-transfer) domain					PDF2_2	10.894	0.036	up	
At3g22760	yes	down?	embryo development ovule and pollen mother specific Tesmin/TSO1-like CXC domain protein					TCX3	-10.78	0.046	down	
At3g63500		down?	embryo development root meristem initiation PHD finger TF	OBE4_1	-9.752	0.008	down	OBE4	-2.29	0.004	down	up
At1g23200	no	down	embryo development seed coat epidermis homogalacturonan methylesterase HIGHLY METHYL ESTERIFIED SEEDS, HMS, PECTIN METHYLESTERASE6, PME6					PME6	-10.71	0.02	down	
AT4G10560	no	up	embryo development ubiquitination RING E3 with DAG-binding PKC C1 domains					MEE53	6.378	0.041	up	
AT3G49240	no	down	embryo development unknown Pentatricopeptide repeat (PPR) protein	EMB1796_1	-3.707	0.0081	down	EMB1796	-3.964	2E-04	down	
AT5G56270	no	down	embryo development WRKY2 TF					WRKY2	-2.39	0.017	down	
AT1G44900	no	down	embryo development, DNA replication, root meristem MINICHROMOSOME MAINTENANCE 2	MCM2_1	-2.378	0.0238	down	MCM2	-2.363	6E-04	down	up
AT4G26330	yes	down	embryo development, subtilisin protease UNFERTILIZED EMBRYO SAC 17	UNE17_2	-20.41	0.0344	down	UNE17	-21.17	0.012	down	
AT5G44790	no	down	embryo endosperm cellularization ethylene signaling esential ATP dependent copper transporter RESPONSIVE-TO-ANTAGONIST 1					RAN1_2	-2.248	4E-05	down	
AT1G66040	no	down	embryo endosperm imprinting ORTH4; ORTHRUS 4; VARIANT IN METHYLATION 4 VIM4 Zinc finger (C3HC4-type RING finger) TF					ORTH4	-2.285	0.009	down	
AT4G28320	no	up	embryo endosperm radicle MAN5; endo-beta-mannase 5 seed germination	MAN5_1	222.48	0.0074	up	MAN5	211.38	0.004	up	
AT5G23260	yes	down	embryo fertilization ovule seed development proanthocyanide synthesis in seed coat	TT16_4	-99.26	0.0242	down	TT16	-19.79	0.004	down	
AT5G13170	no	down	embryo integumentum sucrose efflux transporter	SWEET15_1	-17.65	0.0124	down	SWEET15	-19.08	0.002	down	
AT1G79560	no	down	embryo lethality chloroplast PSII repair protease EMBRYO DEFECTIVE 36; FTSH protease 12					FTSH12	-2.502	0.037	down	down

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G17220	no	down	embryo lethality chloroplast translation initiation factor 2-like					FUG1	-2.324	0.025	down	
AT3G17010	no	up	embryo ovary floral meristem AG activated B3 repeat TF REPRODUCTIVE MERISTEM 22	AT3G17010_1	17.521	0.0343	up	AT3G17010	16.551	0.013	up	
AT2G47990	no	down	embryo ribosome biogenesis 18S EDA13; EDA19; EMBRYO SAC DEVELOPMENT ARREST 13; EMBRYO SAC DEVELOPMENT ARREST 19; SLOW WALKER1					SWA1	-2.883	0.014	down	
AT4G01560	no	down	embryo ribosome biogenesis RPF1 ribosome production factor 1 homolog maternal effect embryo arrest 49					MEE49	-2.556	0.008	down	
AT1G01960	no	down	embryo sac development arrest 10, vesicular transprt cell plate SEC7-like guanine nucleotide exchange protein	BIG3_1	-2.227	0.0153	down	BIG3	-2.349	3E-04	down	
AT2G48140	no	up	embryo sac development arrest 4 AAI Plant lipid transfer protein / seed storage protein / trypsin-alpha amylase inhibitor domain protein	EDA4_1	99.94	0.023	up	EDA4	25.521	0.005	up	down
AT5G18090	no	up	embryo sac differentiation VVD homolog B3 domain repeat TF					AT5G18090	40.868	0.045	up	
AT4G12620	no	down	embryo sac DNA replication orginin complex ORC1B origin of replication complex 1B UNE13; UNFERTILIZED EMBRYO SAC 13	ORC1B_1	-4.433	0.0151	down	ORC1B	-4.765	0.001	down	
AT5G17340	no	up	embryo sac prolamin (Protease inhibitor-seed storage-LTP family9 protein with signal peptide					AT5G17340	43.58	0.041	up	
At4g26740	no	up	embryo seed Ca2+dependent lipid droplet caleosin PEROXYGENASE 1					PXG1	8.9333	0.043	up	
At1g22540	no	down	embryo specific AtNPF5.5 nitrate transporter					NPF5.10	-2.054	0.036	down	
AT5G19310	no	down	embryo stem cell meristem chromatin remodeling small ATPase CHR23 homeotic protein regulator					CHR23	-3.601	0.015	down	
AT4G23660	yes	down	embryo ubiquinin synthesis PPT1 polyprenyltransferase 1	AtPPT1_2	134.34	0.0148	up	AtPPT1	135.39	0.009	up	
AT1G03120	no	up	embryo vascular tissue specific Late embryogenesis abundant (LEA) dehydrin	RAB28_1	18.733	0.031	up	RAB28	17.704	0.011	up	
AT2G35230	yes	up	embryogenesis central cell early endosperm development	IKU1_2	-28.14	0.0115	down	IKU1	-2.122	0.001	down	
AT4G20140	no	up	embryogenesis epidermal differentiation transmembrane LRR RECEPTOR KINASE GASSHO1, GSO1, SCHENGEN 3, SGN3	GSO1_1	27.295	0.0159	up	GSO1	25.783	0.005	up	
AT5G39500	no	down	embryogenesis ER biogenesis GNOM-LIKE1/ERMO1, a member of ARF-GEF	GNL1_1	-3.422	0.0296	down	GNL1	-3.133	3E-04	down	
AT2G25170	no	up	embryogenesis repressor of embryo specific gene PKL chromatin remodeling factor SWI/SNF CHD3					SSL2	44.37	0.041	up	up
AT3G07050	no	down	embryogenesis ribosome biogenesis, meristem, floral organ, leaf etc. development nucleolar GTPase nucleostemin-like 1	NSN1_1	-2.219	0.0182	down	NSN1	-2.35	5E-04	down	up
AT3G19770	no	down	embryogenesis root development vesicular transport VPS9A Vacuolar sorting protein 9 required for ARA7 and ARA6 localization					VPS9A	-2.163	0.02	down	
AT3G47520	no	down	embryogenesis seed development chloroplast C4 cycle photorespiration malate dehydrogenase	MDH_1	-2.421	0.0266	down	MDH	-2.59	0.002	down	
AT2G47790	no	down	embryogenesis seed germination ribosome biogenesis WDR89 homolog GIGANTUS 1; GTS1 CUL4-DDB1 interacting WD40 protein					AT2G47790	-2.511	0.007	down	
AT4G21060	no	up	endomembrane arabinogalactan-protein biosynthesis AGP galactosyltransferase 2; AtGALT2	AT4G21060_2	23.076	0.0322	up	AT4G21060	5.7833	0.021	up	
At5g13860	no	down	endoreduplication vesicular transport multivesicular body ESCRT component	ELCL_1	-3.701	0.0181	down	ELCL	-3.889	8E-04	down	
AT5G60440	no	up	endosperm development suppressor of cellularization AGL62 AGAMOUS-like 62	AGL62_1	38.103	0.0079	up	AGL62	36.026	0.002	up	
AT3G48340	no	up	ER CEP2 cysteine endopeptidase 2					CEP2	10.556	0.034	up	
AT4G01510		up?	ER lipid/sterol transport regulator AVR1 homolog AVR2					ARV2	11.998	0.011	up	?
At1g79940	no	down	ER protein folding Sec63 interacting ATERDJ2A DnaJ / Sec63 Brl domain chaperon					ERDJ2A	-2.613	4E-06	down	
AT5G58000	yes	down?	ER RETICULON 21, RTN21	AT5G58000_2	17.576	0.0182	up	AT5G58000	17.586	0.002	up	
AT4G40042	no	down	ER SCP12+microsomal signal peptidase 12 kDa subunit					AT4G40042	-8.147	0.027	down	down
AT1G29310	no	up	ER SEC61 complex subunit SEC61A1	AT1G29310_2	2.1885	0.0062	up	AT1G29310	2.0641	9E-04	up	
At2g43640	yes	down	ER Signal recognition particle, SRP9/SRP14 subunit	SRP14_2	-13.34	0.0152	down	SRP14	-2.504	0.017	down	
AT2G22810	no	up	ethylene biosynthesis auxin induced ABA repressed ACS4 1-aminocyclopropane-1-carboxylate synthase 4					ACS4	11.034	0.018	up	
AT5G47220	no	up	ethylene signaling EBF2 F-box protein of EIN3 ubiquitin SCF E3	ERF2_1	3.018	0.0039	up	ERF2	2.8643	2E-04	up	
AT3G18980	no	up	ethylene signaling EIN2 uniquitination SCF E3 F-box protein EPT1	ETP1_2	-3.003	0.0026	down	ETP1	-2.82	5E-05	down	
At3g23240	no	up	ethylene signaling EIN3 activated ERF1 ethylene response factor 1	ERF1B_1	17.945	0.0211	up	ERF1B	16.951	0.005	up	
At5g65100	no	up	ethylene transcription unknown Ethylene insensitive 3 domain TF	EIL5_1	56.54	0.0448	up	EIL5	53.688	0.033	up	
AT1G14240	no	up	extracellular ATP hydrolase ENTPD1 ectonucleoside triphosphate diphosphohydrolase 1	APY3_4	163.41	0.0112	up	APY3	14.134	0.004	up	down
AT1G64400	no	up	fatty acid and glycerolipid metabolism long-chain acyl-CoA synthetase 3					LACS3	39.31	0.045	up	up
AT1G01120	no	up	fatty acid cell wall wax synthesis KCS1 3-ketoacyl-CoA synthase 1	KCS1_1	55.247	0.046	up	KCS1	52.344	0.035	up	
AT1G75000	no	down	fatty acid elongation ELO domain protein	AT1G75000_1	-3.06	8E-09	down	AT1G75000	-3.25	6E-14	down	
AT1G77240	no	down	fatty acid synthesis ATP dependent ACYL ACTIVATING ENZYME 2					AEE4	-10.52	0.018	down	
AT1G04220	no	up	fatty acid synthesis very long chain fatty acid KCS2 3-ketoacyl-CoA synthase 2					KCS2	7.0726	0.015	up	
AT3G15870	no	up	fatty acid unsaturated Fatty acid desaturase	ADS3.2_1	59.642	0.0401	up	ADS3.2	56.336	0.029	up	
AT5G22500		up?	fatty alcohol suberin synthesis FAR1 fatty acid reductase 1					FAR1_2	15.755	0.001	up	
AT3G44540	yes	down	fatty alcohol synthesis root wounded tissues FAR4, FATTY ACID REDUCTASE 4	FAR4_3	85.715	0.0323	up	FAR4	12.775	0.005	up	
AT5G27630	yes	up?	fatty asic transport intracellular carrier of acyl-CoA ester ACBP5					ACBP5	6.8906	0.027	up	
AT1G67960	no	up	fertilization pollen tube guidance early embryonic patterning transmembrane DUF747 domain protein					POD1	2.4916	0.036	up	
At4g08850	no	down	fertilization root growth stress responses MDIS1-INTERACTINGLRR RECEPTOR LIKE KINASE2, MIK2	MIK2_2	-2.382	4E-08	down	MIK2	-2.261	9E-11	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT2G25790	no	down	fertilization SKM1; STERILITY-REGULATING KINASE MEMBER 1 LRR receptor kinase					AT2G25790	-2.137	0.038	down	
AT5G10430	no	down	fertilization synergid survival cell wall arabinogalactan protein 4	AGP4_1	-2.122	0.0337	down	AGP4	-2.268	0.003	down	
AT4G34138	no	down	flavonoid 7-O-glucosyltransferase	UGT73B1_1	-3.022	0.0122	down	UGT73B1	-3.19	1E-04	down	
AT3G02420	no	down	flavonoid metabilism dihydroflavonol 4-reductase	AT3G02420_2	-2.514	0.0324	down	AT3G02420	-2.6	0.004	down	
AT4G13550	yes	down	flavonoid metabolism feruloyl esterase A	AT4G13550_3	112.02	0.0239	up	AT4G13550	4.8796	0.006	up	
AT3G21240	yes	up	flavonoid phenylpropanoid biosynthesis 4-COUMARATE:COA LIGASE 2, 4CL2, AT4CL2	4CL2_3	-14.27	0.0013	down	4CL2	-2.565	0.018	down	
AT4G22880	no	down	flavonoid protoanthocyanine synthesis LDOX leucoanthocyanidin dioxygenase	ANS_1	-2.647	0.0031	down	ANS	-2.802	4E-05	down	up
At5g41040		up?	flavonoid, suberin synthesis aliphatic suberin feruloyl-transferase	HHT1_1	92.115	0.0254	up	HHT1	102.3	0.013	up	down
AT4G34135	no	down	flavonol glucosyltransferase	UGT73B2_2	-2.539	4E-05	down	UGT73B2	-2.624	1E-07	down	down
AT3G12680	no	down	floral organ identity AGAMOUS premRNA processing RNA binding ZnF_C3H1 domain factor					HUA1	-2.948	0.039	down	
AT5G03680	no	down	flower 2nd whorl, organ development trihelix PTL TF	PTL_1	-7.617	0.0124	down	PTL	-8.08	3E-04	down	
AT3G61250	no	up	flower organ identify partner of LFY in regulation of AP1 MYB17 TF	AtMYB17_1	19.227	0.0296	up	AtMYB17	18.161	0.011	up	
AT3G54340	no	down	flower organ identity petal & stamen MADS TF AP3					AP3	-38.05	0.046	down	
AT3G07220	no	down	flower stamen development forkhead-associated 2	FHA2_1	-2.666	0.0279	down	FHA2	-2.85	0.002	down	
AT1G51570	no	down	flowering time FT INTERACTING PROTEIN 4, FTIP4, MCTP4, MULTIPLE C2 DOMAIN AND TRANSMEMBRANE REGION PROTEIN 4	AT1G51570_1	-3.01	0.0028	down	AT1G51570	-3.191	2E-05	down	
AT1G68050	no	up	flowering time activator circadian clock FKF SCF E3 F-box protein controlling CBF ubiquitination and CO expression					ADO3	3.5742	0.04	up	down
AT3G15270	no	down	flowering time AP1 LFY Frau regulation SPL5 TF					SPL5	-15.21	0.021	down	
AT5G01040	no	down	flowering time cell wall lignin synthesis LAC8 laccase 8	LAC8_1	-3.234	0.0209	down	LAC8	-3.431	9E-04	down	
AT5G39660	no	up	flowering time FKF substrate cycling DOF factor 2 TF					CDF2	3.1988	0.025	up	
AT3G04610	no	down	flowering time FLC repressor FLK KH RNN binding domain protein					FLK	-2.686	7E-04	down	
AT4G02560	no	down	flowering time LFY repressor LD					LD	-2.335	0.04	down	
AT5G62640	yes	down	flowering time repressor EARLY FLOWERING 5, ELF5 WW domain-binding protein 11 homolog with RNA 3'-terminal phosphate cyclase domain	ELF5_1	-31.25	0.0094	down	ELF5	-2.55	0.002	down	
AT1G55660	yes	down	flowering time repressor ubiquitin SCF E3 LRR repeat F-box protein FLOWERING 2, FOF2	AT1G55660_2	36.809	0.0083	up	AT1G55660	37.396	0.002	up	
AT3G24440	no	down	flowering time vernalization FLC H3K27me3 VERNALIZATION 5; VIL1; VIN3-LIKE 1 PhD TF	VIL1_2	-16.6	0.0064	down	VIL1	-3.841	0.01	down	
At1g19210	no	up	GA DELLA interacting ERF017 DREB subfamily A-5 of ERF/AP2 transcription factor					ERF017	6.1937	0.017	up	
At1g22690	no	down	GA induced cysteine rich protein with signal peptide	GASA9_1	-59.31	0.0419	down	GASA9	-86.34	0.014	down	down
AT5G15230	no	up	GA response redox GASA gibberellin regulated cysteine rich protein with signal peptide	GASA4_1	2.4112	0.0226	up	GASA4	2.2923	0.003	up	down
AT5G09460	no	down	GA signaling DELLA interacting BHLH143 TF					BHLH143	-3.393	0.012	down	
At2g14900	no	up	GA-induced GASA cysteine rich protein with signal peptide					GASA7	7.9194	0.034	up	
AT5G67480	no	down	gametophyte development DNA mismatch repair MutS family BTB AND TAZ DOMAIN protein 4	BT4_2	-28.26	0.008	down	BT4	-3.723	0.008	down	
AT1G60680	no	up	glucose to polyol metabolism fission yeast yak3 aldose reductase ARK13 family YakC homolog	AGD2_1_2	76.322	0.0335	up	AGD2_1	11.17	0.016	up	
AT1G06020	no	up	glycolysis FRUCTOKINASE 3, FRUCTOKINASE 5	AT1G06020_1	12.294	0.049	up	AT1G06020	11.646	0.016	up	
AT3G01590	no	up	glycolysis gluconeogenesis Aldose 1-epimerase					AT3G01590	3.2334	0.011	up	up
AT2G45630	yes	down	glycolysis lactate to pyruvate D-isomer specific 2-hydroxyacid dehydrogenase					AT2G45630	6.7533	0.032	up	down
AT4G26390	no	up	glycolysis Pyruvate kinase					AT4G26390	9.469	0.042	up	up
AT5G63680		up	glycolysis Pyruvate kinase	AT5G63680_3	3.5563	0.0411	up	AT5G63680	3.4854	0.006	up	
AT4G34420	no	up	glycolysis transmembrane Phosphoglycerate mutase					AT4G34420	7.3909	0.029	up	
AT4G23730		up?	glycolysis/neogenesis Aldose 1-epimerase mutarotase					AT4G23730	3.8192	0.018	up	
AT1G55620	yes	down?	Golgi CHLORIDE CHANNEL F; CLCF					CLC-F	-3.891	0.003	down	
AT1G10950	no	down	Golgi endomembrane exporter TMN1	TMN1_1	-2.036	0.03	down	TMN1	-2.166	0.002	down	
AT1G49710	no	down	Golgi FUT12 fucosyltransferase 12					FUT12	-2.502	0.014	down	
AT1G21070	no	up	Golgi nucleotide-sugar transpoter UDP-Rha/UDP-Gal transporter 2; URGT2	AT1G21070_1	139.06	0.015	up	AT1G21070	131.64	0.01	up	
AT4G09810	yes	up	Golgi nucleotide-sugar transpoter UDP-Rha/UDP-Gal transporter 5; URGT5 predicted triose phosphate transporter domain	AT4G09810_3	-30.65	0.0011	down	AT4G09810	-10.13	0.009	down	
AT1G16780		up	Golgi proton pump VHP2;2 Inorganic H pyrophosphatase					AVPL2	5.9691	0.036	up	
AT2G43240	yes	up	Golgi sugar:proton symporter	AT2G43240_2	824.05	0.0004	up	AT2G43240	4.9724	0.015	up	
AT4G33740	no	down	Golgi transmembrane coiled coil protein	AT4G33740_3	-14.66	0.0009	down	AT4G33740	-3.2	4E-04	down	
AT2G30460		up?	Golgi UDP-XYLOSE TRANSPORTER2, UXT2					AT2G30460	18.227	0.001	up	
AT5G62220	no	down	Golgi XLT2; Xyloglucan L-side chain galactosylTransferase position 2					XLT2	-4.16	0.005	down	
At2g36810		down	gravitropism inflorescence stem SGR6; SHOOT GRAVITROPISM 6 ARM repeat protein					SGR6	-2.221	0.007	down	up
AT5G67110	no	down	gynoceum fruit development dehiscence bHLH73 ALCATRAZ	ALC_3	-10.07	0.0446	down	ALC	-10.96	0.014	down	
AT1G54850	no	up	heat shock HSP20 chaperone	ACD22.3_1	16.371	0.0386	up	ACD22.3	15.464	0.015	up	
AT5G20970	no	up	heat shock protein folding transmembrane HSP20 chepaeron with coiled coil domain					AT5G20970	11.652	0.026	up	
AT3G56800	no	up	heat shock signaling CAM3 calmodulin 3					CAM2_2	2.1697	0.005	up	down
AT4G21320	no	up	heat tolerance Coenzyme M (CoM; 2-mercaptoethanesulphonic acid) biosynthesis, COMA domain heat-shock protein HSA32					HSA32	2.0336	0.012	up	down
AT4G23550	no	down	heat tolerance pathogen BAG7 interacting WRKY29 TF					WRKY29	-2.079	0.01	down	
AT1G55775	no	up	heavy matal binding Heavy-Metal-Associated (HMA) domain protein	AT1G55775_1	256.75	0.0062	up	AT1G55775	243.82	0.004	up	
At3g02960	no	down	heavy matal binding HMA domain protein	HIPP08_1	-36.79	0.016	down	HIPP08	-38.87	0.005	down	
AT1G22990	no	up	HEAVY METAL ASSOCIATED ISOPRENYLATED PLANT PROTEIN 22, HIPP22	HIPP22_2	64.472	0.0376	up	HIPP22	61.065	0.028	up	
At3g56891	yes	down	heavy metal bidning Heavy-Metal-Associated (HMA) protein with signal peptide	HIPP45_1	-26.52	0.0058	down	HIPP45	-24.58	9E-04	down	

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AT5G66110		up?	heavy metal detoxifcation HMA domain heavy metal transporter	HIPP27_2	15.976	0.0267	up	HIPP27	12.524	0.007	up	?
