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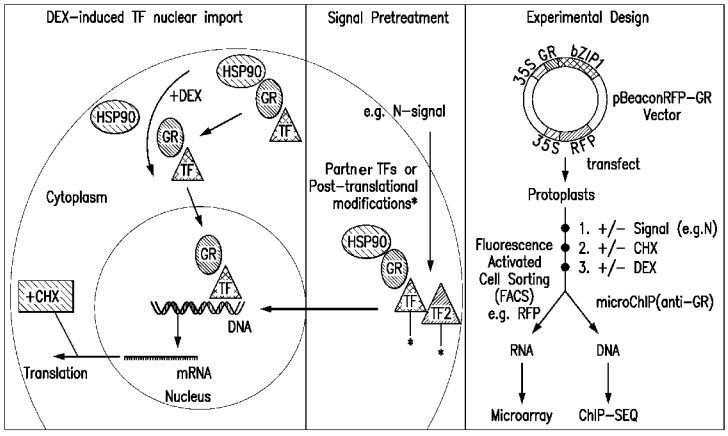


FIG. 1A FIG. 1B FIG. 1C

(57) Abstract: Plant genes regulated by transcription factors that control the gene network response to an environmental perturbation or signal are described. This class of genes responds to the perturbation of a transcription factor and the signal it transduces, but surprisingly, without stable binding of the transcription factor. These genes represent members of the "dark matter" of metabolic regulatory circuits. The invention involves the transgenic manipulation of these "response genes" and/or the genes encoding their regulatory transcription factors in plants so that their respective gene products are either overexpressed or underexpressed in the plant in order to confer a desired phenotype. The invention also relates to a rapid technique named *"TARGET" (ransient ssay eporting enome-wide ffects of ranscription factors)* for determining such "response genes" and their transcription factors by perturbation of the expression of the transcription factors of interest in protoplasts of any plant species.

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TRANSGENIC PLANTS AND A TRANSIENT TRANSFORMATION SYSTEM FOR GENOME-WIDE TRANSCRIPTION FACTOR TARGET DISCOVERY

[0001] This application claims priority benefit to U.S. Provisional Application No. 62/112,923, filed on February 6, 2015 and U.S. Provisional Application No. 62/181,482, filed on June 18, 2015, the disclosures of each of which are hereby incorporated by reference in their entirety.

1. INTRODUCTION

[0002] This invention relates to plant genes regulated by transcription factors that control the gene network response to an environmental perturbation or signal, and the manipulation of the expression of these "response genes" and/or their regulatory transcription factors in transgenic plants to confer a desired phenotype. The invention also relates to a rapid technique named "TARGET" (Transient Assay Reporting Genome-wide Effects of Transcription factors) for determining such "response genes" and their regulatory transcription factors as well as the structure of the involved gene regulatory networks (GRN) - including "transient" targets of transcription factors (TF) - by transiently perturbing the expression of the transcription factors of interest and the signals they transduce in protoplasts of any plant species.

2. BACKGROUND

[0003] Determining the fundamental structure of gene regulatory networks (GRN) is a major challenge of systems biology. In particular, inferring GRN structure from comprehensive gene expression and transcription factor (TF)-promoter interaction datasets has become an increasingly sought after aim in both fundamental and agronomical research in plant biology (Bonneau et al, 2007, Cell 131:1354-1365; Ruffel et al., 2010, Plant Physiol 152:445-452). A crucial step for the assessment of GRN is the identification of the direct TF-target genes.

[0004] Transgenic plant lines expressing tagged versions of the TF-of-interest can be used together with transcriptomic and DNA-binding analyses to obtain high-confidence lists of direct targets (see e.g., Mönke et al., 2012, Nucleic acids research 40:8240-825).

However, the generation of such transgenics can be a limiting factor, especially in large-scale studies or in non-model species.