At5g24580		up	heavy metal transporter HIPP09					HIPP09	6.8578	0.044	up	
AT2G19110	no	down	heavy metal Zn/Cd transporter ATPase					HMA4	-2.225	0.034	down	
AT2G28740	no	down	histine 4					HIS4	-3.344	0.029	down	
AT5G64840	no	down	histone acetylase GCN5	ABCF5_1	-2.512	0.04	down	ABCF5	-2.679	0.003	down	
AT1G67220	no	up	histone acetyltransferase of the CBP family 2					HAC2	5.2936	0.015	up	up
AT1G19330		up	histone deacetylase complex subunit SAP30	AT1G19330_3	93.159	0.0295	up	AT1G19330	6.2477	0.002	up	
AT1G11950	no	up	histone demethylase JmjC domain RING E3 ligase	AT1G11950_1	141.06	0.0176	up	AT1G11950	9.2286	0.014	up	down
AT2G37470	no	up	Histone H2B.4	AT2G37470_1	10.292	0.0223	up	AT2G37470	9.7247	0.005	up	
AT5G59970	no	up	Histone H4	AT5G59970_1	16.758	0.0161	up	AT5G59970	12.184	0.005	up	
AT5G56740	yes	down	histone H4K12 acetyltransferase HAC07; HAC7; HAG02; histone acetyltransferase of the GNAT family 2	HAG2_2 transcription activation	130.21	0.0201	up	HAG2	3.4719	0.049	up	
AT1G04050	yes	up	histone lysine methylase SUVR1 H3K9 nucleolar regulation of rRNA expression	SUVR1_2	-26.13	0.0143	down	SUVR1	-4.777	0.026	down	
AT3G24880		down?	histone modification H4K5 acetylase NuA4 complex component EAF1A	EAF1A_1	-4.149	0.0006	down	EAF1A	-2.349	9E-04	down	
AT1G63470	no	down	hypocotyl elongation AT-hook TF AHL5					AHL5	-2.636	0.01	down	
AT1G75540	no	down	hypocotyl elongation shade avoidance HY5 activator B-box zinc finger transcription factor BBX21	BBX21_1	-2.473	0.0077	down	BBX21	-2.607	1E-04	down	
AT4G37400	no	down	hypoxia haemerythrin/HHE cation-binding domain protein	CYP81F3_1	-6.007	0.023	down	CYP81F3	-6.406	1E-03	down	
AT2G41940	no	up	inflorescence trichome initiation cytokinin/GA regulated ZFP8 zinc finger protein 8 TF					ZFP8	8.9316	0.047	up	
AT2G19800	no	down	inositol phosphate redox myo-inositol oxygenase 2	MIOX2_1	-3.29	0.0047	down	MIOX2	-3.486	4E-05	down	
AT5G26820	no	up	iron chloroplast transporter of iron and antibiotics	IREG3_1	7.4822	0.0455	up	IREG3	7.1974	0.011	up	
AT5G54680	no	down	iron deficiecy homeostasis Helix-Loop-Helix 105; bHLH105; iaa-leucine resistant3 TF	ILR3_1	-2.018	0.0119	down	ILR3	-2.144	5E-04	down	
AT1G80830		up	iron deficiency induced NRAMP1 iron transporter					NRAMP1	2.7167	0.043	up	
AT1G18910	no	up	iron deficiency response negative regulator BRUTUS LIKE 2, BTSL2 haemerythrin/HHE cation-binding RING E3					AT1G18910	5.5504	0.015	up	
AT5G24380	no	down	iron homeostasis Fe-Phytosiderophore transporter homolog AtYSL2					YSL2	-3.051	0.038	down	
AT5G19700	no	up	iron homeostasis, hypocotyl elongation leaf senescence EARLY LEAF SENESCENCE 1, ELS1 MATE transporter					DTX52	8.7998	0.031	up	
AT5G03570	yes	up	iron induced FPN2 FERROPORTIN 2 tonoplast localized nickel/cobalt transport protein	IREG2_1	-119.4	0.0199	down	IREG2	-34.04	0.008	down	
AT5G04950	no	up	iron transport pollen tube growth NAS1 nicotianamine synthase 1					NAS1	43.58	0.04	up	
AT4G16370	no	down	iron transporter, systemic iron signaling	ATOPT3_1	-2.933	3E-05	down	ATOPT3	-3.085	8E-09	down	up
AT3G13610	no	up	iron uptake Fe(II)- and 2-oxoglutarate-dependent dioxygenase F6'H1					F6'H1	3.0444	0.023	up	
AT5G49650		down?	isoprenoid biosynthesis cytosolic XK-2 xylulose kinase-2	XK-2_1	-2.201	0.017	down	XK-2	-2.07	0.004	down	
AT5G58560	no	up	isoprenoid FOLK farnesol kinase	FOLK_1	6.4357	0.0475	up	FOLK	6.0805	0.01	up	
At2g18640	no	up	isoprenoid terpenoid biosynthesis ER GERANYLGERANYL PYROPHOSPHATE SYNTHASE 3, GERANYLGERANYL PYROPHOSPHATE SYNTHASE 4, GGPPS3, GGPS4	GGPP4_1	50.641	0.0482	up	GGPP4	47.835	0.036	up	
AT5G48110	no	down	isoprenoid terpenoid biosynthesis TERPENE SYNTHASE 20, TPS20					AT5G48110	-17.79	0.025	down	
AT1G61120	no	up	isoprenoid terpenoid synthesis defense GERANYLLINALOOL SYNTHASE; GES; terpene synthase 04; TERPENE SYNTHASE 4; TPS4					GES	7.2168	0.033	up	
AT1G30740	yes	down?	isoquinoline biosynthesis FAD dependent oxidoreductase	AT1G30740_2	-64.76	0.0382	down	AT1G30740	-3.831	0.05	down	
AT4G23600		up	JA coronatine induced cysteine lyase invovel in ethylene synthesis CORONATINE INDUCED 1; F9D16.70; F9D16_70; JASMONIC ACID RESPONSIVE 2; JR2					CORI3	14.004	0.022	up	down
AT1G06310	no	down	JA fatty acid oxidation ACX6 acyl-CoA oxidase 6					ACX3.2	-11.35	0.015	down	
At5g07000	no	up	JA hydroxyjasmonate sulfotransferase ST2B	SOT14_1	57.389	0.0422	up	SOT14	54.208	0.031	up	
AT5G43590		up?	JA patatin/phospholipase A2					AT5G43590	49.954	0.034	up	down
At3g57140	no	down	JA patatin/phospholipase A2					SDP1L	-3.976	0.006	down	up
AT5G36670	no	down	JA signaling AT-hook TF with PHD and TPL-binding domain in jasmonate signalling	AT5G36670_2	-620.8	0.0009	down	AT5G36670	-690.9	2E-04	down	down
AT2G44050	no	up	JA signaling chloroplast stroma 6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase					COS1	2.8707	0.025	up	
AT1G73360	no	up	lateral root formation, stomata number, trichome brancing drough tolerance EDT1; ENHANCED DROUGHT TOLERANCE 1; homeodomain GLABROUS 11; HOMEODOMAIN GLABROUS 11	HDG11_1	20.982	0.0252	up	HDG11	19.82	0.009	up	
AT5G10965	no	up	lcRNA	AT5G10965_1	62.288	0.0446	up	AT5G10965	139.42	0.009	up	
AT5G13300	no	down	leaf cotyladeon vein patterning ARF GTPase-activating protein AGD3; ARF-GAP DOMAIN3; ASCULAR NETWORK DEFECTIVE 3; SCARFACE; VAN3					AGD3	-2.096	0.013	down	
AT4G40060	no	down	leaf development ABA circadian clock leucine zipper homeobox HB16 TF					ATHB-16	-4.545	0.02	down	
At3g57130	no	down	leaf development floral meristem BLADE ON PETIOLE 1 BOP1 Ankyrin repeat BTB/POZ domain TF					NPR6	-8.08	0.028	down	
AT3G60390	no	down	leaf development HAT3 homeobox-leucine zipper protein 3	HAT3_1	-9.789	0.0048	down	HAT3	-10.4	2E-04	down	
AT4G01260	no	down	leaf development KNAT1 regulated TF DUF573 domain coiled coil	AT4G01260_1	-16.91	0.0424	down	AT4G01260	-18.46	0.013	down	
AT3G23290	no	up	leaf development suppressor ALOG family LIGHT SENSITIVE HYPOCOTYLS 4, LSH4	LSH4_1	55.163	0.0431	up	LSH4	52.107	0.032	up	
AT1G30210	no	up	leaf development, ribosome biogenesis TCP24 TEOSINTE BRANCHED 1, cycloidea					TCP24	8.0345	0.037	up	down
AT4G14713		up?	leaf growth cell division cyclin D3 repressor TOPless interacting					TIFY4A	105.42	0.013	up	up
AT1G53170	no	up	leaf senescence ABA ERF8 AP2 TF	ERF8_1	58.164	0.0418	up	ERF8	55.304	0.03	up	down
AT5G02760	no	up	leaf senescence negative regulation protein phosphatase 2C 67	AT5G02760_1	7.2538	0.0207	up	AT5G02760	6.8593	0.002	up	
AT2G28400	no	down	leaf senescence regulation, ABA dark SA and pathogen induced Senescence_reg domain protein					AT2G28400	-2.07	0.05	down	down
AT1G29640	no	up	leaf senescence Senescence_reg domain protein					AT1G29640	7.1697	0.015	up	
AT5G66870	no	down	leaf symmmetry apical dominance KNOX repressor ASYMMETRIC LEAVES 2-like 1; LATERAL ORGAN BOUNDARIES DOMAIN GENE 36; LBD36	LBD36_1	-2.352	0.017	down	LBD36	-2.494	0.001	down	
AT2G36120	no	down	leaf vascular patterning DEFECTIVELY ORGANIZED TRIBUTARIES 1 glycine rich protein					DOT1	-4.32	0.018	down	
AT4G16250	no	down	light red/far red signaling phytochrome D	PHYD_1	-2.865	0.0448	down	PHYD	-3.073	0.009	down	
AT2G04560	no	up	lipid A lipopolysaccharie synthesis LpxB glycosyl transferase	LPXB_1	260.04	0.0059	up	LPXB	247.81	0.003	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT5G47720		down?	lipid and amino acid metabolism AACT1 acetoacetyl-CoA thiolase					AT5G47720	-2.312	0.007	down	
AT3G26430	no	down	lipid catabolism GDS(L) lipase	AT3G26430_1	-2.683	0.0011	down	AT3G26430	-2.854	1E-05	down	
AT1G18360	no	up	lipid degradation monoacylglycerol lipase 2 MAGL2					AT1G18360	7.6105	0.024	up	
AT5G08030	yes	down	lipid degradation GDPD6, GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE 6					AT5G08030	37.219	0.049	up	down
AT3G48460	no	up	lipid degradation glucose tolerance SFAR4 GDSL-type esterase	AT3G48460_1	60.715	0.0403	up	AT3G48460	57.574	0.029	up	
AT1G04290	no	up	lipid degradation long-chain acyl-CoA thioester hydrolase	AT1G04290_2	10.211	0.0254	up	AT1G04290	7.4786	0.011	up	
AT5G19290	no	down	lipid degradation monoacylglycerol lipase MAGL16					AT5G19290	-2.757	0.01	down	
AT5G48880	no	up	lipid degradation redox peroxisomal KAT5 peroxisomal 3-keto-acyl-CoA thiolase 2, PKT2					KAT5	13.23	0.025	up	
AT2G36325	no	up	lipid metabolism GDSL esterases and lipase with signal peptide					AT2G36325	45.606	0.04	up	
AT2G29590	no	down	lipid metabolism long-chain acyl-CoA thioester hydrolase					AT2G29590	-4.597	0.023	down	
AT3G50370		down?	lipid transport Apolipophorin-III	AT3G50370_1	-2.178	0.0003	down	AT3G50370	-2.404	3E-11	down	
AT1G06587	no	up	lncRNA					AT1G06587	5.518	0.042	up	
AT5G01732	no	up	lncRNA	AT5G01732_1	59.547	0.0468	up	AT5G01732	56.355	0.035	up	
AT2G07585	no	up	lncRNA	AT2G07585_1	70.553	0.0338	up	AT2G07585	67.216	0.024	up	
AT3G05445	no	down	lncRNA					AT3G05445	-9.358	0.02	down	
AT5G07385	no	down	lncRNA	AT5G07385_1	-102.6	0.0233	down	AT5G07385	-112	0.013	down	
AT2G06465	no	down	lncRNA	AT2G06465_1	-212.8	0.0092	down	AT2G06465	-232.3	0.005	down	
AT5G06665	no	down	lncRNA	AT5G06665_1	-190.1	0.0081	down	AT5G06665	-199.6	0.004	down	
AT2G33050	no	down	lncRNA	AtRLP26_1	-179.8	0.0114	down	AtRLP26	-188.7	0.006	down	
AT3G49580	yes	up	low sulfur stress pathogen ROS signaling LSU1 interactor/activator of chloroplastic superoxide dismutase FSD2					LSU1	2.9516	0.014	up	
AT4G17480	yes	down	lysosomal palmitoyl-protein thioesterase	AT4G17480_3	66.34	0.0378	up	AT4G17480	10.995	0.009	up	up
AT5G22830	no	down	magnesium (Mg) transporter 10 MGT10					MRS2-11	-5.096	0.048	down	up
AT2G04305	no	up	magnesium/Zn2+ CorA transporter homolog	AT2G04305_1	5.626	0.0438	up	AT2G04305	5.3937	0.007	up	
AT4G36950	no	up	MAPK signaling, unknown mitogen-activated protein kinase kinase kinase 21					MAPKKK21	6.6625	0.017	up	down
AT1G47290	no	up	membrane polysaccharide biosynthesis polysaccharide biosynthesis domain transmembrane protein, OE negative effect on auxin transport annotated as 3BETAHSD/D1 3beta-hydroxysteroid-dehydrogenase/decarboxylase	3BETAHSD/D1_1	10.746	0.0066	up	3BETAHSD/D1	3.1967	0.004	up	
AT3G49690	no	up	meristem axillary meristem formation MYB84; myb domain protein 84 RAX3; REGULATOR OF AXILLARY MERISTEMS3	RAX3_1	11.201	0.0406	up	RAX3	10.581	0.012	up	up
AT5G13290	yes	down	meristem CLA3 signaling WUS repression transmembrane protein kinase CORYNE; SOL2; SUPPRESSOR OF LLP1 2	CRN_1	-6.666	0.0492	down	CRN	-5.506	0.027	down	
AT1G63245	no	up	meristem CLAVATA signaling CLAVATA3/ESR-RELATED 14					CLE14	6.4194	0.048	up	down
AT1G05065	no	up	meristem Clavata3 homolog CLE120, CLAVATA3/ESR-related 20	CLE20_1	14.789	0.0265	up	CLE20	14.01	0.007	up	
AT2G39080	no	up	meristem Clavata3 homolog CLE44, CLAVATA3/ESR-related44	AT2G39080_1	3.5399	0.0373	up	AT2G39080	3.3575	0.003	up	
AT1G65380	no	down	meristem organ development CLV2 Leucine-rich repeat (LRR) receptor					CLV2	-4.237	0.032	down	
AT5G05160	no	down	meristem secondary cambium growth RUL1 REDUCED IN LATERAL GROWTH1 LRR kinase					AT5G05160	-2.681	0.007	down	
AT4G13195	no	up	meristem vascular axillary bud formation Clavata3 homolog CLE44 CLAVATA3/ESR-related 44					CLE44	3.3797	0.021	up	down
AT3G20550	no	down	microRNA biogenesis DCL1 parner forkhead domain DAWDLE					DDL	-2.235	0.032	down	
AT2G46040	yes	down?	microsporogenesis pollen development ARID1, AT-RICH INTERACTING DOMAIN 1 ARID and ELM2 domain TF activator	AT2G46040_1	-12.36	0.0258	down	AT2G46040	-5.75	0.002	down	up?
AT2G40070	yes	up	microtubule associated BASIC PROLINE-RICH PROTEIN 1, BPP1	AT2G40070_2	-4.655	0.0162	down	AT2G40070	-2.037	0.046	down	
AT4G13370	no	up	microtubule associated CORD3, CORTICAL MICROTUBULE DISORDERING3	AT4G13370_1	55.209	0.0438	up	AT4G13370	52.153	0.032	up	
AT1G70340	no	down	microtubule associated CORD5, CORTICAL MICROTUBULE DISORDERING5					AT1G70340	-2.325	0.025	down	
AT4G27595	no	up	microtubule associated spectrin SPEC domain coiled coil protein	AT4G27595_2	61.684	0.0393	up	AT4G27595	58.649	0.029	up	
AT5G16730	no	down	microtubule associated weak chloroplast movement under blue light protein (DUF827)	AT5G16730_1	-2.046	0.0001	down	AT5G16730	-2.162	6E-08	down	
AT1G03780	no	down	microtubule cell division chromosome segregation spindle assembly protein targeting protein for Xklp2 (TPX2) protein					TPX2	-2.579	0.018	down	down
AT2G44770	no	up	microtubule cell motility ELMO (EnguLfment and Cell MOtility) domain protein					AT2G44770	2.2972	0.047	up	
AT3G18530		up?	microtubule CLIP-associated protein (CLASP)					AT3G18530	60.659	0.027	up	
AT1G20060		up?	microtubule kinesin motor	AT1G20060_9	120.43	0.0176	up	AT1G20060	7.3772	0.02	up	down
At1g55550	no	down	microtubule Kinesin motor	KIN14T_1	-118.4	0.0197	down	KIN14T	-129.2	0.011	down	
At1g73860	yes	up?	microtubule kinesin motor					KIN14P	-6.186	0.031	down	up
At3g51150		up?	microtubule kinesin motor	KIN7G_1	18.728	0.0311	up	KIN7G	35.87	0.002	up	
AT5G42490	no	up	microtubule kinesin motor with DUF3490 domain					AT5G42490	8.6406	0.024	up	
AT5G55520	no	down	microtubule Kinesin-related domain protein	AT5G55520_1	-1105	0.0002	down	AT5G55520	-5.04	0.001	down	down
At1g75780	no	down	microtubule TUB1 tubulin beta-1 chain					TUBB1	-2.047	0.011	down	
At2g07170	no	down	microtubule unknown ARM/Heat-like repeat	TOR1L2_1	-6.549	0.0396	down	TOR1L2	-7.123	0.009	down	up
AT1G27920	no	up	microtubule-associated protein 65-8					MAP65-8	9.3368	0.019	up	
At2g37420		down	microtubules kinesin KIN5B motor					KIN5B	-2.209	0.038	down	up
AT1G12880	no	down	mitochindion NUDT13 long-chain diadenosinehexaphosphate hydrolase homolog					NUDT12	-6.608	0.037	down	
AT1G09575	no	down	mitochindrion MCU1, MITOCHONDRIAL CALCIUM UPTAKE1 channel					AT1G09575	-2.751	0.043	down	
ATMG00440	no	down	mitochindrion ORF152A	ORF152A_1	-217.2	0.0089	down	ORF152A	-227.9	0.004	down	
AT2G40800	no	up	mitochondrion import inner membrane translocase subunit transmembrane coiled coil protein	AT2G40800_2	15.19	0.0026	up	AT2G40800	3.5964	0.029	up	
ATMG00530	no	down	mitochondrion ORF109	ORF109_1	-142.4	0.0161	down	ORF109	-149.4	0.009	down	
At1g64310	no	down	mitochondrion Pentatricopeptide repeat protein ORGANELLE TRANSCRIPT PROCESSING 71, OTP71	PCMP-E65_1	-11.35	0.049	down	PCMP-E65	-12.4	0.012	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
ATMG00990	no	up	mitochondrion ? NADH dehydrogenase subunit 3	NAD3_1	2.1521	0.0048	up	NAD3	2.0411	0.002	up	
AT5G67590	no	up	mitochondrion 18-kD Fe-S subunit of(NADH dehydrogenase complex I					FRO1_2	2.5621	9E-04	up	
AT3G22300	no	down	mitochondrion 40S ribosomal protein S10					RPS10_2	-4.147	0.001	down	
ATMG00210	no	up	mitochondrion 60S ribosomal protein L5					RPL5_2	2600.2	7E-06	up	
AT1G09794	no	up	mitochondrion 63aa oligopeptide Mature-T-Cell Proliferation I type	AT1G09794_1	8.5945	0.0487	up	AT1G09794	8.1186	0.016	up	
AT2G44880		up?	mitochondrion ABA HYPERSENSITIVE GERMINATION 11, AHG11 nad4 RNA editing Pentatricopeptide repeat (PPR-like) protein					AT2G44880	25.479	0.006	up	
AT4G28620	no	up	mitochondrion ABC TRANSPORTER OF THE MITOCHONDRION 2, ABCB24					ABCB24	45.858	0.041	up	
AT5G64210	no	down	mitochondrion AOX2 alternative oxidase 2 induced during germination					AOX2	-46.92	0.036	down	
AT2G34050	no	up	mitochondrion ATP synthase F1 complex assembly factor	AT2G34050_1	170.39	0.0106	up	AT2G34050	160.96	0.007	up	
AT2G19680	no	up	mitochondrion ATP synthase subunit G	AT2G19680_1	3.5441	0.0107	up	AT2G19680	2.1108	0.007	up	
AT2G07741	no	down	mitochondrion ATPase, F0 complex, subunit A protein	AT2G07741_1	-1585	8E-05	down	AT2G07741	-1728	3E-05	down	
AT4G17420	yes	down	mitochondrion biogenesis AIM24 domain protein					AT4G17420	4.4896	0.027	up	up
AT5G47420	no	up	mitochondrion biogenesis factor AIM24 domain protein					AT5G47420	3.6331	0.01	up	
AT1G55510	no	up	mitochondrion branched chain amino acid degradation SnRK1/starvation induced branched-chain alpha-keto acid decarboxylase E1 beta subunit					BCDH BETA1	2.6647	0.039	up	
AT5G09420	no	down	mitochondrion chloroplast translocon subunit OM64/TOC64					OM64	-2.268	0.012	down	
AT5G08300	no	down	mitochondrion citric acid cycle Succinyl-CoA ligase, alpha subunit					AT5G08300	-2.053	0.01	down	
AT2G15680	no	up	mitochondrion CML30 calmodulin-like 30	CML30_1	22.067	0.0116	up	CML30	20.907	0.003	up	down
AT2G20390	no	up	mitochondrion Coa1 cytochrome oxidase complex IV assembly factor	AT2G20390_2	7.2482	0.0276	up	AT2G20390	5.588	0.01	up	
AT3G13110	no	down	mitochondrion cysteine synthesis sulfur metabolism SERAT2;2 serine acetyltransferase 2;2					SAT3	-2.182	0.019	down	
AT3G22360	no	up	mitochondrion flower specific AOX1B alternative oxidase 1B	AOX1B_1	118.46	0.018	up	AOX1B	111.9	0.012	up	
AT3G07690	no	down	mitochondrion glycolysis transmembrane NAD-dependent glycerol-3-phosphate dehydrogenase (EC 1.1.1.8)					AT3G07690	-2.58	0.036	down	
AT1G53530		up?	mitochondrion Imp protease homolog					AT1G53530	5.4217	0.025	up	
AT1G59510	no	up	mitochondrion inner membrane Histidine kinase-like ATPase CF9					CF9	7.6131	0.039	up	
AT2G30160	no	up	mitochondrion inner membrane substrate carrier					AT2G30160	5.6916	0.045	up	
AT4G28630	no	down	mitochondrion iron homeostasis ATM1; ATP-binding cassette B23; HALF-MOLECULE ABC TRANSPORTER					ABCB23	-6.362	0.015	down	
AT1G80230	no	up	mitochondrion isoform of cytochrome c oxidase subunit 5b					COX5B-2	2.1671	0.014	up	
AT5G11690	no	up	mitochondrion iTRANSLOCASE INNER MEMBRANE SUBUNIT 17-3					TIM17-3	6.0191	0.015	up	
AT5G03770		down?	mitochondrion KDO (3-deoxy-D-manno-octulosonate) transferase	KDTA_1	84.503	0.0272	up	KDTA	12.842	0.003	up	
AT2G31140	no	down	mitochondrion LexA/Signal peptidase					AT2G31140	-2.804	0.017	down	
AT4G32605	no	up	mitochondrion matrix protein family contains members of the MAM33 family which bind to the globular 'heads' of C1Q					AT4G32605	2.7906	0.029	up	
AT5G05990	no	up	mitochondrion matrix protein member of the MAM33 family which bind to the globular 'heads' of C1Q					AT5G05990	4.8646	0.034	up	
AT5G19020	no	down	mitochondrion MEF18 mitochondrial editing factor 18					PCMP-E42_2	-2.49	0.034	down	
At3g18970	no	up	mitochondrion MEF20 mitochondrial pentatricopeptide repeat editing factor 20	PCMP-E93_1	18.129	0.0327	up	PCMP-E93	17.184	0.012	up	
At3g12770	no	down	mitochondrion MEF22 RNA editing factor 22	PCMP-H43_1	-13.91	0.0221	down	PCMP-H43	-14.98	0.004	down	
AT4G30700	no	up	mitochondrion MEF29, MITOCHONDRIAL RNA EDITING FACTOR 29	DYW9_1	29.612	0.0139	up	DYW9	28.097	0.004	up	up
AT4G28580	no	up	mitochondrion Mg2+ transporter pollen development MGT5 magnesium transport 5					MRS2-6	37.146	0.048	up	
AT5G09840	no	down	mitochondrion MITOCHONDRIAL NUCLEASE2, MNU2 RNA processing dsRNA binding OST-HTH domain protein with tRNA/rRNA processing NYN domain	AT5G09840_1	-7.533	0.0015	down	AT5G09840	-8.169	9E-05	down	
AT1G61990	no	up	mitochondrion MTERF transcription termination factor	AT1G61990_1	118.53	0.0212	up	AT1G61990	7.0149	0.024	up	
AT1G02160	no	down	mitochondrion nuclearly encoded Cox19 homolog	AT1G02160_1	-4.996	0.0126	down	AT1G02160	-3.861	0.001	down	
AT2G42210	yes	down	mitochondrion OEP16-3 Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein					ATOEP16-3	2.0811	0.01	up	up
AT5G26780		down?	mitochondrion one carbon pathway serine to glycine conversion, SHM2 serine hydroxymethyltransferase 2					SHM2	-2.204	0.014	down	down
ATMG00600	no	up	mitochondrion ORF106C					ORF106C	5.6868	0.029	up	
ATMG01040	no	up	mitochondrion ORF107F					ORF107F	10.458	0.035	up	
ATMG01060	no	up	mitochondrion ORF107G					ORF107G	9.6963	0.04	up	
AT5G40153	no	down	mitochondrion ORF109	AT5G40153_1	-130.1	0.0141	down	AT5G40153	-140.7	0.007	down	
ATMG01140	no	down	mitochondrion ORF152B	ORF152B_1	-191.3	0.0105	down	ORF152B	-200.7	0.006	down	
ATMG01110	no	down	mitochondrion ORF251 Mitovirus RNA-dependent RNA polymerase					ORF251	-6.956	0.014	down	
AT1G31010	no	up	mitochondrion OSB4 organellar single-stranded DNA binding protein 4	OSB4_1	11.541	0.0136	up	OSB4	11.106	0.002	up	
AT3G09040		up?	mitochondrion Pentatricopeptide repeat (PPR) MEF12, MITOCHONDRIAL RNA EDITING FACTOR 12	AT3G09040_3	159.27	0.0149	up	AT3G09040	20.617	0.001	up	
At5g14580	no	up	mitochondrion polyribonucleotide nucleotidyltransferase					PNP2	5.1141	0.019	up	
AT2G31290	no	down	mitochondrion PORR domain RNA processing protein					AT2G31290	-3.706	0.027	down	
AT3G16890	yes	down	mitochondrion PPR40 pentatricopeptide repeat (PPR) affecting complex III	PPR40_2	18.018	0.0338	up	PPR40	17.07	0.013	up	
AT1G12300	no	up	mitochondrion RNA editing RESTORER-OF-FERTILITY-LIKE 2, RFL2 pentatricopeptide repeat protein					AT1G12300	5.7597	0.045	up	up
At2g22410	no	up	mitochondrion RNA editing SLO1, SLOW GROWTH 1 Pentatricopeptide repeat protein					PCMP-E28	6.9911	0.042	up	
AT1G62720	no	up	mitochondrion RNA processing pathogen seed germonation NOVEL GENE 1, PENTATRICOPEPTIDE REPEAT PROTEIN 2, PPR2					AT1G62720	8.6568	0.021	up	
AT5G60870	yes	up?	mitochondrion RUG3 REGULATOR OF CHROMOSOME CONDENSATION 1 (RCC1) domain repeat protein	AT5G60870_4	24.771	0.0045	up	AT5G60870	5.5956	0.019	up	
AT1G30370	no	up	mitochondrion seed viability mitochondrial acylhydrolase AtDLAH	AT1G30370_1	61.964	0.0386	up	AT1G30370	58.531	0.028	up	
AT3G18580	no	up	mitochondrion single-stranded DNA binding					AT3G18580	9.444	0.018	up	
AT3G61360	no	down	mitochondrion SLO3, SLOW GROWTH3 pentatricopeptide repeat protein					AT3G61360	-3.233	0.011	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G78180	no	up	mitochondrion substrate carrier protein					AT1G78180	6.542	0.045	up	
AT1G14688	no	up	mitochondrion SUMO E3 ligase activator of NFKB 1 (MULAN, also known as GIDE)					AT1G14688	36.797	0.05	up	
AT2G17130	yes	down	mitochondrion TCA cycle ISOCITRATE DEHYDROGENASE SUBUNIT 2	IDH2_1	512.07	0.0016	up	IDH2	2.0482	0.035	up	
AT2G43180	yes	down?	mitochondrion TCA cycle Isocitrate lyase	AT2G43180_1	169.76	0.0107	up	AT2G43180	6.1468	0.041	up	
AT3G47833	no	up	mitochondrion TCA cycle SDH7 succinate dehydrogenase subunit					SDH7A	3.5674	0.042	up	
AT2G35010	no	up	mitochondrion TO1 thioredoxin O1 salt sed germination					ATO1	2.297	0.045	up	
AT1G62120	no	up	mitochondrion transcription termination factor MTERF	AT1G62120_1	64.162	0.0373	up	AT1G62120	60.606	0.027	up	
AT1G62490	no	up	mitochondrion transcription termination factor MTERF	AT1G62490_1	66.45	0.0357	up	AT1G62490	62.769	0.026	up	
AT1G21150		up?	mitochondrion transcription terminator factor MTERF					AT1G21150	25.957	0.005	up	
AT5G67290	no	down	mitochondrion tRNA GidA methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase enzyme TrmFO	AT5G67290_1	-2.945	0.0257	down	AT5G67290	-3.162	0.002	down	
AT4G02930	no	down	mitochondrion TUF1/M Tu translation elongation factor					TUFA_1	-2.011	5E-06	down	
AT4G23885	no	down	mitochondrion unknown 77aa oligopeptide					AT4G23885	-2.192	0.04	down	
AT2G04940	no	up	mitochondrion yeast Slm35 homolog implicated in mitochondrial TOR signaling					AT2G04940	7.0811	0.032	up	
AT1G22800	no	up	mitochondrion, homolog of NDUFAF5 NADH dehydrogenase (ubiquinone) complex I, assembly factor 5	AT1G22800_1	331.53	0.0051	up	AT1G22800	316.3	0.003	up	up
At4g14170		up	mitochondrion, RNA editing MITOCHONDRIAL EDITING FACTOR 32	PCMP-E17_2	17.565	0.0199	up	PCMP-E17	21.189	0.002	up	down
AT1G47580	no	up	mitochondrionndhD-1 RNA editing DYW1 Pentatricopeptide repeat (PPR) factor	DYW1_1	19.24	0.0283	up	DYW1	18.174	0.01	up	
AT3G20650		up	mRNA capping enzyme ABD1 mRNA (guanine-N7)-methyltransferase homolog	AT3G20650_2	59.593	0.0417	up	AT3G20650	3.0515	0.025	up	
AT2G01730	yes	down	mRNA cleavage and polyadenylation specificity factor 73 kDa subunit-II	CPSF73-II_1	182.48	0.0097	up	CPSF73-II	5.927	0.041	up	
AT2G38680	no	up	mRNA decapping 7-methyl GMP-specific nucleotidase	AT2G38680_1	9.2107	0.0318	up	AT2G38680	8.7501	0.006	up	
AT3G07750	no	up	mRNA degradation exosome component 7 RRP42-like 3'-5' exonuclease					AT3G07750	3.6089	0.014	up	
AT5G13570	no	up	mRNA degradation transgene silencing ATDCP2; decapping 2; INCREASED TRANSGENE SILENCING 1; ITS1; T6I14.5; TDT; TRIDENT	TDT_1	6.5349	0.0383	up	TDT	6.2046	0.006	up	
AT2G19560	yes	down?	mRNA export TREX2 complex subunit, ethylene signaling EIN2 interacting negative regulator EER5 AtTHP1; ectopic expression of seed storage proteins 1; ENHANCED ETHYLENE RESPONSE 5; ESSP1;					EER5	3.2664	0.034	up	
AT2G29190	no	down	mRNA translation 3'-UTR binding PUM2 ARM repeat protein					APUM2	-2.985	3E-04	down	
AT5G09610	no	down	mRNA translation 3'-UTR binding PUM21 ARM repeat protein					APUM21	-3.33	0.043	down	
AT4G02940	no	down	mRNA stability flwoering time ALKBH10B RNA N6-methyladenosine demethylase	AT4G02940_1	-2.173	0.002	down	AT4G02940	-2.303	2E-05	down	
AT3G05932		up	nat-siRNA for the germin-like protein 8 gene	AT3G05932_3	333.79	0.0037	up	AT3G05932	3.9804	0.031	up	up
AT3G52072		up	ncRNA	AT3G52072_6	73.427	0.0375	up	AT3G52072	17.614	0.004	up	up
AT2G45245	no	up	ncRNA					AT2G45245	6.9898	0.043	up	down
AT2G32795		up	ncRNA	AT2G32795_1	61.364	0.0403	up	AT2G32795	58.069	0.029	up	down
AT3G05905	no	up	ncRNA	AT3G05905_2	129.09	0.0163	up	AT3G05905	9.2242	0.015	up	
AT5G20225	no	up	ncRNA					AT5G20225	6.6423	0.041	up	
AT2G35637	no	up	ncRNA					AT2G35637	8.4807	0.021	up	
AT5G38212	no	up	ncRNA	AT5G38212_1	10.951	0.02	up	AT5G38212	2.8248	0.035	up	
AT1G78990	no	up	ncRNA	AT1G78990_1	17.625	0.035	up	AT1G78990	16.835	0.013	up	
AT5G01935	no	up	ncRNA	AT5G01935_1	26.188	0.0174	up	AT5G01935	24.812	0.005	up	
AT2G05995	no	up	ncRNA	AT2G05995_1	52.86	0.0457	up	AT2G05995	49.929	0.034	up	
AT3G58795	no	up	ncRNA	AT3G58795_1	64.51	0.0376	up	AT3G58795	61.297	0.027	up	
AT1G26218	no	up	ncRNA	AT1G26218_1	62.479	0.0385	up	AT1G26218	59.191	0.028	up	
AT1G20691	no	up	ncRNA	AT1G20691_1	56.539	0.0494	up	AT1G20691	53.256	0.037	up	
AT3G46658	no	up	ncRNA	AT3G46658_1	152.45	0.0125	up	AT3G46658	144.38	0.008	up	
AT5G00875		up	ncRNA	AT5G00875_2	133.01	0.0152	up	AT5G00875	140.18	0.009	up	
AT4G37553	no	up	ncRNA	AT4G37553_3	84.655	0.027	up	AT4G37553	110.8	0.012	up	
AT1G48698		up	ncRNA	AT1G48698_2	58.564	0.0481	up	AT1G48698	107.47	0.013	up	
AT3G52748	no	up	ncRNA					AT3G52748	43.542	0.04	up	
AT1G07943	no	up	ncRNA					AT1G07943	43.558	0.04	up	
AT2G37555	no	up	ncRNA					AT2G37555	51.864	0.038	up	
AT3G54625	no	down	ncRNA	AT3G54625_2	-198	0.0074	down	AT3G54625	-12.38	0.012	down	up
AT1G17232	no	down	ncRNA	AT1G17232_1	-191.7	0.0081	down	AT1G17232	-207.4	0.004	down	up
AT4G06780	no	down	ncRNA					AT4G06780	-15.25	0.032	down	
AT1G58808	no	down	ncRNA					AT1G58808	-7.461	0.027	down	
AT3G03702	no	down	ncRNA					AT3G03702	-5.156	0.048	down	
AT5G23155		down	ncRNA					AT5G23155	-4.434	0.038	down	
AT5G01215	no	down	ncRNA					AT5G01215	-2.881	0.034	down	
AT5G00780	no	down	ncRNA	AT5G00780_3	-27.88	0.0175	down	AT5G00780	-12.47	0.013	down	
AT1G80325	no	down	ncRNA	AT1G80325_1	-4.04	0.0314	down	AT1G80325	-2.826	0.008	down	
AT1G08547	no	down	ncRNA	AT1G08547_1	-56.82	0.045	down	AT1G08547	-59.22	0.027	down	
AT5G59732	no	down	ncRNA	AT5G59732_1	-1317	0.0002	down	AT5G59732	-1381	8E-05	down	
AT5G45475	no	down	ncRNA	AT5G45475_1	-81.77	0.0005	down	AT5G45475	-89.49	4E-05	down	
AT4G36032	no	down	ncRNA	AT4G36032_1	-21.03	0.0109	down	AT4G36032	-22.76	9E-04	down	
AT3G52605	no	down	ncRNA	AT3G52605_1	-9.892	0.013	down	AT3G52605	-10.56	0.001	down	
AT3G54290	no	down	ncRNA	AT3G54290_1	-5.964	0.0105	down	AT3G54290	-6.423	4E-04	down	
AT2G06795	no	up	ncRNA of ABORTED MICROSPORES basic helix-loop-helix (bHLH) TF					AT2G06795	43.545	0.041	up	
AT1G16489	no	up	ncRNA of MYB58 activator of lignin synthesis					AT1G16489	20.446	0.004	up	
AT5G03585	no	up	ncRNA of NIC2 nicotinamidase 2					AT5G03585	5.2632	0.046	up	
AT4G25719	no	down	ncRNA of QC glutaminyl cyclase					AT4G25719	-9.479	0.011	down	
AT2G46572	no	up	ncRNA, cell wall laccase 6 down	AT2G46572_3	20.986	0.025	up	AT2G46572	27.942	0.004	up	up
AT4G37895	no	down	ncRNA, nat-siRNA of EMBRYO SAC DEVELOPMENT ARREST 40	AT4G37895_1	-17.23	0.0328	down	AT4G37895	-17.86	0.009	down	
AT5G02895	no	down	ncRNA, nat-siRNA of Curculin-like (mannose-binding) lectin	AT5G02895_1	-17	0.03	down	AT5G02895	-17.94	0.006	down	
AT1G12110	no	up	nitrate signaling root stomatal closure CHL1-1; CHLORATE/NITRATE TRANSPORTER; CHLORINA 1	NPF6.3_1	5.015	0.0362	up	NPF6.3	4.6689	0.008	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT5G60780	no	up	nitrate transprot high affinity NRT2.3 nitrate transporter 2.3	NRT2.3_1	30.778	0.0124	up	NRT2.3	29.076	0.004	up	
AT1G09480	yes	down?	nitrogen repression NmrA is a negative transcriptional regulator domain protein	AT1G09480_1	-9.743	0.0233	down	AT1G09480	-8.999	0.002	down	
AT1G55180	yes	up	nitrogen signaling PLDEPSILON phospholipase D alpha 4					PLDALPHA4	-2.903	0.046	down	up
At1g72140	no	down	nitrogen transport root Tonoplast localized pH dependent low affinity nitrogen transporter NPF5.12.	NPF5.12_1	-39.29	0.0014	down	NPF5.12	-41.81	8E-05	down	
AT1G54385		up	nuclear envelop SUN1/2 interacting actin colocalized SINE1 ARM repeat membrane protein	AT1G54385_1	9.3671	0.0485	up	AT1G54385	9.8325	0.008	up	up
AT3G59020	no	down	nuclear export exportin Cse1 (importin-alpha re-exporter)					AT3G59020	-2.098	3E-04	down	
AT3G54380	yes	down?	nuclear export SAC3_GANP domain protein					SAC3C	-2.141	0.036	down	
AT1G68910		down?	nuclear export/import RAN_GAP anchor protein					WIT2	-2.327	0.006	down	up
AT4G09310	no	up	nuclear import chromosome segregation Ran GTPase binding protein with microtubule binding LisH and SPRY SPla and the RYanodine Receptor domains					AT4G09310	3.2925	0.047	up	
AT4G09200	no	up	nuclear import CRA domain Ran-bidning protein with SPla and the RYanodine Receptor, LisH and CTLH domains					AT4G09200	3.8003	0.024	up	
At5g03070	no	down	nuclear import IMPA-9 importin alpha					IMPA9	-4.887	0.018	down	
AT1G69680	no	up	nuclear import MOG1 RAN GTPase GAP					AT1G69680	2.0178	0.043	up	
AT5G26190	no	up	nuclear import PHD finger repeat Ran-binding protein	AT5G26190_1	68.762	0.0351	up	AT5G26190	64.954	0.025	up	
AT5G03360	no	up	nuclear pore associated Protein kinase C conserved region 1 (C1) domain repeat protein	AT5G03360_1	18.085	0.0347	up	AT5G03360	17.083	0.013	up	
AT5G18750	no	down	nuclear pore protein folding DNAJ and DUF3444 domain protein					AT5G18750	-3.172	0.045	down	
AT2G05120	yes	down	nuclear pore subunit nucleoporin NUP133/150 homolog	AT2G05120_2	12.817	0.013	up	AT2G05120	5.7747	0.004	up	down
AT2G15240	no	up	nuclear transport NUC-50 nuclear inner transmembrane protein					AT2G15240	3.4408	0.012	up	
AT4G34570	yes	up?	nucleotide DNA synthesis thymidylate synthase 2	THY-2_2	129.32	0.0245	up	THY-2	3.5697	0.037	up	
AT3G11020	no	down	osmotic salt stress signaling RCD1 interacting DREB2B TF					DREB2B	-3.309	0.004	down	
AT2G21620		down?	osmotic stress induced universal stress protein UspA	RD2_2	-2.151	0.0114	down	RD2	-2.317	2E-04	down	
AT2G38750		up?	osmotic stress regulating MYB30 controlled Ca2+-dependent Golgi annexin4					ANN4	8.3965	0.023	up	
At4g11230	no	down	osmotic stress ROS root specific NADPH-oxidase RbohI					RBOHI	-5.754	0.024	down	
At1g51170	no	down	ovule integumentum development UNC UNICORN AGC2 kinase 3; AGC2-3;					UNC	-3.271	0.014	down	
AT1G11130	yes	down	ovule stem cell floralorgan development transmembrane STRUBBELIG LRR receptor kinase SCM, SCRAMBLED, SRF9, STRUBBELIG, STRUBBELIG-RECEPTOR FAMILY 9					SUB	-2.531	0.02	down	
AT5G17170	yes	down	oxidative salt stress enhancer of sos1 chloroplast rubredoxin with N-term PDZ domain	ENH1_2	-20.56	0.0489	down	ENH1	-21.5	0.022	down	
AT2G33550	no	down	pathogen ASR3 (ARABIDOPSIS SH4-RELATED3) transcription repressor of a set of flg22-induced genes MPK4 substrate					ASR3	-2.18	0.035	down	
AT1G21880	yes	up?	pathogen bacterial peptidoglycan sensing	LYM1_2	-796.5	0.0005	down	LYM1	-2.644	0.014	down	down?