[0005] Another major challenge in systems biology is the generation of gene regulatory networks (GRNs) that describe, and ideally, predict how the network will respond to perturbation. Currently, the global structure of a GRN is modeled by inferring regulatory relationships between transcription factors (TFs) and their target genes from genomic data (Krouk et al., 2010, Genome Biology 11:R123; Brady et al., 2011, Molecular Systems Biology 7:459; Petricka et al., 2011, Trends in Cell Biology 21:442). While diverse experimental approaches have been devised to validate interactions between specific TFs and their targets (Matallana-Ramirez et al., 2013, Molecular Plant 6 (5): 1438-1452; Bargmann et al., 2013, Molecular Plant 6(3):978; Gorte et al., 2011, Plant Transcription Factors, vol. 754, pp. 119-141; Iwata et al., 2011, Plant Transcription Factors, vol. 754, pp. 107-117; Wehner et al., 2011, Frontiers in Plant Science 2:68), the "gold standard" in the field has been to identify primary TF-targets as genes that are both transcriptionally regulated *and* whose promoter region is bound by the TF of interest (Oh et al., 2009, The Plant Cell Online 21:403). However, a GRN built purely on this "gold standard" rule (Reeves et al., 2011, Plant Molecular Biology 75:347; Gorski et al., 2011, Nucleic Acids Research 39:9536; Hull et al., 2013, BMC Genomics 14:92; Fujisawa et al., 2011, Planta 235:1107), renders a static network that only includes targets stably bound by a TF under the studied conditions, and likely underestimates the dynamic interactions occurring *in vivo*.

[0006] For example, in higher plants, fluctuating nitrogen levels in the soil cause rapid and dramatic changes in plant gene expression. Nitrogen is both a metabolic nutrient and signal that broadly and rapidly reprograms genome-wide responses. While genomic responses to nitrogen have been studied for many years, only a small number of genes in nitrogen genome-wide reprogramming have been identified. The unidentified genes represent the so-called "dark matter" of such metabolic regulatory circuits, a crucial problem in understanding system-wide genetic regulation in many fields.

3. SUMMARY

[0007] Plant genes regulated by transcription factors that control the gene network response to an environmental perturbation or signal (e.g., nitrogen, water, sunlight,

oxygen, temperature) are described. These genes respond rapidly to their environment, but surprisingly, there is no evidence of direct transcription factor interaction. More particularly, the large class of genes described herein (and exemplified in Tables 1, 2, 19, 20, and 23) respond to the perturbation of a regulatory transcription factor and the signal it transduces, but in fact are not stably bound to the transcription factor, and yet are most relevant to the signal induced in vivo – in other words, they represent members of the "dark matter" of metabolic regulatory circuits. The invention involves the transgenic manipulation of these "response genes" and/or the genes encoding their regulatory transcription factors in plants so that their respective gene products are either overexpressed or underexpressed in the plant in order to confer a desired phenotype; e.g., increased N usage (to enhance plant growth/biomass) or N storage/yield (to enhance N storage and/or protein accumulation in seeds of seed crops).

[0008] The invention is based, in part, on the development of a rapid technique named "TARGET" (Transient Assay Reporting Genome-wide Effects of Transcription factors) that uses transient transformation of a plasmid containing a glucocorticoid receptor (GR)-tagged TF in protoplasts to study the genome-wide effects of TF activation. The TARGET system can be used to rapidly retrieve information on direct TF target genes in less than two week's time. The technique can be used as a part of various experimental designs, as show in Figure 1. The core of the technique makes use of an isolated nucleic acid molecule encoding a chimeric protein comprising a transcription factor fused to a domain comprising an inducible cellular localization signal and an independently expressed selectable marker. A host cell such as a plant protoplast may then be transiently transfected with the nucleic acid molecule. The selectable marker allows for the determination of which cells have been successfully transfected. The TF-inducible signal fusion is sequestered in one cellular location until this retention mechanism is released through treatment with a localization- inducing signal, such as a small molecule. To determine the transcription factor response in the presence of an environmental signal, pre-treatment with such a signal may optionally be performed before the treatment with the cellular localization-inducing signal. mRNA transcripts may then be measured by microarray analysis or other suitable method in those cells identified to be successfully transfected by means of the selectable marker. To

distinguish between primary and secondary response genes, a translation inhibitor such as cyclohexamide may optionally be used to inhibit translation of mRNA. Likewise, to determine the binding properties of the transcription factors to their target sequences, an additional step of ChIP-Seq analysis may be optionally added concurrently to microarray analysis which detects mRNAs of TF targets. ChIP-Seq analysis may be done on the same cell samples as the microarray analysis.