At5g03140	no	down	pathogen L-type lectin receptor kinase VIII.2; LecRK-VIII.2					LECRK82	-5.043	0.037	down	
AT2G38540	no	up	pathogen AAI domain epidermal cell specific PR14 Ca2+/CAM binding LP1 lipid transfer protein 1	LTP1_1	21.902	0.0136	up	LTP1	20.689	0.003	up	
AT1G53920	no	up	pathogen Altenaria transmembrane GDSL-MOTIF LIPASE 5, GLIP5					GLIP5	10.316	0.037	up	
AT1G49050	yes	up	pathogen aspartate protease of BAG6, transmembrane xylanase inhibitor	APCB1_3	-8.989	0.021	down	APCB1	-2.078	0.005	down	
AT5G67385	yes	down	pathogen AtSR1/CAMTA3 interacting E3 ligase BTB subunit positive regulator of defense; NCH1, NRL PROTEIN FOR CHLOROPLAST MOVEMENT1	AT5G67385_2	123.47	0.0171	up	AT5G67385	123.8	0.01	up	down
AT5G18370	no	up	pathogen autoimmunity DSC2 TIR-NBS-LRR disease resistance protein	AT5G18370_1	5.7562	0.0374	up	AT5G18370	5.3863	0.007	up	
At1g26380	no	down	pathogen auxin 4-hydroxy indole-3-carbonyl nitrile (4-OH-ICN) phytoallexin systhesis FOX1					FOX1	-3.058	0.047	down	
AT1G59218	no	down	pathogen CC-NBS-LRR protein RDL6	RDL6_2_2	-523.4	0.0021	down	RDL6_2	-4.228	0.024	dow n	
At5g45180	no	up	pathogen cell death FMO1 homolog flavin-dependent monooxygenase					FMO2	10.116	0.018	up	
At5g07680	no	down	pathogen cell death miR164 traget NAC4, NAC79/NAC80 TF					NAC079	-3.383	0.008	down	
AT4G28250		down?	pathogen cell expanion nematode-induced syncytia formation root EXPB3 expansin B3					EXPB3	-2.104	0.028	down	
AT1G21240		up?	pathogen cell wall associated WAK3 kinase					WAK3	12.585	0.024	up	down
AT1G78830	no	down	pathogen cell wall Curculin-like mannose-binding lectin	AT1G78830_1	-2.023	5E-06	down	AT1G78830	-2.143	2E-09	down	
AT1G21250	no	up	pathogen cell wall GRP3 interacting oligogalacturonide receptor kinase WAK1					WAK1	8.1342	0.03	up	
AT4G19810	no	up	pathogen ChiC Class V exochitinase	AT4G19810_2	70.933	0.0335	up	AT4G19810	67.002	0.023	up	
AT3G09590	no	down	pathogen cysteine-rich secretory proteins, antigen 5, and pathogenesis-related 1 protein with signal peptide					AT3G09590	-41.07	0.042	down	
At3g57030	no	up	pathogen defense alkaloid strictosidine synthase	SSL10_1	5.8163	0.0278	up	SSL10	5.4961	0.002	up	
AT3G15810	no	up	pathogen defense LURP-one-related protein					AT3G15810	4.5332	0.023	up	
AT2G45220	no	down	pathogen defense pectin methylesterase 17	PME17_1	-2.423	0.0029	down	PME17	-2.583	1E-04	down	
AT4G33925	yes	up	pathogen DNA repair SSN2 (suppressor of sni1 2), a suppressor of SNI1 (AT4G18470)/**unknown protein**	AT4G33925_2	50.357	0.0489	up	AT4G33925	47.784	0.037	up	down
At5g64890	no	up	pathogen elicitor peptide PROPEP2	PEP2_1	61.986	0.039	up	PEP2	58.554	0.028	up	down
AT1G12460	yes	up	pathogen elicitor-induced PM LRR receptor kinase	AT1G12460_1	-14.82	0.0027	down	AT1G12460	-10.44	0.002	down	down?
AT5G40990	no	down	pathogen ethylene/SA induced antimicrobial GLIP1 GDSL lipase 1	GLIP1_1	-15.87	0.0105	down	GLIP1	-17.1	0.001	down	
AT3G02910	no	down	pathogen Gamma-glutamyl cyclotransferase, AIG2-like avirulence protein					AT3G02910	-2.07	0.049	down	
AT2G43910	no	up	pathogen glucosinolate/thiocyanate metabolism HARMLESS TO OZONE LAYER 1 methylase					ATHOL1	14.2	0.019	up	
AT3G15395	no	up	pathogen HrpN-hairpin interacting transmembrane 59aa oligopeptide					AT3G15395	10.167	0.007	up	down
AT2G21110	no	up	pathogen induced Dirigent domain protein with signal peptide					DIR4	7.5966	0.039	up	
AT1G18250	no	down	pathogen induced PR5 Thaumatin with signal peptide	ATLP-1_1	-1055	0.0002	down	ATLP-1	-3.194	0.031	down	up
AT3G55970		up?	pathogen JA inactivation JASMONATE-INDUCED OXYGENASE3	JRG21_1	17.195	0.0156	up	JRG21	17.435	0.002	up	down
AT5G18860	no	down	pathogen JA induced apopalstic purine/ATP nucleoside hydrolase					AT5G18860	-3.739	0.019	down	
AT3G15210	no	up	pathogen JA response negative regulator ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4; RAP2.5; RELATED TO AP2 5 TF					ERF4	2.7274	0.017	up	
At3g15356	no	down	pathogen JA,ethylene, chtin upregulated lectin-like protein					LEC	-2.196	0.004	down	

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At2g18370	no	up	pathogen lipid transfer protein (PR-14)	LTP8_1	77.734	0.0295	up	LTP8	73.427	0.021	up	
AT1G77630	no	down	pathogen LYM3 lysin-motif protein mediating bacterial peptidoglycan sensing and immunity to bacterial infection	LYM3_1	-7.461	0.0375	down	LYM3	-8.097	0.007	down	
AT2G17120	no	down	pathogen LysM domain secreted bacterial cell wall degrading LYM2 protein					LYM2	-2.334	0.029	down	
AT2G39200	no	down	pathogen MLO12 Seven transmembrane MLO	MLO12_1	-3.654	0.0092	down	MLO12	-3.902	3E-04	down	
AT1G10170	yes	down	pathogen negative regulator of defence response homologue of the putative human transcription repressor NF-X1	ATNFXL1_4	-9361	2E-07	down	ATNFXL1	-2.276	5E-06	down	up
AT1G14960	no	down	pathogen Pathogenesis-related protein Bet v I PR-10 domain protein					AT1G14960	-12.64	0.028	down	down
AT5G06870	no	down	pathogen PGIP2 polygalacturonase inhibiting protein 2	PGIP2_1	-2.032	0.0142	down	PGIP2	-2.146	4E-04	down	
AT2G18660	no	up	pathogen PLANT NATRIURETIC PEPTIDE A, PNP-A	EGC2_1	55.014	0.0036	up	EGC2	52.126	6E-04	up	down
AT2G46440	yes	down	pathogen positive regulator of fungal resistance CNGC11 cyclic nucleotide-gated channel	CNGC11_2	84.512	0.027	up	CNGC11	79.831	0.019	up	
AT5G43580	no	down	pathogen PR6 UPI UNUSUAL SERINE PROTEASE INHIBITOR					AT5G43580	-2.099	0.006	down	
AT1G61750	no	up	pathogen Proline-rich membrane anchor 1 Stress-antifung domain cys-rich protein with signal peptide					CRRSP1	45.737	0.038	up	
AT5G43470	no	down	pathogen RCY1; RECOGNITION OF PERONOSPORA PARASITICA 8; RESISTANT TO CMV(Y) 1	RPP8_4	-16.9	0.0093	down	RPP8	-10.9	0.005	down	
AT1G10210	no	up	pathogen regative regulation of MPK6-activated defense response					MPK1	6.3244	0.029	up	up
At1g44830	no	down	pathogen regulator of pctin deposition DREB family of AP2/ERF104					ERF014	-12.02	0.015	down	
AT1G20160	yes	down	pathogen response attenuation MYB30 endosomal tethering CO2 RESPONSE SECRETED PROTEASE, CRSP,SBT5.2(B)	CRSP_2	-28.28	0.0219	down	CRSP	-30.4	0.006	down	
AT3G07040	no	up	pathogen RPM1 NB-ARC domain-containing disease resistance, RESISTANCE TO PSEUDOMONAS SYRINGAE 3; RPS3	RPS3_1	3.0125	0.0059	up	RPS3	2.8502	2E-04	up	
AT2G04410	no	down	pathogen RPM1-interacting protein 4 (RIN4) homolog with AvrRpt-cleavage domain	AT2G04410_1	-3.146	0.0279	down	AT2G04410	-3.382	0.003	down	
AT1G12210	yes	up	pathogen RPS5-like RFL1 NB-ARC LRR receptor	RFL1_1	-845.8	0.0008	down	RFL1	-2.583	0.024	down	down
AT4G01250	no	down	pathogen SA JA senescence WRKY22 TF					WRKY22	-3.106	0.006	down	
AT4G12470	no	down	pathogen SAR AZI1 (AZELAIC ACID INDUCED 1) proline-rich protein	AZI1_1	-2.088	5E-05	down	AZI1	-2.206	3E-08	down	
AT1G68600	no	up	pathogen SAR/SA p-hydroxybenzoic acid efflux pump subunit AaeB (pHBA efflux pump protein B) whose substrates are p-hydroxybenzoic acid (pHBA), 6-hydroxy-2-naphthoic and 2-hydroxycinnamate.	ALMT5_1	59.693	0.04	up	ALMT5	56.386	0.029	up	
AT1G63580	no	down	pathogen secreted Stress-antifung domain protein	CRRSP6_1	-94.69	0.0254	down	CRRSP6	-98.6	0.015	down	
AT5G18520	no	down	pathogen seven transmembrane receptor trimeric G-couped candidate	AT5G18520_1	-2.101	0.0174	down	AT5G18520	-2.221	3E-04	down	
AT1G17600	no	up	pathogen SOC3 TIR-NB-leucine-rich repeat (TNL) protein					AT1G17600	9.5563	0.013	up	
AT1G10300	no	up	pathogen stomatal defense response Nucleolar GTP-binding protein 1 (NOG1)	AT1G10300_3	303.01	0.0042	up	AT1G10300	42.26	2E-04	up	up
AT1G12280	no	up	pathogen suppressor of mkk1 mkk2 2 SUMM2 LRR and NB-ARC domains-containing disease resistance protein	AT1G12280_2	192.89	0.0093	up	AT1G12280	21.317	0.001	up	
AT4G16890		up	pathogen SUPPRESSOR OF NPR1-1					SNC1	-2.418	0.019	down	up?
At5g45070	no	up	pathogen TIR domain containing PP2-A8 phloem protein 2-A8	PP2A8_1	84.472	0.0272	up	PP2A8	79.792	0.019	up	
AT5G45770	no	up	pathogen transmembrane LRR receptor RLP55 with signal peptide	RLP55_1	19.804	0.0275	up	RLP55	18.707	0.01	up	
AT1G01310	no	up	pathogen transmembrane SCP / Tpx-1 / Ag5 / PR-1 / Sc7 family of extracellular domain protein					AT1G01310	12.194	0.026	up	up
AT3G46510	no	down	pathogen ubiquitin ligase of FLS2 receptor	PUB13_1	-2.185	0.0038	down	PUB13	-2.32	9E-05	down	
AT4G23515	no	up	pathogen unknown transmembrane Toll - interleukin 1 - resistance domain protein	AT4G23515_2	16.635	0.026	up	AT4G23515	15.714	0.007	up	
At5g18525	no	down	pathogen vacuole targeting Beach domain and WD40 repeat protein kinase					GFS12	-2.327	0.041	down	
AT2G25620	no	down	pathogen viral defense flowering time DNA binding PP2C	AtDBP1_2	-501.2	0.001	down	AtDBP1	-3.4	0.035	down	down
AT1G07730	no	up	pathogen, Dirigent domain protein with signal peptide					DIR25	6.9209	0.041	up	down
AT2G32680	no	up	pathogen/BR signaling SOBIR1-BABK1 interacting transmembran LRR RLP23 receptor like protein 23	AtRLP23_1	59.736	0.0406	up	AtRLP23	56.429	0.03	up	
AT2G22860	no	up	peptide growth factor PSK2 phytosulfokine 2	PSK2_1	13.073	0.0422	up	PSK2	12.417	0.013	up	
AT1G13245	no	up	peptide ligand growth factor DEVIL 4; DVL4; ROTUNDIFOLIA like 17					RTFL17	7.1387	0.043	up	down
AT1G68825		up	peptide ligand growth factor DEVIL 5; DVL5; ROTUNDIFOLIA like 15					DVL5	10.017	0.035	up	
AT1G17235	no	down	peptide ligand growth factor DEVIL, ROTUNDIFOLIA LIKE 11, RTFL11					RTFL11	-10.7	0.031	down	
AT5G46050	yes	up	peptide transporter 3 NPF5.2; NRT1/ PTR family 5.2 pathogen wounding salt stress					NPF5.2	8.2262	0.03	up	
AT2G24580	no	up	peroxisomal Sarcosine oxidase (SOX)					AT2G24580	7.6751	0.031	up	
AT3G07490	no	up	peroxisome ARF-GAP domain 11; AtCML3; calmodulin-like 3; CML3	AGD11_2	50.645	0.0478	up	AGD11	60.63	0.027	up	
AT1G79810		up?	peroxisome biogenesis PEX2 RING E3 suppressor of det1 mutation					PEX2	4.0779	0.016	up	
AT3G02400	yes	down	peroxisome division repressor forkhead-associated (FHA) AT-hook TF of PEX11	AT3G02400_1	-4.35	0.0032	down	AT3G02400	-4.451	3E-05	down	
AT5G16370	no	down	peroxisome lipid beta oxidation AAE5 acyl activating enzyme 5	AAE5_1	-2.551	0.001	down	AAE5	-2.717	8E-06	down	
AT4G33905	no	up	peroxisome Mpv17_PMP22 domain 22 kDa peroxisomal membrane protein (PMP22)	AT4G33905_1	132.02	0.0153	up	AT4G33905	125.95	0.01	up	
AT5G22890	no	down	pH and ALU tolerance STOP2 TF					AT5G22890	-16.27	0.022	down	
AT3G15240	no	up	phenylpropanoid biosynthesis bHLH-MYC_N domain TF	AT3G15240_1	50.622	0.0482	up	AT3G15240	47.816	0.036	up	
AT1G65060	no	up	phenylpropanoid flavonoid biosynthesis, pathogen the last step of the general phenylpropanoid pathway	4CL3_1	78.444	0.0299	up	4CL3	74.534	0.021	up	up
AT4G26220	no	down	phenylpropanoid flavonoid lignin CAFFEOYL COENZYME A ESTER O-METHYLTRANSFERASE 7, CCOAOMT7					AT4G26220	-5.11	0.029	down	
AT3G24503	no	up	phenylpropanoid flavonoid synthesis sinapaldehyde dehydrogenase aldehyde dehydrogenase 2C4; ALDH1A; REDUCED EPIDERMAL FLUORESCENCE1; REF1					ALDH2C4	4.749	0.043	up	
AT5G63600	no	up	phenylpropanoid flavonol synthase 5 FLS5	FLS5_2	26.011	0.019	up	FLS5	18.158	0.004	up	up
AT5G63580		up	phenylpropanoid flavonol synthesis FLS2 flavonol synthase 2					FLS2_2	109.7	0.012	up	
AT5G04230	no	up	phenylpropanoid PAL3 phenyl alanine ammonia-lyase 3	PAL3_1	17.453	0.0369	up	PAL3	16.527	0.014	up	
AT3G10340	no	up	phenylpropanoid synthesis PAL4 phenylalanine ammonia-lyase 4	PAL4_1	12.681	0.0398	up	PAL4	11.979	0.011	up	
AT4G15500	no	up	phenylpropanoid synthesis sinapic acid:UDP-glucose glucosyltransferase	UGT84A4_1	15.429	0.0207	up	UGT84A4	14.626	0.005	up	
AT1G10155	no	up	phloem sap Phloem protein 2 (PP2) A10					ATPP2-A10	7.2659	0.05	up	
AT3G20570	no	up	pholem sieve element specific copper binding ENODL9 early nodulin-like protein 9					ENODL9	11.253	0.032	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G68320	no	up	phosphate starvation induced GA biosynthesis regulator MYB62 myb domain protein 62 TF					MYB62	39.295	0.045	up	
AT3G47420	no	up	phosphate starvation-induced glycerol-3-phosphate permease G3Pp1	ATPS3_3	19.103	0.0124	up	ATPS3	18.217	0.002	up	up
At4g22550	no	down	phosphatidic acid phosphatase LIPID PHOSPHATE PHOSPHATASE BETA, LPPBETA	LPPB_1	-9.151	0.0453	down	LPPB	-9.87	0.009	down	
AT3G56600	no	up	phosphatidylinositol signaling PI4K GAMMA 1 homolog Phosphatidylinositol 3-kinase	AT3G56600_2	90.146	0.0302	up	AT3G56600	133.34	0.009	up	
AT2G31830	yes	up?	phosphatidylinositol signaling 5-inositol-polyphosphate phosphatase	AT2G31830_1	89.71	0.0256	up	AT2G31830	8.1078	0.029	up	down
AT3G18050	no	up	phosphatidylinositol signaling glycosylphosphatidylinositol-anchored PM protein	AT3G18050_1	55.116	0.044	up	AT3G18050	52.061	0.033	up	
At5g56160	no	up	phosphatidylinositol signaling G prtein interactin SEC14 phosphatidylinositol transfer protein	SFH14_2	99.061	0.0266	up	SFH14	6.731	0.023	up	
AT1G73200	no	down	phosphatidylinositol signaling transmembrane Pleckstrin homology domain protein					AT1G73200	-2.144	0.016	down	
At2g18180		up?	phosphoinositide signaling effector SEC14 homolog SFH10					SFH10	16.002	0.014	up	
AT2G19400	no	up	phosphoinositol signaling AGC protein kinase					AT2G19400	7.0676	0.027	up	
At5g63990	no	up	phosphoinositol signaling inositol monophosphatase	SAL3_1	14.613	0.016	up	SAL3	7.0501	0.014	up	
At2g40116	no	up	phosphoinositol signaling Phosphoinositide-specific phospholipases C					PLC6	9.3064	0.044	up	
AT5G41120	yes	up	phospholipid biosynthesis Alpha/beta hydrolase fold glycerolphosphate, 1-acylglycerolphosphate, or 2-acylglycerolphosphoethanolamine acyltransferase	AT5G41120_1	130.54	0.0187	up	AT5G41120	12.261	0.006	up	
AT3G48180	no	down	phospholipid metabolism CDP-diacylglycerol—glycerol-3-phosphate 3-phosphatidyltransferase					AT3G48180	-4.088	0.011	down	
AT3G44610	no	up	phospholipid signaling AGC1-12, AGCVIII KINASE 1-12	AT3G44610_1	61.725	0.04	up	AT3G44610	59.101	0.03	up	
AT4G11840	yes	down?	phospholipid signaling vesicular transport Phosphatidylcholine-hydrolyzing phospholipase D3	PLDGAMMA3_1	-6.57	0.0382	down	PLDGAMMA3	-3.2	0.033	down	
At3g44830	no	up	phospholipid synthesis phospholipid:diacylglycerol acyltransferase					PDAT2	39.302	0.045	up	
AT1G13210	no	down	phospholipid transporting ACA.l autoinhibited Ca2+/ATPase II					ALA11	-2.057	3E-04	down	
AT1G69935	no	down	photomorphogenesis negative regulator COP1 interactor					SHW1	-4.193	0.017	down	
AT5G58330		down?	photorespiration C4 cycle NADP-DEPENDENT MALATE DEHYDROGENASE					AT5G58330	-2.325	0.041	down	
AT5G04190	no	up	phototropin PHOT1 phosphorylated PKS4					PKS4	40.977	0.048	up	down
AT1G14280	no	up	PhyA signaling leaf development hypocotyl phototropism PKS2 phytochrome kinase substrate 2	PKS2_1	57.472	0.0425	up	PKS2	54.289	0.031	up	
AT5G02200	yes	down?	phytochrome A signaling FAR-RED-ELONGATED HYPOCOTYL1-LIKE, FHL required for Pfr PhyA nuclear accumulation	FHL_2	24.614	0.0244	up	FHL	7.0893	0.026	up	
AT1G18520	no	up	plasma membrane TET11 tetraspanin11	TET11_1	57.448	0.0416	up	TET11	54.267	0.031	up	
AT4G28050	no	up	plasma membrane TET7 tetraspanin11	TET7_1	52.899	0.0455	up	TET7	49.968	0.034	up	
At4g03100	no	up	polar cell growth Cdc42/Rac interacting Rho GTPase activating protein	ROPGAP2_1	113.93	0.0186	up	ROPGAP2	107.92	0.013	up	up
AT2G20430	no	up	polar cell growth CRIB (for Cdc42/Rac-interactive binding) motif containing RIC6 ROP-interactive CRIB motif-containing protein 6					RIC6	39.319	0.046	up	
AT5G55590	no	up	pollen cell wall pectin lyase QRT1	QRT1_2	89.605	0.0307	up	QRT1	20.3	0.003	up	
AT4G26440	no	up	pollen development cold WRKY34 WRKY DNA-binding protein 34 TF					WRKY34	45.669	0.038	up	
AT5G56450	no	up	pollen development PM ATP transporter	AT5G56450_1	30.225	0.007	up	AT5G56450	28.893	0.001	up	
AT2G31500	no	up	pollen K+ influxi Ca2+ signaling CPK24 calcium-dependent protein kinase 24					CPK24	13.352	0.022	up	
AT1G49490	yes	down	pollen tube growth LRR receptor of RALF4 growth peptide					AT1G49490	10.557	0.031	up	
AT5G58040		down?	polyadenylation cleavage complex subunit FIPS5; homolog of yeast FIP1	FIPS5_1	-3.675	0.0002	down	FIPS5	-2.515	2E-06	down	
AT4G29820	no	up	polyadenylation cleavage complex subunit CFIM-25	CFIS1_1	4.336	0.0101	up	CFIS1	4.1453	7E-04	up	
AT3G59050	no	up	polyamine metabolism ROS signaling spermidine oxidase PAO3 polyamine oxidase 3					PAO3	3.0038	0.034	up	
AT5G13700	no	down	polyamine oxidase 1	PAO1_1	-2.53	0.0468	down	PAO1	-2.679	0.003	down	
At5g15950		up	polyamine spermidine biosynthesis S-adenosylmethionine decarboxylase SAMDC2					SAMDC2	9.9234	0.014	up	up
AT5G11530	no	down	polycomb 1 histone H3K27me3					EMF1	-2.07	0.021	down	up
At5g67100	no	down	polycomb 2 interacting ICU2 DNA-directed DNA polymerase	POLA_2	-2.814	0.0196	down	POLA	-2.142	0.018	down	
AT1G10095	yes	down?	posttranlational protein modification protein prenyltransferase					AT1G10095	7.3059	0.042	up	
AT1G67880	no	up	posttranslational protein modification eta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	AT1G67880_1	10.049	0.0426	up	AT1G67880	9.4932	0.012	up	
AT1G06970	no	up	potassium efflux ATCHX14; cation/hydrogen exchanger 14 regulating K+ desitributon essential for growth					CHX14	7.0881	0.031	up	
At3g02050	no	down	potassium KUP3 K+ uptake transporter 3					POT4	-2.223	0.018	down	
AT1G30450		down?	potassium transport cation-chloride co-transporter 1					CCC1	-2.138	0.039	down	down?
AT1G04690	no	up	potassium transport vacuolar K+ CHANNEL BETA SUBUNIT PROTEIN; KV-BETA1; potassium channel beta subunit 1	KAB1_1	2.3629	0.0054	up	KAB1	2.2424	3E-04	up	
At5g14880	no	down	Potassium transporter KUP8	POT8_1	-74.3	0.0336	down	POT8	-77.39	0.02	down	
AT3G17630	no	up	potassium transporter, endomembrane pollen tube CHX19 cation/H+ exchanger 19					CHX19	7.2972	0.032	up	
AT2G30240	no	up	potassium transporter, PM CATION/H+ EXCHANGER 13; CHX13					CHX13	7.4404	0.03	up	
AT5G53140	no	down	PP2C protein phosphatase 2C 76	AT5G53140_1	-507.7	0.0023	down	AT5G53140	-2.275	0.002	down	up
AT1G09160	no	up	PP2C-5 protein phosphatase 2C 5	AT1G09160_1	355.87	0.0032	up	AT1G09160	7.54	0.007	up	down
AT5G14710	no	down	Proteasome assembly chaperone 3					AT5G14710	-3.88	0.022	down	
At2g03890	yes	up	proteasome phosphoinositide signaling UFD1 and RPN10 ubiquitin domain phosphoinositide 3/4-kinase	PI4KG7_2	-22.53	0.001	down	PI4KG7	-4.006	4E-04	down	
At1g76400		down?	proteasome RPN1 subunit ER N-oligosaccharyl transferase riboforin					OST1A	-2.124	0.001	down	
AT2G20580	no	down	proteasome RPN1A 26S proteasome regulatory subunit S2 1A, embryogenesis, growth, trichome development					RPN1A	-2.067	0.003	down	
At4g15165	no	up	proteasome subunit alpha type-4-B					PAC2	43.163	0.044	up	
AT5G62780	no	up	protein folding DnaJ chaperone					AT5G62780	7.9705	0.035	up	
AT2G35540	no	down	protein folding DNAJ chaperone with DUF3444 domain					AT2G35540	-2.106	0.007	down	
AT1G10350	no	down	protein folding DNAJ heat shock chaperone					AT1G10350	-3.448	0.04	down	
AT1G12270	no	down	protein folding stress-induced Hsp90/Hsp70 co-chaperone carboxylate clamp (CC)-tetratricopeptide repeat (TPR) protein HOP1	HOP1_1	-2.506	0.0046	down	HOP1	-2.673	1E-04	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G79030	yes	down	protein folding transmembrane DNAJ protein with Jiv90 Cleavage inducing molecular chaperone domain	AT1G79030_2	35.049	0.0097	up	AT1G79030	5.9742	0.04	up	
AT1G72416	yes	up	protein folding transmembrane DnaJ chaperon	AT1G72416_2	73.496	0.0373	up	AT1G72416	4.894	0.039	up	
AT5G42760	yes	up?	protein phosphatase 2A leucine carboxymethyltransferase					AT5G42760	8.8523	0.025	up	
AT1G13460	no	up	Protein phosphatase 2A regulatory B subunit BR signaling peroxisome	B'THETA_1	84.505	0.0324	up	B'THETA	8.9381	0.019	up	
AT3G05580	yes	down	Protein phosphatase 2A TOPP9					TOPP9	2.8246	0.034	up	
AT1G48040	no	up	protein phosphatase 2C 13, AtPP2C13					AT1G48040	3.5489	0.025	up	
AT1G68410	no	up	protein phosphatase 2C 15	AT1G68410_4	136.75	0.0218	up	AT1G68410	2.1648	0.009	up	
AT5G10740	no	down	protein phosphatase 2C 69					AT5G10740	-2.559	0.015	down	
AT1G48740	yes	up?	protein posttranslational modification Prolyl 4-hydroxylase alpha subunit	AT1G48740_1	98.022	0.0245	up	AT1G48740	94.022	0.017	up	
AT5G43660		up?	protein posttranslational modification Prolyl 4-hydroxylase alpha subunit	AT5G43660_4	74.726	0.0313	up	AT5G43660	149.04	0.008	up	
At3g22180	no	down	proteinCys- palmitoyltransferase membrane-bound zf-DHHC domain protein	PAT20_1	-8.598	0.0236	down	PAT20	-9.378	0.004	down	
AT4G01575	no	up	proteolysis transmembrane KAZAL-TYPE PROTEINASE INHIBITOR 2, KPI-2 with signal peptide	AT4G01575_1	60.144	0.04	up	AT4G01575	57.227	0.029	up	
AT5G61540	no	down	proteolysis Asparaginase_2	AT5G61540_1	-286.9	0.0047	down	AT5G61540	-4.696	0.011	down	
AT1G22080	no	up	proteolysis Cysteine proteinase					AT1G22080	8.9281	0.042	up	
AT1G59970	no	up	proteolysis extracellular matrix peptodoglycan binding Zinc-dependent metalloprotease					5MMP	8.9932	0.015	up	
AT2G25740	yes	up?	proteolysis human CRBN-like ATP-dependent nuclear LON protease	AT2G25740_2	3.5798	0.0167	up	AT2G25740	2.2638	0.019	up	down
AT1G67690	no	up	proteolysis humanTHOP1 thimet oligopeptidase 1 homolog					AT1G67690	6.8844	0.026	up	
AT1G32940	yes	down	proteolysis root PECTIN METHYLESTERASE17 processing serine protease	SBT3.5_1	641.46	0.001	up	SBT3.5	2.1495	0.018	up	down
AT3G30770	no	up	proteolysis RVP_2 domain aspartyl protease	AT3G30770_1	9.6464	0.0158	up	AT3G30770	9.1403	0.002	up	
AT1G32960	no	down	proteolysis SAR-induced Subtilase	SBT3.3_1	-2.656	0.0412	down	SBT3.3	-2.83	0.003	down	
AT5G42240	no	up	proteolysis scpl42 serine carboxypeptidase-like 42 with signal peptide	SCPL42_1	235.58	0.0067	up	SCPL42	222.55	0.004	up	
AT2G27920	yes	down	proteolysis serine carboxypeptidase-like 51					SCPL51	44.407	0.04	up	down
AT1G63280	no	up	proteolysis Serpin (SERine Proteinase INhibitor)					AT1G63280	48.008	0.037	up	
AT4G20850	no	down	proteolysis Tripeptidyl peptidase II					TPP2_2	-2.423	2E-06	down	
AT3G45310	no	up	proteolysis unknown cysteine peptidase	AT3G45310_1	57.384	0.0418	up	AT3G45310	13.817	0.019	up	
AT4G17050	no	down	purine catabolism UGLYAH ureidoglycine aminohydrolase					UGLYAH	-2.037	0.031	down	
AT4G34890	no	down	purine catabolism XDH1 xanthine dehydrogenase 1					XDH1	-2.065	6E-04	down	
AT4G04955		down?	purine metabolism allantoinase					ALN	-4.291	0.02	down	
AT2G23890	no	up	purine nucleotide metabolism purine specific 5'-nucleotidase	AT2G23890_2	72.456	0.0453	up	AT2G23890	3.6932	0.046	up	up
AT1G32380		up?	purine synthesis PRS2 phosphoribosyl pyrophosphate (PRPP) synthase 2	PRS2_1	13.237	0.0132	up	PRS2	7.8487	0.003	up	
AT1G78590	yes	down?	redox ABA signaling NADK3 NAD(H) kinase 3					NADK3	3.0259	0.04	up	
AT5G11540	no	up	redox ascorbate biosynthesis GulLO3 D-arabinono-1,4-lactone oxidase	GULLO3_1	33.69	0.01	up	GULLO3	31.827	0.003	up	
AT1G75270	no	up	redox ascorbate-glutathione cycle DHAR2 dehydroascorbate reductase 2					DHAR2	2.0995	0.04	up	
AT2G02930	no	down	redox ATGSTF3; GLUTATHIONE S-TRANSFERASE 16	GSTF3_1	-2.482	0.041	down	GSTF3	-2.636	0.002	down	
AT5G47390	no	down	redox cell expansion leaf development KUA1; KUODA1 MYB hypocotyl elongation-related; MYBH TF	AT5G47390_1	-3.092	0.022	down	AT5G47390	-3.278	0.001	down	
At3g49110	no	up	redox cellwall pathogen defense Class III peroxidase Perx33					PER33	6.7311	0.039	up	
AT1G07700		up	redox chloroplast Thioredoxin-like 4 with signal peptide	AT1G07700_3	184.08	0.0096	up	AT1G07700	7.002	0.022	up	
AT5G25090	no	down	redox Cu-binding phytocyanin					ENODL13	-9.144	0.014	down	
AT2G28420	no	up	redox detoxification Glyoxalase_2 domain protein	AT2G28420_1	61.951	0.0384	up	AT2G28420	58.519	0.028	up	
AT2G47780	no	up	redox drough tolerance lipid droplet LD-ASSOCIATED PROTEIN 2, LDAP2, SMALL RUBBER PARTICLE PROTEIN2, SRP2					AT2G47780	7.5265	0.033	up	
AT1G72280	no	up	redox ER secretory pathway AERO1; endoplasmic reticulum oxidoreductins 1	AERO1_1	2.7042	0.0454	up	AERO1	2.5694	0.01	up	
AT5G37830	no	down	redox glutathione metabolism OXP1 oxoprolinase 1					OXP1	-2.314	0.013	down	
AT1G78340	no	up	redox GLUTATHIONE S-TRANSFERASE TAU 22	GSTU22_1	14.32	0.0218	up	GSTU22	13.671	0.003	up	
AT5G41220	no	down	redox GSTT3 glutathione S-transferase THETA 3	GSTT3_1	-6.586	0.0008	down	GSTT3	-5.246	1E-05	down	
AT4G36910	no	up	redox JA ethylene thrioredoxin modulating cystathionine beta-synthase domain-containing protein CBSX1; CDCP2; CYSTATHIONE [BETA]-SYNTHASE DOMAIN-CONTAINING PROTEIN 2; LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 2					CBSX1	4.6942	0.015	up	
AT3G27620	no	down	redox mitochondrion AOX1C alternative oxidase 1C					AOX1C	-4.746	0.044	down	up
At2g03050	no	up	redox mitochondrion transcription terminator SINGLET OXYGEN-LINKED DEATH ACTIVATOR 10; SOLDAT10					MTERF1	37.15	0.049	up	down
AT4G38420		down	redox Multicopper oxidase SKS9	sks9_1	-2.151	0.0187	down	sks9	-2.193	2E-04	down	
AT3G10930	no	up	redox negative modulator of ROS signaling IDA-LIKE7, IDL7 secreted signaling peptide	AT3G10930_1	6.1248	0.0262	up	AT3G10930	5.7882	0.002	up	
AT4G09320	no	up	redox nucleotide synthesis peroxidase-interacting NDPK1 nucleoside diphosphate kinase	NDK1_1	2.1822	0.0004	up	NDK1	2.0495	1E-04	up	
AT3G56090	no	up	redox oxidative damage proteion iron storage ferritin 3	FER3_1	37.366	0.0079	up	FER3	35.394	0.002	up	
At2g38390	no	up	redox peroxidase 23 with signal peptide	PER23_1	31.617	0.0116	up	PER23	30.023	0.003	up	down
At4g37520	yes	up	redox Peroxidase 5	PER50_1	-128.7	0.0142	down	PER50	-2.007	0.035	down	
At5g40150	no	down	redox Peroxidase 63					PER63	-4.245	0.033	down	
At2g38380	no	up	redox peroxidase PER22	PER22_1	7.6047	0.0246	up	PER22	7.334	0.004	up	
AT5G14130	yes	up?	redox peroxidase PER55					AT5G14130	7.3018	0.032	up	
At5g19880	no	up	redox peroxidase PER58 with signal peptide					PER58	7.1668	0.033	up	
AT3G02870	yes	down?	redox phosphoinositol Inositol monophosphatase; ascorbate synthesis L-galactose-1-phosphate phosphatase					VTC4	-2.031	0.014	down	down?
AT3G47720	no	up	redox RCD1-like SRO4 ADP-ribosylation	SRO4_1	33.472	0.0045	up	SRO4	31.622	5E-04	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT1G23010	no	down	redox root cupredoxin controlling cell division by phosphate starvation	LPR1_1	-6.748	0.035	down	LPR1	-7.278	0.007	down	up
AT1G34570	no	up	redox ROS protection of ribosome Yae1_N domain essential protein					AT1G34570	4.4086	0.028	up	
AT5G06430	no	up	redox thrioredoxin	AT5G06430_1	15.797	0.0397	up	AT5G06430	14.922	0.016	up	
AT4G23340	no	down	redox unknown 2-oxoglutarate/Fe(II)-dependent dioxygenase	AT4G23340_2	-17.93	0.0351	down	AT4G23340	-9.109	0.04	down	
AT5G50350	no	down	redox unknown coiled coil protein	AT5G50350_1	-6.385	0.0023	down	AT5G50350	-6.896	2E-04	down	
AT4G31840	no	down	redox unknown transmembrane plantacyanin					ENODL15	-4.019	0.023	down	
AT3G60270	no	up	redox, plastocyanin family with cupredoxin domain					AT3G60270	41.453	0.042	up	down
AT3G27200	no	up	redox, transmembrane cupredoxin, plastocyanin family with cupredoxin domain					AT3G27200	39.326	0.045	up	
AT2G46740	no	down	redoxc ascorbate biosynthesis GulLO5 D-arabinono-1,4-lactone oxidase					GULLO5	-10.12	0.014	down	
AT1G30330	no	down	reproduction auxin JA synthesis root development microRNA167 regulated ARF6 TF, which acts together with ARF8 and AS1/2	ARF6_1	-3.401	0.0021	down	ARF6	-2.678	1E-04	down	down
AT1G11303	no	up	reproduction bulb lectin S-locus glycoprotein transmembrane receptor kinase					AT1G11303	8.9378	0.013	up	
AT3G50570	yes	down?	reproduction embryo sac specific MYB98 regulated Prolamin_like domain protein					AT3G50570	-9.561	0.05	down	
AT5G59370	no	down	reproductive tissue embryo pollen specific actin	ACT4_2	-57.49	0.0059	down	ACT4	-60.04	0.001	down	
AT4G27330	no	down	reproductive tissues macro/microsporogenesis SPOROCYTELESS					SPL	-38.8	0.045	down	
AT5G59850	no	up	ribosome 40S ribosomal protein S15a-1					RPS15AA_2	2.196	0.038	up	
AT4G29430	no	up	ribosome 40S ribosomal protein S15a-5					RPS15AE	4.3059	0.038	up	
At3g57490	no	up	ribosome 40S ribosomal protein S2-4	RPS2D_1	8.1757	0.0142	up	RPS2D	7.7962	0.001	up	
At2g45710	no	up	ribosome 40S ribosomal protein S27-1	RPS27A_1	12.709	0.0173	up	RPS27A	12.141	0.003	up	
At5g39850	no	down	ribosome 40S ribosomal protein S9-2					RPS9C	-2.142	0.019	down	
AT4G02720	no	down	ribosome 45S RNA silencing MAS2 (MORPHOLOGY OF AGO1-52 SUPPRESSED2)	AT4G02720_1	-4.869	0.0018	down	AT4G02720	-5.125	1E-05	down	
AT3G49725	no	down	ribosome 50S GTPase GTP-binding HflX-like protein					AT3G49725	-3.208	0.028	down	up
At3g11250	no	up	ribosome 60S acidic ribosomal protein P0-3					RPP0C	3.6088	0.024	up	
At1g32990	no	up	ribosome 60S ribosomal protein L11-1	RPL11_1	11.605	0.0395	up	RPL11	10.989	0.012	up	
At5g48760		up	ribosome 60S ribosomal protein L13a-4					RPL13AD	4.3476	0.011	up	down
At2g19740	no	down	ribosome 60S ribosomal protein L31-1					RPL31A	-2.086	0.024	down	
At1g18540	no	down	ribosome 60S ribosomal protein L6-1					RPL6A	-2.111	0.008	down	
At3g51190	no	up	ribosome 60S ribosomal protein L8-2					RPL8B	10.112	0.02	up	
AT5G06110	no	up	ribosome associated RF1B, ZUOTIN-RELATED FACTOR 1B, DNAJC2 DnaJ heat shock protein family (Hsp40) member C2 homolog	AT5G06110_2	-2.198	0.0081	down	AT5G06110	-2.402	4E-06	down	up
AT3G15030	no	up	ribosome biogenesis cell division leaf development TCP4 TCP family transcription factor 4					TCP4	56.358	0.029	up	down
AT4G21130	no	down	ribosome biogenesis embryo lethality U3-55K RRP9 ribosomal RNA processing 9, U3 small nucleolar RNA binding protein	EMB2271_1	-15.49	0.0075	down	EMB2271	-16.93	0.001	down	
AT3G62210	no	up	ribosome biogenesis embryo sac development arrest 32 transmembrane NYN domain nuclease					EDA32	8.301	0.025	up	
AT1G54770	no	down	ribosome biogenesis Fcf2 pre-rRNA processing protein					AT1G54770	-2.37	0.026	down	
AT5G18180	no	up	ribosome biogenesis GAR1 domain protein involved in maturation of box H/ACA snoRNPs complex					AT5G18180	6.8653	0.04	up	
AT5G30495	no	up	ribosome biogenesis pre-rRNA processing Fcf2 domain potein	AT5G30495_2	77.044	0.0425	up	AT5G30495	8.6256	0.013	up	
AT4G35370	no	up	ribosome biogenesis Pwp1 assembly factor WD40 protein					AT4G35370	9.721	0.026	up	
At1g74250	no	down	ribosome biogenesis REIL maturation factor interacting DNAJ protein JJJ1	JJJ1_1	-2.005	8E-05	down	JJJ1	-2.128	8E-08	down	
AT5G66180	yes	down	ribosome biogenesis ribosomal RNA methyltransferase NOL1-NOP2					AT5G66180	3.7868	0.012	up	
AT4G32175	no	up	ribosome biogenesis rRNA processing exosome component RRP40 homolog					AT4G32175	7.804	0.013	up	
AT3G22660	no	down	ribosome biogenesis rRNA processing protein Ebp2 homolog					EBP2	-2.371	0.011	down	
AT3G19440	yes	down	ribosome biogenesis rRNA Pseudouridine synthase	AT3G19440_2	73.253	0.0319	up	AT3G19440	7.5735	0.017	up	
AT3G20420	no	up	ribosome biogenesis rRNA spacer double-stranded RNA binding / ribonuclease III ATRTL2; RNAse THREE-like protein 2					RTL2	4.2425	0.009	up	
AT5G42540	no	down	ribosome biogenesis silencing suppressor	XRN2_2	-86.88	0.0275	down	XRN2	-2.112	0.002	down	up
AT5G35400	yes	up	ribosome biogenesis, tRNA telomer Pseudouridine synthase I, TruA	AT5G35400_1	-4.247	0.044	down	AT5G35400	-4.506	0.008	down	
AT1G33040	no	down	ribosome nascent polypeptide-associated complex (NAC) subunit alpha-like protein 5 NACA5					NACA5	-2.094	0.002	down	
AT1G80410	no	down	ribosome protein N-terminalacetylation NatA N-terminal acetyltransferase	EMB2753_1	-3.587	0.0025	down	EMB2753	-2.022	0.004	down	
AT5G09770	no	up	ribosome Ribosomal_L17 domain protein					AT5G09770	2.1753	0.017	up	
AT3G45020		up	ribosome Ribosomal_L18 protein					AT3G45020	6.0832	0.044	up	
AT3G22450		up	ribosome Ribosomal_L18 protein					AT3G22450	15.111	0.008	up	
AT4G39880	no	down	ribosome Ribosomal_L23 protein					AT4G39880	-2.471	0.046	down	
AT2G24990	no	down	ribosome RNA processing atypical RIO kinase with coiled coil domain					AT2G24990	-2.916	0.046	down	
AT5G64420	no	down	ribosome rRNA gene repeat replication DNA polymerase V					AT5G64420	-2.122	0.022	down	
AT2G48160		down?	RNA pol II CTD interacting trithorax PWWP domain HUA2 homolog HUA2 LIKE 2, HULK2, SL3					AT2G48160	-2.205	0.006	down	
AT1G17440	no	down	RNA pol II TFIID subunit ethylene cytokinin signaling inhibitor TBP-associated factor TAF12 CKH1; CYTOKININ-HYPERSENSITIVE 1; ENHANCED ETHYLENE RESPONSE 4	TAF12B_2	-3.02	0.0009	down	TAF12B	-2.636	3E-04	down	
AT1G54140	no	down	RNA pol II TFIID TATA binding protein associated factor 21kDa subunit					TAF9	-2.218	0.005	down	
AT5G12840	no	down	RNA polI CCAAT-binding complex subunit ATHAP2A; AtNFYA1; EMB2220; EMBRYO DEFECTIVE 2220; HAP2A; NFYA1; nuclear factor Y	NFYA1_2	-6.373	0.0205	down	NFYA1	-3.461	0.009	down	
AT2G27470	no	down	RNA polII CCAAT-box binding NF-Y complex subunit	NF-YB11_1	-2.827	0.0077	down	NF-YB11	-3.005	6E-05	down	
AT3G23590	no	down	RNA polII MEDIATOR subunit MED33A regulation of phenylpropanoid homeostasis					MED33A	-3.099	0.014	down	
AT3G10070	no	down	RNA polII TFIID TAFII58; TATA-ASSOCIATED FACTOR II 58; TBP-associated factor 12	TAF12_1	-4.086	0.0313	down	TAF12	-4.431	0.006	down	
AT1G18040	no	down	RNA polII TFIIH kinase					CDKD-3	-4.025	0.011	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT2G43970		down?	RNA polIII transcript 3' binding La RRM domain RNA binding protein					LARP6B	-2.088	7E-09	down	
AT5G52090	no	up	RNA procesing (+)RNA virus helicase core domain protein					AT5G52090	45.723	0.038	up	
AT1G20000	no	up	RNAP II TFIID subunit TAF28	TAF11B_1	53.487	0.0467	up	TAF11B	50.791	0.035	up	
At5g47640	no	up	RNAPII CCAAT binding complex subunit NF-YB2 nuclear factor Y, subunit B2	NFYB2_1	18.756	0.0134	up	NFYB2	17.719	0.002	up	
At5g38140	no	up	RNAPII CCAATbox TF complex subunit NF-YC12 nuclear factor Y, subunit C12	NFYC10_1	12.05	0.0484	up	NFYC10	11.381	0.018	up	
AT4G10090	no	up	RNAPII elongator complex subunit 6, tRNA maturation auxin response					ELP6	6.9926	0.032	up	
AT2G14850	no	up	RNAPII SAGA complex core subunit Hfi1 (known as Transcriptional adapter 1, Tada1 in higher eukaryotes)	AT2G14850_1	14.632	0.0453	up	AT2G14850	13.822	0.019	up	
AT1G73690	no	up	RNAPII TFIIH kinase CDKD;1					CDKD-1	4.4348	0.013	up	
AT2G13640	no	up	RNAPII transcription elongation factor S-II	AT2G13640_1	38.11	0.0077	up	AT2G13640	36.069	0.002	up	
AT4G18720	no	up	RNAPII transcription elongation factor S-II					AT4G18720	45.705	0.039	up	
AT1G30455	no	up	RNApolIII MEE 65 homolog maternal effect embryo arrest 65 BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIBa	AT1G30455_1	20.614	0.015	up	AT1G30455	19.474	0.004	up	
AT4G35290	yes	up?	root amino acid gated channel GLUR2 glutamate receptor 2	GLR3.2_2	-23.15	0.0241	down	GLR3.2	-25.43	0.006	down	
AT5G60920		down	root cell elongation COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein	COB_1_2	-2.053	0.002	down	COB_1	-2.156	2E-05	down	down
At3g16430		up	root cell wall scopolin glucosidase stimulating JAL31 jacalin-related lectin 31					PBP2	9.4766	0.038	up	down
AT1G02900	no	up	root elongation lateral root development, negative regulator BR antagonist peptide	RALF1_1	19.485	0.0283	up	RALF1	18.527	0.01	up	down
AT2G24610	no	down	root gravitropism Cyclic Nucleotide-Gated Channel CNGC14	ATCNGC14_2	-28.6	0.0111	down	ATCNGC14	-21.33	0.003	down	down
AT2G22680	no	down	root gravitropism WAV3 homolog 1 WANH1 E3 ligase					AT2G22680	-3.351	0.013	down	
AT1G26150		down?	root growth PERK10 proline-rich extensin-like receptor kinase 10	PERK10_1	-2.22	0.0429	down	PERK10	-2.463	1E-04	down	
AT3G25640		up?	root hydrotropisms, MIZU-KUSSEI-like protein unknown DUF617 domain protein	AT3G25640_1	10.048	0.0452	up	AT3G25640	11.983	0.006	up	
AT1G11000	no	up	root mechanosensing thigmotropism MLO4 Seven transmembrane MLO family protein					MLO4	20.882	0.008	up	
AT5G51451	no	up	root meristem growth factor RGF5					RGF5	6.0291	0.032	up	
AT3G51290	yes	down	root meristem maintenance inhibited by P-starvation Rho (Ras homology) subfamily of Ras-like small GTPases	AT3G51290_2	15.505	0.0432	up	AT3G51290	17.604	0.013	up	
AT1G34670	no	up	root negative regulator of lateral root development MYB93 TF	AtMYB93_1	19.458	0.0286	up	AtMYB93	18.563	0.01	up	
AT5G38030	no	up	root nematode-induced MATE drug/sodium antiporter					DTX30	7.3903	0.033	up	
At3g60490	no	up	root stele DREB subfamily A-4 of ERF/AP2 TF ERF35, predicted regulator of TOM6 (TARGET OF MONOPTEROS 6)	ERF035_1	38.812	0.0017	up	ERF035	36.82	1E-04	up	down
AT3G22270	no	down	root stem cell nieche JA regulation Topoisomerase II-associated protein PAT1H1 interactor of JAZ NINJA					AT3G22270	-2.055	0.043	down	
At5g51890	no	up	root tracheary element lignification peroxidase 66					PER66	11.106	0.031	up	
AT5G01510	no	up	root UV perception RUS5 DUF647 domain protein	RUS5_1	34.049	0.0054	up	RUS5	32.462	7E-04	up	
AT5G51590	no	up	root vascular patterning AHL4; AT-HOOK MOTIF NUCLEAR LOCALIZED PROTEIN 4					AHL4	37.135	0.049	up	
AT3G58810	yes	down	root Zn2+ efflux transporter					MTPA2	10.571	0.033	up	
AT3G19430	no	up	Root_cap domain protein of unknown function					AT3G19430	9.1431	0.045	up	down
AT5G17860	no	down	ROS Ca2+ signaling induction of senescence transmembrane sodium/calcium exchanger	CCX1_2	-4.07	0.0297	down	CCX1	-4.186	0.004	down	down
AT2G43840	no	up	SA synthesis pABA acylglucosyltransferase	UGT74F1_2	75.589	0.0308	up	UGT74F1	71.406	0.022	up	
AT5G38020		up?	SA, SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri) or to SAM:benzoic acid carboxyl methyltransferase (BAMT)	AT5G38020_2	80.052	0.0288	up	AT5G38020	86.329	0.017	up	?