[0009] While not intending to be bound to any theory of operation, using the TARGET system, gene networks have been identified that are regulated by TFs via transient associations with the target gene. Unexpectedly, these transient TF targets were found to be biologically relevant in controlling responsiveness to the applied signal/pertubation/cue. The target genes of interest are referred to herein as "response genes" that are regulated by what is referred to herein as their transiently associated "touch and go" or "hit and run" transcription factors. Conventional wisdom has focused on the "Golden Set" of genes stably bound and regulated by a TF, and has failed to uncover these transient associations described herein.

[0010] As a proof-of-principle candidate, the well-studied transcription factor, Abscicic acid insensitive 3 (ABI3) was investigated using *TARGET*, as described in more detail herein in Section 6 (Example 1). The *de novo* identification of the abscisic acid response element (ABRE) and a majority of the previously classified direct targets was established by use of the *TARGET* method, confirming its applicability. The *TARGET* system was then further modified, as described in further detail in Sections 7 and 10 (Examples 2 and 5), to identify genes transiently bound and regulated by the TF of the system in response to an environmental signal. These modifications allowed for the discovery of a "hit-and-run" ("touch-and-go") mode-of-action for a proof-of-principle transcription factor candidate, bZIP1, where bZIP1 "hits" its target, initiates transcription, then dissociates ("run"), leaving the transcription going on even without bZIP1 binding to the promoter. As evidence that transcription of a gene initiated by "the Hit" continues after "the Run," an affinity-tagged UTP was used to label and capture newly synthesized mRNA, as described in Section 11 (Example 6). By adding this UTP affinity label at a time-point when bZIP1 is not detectably bound, it was determined that response genes were still actively transcribed. Section 12 (Example 7) describes the discovery that the

transient TF-targets detected specifically in the TARGET cell-based system make a unique contribution to understanding how signal transduction occurs in planta, while eluding detection in planta.

[0011] In Section 8 (Example 3), a method for identifying nitrogen-regulated connections conserved across model species and crops is detailed. This method is a rapid way to assess whether the function of a gene of interest is conserved across species and enables the enhancement of the translational discoveries of the *TARGET* system. The method of Section 8 may be used as an alternative or supplement to using the *TARGET* system directly in protoplasts of crops or other plant species. Section 9 (Example 4) also describes a method for identifying networks conserved across species to identify translational targets that may be used as an alternative or supplement to the *TARGET* system.

[0012] One advantage of the TARGET system is the ability to study gene regulatory networks and targets of transcription factors in a transient assay system, which means the method can be applied to plants that cannot be stably transformed. Protoplasts can be made from any plant species, and a transcription factor of interest can be transiently expressed to identify its targets genome-wide. Target genes of transcription factors can be rapidly identified because the method does not rely on the use of transgenic plants, which normally have to be stably transformed. Also, the TARGET technique allows for cross-species studies in order to analyze evolutionary conserved networks using genes from a poorly characterized plant genus or species in a better characterized model genus, such as Arabidopsis, which has a fully sequenced genome and has microarray chip data available. This also has important implications for translational studies of gene function, from data-rich models (e.g. Arabidopsis) to data-poor crops. By providing the ability to do reciprocal cross species genetic network comparisons, the TARGET technique allows for the determination of TF-target connections that are evolutionarily conserved and therefore likely the most important elements of transcription factor networks. The optional modifications to the TARGET system confers the further advantage of the ability to detect gene networks that are controlled transiently in response to environmental signals by TF interactions that have been previously ignored. TF regulation is not always associated with stable TF binding. The TARGET system

uncovers TF targets that would otherwise be missed in other systems that require TF binding to identify gene targets. The TARGET system allows for the identification of the functional mode of action for any TF within and across species.

[0013] The most recent advance in the field of nitrogen-signaling uncovered a master transcription factor, NLP7, which when mutated, affects >58% of the nitrogen-responsive genes in plants, yet can be shown to bind to only 10% of these targets. This conundrum represents a general problem in the field of transcription, and a particular problem in metabolic signaling, where TF binding is a poor indicator of system-wide gene regulation. In fact, most GRN studies have focused on determining when and how TF binding does, or does not, result in activation of its target genes. Such TF-binding approaches have missed the "dark matter" of signal transduction. The *TARGET* system has revealed that the largest class of genes responding to the perturbation of a TF and a signal it transduces are in fact not stably bound to the TF, and this class of genes which has the most relevance to the signal transduced has been missed in all TF studies to date. Several unique aspects of the system described enable the discovery of this large set of primary TF targets that are regulated by, but do not stably bind to the TF.

[0014] The tables provided herein list transcription factors and response genes for which expression may be modified in transgenic plants to produce desired phenotypes.

[0015] Provided herein are transgenic plants that ectopically express genes that increase the nitrogen use efficiency (NUE) of the plants. In one embodiment, the transgenic plant of the present invention contains a heterologous gene construct comprising a polynucleotide encoding HHO5 and/or WRKY28, wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

[0016] Provided herein is a transgenic plant engineered to ectopically express/overexpress HHO5 or an ortholog of HHO5, such as described in Table 37, infra, wherein the transgenic plant expressing/overexpressing HHO5 or the ortholog exhibits increased nitrogen use efficiency. In another embodiment, provided herein is a transgenic plant engineered to ectopically express/overexpress a protein with at least 80%, 85%, 90%, 95%, 97%, 99% homology/identity to HHO5, wherein the transgenic plant expressing/overexpressing protein/polypeptide with at least 80%, 85%, 90%, 95%, 97%, 99% homology/identity exhibits increased nitrogen use efficiency.

[0017] In another embodiment, provided herein is a transgenic plant containing a heterologous gene construct comprising a polynucleotide encoding HHO5, an ortholog of HHO5, such as described in Table 37, infra, or a protein with at least 80%, 85%, 90%, 95%, 97%, 99% homology/identity to HHO5, wherein the transgenic plant expressing the HHO5, ortholog, or protein with at least 80%, 85%, 90%, 95%, 97%, 99% homology/identity exhibits increased nitrogen use efficiency.

[0018] In another embodiment, the transgenic plant of the present invention ectopically expresses one or more transcription factor genes conserved in Arabidopsis and Maize, wherein said one or more transcription factor genes comprises a polynucleotide that encodes AT5G44190, AT2G20570, AT1G01060, AT2G46830, AT5G24800, AT2G22430, AT1G68840, AT1G53910, AT1G80840, AT3G04070, AT1G77450, AT1G01720, AT3G01560, AT2G38470, AT3G60030, and/or AT5G49450, and wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

[0019] In another embodiment, the transgenic plant of the present invention ectopically expresses one or more transcription factor genes conserved in Arabidopsis and Maize, wherein said one or more transcription factor genes comprises a polynucleotide that encodes GRMZM2G026833, GRMZM2G087804, GRMZM2G409974, GRMZM2G026833, GRMZM2G087804, GRMZM2G474769, GRMZM2G145041, GRMZM2G181030, GRMZM2G014902, GRMZM2G170148, GRMZM2G103647, GRMZM2G098904, GRMZM2G122076, GRMZM2G041127, GRMZM2G018336, GRMZM2G110333, GRMZM2G148333, GRMZM2G120320, GRMZM2G176677, GRMZM2G031001, GRMZM2G123667, GRMZM2G054252, GRMZM2G167018, GRMZM2G127379, GRMZM2G180328, GRMZM2G159500, GRMZM2G104400, GRMZM2G025215, GRMZM2G012724, GRMZM2G054125, GRMZM2G169270, GRMZM2G081127, GRMZM2G133646, GRMZM2G101499, GRMZM2G093020, , GRMZM2G361611, GRMZM2G444748, and/or GRMZM2G092137, and wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

[0020] In an embodiment, the transgenic plant of the present invention is a species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable. In another embodiment, the transgenic plant of the present invention is a species of one of the following genuses:

Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arabidopsis, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea, or Zinnia.