AT2G30360	no	down	salt pH Plasmamembrane proton transporter ATPase kinase SOS2 interacting protein SIP4	CIPK11_1	-2.629	0.0048	down	CIPK11	-2.784	6E-05	down	down
At3g45410	no	up	salt stress induced ethylene repressed L-type lectin receptor kinase I.3; LecRK-I.3	LECRK13_1	68.663	0.0349	up	LECRK13	64.857	0.025	up	
AT3G28610	no	down	salt stress regulated AAA ATPase with signal peptide	AT3G28610_1	-17.42	0.0354	down	AT3G28610	-19.22	0.01	down	
AT3G51960		up	salt tolerance ATBZIP24, BASIC LEUCINE ZIPPER 24, BZIP24 TF					ATBZIP24	8.1752	0.025	up	
AT1G66230	no	up	salt tolerance negative regulation of PP2Cs MYB20 TF	MYB20_1	56.434	0.0439	up	MYB20	53.413	0.033	up	
AT1G62000	no	up	seed coat mucilage protein	AT1G62000_1	75.477	0.0309	up	AT1G62000	71.295	0.022	up	
AT3G13540	no	down	seed endosperm coat mucilage formation negative regulation of trichome branching MYB5 TF	MYB5_1	-56.93	0.0383	down	MYB5	-61.76	0.022	down	
AT1G15320	yes	up	seed germination dormancy DOG1 domain TF	AT1G15320_2	57.415	0.0418	up	AT1G15320	14.91	0.017	up	
AT1G09970	no	down	seed germination oxidative stress tolerance RLK7 LRR XI-23 Leucine-rich receptor kinase	LRR XI-23_1	-4.413	0.0003	down	LRR XI-23	-2.878	2E-06	down	
AT2G46590	no	down	seed germination viability DOF AFFECTING GERMINATION 2 DAG2 Dof-type zinc finger TF					DOF2.5	-2.123	0.039	down	
AT5G09530	no	up	seed germination/growth positive regulator transmembrane PELPK1 hydroxyproline-rich glycoprotein	AT5G09530_1	18.242	0.0038	up	AT5G09530	17.236	2E-04	up	
AT3G61880	yes	up?	seed pod development fertilization independent unknown Cytochrome P450 CYP78A9	CYP78A9_2	50.626	0.0481	up	CYP78A9	6.9856	0.042	up	down
AT2G23510	no	down	seed specific spermidine disinapoyl acyltransferase					SDT	-9.657	0.044	down	
AT4G27160	no	down	seed storage albumin 3	AT2S3_1	-119.4	0.0199	down	AT2S3	-125.3	0.011	down	
AT3G54320		down?	seed storage compounds positive regulator of LEC, AP2/ERWEBP TF ACTIVATOR OF SPO(MIN)::LUC1; ASML1; ATWRI1; WRI; WRINKLED; WRINKLED 1					WRI1	14.885	0.019	up	
AT1G62710	no	up	seed storage protein processing vacuolar cysteine protease BETA-VPE beta vacuolar processing enzyme	bVPE_1	59.184	0.0431	up	bVPE	56.054	0.032	up	
AT3G62020	yes	down	seed strorage Cupin_1 domain germin with signal peptide					GLP10	10.544	0.02	up	
AT2G26170	yes	down	shoot branching negative regulator of genes in flavonoid synthesis MAX1, MORE AXILLARY BRANCHES 1					CYP711A1	9.4693	0.041	up	
AT1G77932	no	up	shoot meristem growth WUS repressor FAF domain Fantastic Four meristem regulator homolog					AT1G77932	45.669	0.038	up	
At1g72010	no	down	shoot meristem leaf development DELLA intarcting TCP22 TF					TCP22	-2.897	0.029	down	
AT5G19260	no	down	shoot meristem WUS repressor FANTASTIC FOUR 3					FAF3	-8.165	0.027	down	
AT3G06020	no	down	shoot meristem WUS repressor FANTASTIC FOUR 4	FAF4_1	-140.8	0.0148	down	FAF4	-153.5	0.007	down	
AT1G15215		down?	silecing DNA methylation factor DNA-binding transcription factor 1; DTF1; SAWADEE homeodomain homolog 1					AT1G15215	-2.889	0.012	down	
AT1G80740	no	up	silencing CHROMOMETHYLASE 1; DMT4; DNA METHYLTRANSFERASE 4	CMT1_1	52.935	0.0456	up	CMT1	50.003	0.034	up	
AT3G46580	no	up	silencing DNA methylation MBD5 methyl-CPG-binding domain protein 5					MBD5	12.2	0.023	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT4G15417	yes	up	silencing dsRNA processing Rnase III	ATRTL1_2	59.662	0.0411	up	ATRTL1	56.357	0.03	up	
AT2G32940	no	up	silencing heterochomomatic siRNA DNA methylation AGO6 Argonaute	AGO6_1	10.621	0.0392	up	AGO6	10.034	0.01	up	
AT1G05910	no	down	silencing inhibitor Bromodomain and ATPase BRAT1					AT1G05910	-3.597	0.009	down	
At3g02950	no	down	silencing mRNA import siRNA THO7 Tho complex subunit 7/Mft1p					THO7B	-4.565	0.024	down	
At5g16790		down	silencing mRNA import siRNA THO7 Tho complex subunit 7/Mft1p					THO7A	-4.73	0.011	down	
AT5G02950	yes	up	silencing MSI4/FVE histone deacetylase complex interacting PWP domain protein	AT5G02950_2	13.576	0.0275	up	AT5G02950	11.662	0.002	up	up
AT3G17712	yes	up?	silencing NRDE2 NRDE-2, necessary for RNA interference	AT3G17712_1	17.47	0.0321	up	AT3G17712	4.8484	0.049	up	up
AT3G17310		up?	silencing repeat siRNA non-CG DNA methylation AtDRM3; domains rearranged methyltransferase 3					DRM3	4.1524	0.041	up	down?
AT5G58130	no	down	silencing repressor ROS3 RNA binding protein required for DNA demethylation					ROS3	-2.527	0.045	down	
AT3G11770	no	down	silencing RISK AGO associated RICE1 3'-5' exonuclease degrading uridylated RNAs					AT3G11770	-2.683	0.047	down	
AT1G15340	no	down	silencing siRNA MBD10 methyl-CPG-binding domain					MBD10	-2.115	2E-08	down	up
AT3G42670	no	down	silencing SWI/SNF CHR38 ATPase subunit CLASSY1	CHR38_4	-6.789	0.0335	down	CHR38	-5.096	0.003	down	up
AT2G16390	yes	up?	silencing SWI/SNF2 CHR35; DEFECTIVE IN MERISTEM SILENCING 1; DEFECTIVE IN RNA-DIRECTED DNA METHYLATION 1; DMS1	DRD1_1	93.845	0.0286	up	DRD1	6.5968	0.006	up	
AT3G23780	no	down	silencing transposon facultative heterochromatin C-methylation RNA polymerase IV	NRPD2_2	-177.4	0.0091	down	NRPD2	-2.943	0.014	down	up
AT2G41850	no	up	silique/seed abscission ADPG2; ARABIDOPSIS DEHISCENCE ZONE POLYGALACTURONASE 2	ADPG2_1	16.595	0.0098	up	ADPG2	15.679	0.001	up	
AT3G17740	no	down	siRNA mediated silencing NRDE-2, necessary for RNA interference, domain	AT3G17740_1	-3.375	0.0318	down	AT3G17740	-3.619	0.006	down	
AT5G45150		up?	siRNA mediated silencing RTL2 homolog	RTL3_2	66.995	0.0409	up	RTL3	106.99	0.013	up	down
AT5G60550	no	up	SnRK1 activating protein kinase SNAK1					GRIK2	3.2802	0.03	up	
AT1G79400	no	up	sodium transport salt tolerance CHX2 cation/H+ exchanger 2	CHX2_1	56.184	0.0438	up	CHX2	53.405	0.032	up	
AT4G10060	no	up	sphingolipid metabolism ER non-lysosomal glucosylceramidase	AT4G10060_1	21.249	0.0141	up	AT4G10060	20.072	0.004	up	
AT4G22330	no	up	sphingolipid signaling salt pathogen tolerance Acyl-CoA independent ceramide synthase					ATCES1	2.0776	0.027	up	
AT1G21790	no	up	sphingolipid signaling transmembrane essential TLC (TRAM, LAG1 and CLN8 homology domain) protein acyl-CoA-dependent ceramide synthesis	AT1G21790_1	4.535	0.0405	up	AT1G21790	4.2856	0.004	up	
AT3G55200		down	spliceosome 17S U2 snRNP atSAP130a splicing factor 3B subunit 3	AT3G55200_1	-2.811	0.0452	down	AT3G55200	-2.341	0.015	down	
AT1G09770	no	down	spliceosome activating NTC complex core subunit CDC5	CDC5_1	-2.178	0.0037	down	CDC5	-2.314	7E-05	down	
AT1G58470	no	up	spliceosome asociated AtRNPA/B_7 RBP1; RNA-binding protein 1					RBP1	7.805	0.026	up	
AT2G42510	yes	down	spliceosome assembly	AT2G42510_1	111.66	0.0192	up	AT2G42510	41.56	0.001	up	up
AT3G59810	no	up	spliceosome associated Lsm core protein atLSM6a U6 snRNA-associated Sm-like protein LSm6	LSM6A_3	149.37	0.0134	up	LSM6A	6.851	0.007	up	
AT2G14285	no	up	spliceosome associeted Sm core protein SmF Small nuclear ribonucleoprotein family protein					AT2G14285	6.4125	0.048	up	
AT1G53720		down?	spliceosome B-complex associated interacts also with BRZ1					CYP59	-2.373	0.002	down	down
AT5G15270	yes	up?	spliceosome HnRNA K homology RNA-binding domain repeat protein	AT5G15270_1	18.494	0.0067	up	AT5G15270	3.4886	0.006	up	
AT5G40490	yes	up	spliceosome hnRNP A/B-8a protein HLP1, RBGD5, RNA-BINDING GLYCINE-RICH PROTEIN D5	AT5G40490_1	-22.1	0.0176	down	AT5G40490	-2.483	0.041	down	
AT3G07590	no	up	spliceosome Sm cor eatSmD1-a Small nuclear ribonucleoprotein	AT3G07590_1	13.456	0.0118	up	AT3G07590	5.3599	0.015	up	
AT5G22480	no	up	spliceosome U2 snRNP atSPF30 survival of motor neuron-related-splicing factor 30 interacting ZPR1 protein	AT5G22480_1	2.851	0.0352	up	AT5G22480	2.7166	0.008	up	
AT1G20960	no	down	spliceosome U5 snRNP atU5-200-2a EMB1507 BRR DExH-box ATP-dependent RNA helicase DExH12					BRR2A	-2.01	6E-08	down	
AT4G03430	no	down	spliceosome U5 snRNP subunit atU5-102KD, STABILIZED 1 (STA1); EMB2770	STA1_1	-2.1	0.0003	down	STA1	-2.09	6E-06	down	up
At5g42920	yes	up	spliceosome, mRNA export, siRNA silencing	THO5B_1	-147.5	7E-10	down	THO5B	-2.425	0.01	down	down
AT2G19270	no	down	splicing MAD2B interacting PRCC domain protein					AT2G19270	-2.011	0.017	down	
AT4G38590		up?	splicing PRP1_N domain D-galactoside binding lectin domain O-Glycosyl hydrolases					BGAL14	17.826	0.005	up	
AT1G80000	yes	down?	splicing RNA export exon junction complex CASC3 (cancer susceptibility candidate gene 3 protein) homolog	AT1G80000_4				AT1G80000	-2.576	0.046	down	
AT5G12280	no	up	splicing unknown Suppressor-of-White-APricot splicing regulator and ubiquitin domain protein					AT5G12280	11.651	0.025	up	
AT3G01530	no	up	stamen development filament elongation GA/JA induced MYB057 TF	MYB57_1	17.516	0.0339	up	MYB57	16.546	0.012	up	
AT2G21590		up	starch biosynthesis APL4 large subunit of ADP-glucose pyrophosphorylase	APL4_7	29.69	0.0185	up	APL4	10.573	0.009	up	down
AT2G40840	no	down	starch degradation DPE2 disproportionating enzyme 2	DPE2_1	-2.564	0.0338	down	DPE2	-2.75	0.004	down	
AT5G19220	no	up	starch synthesis APL1 ADP glucose pyrophosphorylase large subunit 1					ADG2	10.041	0.04	up	
AT1G11720	yes	up	starch synthesis, transient starch SS3 starch synthase 3	ATSS3_2	267.97	0.0055	up	ATSS3	11.759	0.002	up	
AT4G39410	no	down	stem development flowering lignin synthesis WRKY13 TF					WRKY13	-3.442	0.021	down	
AT2G23910	no	up	steroid metabolism 3-beta-hydroxy-delta5-steroid dehydrogenase	AT2G23910_3	15.487	0.0295	up	AT2G23910	14.659	0.008	up	up?
AT1G78480	no	down	sterol biosynthesis membrane-bound Prenyltransferase	AT1G78480_1	-10.43	0.0349	down	AT1G78480	-11.32	0.006	down	
AT4G22755	no	up	sterol biosynthesis transmembrane sterol desaturase	SMO1-3_1	25.985	0.0211	up	SMO1-3	24.635	0.008	up	
AT5G57240	no	up	sterol transport Pleckstrin homology (PH) domain ORP4C OSBP(oxysterol binding protein)-related protein 4C	ORP4C_2	81.36	0.0338	up	ORP4C	7.5696	0.029	up	down
AT2G46890	no	up	sterol/BR biosynthesis transmembrane 3-oxo-5-alpha-steroid 4-dehydrogenase	AT2G46890_1	19.725	0.0183	up	AT2G46890	18.74	0.005	up	
AT3G47350	yes	down?	sterol/BR synthesis HSD2 hydroxysteroid dehydrogenase 2	ATHSD2_1	2.7419	0.0224	up	ATHSD2	2.5849	0.002	up	
AT1G75640	no	up	stomata bilateral symmetry Leucine-Rich Repeat Receptor-Like Kinase MUSTACHES (MUS)					AT1G75640	7.359	0.032	up	
AT3G05030		down?	stomata closure K+ uptake vacuolar NHX2 sodium hydrogen exchanger 2					NHX2	-2.322	0.033	down	
AT5G24030	yes	up	stomatal closure ABA pathogen anion transport, NH3/chlorate channel SLAH3					SLAH3	-2.997	0.017	down	down
AT4G31805	no	up	stomatal differentiation asymmetric cell division WRKY TF POLAR; POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND REDISTRIBUTION					POLAR	9.1037	0.014	up	
AT3G54540	no	down	stomatal opening RIN4 interacting ABC transporter ATGCN4, ATP-BINDING CASSETTE F4, GCN4, GENERAL CONTROL NON-REPRESSIBLE 4	ABCF4_1	-2.232	0.0285	down	ABCF4	-2.262	7E-04	down	up
AT1G80180	no	down	stomatal patterning/division MAPK3/6 substrate	AT1G80180_1	-3.926	0.0017	down	AT1G80180	-4.188	1E-05	down	down
AT1G13170	yes	up	strerol transport ORP1D OSBP(oxysterol binding protein)					ORP1D	-2.505	0.019	down	

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AT2G32160	no	up	stress defense yeast meiotic N2227 domain protein homolog	AT2G32160_2	13.958	0.0148	up	AT2G32160	5.9412	0.02	up	down
AT1G29230	no	up	stress signaling CBL-interacting protein kinase 18;SNF1-RELATED PROTEIN KINASE 3.20; SnRK3.20; WL1; WPL4-LIKE 1	CIPK18_1	95.827	0.0234	up	CIPK18	90.52	0.016	up	
AT2G01670	no	up	stress signaling NUcleoside Diphosphate hydrolase NUDIX17					NUDT17	7.7299	0.029	up	
AT2G04430	yes	up?	stress signaling NUcleoside Diphosphate hydrolase NUDIX5	NUDT5_2	69.724	0.037	up	NUDT5	12.197	0.014	up	
AT5G45940		up?	stress signling CoA pyrophosphatase,ppGpp pyrophosphohydrolase and NADH pyrophosphatase					NUDT11	14.365	0.017	up	
AT3G52340	yes	up?	sucrose biosynthesis Sucrose-6-phosphate phosphohydrolase SPP2					SPP2_2	5.7903	0.032	up	up?