[0021] In an embodiment, a transgenic plant-derived commercial product is derived from a transgenic plant of the present invention. In one embodiment, the transgenic plant is a tree and the transgenic plant-derived commercial product is pulp, paper, a paper product, or lumber. In another embodiment, the transgenic plant is tobacco and the transgenic plant-derived commercial product is a cigarette, cigar, or chewing tobacco. In another embodiment, the transgenic plant is is a crop and the transgenic plant-derived commercial product is a fruit or vegetable. In another embodiment, the transgenic plant is is a grain and the transgenic plant-derived commercial product is bread, flour, cereal, oat meal, or rice. In another embodiment, the transgenic plant-derived commercial product is a biofuel or plant oil.

3.1. TERMINOLOGY

[0022] Units, prefixes, and symbols may be denoted in their SI accepted form. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxyl orientation, respectively. Numeric ranges recited within the specification are inclusive of the numbers defining the range and include each integer within the defined range. Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes. Unless otherwise provided for, software, electrical, and electronics terms as used herein are as defined in The New IEEE Standard Dictionary of Electrical and Electronics Terms (5th edition, 1993). The terms defined below are more fully defined by reference to the specification as a whole.

[0023] As used herein, the term "agronomic" includes, but is not limited to, changes in root size, vegetative yield, seed yield or overall plant growth. Other agronomic properties include factors desirable to agricultural production and business.

[0024] By "amplified" is meant the construction of multiple copies of a nucleic acid sequence or multiple copies complementary to the nucleic acid sequence using at least one of the nucleic acid sequences as a template. Amplification systems include the polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario), Q-Beta Replicase systems, transcription-based amplification system (TAS), and strand displacement amplification (SDA). See, *e.g.*, Diagnostic Molecular Microbiology: Principles and Applications, D. H. Persing *et al.*, Ed., 1993, American Society for Microbiology, Washington, D.C.. The product of amplification is termed an amplicon.

[0025] As used herein, "antisense orientation" includes reference to a duplex polynucleotide sequence that is operably linked to a promoter in an orientation where the antisense strand is transcribed. The antisense strand is sufficiently complementary to an endogenous transcription product such that translation of the endogenous transcription product is often inhibited.

[0026] In its broadest sense, a "delivery system," as used herein, is any vehicle capable of facilitating delivery of a nucleic acid (or nucleic acid complex) to a cell and/or uptake of the nucleic acid by the cell.

[0027] The term "ectopic" is used herein to mean abnormal subcellular (*e.g.*, switch between organellar and cytosolic localization), cell-type, tissue-type and/or developmental or temporal expression (*e.g.*, light/dark) patterns for the particular gene or enzyme in question. Such ectopic expression does not necessarily exclude expression in tissues or developmental stages normal for said enzyme but rather entails expression in tissues or developmental stages not normal for the said enzyme.

[0028] By "endogenous nucleic acid sequence" and similar terms, it is intended that the sequences are natively present in the recipient plant genome and not substantially modified from its original form.

[0029] The term "exogenous nucleic acid sequence" as used herein refers to a nucleic acid foreign to the recipient plant host or, native to the host if the native nucleic acid is

substantially modified from its original form. For example, the term includes a nucleic acid originating in the host species, where such sequence is operably linked to a promoter that differs from the natural or wild-type promoter.

[0030] By "encoding" or "encoded", with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequences (*e.g.*, introns) within translated regions of the nucleic acid, or may lack such intervening non-translated sequences (*e.g.*, as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the "universal" genetic code. However, variants of the universal code, such as are present in some plant, animal, and fungal mitochondria, the bacterium Mycoplasma capricolum, or the ciliate Macronucleus, may be used when the nucleic acid is expressed therein.