At3g54270	no	up	sucrose synthesis Sucrose-6-phosphate phosphohydrolase	SPP3A_1	8.4313	0.0493	up	SPP3A	8.0425	0.013	up	
AT1G07340	no	up	sugar hexose transporter male gametophyte STP2 sugar transporter 2	STP2_1	73.294	0.0321	up	STP2	69.236	0.023	up	
AT3G47800	no	down	sugar metabolism Aldose 1-epimerase (EC 5.1.3.3) (mutarotase)					AT3G47800	-2.472	0.003	down	
At5g14470	no	down	sugar metabolism galactokinase 2; GALK2	GLCAK2_1	-2.967	0.0014	down	GLCAK2	-3.15	7E-06	down	
AT5G39970	yes	up?	sugar metabolism glucose/sorbosone dehydrogenase (_to gluconolactone)	AT5G39970_3	-36.51	2E-05	down	AT5G39970	-21.38	6E-06	down	
AT1G47840	no	up	sugar metabolism sensing hexokinase 3					HXK3	5.825	0.046	up	
AT4G32272	yes	down	sugar metabolism Triose-phosphate Transporter					AT4G32272	5.1683	0.043	up	down
AT4G10960	no	down	sugar metabolism UDP-D-glucose/UDP-D-galactose 4-epimerase 5					UGE5	-11.2	0.026	down	
AT5G40510		up?	sugar sucrose catabolism transmembrane sucrase					AT5G40510	6.8579	0.033	up	
AT1G50310	no	up	sugar transpor SUGAR TRANSPORTER 9,STP9	STP9_1	77.698	0.0305	up	STP9	13.724	0.005	up	
AT3G16690		up?	sugar transport growth under stress conditions vacuolar sugar carrier AtSWEET16					SWEET16	58.786	0.029	up	down
AT1G22710	no	up	sugar transport phloem loading SUC2 sucrose-proton symporter 2	SUC2_1	82.806	0.0279	up	SUC2	78.648	0.019	up	
AT1G11260	no	down	sugar transport STP1 H+/hexose cotransporter					STP1	-2.014	2E-06	down	
AT3G46180	no	up	sulfate metabolism PAPS transporter SLC35B2 solute carrier family 35 member B2 homolog					UTR5	8.7754	0.012	up	
AT5G24655	no	up	sulfur deficiency RESPONSE TO LOW SULFUR 4 92aa coiled coil oligopeptide	LSU4_1	91.308	0.0253	up	LSU4	86.252	0.017	up	
AT4G39940	no	up	sulfur metabolism PAPS synthesis ADENOSINE-5'-PHOSPHOSULFATE (APS) KINASE 2					APK2	6.344	0.046	up	
AT3G49570	no	down	sulfure deficiency induced coiled coil LSU3 protein					LSU3	-2.971	0.033	down	
At5g48850	no	up	SULPHUR DEFICIENCY-INDUCED 1 tetratrico peptide repeat (TPR) coiled coil protein					SDI1	3.6027	0.046	up	
AT1G61740	no	up	taurine metabolism transmembrane sulfoacetate exporter	AT1G61740_1	6.1494	0.0476	up	AT1G61740	5.8689	0.01	up	
AT1G48820	no	up	terpenoid synthesis terpene synthase					AT1G48820	7.3007	0.037	up	
AT1G45110	no	up	tetrapyrrole metabolism Tetrapyrrole methytransferase					AT1G45110	7.3355	0.026	up	
AT4G29760	no	up	thermotolerance HEAT-INDUCED TAS1 TARGET 4; HTT4	AT4G29760_1	67.975	0.0354	up	AT4G29760	64.539	0.025	up	
AT2G33735	no	up	thermotoleranceprotein foldin HEAT-INDUCED TAS1 TARGET1, HTT1 DNAJ chaperon					AT2G33735	6.9663	0.035	up	
AT3G21430	no	up	transc ription telomer SIN3 repressor interacting MYB TF ALWAYS EARLY 3; ATALY3					ALY3_2	2.1754	0.038	up	
AT5G49420	no	up	transciption AGAMOUS-LIKE 84, AGL84 TF					AT5G49420	7.7818	0.031	up	
AT1G48610	yes	down	transcription AT-hook high mobility group non-histone chromosomal protein HMG-I(Y).					AT1G48610	6.5007	0.039	up	down?
AT3G60870	no	up	transcription AT-hook TF AHL18	AHL18_1	14.633	0.0455	up	AHL18	13.822	0.019	up	
At4g28140	no	down	transcription DREB subfamily A-6 of ERF/AP2 ERF54					ERF054	-3.685	0.01	down	down
AT3G48920	no	up	transcription MYB DOMAIN PROTEIN 45, MYB45 TF	AtMYB45_1	14.002	0.0262	up	AtMYB45	13.397	0.005	up	
AT2G34440	no	up	transcription AGAMOUS-LIKE 29, AGL29 TF					AGL29	8.5548	0.049	up	
AT2G26880	no	up	transcription AGL41 AGAMOUS-like 41 TF					AGL41	41.004	0.047	up	
AT4G17950	no	down	transcription AHL13, AT-HOOK MOTIF NUCLEAR LOCALIZED PROTEIN 13					AHL13	-2.053	0.015	down	
AT5G43850	no	up	transcription arabinose-binding AraC_domain TF					ARD4	2.5357	0.039	up	
AT2G45850		up?	transcription AT_hook AHL9 TF					AHL9	7.6295	0.036	up	
AT5G52890		up?	transcription AT_hook domain TF	AT5G52890_2	97.257	0.0236	up	AT5G52890	107.5	0.012	up	
AT5G46915	no	up	transcription B3 domain repeat TF					AT5G46915	45.665	0.038	up	
AT4G20970	no	up	transcription basic helix-loop-helix (bHLH) BHLH162 TF					AT4G20970	6.3125	0.043	up	
AT4G15250	no	up	transcription BBX9 B-box type zinc finger CCT domain TF					COL11	46.141	0.039	up	
AT3G02160		up	transcription bromodomain BTP domain TF					AT3G02160	48.38	0.036	up	
AT3G16490	no	up	transcription calmodulin binding DUF4005 and IQ domain protein IQD26					IQD26	10.105	0.037	up	
AT5G14370	no	down	transcription CCT (CONSTANS, CO-like, and TOC1) domain TF					AT5G14370	-2.724	0.01	down	
AT1G50590		up?	transcription cell death pirin					AT1G50590	8.9618	0.022	up	
AT1G29220	no	down	transcription cell death SAP30-binding transcriptional co-repressor with HCNGP and coiled coil domains					AT1G29220	-2.04	0.043	down	
At5g59450	no	down	transcription cell division SCL11 GRAS TF					SCL11	-2.91	0.044	down	
AT4G00980	no	up	transcription chromatin binding DEKc and ssDNA-binding transcriptional regulator domain LTR type gag-polypeptide	AT4G00980_1	59.01	0.041	up	AT4G00980	56.007	0.03	up	
AT3G14880		down?	transcription DOG1 domain TGA/PERIANTHIA-like TF					AT3G14880	-7.059	0.031	down	
At4g31640	no	down	transcription double B3 domain TF with coiled coil motive					REM5	-49.94	0.033	down	
AT5G59140	no	up	transcription elongation factor B (SIII) complex elongin C regulatory subunit					AT5G59140	2.164	0.024	up	
AT1G03800	no	up	transcription ERF010 (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor	ERF10_1	23.582	0.0119	up	ERF10	22.278	0.002	up	
At1g77200	no	up	transcription ERF037 DREB subfamily A-4 of ERF/AP2 transcription factor	ERF037_1	62.004	0.0391	up	ERF037	58.571	0.029	up	
AT1G14687	no	up	transcription flower development homeobox 32 ZF-HD_dimer domain protein					ZHD14	8.3825	0.048	up	down
At1g71450	no	up	transcription flower senescence ERF021 DREB subfamily A-4 of ERF/AP2 transcription factor	ERF021_1	131.38	0.0156	up	ERF021	124.29	0.01	up	
AT3G06740	no	up	transcription GATA15 ZnF_GATA domain TF					GATA15	7.5356	0.035	up	

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AT4G34680	no	up	transcription GATA3 GATA transcription factor 3	GATA3_2	102.23	0.0225	up	GATA3	141.87	0.009	up	
AT4G18150	no	down	transcription GBF1-like co-activator DUF1296 domain proetin					AT4G18150	-12.17	0.021	down	
AT1G18860	no	up	transcription group II-B ATWRKY61, WRKY DNA-BINDING PROTEIN 61					WRKY61	7.2973	0.027	up	
AT5G66350	yes	up?	transcription gynoeceum, stamen and leaf development SHI, SHORT INTERNODES DUF702 domain TF	SHI_1	56.321	0.0492	up	SHI	88.42	0.016	up	
AT3G27420	no	up	transcription H3-AC binding Bromodomain extra-terminal - transcription regulation TF	AT3G27420_1	32.346	0.0027	up	AT3G27420	30.716	2E-04	up	
AT3G03260	yes	down	transcription HOMEODOMAIN GLABROUS 8 TF with START lipid-binding domain in StAR and phosphatidylcholine transfer protein	HDG8_1	84.616	0.0268	up	HDG8	6.2987	0.037	up	up
AT5G28210	no	up	transcription initiation mRNA capping enzyme RNA guanylyltransferase and 5'-phosphatase RNGTT, HCE; HCE1; hCAP; CAP1A	AT5G28210_1	17.035	0.0373	up	AT5G28210	16.128	0.014	up	
AT4G00210	no	up	transcription lateral organ boundaries (LOB) domain TF	LBD31_1	11.639	0.0386	up	LBD31	10.995	0.011	up	
AT2G16400	no	up	transcription leaf development KNAT-interacting BLH7 TF					BLH7	2.6044	0.049	up	
At5g19790	no	up	transcription low potassium regulated RAP2.11 ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor	RAP2-11_1	93.639	0.0242	up	RAP2-11	88.456	0.016	up	
AT5G27580	no	down	transcription MADS TF AGAMOUS-LIKE 89, AGL89	AGL89_1	-53.91	0.0475	down	AGL89	-56.2	0.029	down	
AT5G12980	no	down	transcription mRNA turn over RCD1/CAF40 homolog	AT5G12980_1	-4.584	0.0309	down	AT5G12980	-4.953	0.004	down	
AT4G09460	no	up	transcription MYB DOMAIN PROTEIN 6, MYB6 TF	MYB6_1	116.29	0.0184	up	MYB6	109.86	0.012	up	
At2g01060	yes	down	transcription MYB TF PHL7	PHL7_1	131.87	0.0152	up	PHL7	3.8727	0.008	up	
AT3G10590	no	down	transcription MYB TF with 2 SANT domains					AT3G10590	-10.48	0.015	down	
AT4G13480	no	down	transcription MYB79 TF					AtMYB79	-15.79	0.027	down	
AT5G22240	no	up	transcription negative regulation of cell differentiation ovate AtOFP10 repressor TF	OFP10_1	100.26	0.0223	up	OFP10	94.701	0.015	up	
AT5G04820	no	up	transcription negative regulation of cell differentiation ovate AtOFP13 repressor TF	OFP13_1	17.336	0.0358	up	OFP13	16.555	0.014	up	
AT1G20640		down?	transcription nitrogen controlled GAF, RWP-RK and PB1 dimerization domain TF					NLP4	-2.393	0.021	down	up
AT3G47680	no	up	transcription No Apical Meristem and SANT domain MYB TF					AT3G47680	2.4675	0.049	up	
AT3G60670	no	up	transcription PLATZ transcription factor					AT3G60670	42.104	0.043	up	
AT1G18750		up?	transcription pollendevelopment AGL65 TF					AGL65	5.8123	0.044	up	
AT5G27030		down?	transcription repressor LEUNING-like TPR3 TOPLESS-related 3					TPR3_2	-2.187	0.002	down	up
AT4G00850	no	up	transcription reproductive male female and organ development SSXT domain coactivator GRF1-interacting factor 3	GIF3_1	139.12	0.0145	up	GIF3	7.1102	0.021	up	
AT1G60880	no	up	transcription root specific AGAMOUS-LIKE-56, AGL56					AGL56	43.55	0.04	up	
At3g53370	no	up	transcription S1FA TF	S1FA1_2	18.518	0.016	up	S1FA1	14.254	0.003	up	
AT2G47820	no	down	transcription SANT domain MYB TF	AT2G47820_1	-449.7	0.0017	down	AT2G47820	-5.131	0.001	down	
AT5G50570	no	up	transcription SPL13A Squamosa promoter-binding protein-like TF	SPL13B_1_2	103.49	0.0221	up	SPL13B_1	104.73	0.013	up	down
At1g16070	yes	down	transcription TLP8 tubby like TF	TULP8_1	-11.24	0.0467	down	TULP8	-5.772	0.031	down	
AT1G14490	no	up	transcription transmembrane AT-hook TF	AT1G14490_2	12.796	0.0376	up	AT1G14490	6.0103	0.039	up	
AT3G56390	no	up	transcription trichome differentiation ZPF5 interacting inhibitor TRICHOME RELATED PROTEIN, TRP TF	AT3G56390_1	60.382	0.0399	up	AT3G56390	57.555	0.029	up	
AT1G31310	no	up	transcription unknown MYB TF	AT1G31310_1	51.259	0.0487	up	AT1G31310	48.495	0.037	up	
AT3G60520		up?	transcription unknown PHD zinc finger TF					AT3G60520	9.4899	0.018	up	down
AT4G22070	no	down	transcription WRKY31 WRKY DNA-binding protein 31					WRKY31	-3.633	0.019	down	down
AT2G40740	yes	up?	transcription WRKY55 TF	WRKY55_2	79.953	0.0288	up	WRKY55	79.816	0.018	up	
AT3G62340	no	up	transcription WRKY68 groupII-C TF					WRKY68	6.1632	0.047	up	
AT2G31600	yes	up	transcription zf-C3Hc3H domain TF	AT2G31600_3	74.676	0.0315	up	AT2G31600	7.1733	0.027	up	
AT2G14825	no	up	transcription zf-UBP domain TF					AT2G14825	7.8234	0.017	up	
AT5G60470	no	down	transcription ZnF_C2H2 domain repeat TF	AT5G60470_1	-3.999	0.042	down	AT5G60470	-4.484	3E-05	down	
AT5G15480	no	up	transcription ZnF_C2H2 domain TF	AT5G15480_1	14.066	0.0472	up	AT5G15480	13.287	0.02	up	
AT1G48150	no	up	transcription, AGAMOUS-LIKE 74, AGL74 TF					AT1G48150	11.657	0.027	up	
AT1G29370		down?	transcription, GBF1-interacting protein 1-like DUF1296 domain protein with coiled coil domain					AT1G29370	-2.268	5E-06	down	down
AT2G24645		up?	transcription, unknown B3 domain TF					AT2G24645	54.241	0.03	up	down
AT3G25560	yes	up?	translation RIBOSOMAL PROTEIN L10 A interacting transmembrane LRR kinase with signal peptide					NIK2	5.9297	0.045	up	up
AT3G16040	no	up	translation 64aa oligopeptide Translation machinery associated TMA7					AT3G16040	6.8592	0.045	up	
AT4G30690	no	up	Translation initiation factor 3	AT4G30690_1	177.47	0.0101	up	AT4G30690	167.66	0.006	up	
AT4G11420	no	down	translation initiation factor eIF-3 subunit 10 (EIF3A)	TIF3A1_1	-2.151	0.0016	down	TIF3A1	-2.282	2E-05	down	
AT4G38710	yes	up	translation initiation factor eIF-4B					AT4G38710	-2.002	0.009	down	
AT3G44770	no	up	transmembrane DUF626 domain protein					AT3G44770	2.6406	0.04	up	
AT1G75140	no	up	transmembrane protein with signal peptide	AT1G75140_1	9.6277	0.0197	up	AT1G75140	9.1856	0.003	up	
AT4G36925	yes	up	transmembrane protein with signal peptide	AT4G36925_1	52.905	0.0456	up	AT4G36925	49.973	0.034	up	
AT3G24255	yes	up?	transposition reverse transcriptase					AT3G24255	-6.804	0.045	down	down
AT2G36355		up?	transriptin wheat TaSRG salt stress induced TF Transcrip_act domain protein homolog					AT2G36355	13.6	0.02	up	up
AT5G13920	yes	up?	transription ZnF_C2HC and zf-GRF domain putative TF	AT5G13920_2	93.523	0.0245	up	AT5G13920	88.343	0.016	up	
AT5G56960	yes	down	transription basic helix-loop-helix (bHLH) BHLH41 EN51 TF					AT5G56960	37.146	0.048	up	
AT5G65140		up?	trehalose TPPJ trehalose-6-phosphate phosphatase J					TPPJ	62.881	0.026	up	
AT5G10100	yes	up?	trehalose-6-phosphate phosphatase I	TPPI_1	55.146	0.0441	up	TPPI	7.6095	0.036	up	
AT1G78580		up	TREHALOSE-6-PHOSPHATE SYNTHASE 1					TPS1	13.27	0.02	up	
AT1G14460	no	up	trichome branching STICHEL homolog DNA_pol3_gamma3 domain AAA ATPase					AT1G14460	5.985	0.026	up	up

TAIR locus	Altered coding	Predicted effect on gene function	Pathw ay	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
At1g19835	no	down	trichome cell shape 1 (tcs1) controlling trichome branch number microtubule binding coiled coil protein	FPP4_5	-2.519	0.0197	down	FPP4	-2.372	9E-04	down	up
AT5G52600	no	up	trichome development GL1 partner MYB82 TF	MYB82_1	21.316	0.0302	up	MYB82	20.17	0.011	up	
AT4G38600		down	trichome development GL3 and EGL3 HECT ubiquitin ligase 3 KAKTUS; UBIQUITIN-PROTEIN LIGASE 3; UBIQUITIN_PROTEIN LIGASE; UPL3					UPL3	-2.168	1E-05	down	
AT4G00480	yes	down?	trichome root hair differentiation MYC1 TF					ATMYC1	-16.96	0.031	down	
AT5G20040	yes	up?	tRNA isopentenyltransferase AtIPT9					ATIPT9	4.483	0.048	up	
AT1G09620	no	down	tRNA LARS leucyl-tRNA synthetase	AT1G09620_1	-2.233	0.0137	down	AT1G09620	-2.377	0.001	down	
AT5G38290	no	up	tRNA Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH)	AT5G38290_1	68.753	0.0345	up	AT5G38290	64.946	0.024	up	
AT5G13240	yes	down	tRNA strarvation stress induced RNA polIII negative regulator MAF1 with signal peptide					AT5G13240	4.117	0.038	up	up
AT1G70220	no	up	tRNA synthesis transmembrane Anticodon-binding domain putative tRNA synthase					AT1G70220	6.926	0.038	up	
AT2G28450	no	down	tRNA TRM2B, TRNA METHYLTRANSFERASE 2B	AT2G28450_1	-2.008	0.0198	down	AT2G28450	-2.106	0.003	down	
At1g75200	no	down	tRNA TYW1 tRNA-yW synthesizing protein 1	TYW1_1	-3.366	0.0139	down	TYW1	-3.614	7E-04	down	
AT3G62850	no	up	tRNA/rRNA processing NYN and ZnF_C2H2 domain protein	AT3G62850_1	122.94	0.017	up	AT3G62850	116.14	0.011	up	
AT3G02370	no	up	tRNA-splicing endonuclease subunit	AT3G02370_1	18.851	0.0162	up	AT3G02370	12.232	0.004	up	up
AT4G39240	no	up	ubiquiination SCF E3 Kelch repeat F-box protein	AT4G39240_1	10.025	0.0088	up	AT4G39240	9.5298	7E-04	up	
AT5G01070	no	down	ubiquiination transmembrane RINGv domain E3					AT5G01070	-9.91	0.038	down	
AT4G32270	no	up	ubiquitin	AT4G32270_1	91.031	0.026	up	AT4G32270	86.23	0.017	up	
AT1G65350	no	down	ubiquitin 13					UBQ13	-34.71	0.034	down	
AT4G05230	no	down	ubiquitin poly_UBI					AT4G05230	-49.94	0.033	down	
AT2G32350	no	up	ubiquitin polyUbi	AT2G32350_1	14.071	0.0489	up	AT2G32350	13.292	0.021	up	
AT1G80690	yes	down	ubiquitin protease PPPDE superfamily (after Permuted Papain fold Peptidases of DsRNA viruses and Eukaryotes)					AT1G80690	39.314	0.045	up	
AT2G24510	no	down	ubiquitin SCF E3 F-box associated domain protein	AT2G24510_1	-42.53	0.0154	down	AT2G24510	-44.03	0.005	down	
AT5G14160	no	up	ubiquitin SCF E3 C-type lectin (CTL) domain transmembrane F-box protein	AT5G14160_1	20.393	0.0261	up	AT5G14160	19.263	0.009	up	
AT1G16930	no	down	ubiquitin SCF E3 LRR repeat F-box protein	AT1G16930_2	-38.05	8E-05	down	AT1G16930	-41.11	2E-06	down	
AT1G65650	no	up	ubiquitin transcription proteasome UCH2 UBIQUITIN C-TERMINAL HYDROLASE 2					UCH2	5.1634	0.03	up	
At1g23410	no	down	Ubiquitin-40S ribosomal protein S27a-1	RPS27AA_1	-94.75	0.0254	down	RPS27AA	-103.4	0.014	down	
AT3G25880	yes	down	Ubiquitin-activating enzyme (E1 enzyme)					AT3G25880	17.48	0.012	up	
AT3G27640		up?	ubiquitination CUL4-DDB1 substrate adaptor WD40 protein	AT3G27640_1	63.996	0.0424	up	AT3G27640	88.8	0.017	up	down
AT4G00070		up?	ubiquitination RING E3	AT4G00070_1	21.901	0.0245	up	AT4G00070	7.8816	0.017	up	
AT5G41400	no	up	ubiquitination RING E3					AT5G41400	37.71	0.048	up	
AT1G27910	no	up	ubiquitination ARM repeat U-box E3					PUB45	5.6605	0.026	up	
AT1G26830	no	down	ubiquitination BTB domain CUL3 E3 ligases					CUL3A	-2.006	0.007	down	
AT1G30860	no	up	ubiquitination coiled coil domain RING E3	AT1G30860_1	35.803	0.0089	up	AT1G30860	33.938	0.003	up	
AT4G01023	yes	down?	ubiquitination coiled coil RING E3	AT4G01023_3	-18.18	0.0298	down	AT4G01023	-5.243	0.035	down	
AT3G13590	no	up	ubiquitination DAG binding C1 domain repeat PHD zinc finger RING E3	AT3G13590_1	55.162	0.0435	up	AT3G13590	52.106	0.032	up	
AT3G16090	no	down	ubiquitination ERAD (Endoplasmic reticulum-associated degradation)Hrd1A RING/U-box E3					HRD1A	-3.189	0.045	down	
AT2G15530	yes	up	ubiquitination flowering time FT activation MBR1 MED25 BINDING RING-H2 PROTEIN 1	AT2G15530_1	-61.88	0.0403	down	AT2G15530	-3.494	0.026	down	down?
AT3G26750	no	up	ubiquitination HECT E3 ligase					AT3G26750	10.008	0.038	up	
AT1G76410	no	down	ubiquitination membrane-bound RING E3					ATL8	-4.314	0.043	down	down
AT2G12550	no	up	ubiquitination negative regulator NUB1, which targets NEDD8 for proteasomal degradation					AT2G12550	4.0584	0.017	up	
AT5G55800	no	down	ubiquitination PHD zinc finger repeat RING E3					AT5G55800	-9.876	0.035	down	
AT3G54130	no	up	ubiquitination polyUbi binding Josephin domain protein	AT3G54130_1	9.6212	0.0105	up	AT3G54130	9.1478	1E-03	up	
AT3G28620	no	up	ubiquitination RING E3	AT3G28620_1	54.319	0.0477	up	AT3G28620	52.039	0.035	up	
AT2G24480	no	down	ubiquitination RING E3					AT2G24480	-15.33	0.032	down	
AT4G11360	no	up	ubiquitination RING E3 chitin and cadmium induced RING-H2 finger A1B					RHA1B	6.5602	0.013	up	down
AT5G01880	no	down	ubiquitination RING E3 DAF-Like gene 2					ATL74	-17.71	0.026	down	
AT4G00335		up	ubiquitination RING E3 RHB1A, RING-H2 FINGER B1A					RHB1A	6.6097	0.021	up	
AT1G72175	no	up	ubiquitination RING E3 with DUF1232 domain	AT1G72175_1	36.247	3E-05	up	AT1G72175	3.7251	0.008	up	
AT2G43220	no	down	ubiquitination RING E3 with Protein kinase C conserved region 1 (C1) domain repeats and PHD zinc fingers	AT2G43220_1	-9.491	0.0374	down	AT2G43220	-10.33	0.008	down	
AT5G37930	no	up	ubiquitination RING E3 with ZnF_C2H2 domain					AT5G37930	3.6125	0.025	up	
AT4G13960	no	down	ubiquitination SCF E3 F-box protein	AT4G13960_4	-211.7	0.0076	down	AT4G13960	-10.34	0.02	down	
AT2G32470	no	up	ubiquitination SCF E3 F-box interacting FBA_3 domain protein					AT2G32470	14.423	0.027	up	
AT1G67455		up?	ubiquitination SCF E3 F-box protein					AT1G67455	13.295	0.021	up	
AT2G17830	no	up	ubiquitination SCF E3 F-box protein					AT2G17830	3.2693	0.035	up	
AT1G25211	no	up	ubiquitination SCF E3 F-box protein					AT1G25211	4.4931	0.047	up	
AT1G48060	no	up	ubiquitination SCF E3 F-box protein					AT1G48060	5.66	0.038	up	
AT3G17620	no	up	ubiquitination SCF E3 F-box protein					AT3G17620	7.675	0.026	up	
AT3G23260	no	up	ubiquitination SCF E3 F-box protein					AT3G23260	7.2024	0.027	up	
AT3G47150	no	up	ubiquitination SCF E3 F-box protein	AT3G47150_1	18.779	0.0349	up	AT3G47150	17.765	0.015	up	
AT1G20940	no	up	ubiquitination SCF E3 F-box protein	AT1G20940_1	50.659	0.0478	up	AT1G20940	47.853	0.036	up	
AT2G16300	no	up	ubiquitination SCF E3 F-box protein	AT2G16300_1	67.082	0.0358	up	AT2G16300	64.023	0.025	up	
AT3G27290	no	up	ubiquitination SCF E3 F-box protein	AT3G27290_1	123.02	0.0169	up	AT3G27290	116.22	0.011	up	
AT1G23770	no	up	ubiquitination SCF E3 F-box protein	AT1G23770_1	122.52	0.0171	up	AT1G23770	116.06	0.012	up	
AT1G46984	no	up	ubiquitination SCF E3 F-box protein					AT1G46984	37.23	0.049	up	
AT1G49610	no	up	ubiquitination SCF E3 F-box protein					AT1G49610	41.449	0.043	up	
AT2G03610	no	down	ubiquitination SCF E3 F-box protein					AT2G03610	-7.243	0.035	down	
AT3G03030	no	down	ubiquitination SCF E3 F-box protein					AT3G03030	-3.335	0.045	down	
AT5G38396	no	down	ubiquitination SCF E3 F-box protein	AT5G38396_1	-98.69	0.0243	down	AT5G38396	-107.7	0.014	down	
AT3G16210	no	down	ubiquitination SCF E3 F-box protein	AT3G16210_1	-13.12	0.0443	down	AT3G16210	-14.09	0.013	down	
AT2G02350		down?	ubiquitination SCF E3 F-box protein SKIP3, SKP1 INTERACTING PARTNER 3					SKIP3	-2.799	0.014	down	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT3G25750		up?	ubiquitination SCF E3 F-box protein with DUF295 domain	AT3G25750_1	87.888	0.0311	up	AT3G25750	150.16	0.008	up	
AT5G50450	no	down	ubiquitination SCF E3 F-box protein with TPR SEL1 and zf-MYND zinc finger domains					AT5G50450	-14.11	0.019	down	down
At4g21510	no	up	ubiquitination SCF E3 F-BOX STRESS INDUCED 2, FBS2: **no F-box motive**	SKIP27_2	25.142	0.0284	up	SKIP27	14.719	0.01	up	?
AT2G44700	no	up	ubiquitination SCF E3 Kelch repeat F-box protein	AT2G44700_1	22.678	0.0221	up	AT2G44700	21.421	0.007	up	
At4g03030	no	down	ubiquitination SCF E3 Kelch repeat F-box protein					OR23	-2.017	0.006	down	
AT5G48980	no	down	ubiquitination SCF E3 Kelch-repeat F-box protein					AT5G48980	-5.625	0.046	down	
AT1G52650	no	up	ubiquitination SCF E3 LRR F-box protein	AT1G52650_1	82.56	0.0279	up	AT1G52650	78.211	0.019	up	
AT1G32375	no	up	ubiquitination SCF E3 LRR F-box protein	AT1G32375_2	77.977	0.0299	up	AT1G32375	77.289	0.019	up	
AT4G02740	yes	down?	ubiquitination SCF E3 LRR F-box protein	AT4G02740_2	-4.894	0.0197	down	AT4G02740	-3.921	0.004	down	
AT4G10400	no	down	ubiquitination SCF E3 LRR F-box protein					AT4G10400	-4.122	0.01	down	up
AT1G51370	no	up	ubiquitination SCF E3 LRR repeat F-box protein	AT1G51370_2	328.25	0.0036	up	AT1G51370	5.5814	0.033	up	
AT3G60790	no	up	ubiquitination SCF E3 LRR repeat F-box protein					AT3G60790	9.4748	0.037	up	
AT5G38590	yes	up	ubiquitination SCF E3 LRR repeat F-box protein					AT5G38590	17.632	0.011	up	
At4g05460	no	up	ubiquitination SCF E3 LRR repeat F-box protein	SKIP19_1	7.5112	0.0375	up	SKIP19	7.1333	0.008	up	
AT3G58980	no	up	ubiquitination SCF E3 LRR repeat F-box protein	AT3G58980_1	11.472	0.0426	up	AT3G58980	10.88	0.012	up	
AT1G78760	no	up	ubiquitination SCF E3 LRR repeat F-box protein	AT1G78760_1	35.306	0.0092	up	AT1G78760	33.405	0.003	up	
AT2G42730	no	up	ubiquitination SCF E3 LRR repeat F-box protein	AT2G42730_1	56.041	0.0492	up	AT2G42730	52.925	0.037	up	
AT4G09920		down?	ubiquitination SCF E3 LRR repeat F-box protein					AT4G09920	-10.39	0.037	down	
AT5G60610	no	down	ubiquitination SCF E3 LRR repeat F-box protein	AT5G60610_2	-13.99	0.0037	down	AT5G60610	-9.799	0.001	down	up
AT1G26890	yes	down	ubiquitination SCF E3 LRR repeat F-box protein	AT1G26890_3	64.65	0.0429	up	AT1G26890	7.6477	0.035	up	
AT1G13570	yes	down	ubiquitination SCF E3 LRR repeat F-box protein	AT1G13570_3	142.58	0.0145	up	AT1G13570	3.4522	0.037	up	
AT1G05080	no	down	ubiquitination SCF E3 LRR repeat F-box protein					AT1G05080	-5.402	0.047	down	
AT4G29420	no	down	ubiquitination SCF E3 LRR repeat F-box protein	AT4G29420_1	-9.591	0.0168	down	AT4G29420	-10.39	0.002	down	
AT3G60040	yes	down	ubiquitination SCF E3 LRR repeat F-box protein with pentatricopeptide repeats and Rtv3 Reverse transcriptase-like domain	AT3G60040_2	121.35	0.0174	up	AT3G60040	5.4324	0.028	up	
AT1G64540	no	down	ubiquitination SCF E3 LRR repeat F-box proteins					AT1G64540	-4.778	0.038	down	
AT4G34470	no	down	ubiquitination SCF E3 SKP1 subunit ASK12					ASK12	-4.414	0.039	down	
AT3G60020	no	up	ubiquitination SCF E3 SKP5 subunit					ASK5_1	41.409	0.042	up	
AT3G03726	yes	up	ubiquitination SCF E3 transmembrane F-boxn protei with C-type lectin (CTL) or carbohydrate-recognition domain (CRD)					AT3G03726	-38.8	0.045	down	
AT1G22500	no	up	ubiquitination sugar signaling light ascorbate induced transmembrane RING E3 with signal peptide TOXICOS EN LEVADURA 15					ATL15	5.6734	0.047	up	
AT2G20030	no	up	ubiquitination transmembrane RING E3 with signal peptide	ATL12_1	22.073	0.0238	up	ATL12	20.868	0.008	up	
AT5G17600	no	up	ubiquitination transmembrane RING E3					ATL52	39.524	0.047	up	
AT5G43420	no	down	ubiquitination transmembrane RING E3					ATL16	-2.385	0.04	down	
AT2G26135	no	up	ubiquitination transmembrane RING E3 with Reverse transcriptase-like and IMR domains	AT2G26135_1	29.606	0.014	up	AT2G26135	27.966	0.004	up	
AT4G09130	no	up	ubiquitination transmembrane RING E3 with signal peptide	ATL37_1	73.609	0.0327	up	ATL37	69.888	0.023	up	
AT4G09120	no	up	ubiquitination transmembrane RING E3 with signal peptide					ATL36	37.847	0.048	up	
AT1G50440	no	up	ubiquitination transmembrane RINGv E3	AT1G50440_2	68.366	0.04	up	AT1G50440	5.5102	0.037	up	
AT1G70360	yes	down	ubiquitination transmembrane SCF E3 F-box protein	AT1G70360_2	158.07	0.0116	up	AT1G70360	38.281	0.002	up	down
AT5G56150		down?	ubiquitination UBC30 ubiquitin-conjugating enzyme 30					UBC30	-2.043	0.003	down	
At3g61390		up?	ubiquitination UBOX E3 with coiled coil					PUB36	109.73	0.012	up	
AT5G24680	no	up	ubiquitination UfSP1/2,cysteine peptidase homolog required for the processing and activation of Ubiquitin fold modifier 1 (Ufm1, IPR005375) and for its release from conjugated cellular proteins	AT5G24680_1	9.4901	0.0362	up	AT5G24680	9.0115	0.008	up	
AT1G01680	no	up	ubiquitination universal stress protein UspA domain U-box E3					PUB54	5.6284	0.019	up	
AT5G06490	no	down	ubiquitination unknown membrane-bound RING E3	ATL71_1	-30.63	0.0194	down	ATL71	-32.05	0.005	down	
AT5G37230	no	down	ubiquitination unknown RING E3	AT5G37230_1	-67.19	0.038	down	AT5G37230	-73.28	0.021	down	
At2g40640	yes	down?	ubiquitination unknown RING/U-box E3 ligase	PUB63_7	66.451	0.0358	up	PUB63	3.173	0.04	up	down
AT4G27390	no	up	uknown transmembrane protein					AT4G27390	6.3417	0.031	up	
AT5G06890	no	down	uniquitin					AT5G06890	-12.3	0.049	down	
AT5G49000	yes	up	uniquitination SCF E3 Kelch repeat F-box protein					AT5G49000	-3.001	0.045	down	
At1g21760	yes	up?	uniquitination SCF E3 temperature changed induced F-box protein	SKIP32_1	5.1006	0.0033	up	SKIP32	4.904	1E-04	up	
AT2G34355	no	up	unknonw Nodulin-like Major Facilitator Superfamily (MFS) transmembrane transporter					AT2G34355	5.0573	0.049	up	
AT1G62660		up?	vacuolar ATBETAFRUCT4 invertase homolog					BFRUCT3	9.796	0.02	up	
AT4G33400	no	up	vacuolar degradation of Fruc1,6-biphosphatase VID27 domain protein	AT4G33400_1	34.63	0.0097	up	AT4G33400	32.995	0.003	up	
AT1G02530	yes	down	vacuolar fission yeast leptomycin efflux transporter Pmd1 homolog P-glycoprotein transporter	ABCB12_1	240.18	0.007	up	ABCB12	5.2554	0.045	up	
AT1G79410	no	up	vacuolar OCT5 organic cation/carnitine transporter5					43378	6.1899	0.022	up	
At2g36830	no	down	vacuolar water H2O2 transporter aquaporin					TIP1-1	-6.565	0.028	down	
AT1G55720	yes	up?	vacuole low affiry CAX6 cation/proton exchanger	ATCAX6_1	16.945	0.0359	up	ATCAX6	16.007	0.013	up	
At4g17340	no	down	valuolar DELTA-TIP2 tonoplast intrinsic protein 2;2	TIP2-2_1	-88.01	0.0245	down	TIP2-2	-92.42	0.014	down	
AT2G14690	no	up	vascular budnle cell wall xylanase, AtXyn1,					AT2G14690	7.3007	0.033	up	
AT1G20700		up?	vascular meristem differentiation WOX14 peptide growth factor	WOX14_2	10.735	0.0493	up	WOX14	8.7023	0.018	up	
AT3G10640	yes	down	vasicular transport Snf7 coiled coil subunit of the ESCRT-III complex that is required for endosome-mediated trafficking					VPS60.1	2.8108	0.011	up	
AT1G60530	no	down	vesicle trafficking dynamin GTPase	DRP4A_1	-18.32	0.024	down	DRP4A	-19.92	0.004	down	
At4g00170	yes	down	vesicle transport Vesicle-Associated Membrane Protein-associated (VAMP-associated) protein family of 33 kDa (VAP33) homolog	PVA13_1	174.74	0.0104	up	PVA13	9.1866	0.008	up	
AT5G03540	yes	down?	vesicle transport, exocytosis, tracheal differentiation	ATEXO70A1_1	-2.921	0.0497	down	ATEXO70A1	-2.117	0.019	down	down
AT1G68110	no	up	vesicular trafficking CLAP, CLATHRIN ASSEMBLY PROTEIN	AT1G68110_1	52.887	0.0465	up	AT1G68110	49.969	0.035	up	
AT4G35380	yes	up	vesicular trafficking post-Golgi ARF guanine-nucleotide exchange factor BIG4/Sec7-like	BIG4_1	-5.598	0.0041	down	BIG4	-2.154	0.031	down	
AT3G06540	no	down	vesicular trafficking REP Rab escort protein	REP_1	-2.479	0.0052	down	REP	-2.636	9E-05	down	
AT1G71300	yes	up	vesicular trafficking vacuolar protein sorting 52 homolog					AT1G71300	7.2014	0.031	up	
AT3G29100		up?	vesicular trafficking v-SNARE subunit VTI13 vesicle transport V-snare 13	VTI13_3	90.711	0.025	up	VTI13	152.21	0.008	up	
AT1G43890	no	down	vesicular transfficking Golgi RAB GTPASE HOMOLOG C1, RAB18, RAB18-1					RAB18	-38.78	0.037	down	
AT1G08270		up?	vesicular transport Vacuolar protein sorting-associated protein 4					AT1G08270	6.6522	0.017	up	

TAIR locus	Altered coding	Predicted effect on gene function	Pathway	CLC Bio mRNA isoform (DAS)	prl2 DAS Fold change	prl2 DAS P-value	prl2 DAS change	prl2 CLC Bio Gene Name	prl2 DE Fold change	prl2 DE P-value)	prl2 DE change	prl1 Predicted effect on gene function
AT2G25530	yes	up	vesicular transport ATPase family gene 1	AT2G25530_1	93.067	0.0251	up	AT2G25530	10.608	0.008	up	
AT5G16300		down?	vesicular transport COG1 component of oligomeric golgi complex 1					AT5G16300	-2.197	0.001	down	
AT3G07100	no	down	vesicular transport ER to Golgi cell size male transmission ENDOPLASMIC RETICULUM MORPHOLOGY 2; SEC24A					ERMO2	-2.055	3E-05	down	
AT5G43670	no	up	vesicular transport ER to Golgi COPII Sec23 subunit	AT5G43670_1	7.2069	0.0279	up	AT5G43670	6.81	0.004	up	
AT4G29440	yes	down	vesicular transport ESCRT complex Regulator of Vps4 activity in the MVB pathway	AT4G29440_1	-3.181	0.0117	down	AT4G29440	-2.272	0.004	down	
AT5G50380	no	down	vesicular transport EXO70F1 exocyst subunit exo70 family protein F1	ATEXO70F1_1	-2.01	0.0071	down	ATEXO70F1	-2.14	4E-04	down	
AT4G31540	no	down	vesicular transport EXO70G1 exocyst subunit exo70 family protein G1	ATEXO70G1_1	-67.63	0.0361	down	ATEXO70G1	-71.03	0.022	down	
AT2G21540	no	down	vesicular transport flower specific phosphatidylcholin transfer proteon SEC13-like 3					SFH3	-10.41	0.038	down	down?
AT1G56590	no	up	vesicular transport fromGolgi to vacuole ZIP4 Clathrin adaptor complexes medium subunit					AP3M	2.9438	0.028	up	
AT2G33470	no	up	vesicular transport GLTP1 glycolipid transfer protein 1					GLTP1	2.3981	0.023	up	down
AT5G45750	no	up	vesicular transport Golgi cell polarity RABA1c RAB GTPase homolog A1C					RABA1C	2.2801	0.025	up	
At2g40380	no	down	vesicular transport Golgi PRA1.B2 prenylated RAB acceptor 1.B2					PRA1B2	-2.503	0.022	down	
At3g13710	no	up	vesicular transport GOLGI Rab GTPase Receptor PRA1.F4	PRA1F4_1	178.09	0.01	up	PRA1F4	169.78	0.006	up	down
AT1G13340	no	up	vesicular transport ISt1 regulator of Vps4 oligomerization in the MVB pathway					AT1G13340	2.3795	0.043	up	
At1g33475		down?	vesicular transport membrane bound Longin domain R-SNARE protein					PHYL1.2	-7.967	0.021	down	down
AT1G03050	no	down	vesicular transport PtdIns(4,5)P2 and PtdIns(1,4,5)P3 binding ENTH (Epsin N-terminal homology) domain protein					AT1G03050	-10.95	0.035	down	
AT1G16225	yes	up	vesicular transport Q-SNARE Target SNARE coiled-coil domain protein	AT1G16225_3	-164.6	0.013	down	AT1G16225	-11.78	0.038	down	
AT3G09910		up?	vesicular transport RAB18 GTPase					RABC2B	6.314	0.041	up	
AT1G14820		up?	vesicular transport Sec14 phosphatidylinositol transport membrane protein G-protein interaction					AT1G14820	9.578	0.021	up	up
AT1G47550	no	down	vesicular transport SEC3A exocyst complex component sec3A	SEC3A_2	-3.512	0.0457	down	SEC3A	-2.412	0.006	down	
AT4G20410	yes	up	vesicular transport Soluble NSF attachment protein, SNAP for SNARE	GSNAP_1	2.444	0.0481	up	GSNAP	2.3415	0.009	up	
AT1G08190	no	up	vesicular transport to vacuole VPS41 (vacuolar protein sorting 41) homolog	ZIP2_1	3.6641	0.0389	up	ZIP2	3.4683	0.005	up	down
AT2G27900	no	up	vesicular transport Vacuolar protein sorting-associated protein 54 EARP complex subunit endocytic recycling	AT2G27900_1	72.486	0.045	up	AT2G27900	2.0293	0.05	up	
AT2G33110		down?	vesicular transport VAMP723, VAMP723, VESICLE-ASSOCIATED MEMBRANE PROTEIN 723					VAMP723	-2.221	0.024	down	
AT3G14910	no	up	vesicular transprot exocytosis RAB3GAP2 RAB3 GTPase activating non-catalytic protein subunit 2 homolog					AT3G14910	3.9624	0.02	up	
AT4G27690		up?	vesicular transprot VPS26B vacuolar protein sorting 26B					VPS26B	4.0816	0.028	up	
AT1G57770	no	up	vitamin A1 retinol metabolism all-trans-retinol 13,14-reductase	AT1G57770_1	41.099	0.0062	up	AT1G57770	38.824	0.002	up	
AT1G51560	no	up	vitamin B6 pyridoxin synthesis Pyridoxamine 5'-phosphate oxidase					AT1G51560	6.7992	0.014	up	
At2g38230	no	down	vitamin B6 synthesis development stress response PDX1.1 pyridoxine biosynthesis 1.1					PDX11	-2.55	0.042	down	
AT1G50480	no	down	vitamin B9 folate synthesis THFS 10-formyltetrahydrofolate synthetase	THFS_1	-2.044	0.0008	down	THFS	-2.174	2E-05	down	
AT1G48320	no	down	vitamin K phylloquinone synthesis peroxisome DHNA-CoA (1,4-dihydroxy-2-naphthoyl-CoA) thioesterase 1					DHNAT1	-2.809	0.026	down	
AT5G48950	yes	down	vitamin K1 phylloquinone biosynthesis peroxisomeDHNAT2, DHNA-CoA (1,4-dihydroxy-2-naphthoyl-CoA) thioesterase	DHNAT2_2	80.207	0.0341	up	DHNAT2	7.9778	0.027	up	
AT1G20850	no	up	xylem development XCP2 xylem cysteine peptidase 2	XCP2_1	154.44	0.0127	up	XCP2	146.08	0.008	up	
AT4G18780	no	up	xylem differentiation pathogen ABA tolerance cell wall CESA8; CELLULOSE SYNTHASE 8; CESA8; F28A21.190; F28A21_190; IRREGULAR XYLEM 1; LEAF WILTING 2; LEW2					CESA8	39.355	0.048	up	
AT4G29720	no	up	xylem differentiation salt tolerance polyamine metabolism PAO5 polyamine oxidase 5	PAO5_1	116.11	0.018	up	PAO5	109.68	0.012	up	
AT4G35350	no	up	xylem vessel formation tracheary element vacuolar XCP1 xylem cysteine peptidase 1	XCP1_1	17.762	0.0332	up	XCP1	17.651	0.011	up	
AT2G16770	no	up	zic deficiency adaptation bZIP23 TF	BZIP23_2	11.211	0.0333	up	BZIP23	7.0953	0.019	up	

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9. ERKLÄRUNG

Ich versichere, daß ich die von mir vorgelegte Dissertation selbständig angefertigt, die benutzten Quellen und Hilfsmittel vollständig angegeben und die Stellen der Arbeit - einschließlich Tabellen, Karten und Abbildungen -, die anderen Werken im Wortlaut oder dem Sinn nach entnommen sind, in jedem Einzelfall als Entlehnung kenntlich gemacht habe; daß diese Dissertation noch keiner anderen Fakultät oder Universität zur Prüfung vorgelegen hat; daß sie - abgesehen von unten angegebenen Teilpublikationen - noch nicht veröffentlicht worden ist sowie, daß ich eine solche Veröffentlichung vor Abschluß des Promotionsverfahrens nicht vornehmen werde.

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