[0031] When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon preferences of the intended host where the nucleic acid is to be expressed. For example, although nucleic acid sequences of the present invention may be expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray *et al.*, 1989, Nucl. Acids Res. 17: 477-498). Thus, the maize preferred codon for a particular amino acid may be derived from known gene sequences from maize. Maize codon usage for 28 genes from maize plants is listed in Table 4 of Murray *et al.*, *supra*.

[0032] By "fragment" is intended a portion of the nucleotide sequence. Fragments of the modulator sequence will generally retain the biological activity of the native suppressor protein. Alternatively, fragments of the targeting sequence may or may not retain biological activity. Such targeting sequences may be useful as hybridization probes, as antisense constructs, or as co-suppression sequences. Thus, fragments of a nucleotide sequence may range from at least about 20 nucleotides, about 50 nucleotides, about 100 nucleotides, and up to the full-length nucleotide sequence of the invention.

[0033] As used herein, "full-length sequence" in reference to a specified polynucleotide or its encoded protein means having the entire amino acid sequence of, a

native (non-synthetic), endogenous, biologically active form of the specified protein. Methods to determine whether a sequence is full-length are well known in the art including such exemplary techniques as northern or western blots, primer extension, S1 protection, and ribonuclease protection. See, *e.g.*, Plant Molecular Biology: A Laboratory Manual, Clark, Ed., 1997, Springer-Verlag, Berlin. Comparison to known full-length homologous (orthologous and/or paralogous) sequences can also be used to identify full-length sequences of the present invention. Additionally, consensus sequences typically present at the 5' and 3' untranslated regions of mRNA aid in the identification of a polynucleotide as full-length. For example, the consensus sequence ANNNNAUGG, where the underlined codon represents the N-terminal methionine, aids in determining whether the polynucleotide has a complete 5' end. Consensus sequences at the 3' end, such as polyadenylation sequences, aid in determining whether the polynucleotide has a complete 3' end.

[0034] The term "gene activity" refers to one or more steps involved in gene expression, including transcription, translation, and the functioning of the protein encoded by the gene.

[0035] The term "genetic modification" as used herein refers to the introduction of one or more exogenous nucleic acid sequences as well as regulatory sequences, into one or more plant cells, which in certain cases can generate whole, sexually competent, viable plants. The term "genetically modified" or "genetically engineered" as used herein refers to a plant which has been generated through the aforementioned process. Genetically modified plants of the invention are capable of self-pollinating or cross-pollinating with other plants of the same species so that the foreign gene, carried in the germ line, can be inserted into or bred into agriculturally useful plant varieties.

[0036] As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species, one or both are substantially modified from their original form. A

heterologous protein may originate from a foreign species or, if from the same species, is substantially modified from its original form by deliberate human intervention.

[0037] By "host cell" is meant a cell that contains a vector and supports the replication and/or expression of the vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, plant, insect, amphibian, or mammalian cells. Preferably, host cells are monocotyledonous or dicotyledonous plant cells. A particularly preferred monocotyledonous host cell is a maize host cell.

[0038] The term "introduced" in the context of inserting a nucleic acid into a cell, means "transfection" or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (*e.g.*, chromosome, plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (*e.g.*, transfected mRNA).

[0039] The term "isolated" refers to material, such as a nucleic acid or a protein, which is: (1) substantially or essentially free from components which normally accompany or interact with it as found in its natural environment. The isolated material optionally comprises material not found with the material in its natural environment; or (2) if the material is in its natural environment, the material has been synthetically altered or synthetically produced by deliberate human intervention and/or placed at a different location within the cell. The synthetic alteration or creation of the material can be performed on the material within or apart from its natural state. For example, a naturally-occurring nucleic acid becomes an isolated nucleic acid if it is altered or produced by non-natural, synthetic methods, or if it is transcribed from DNA which has been altered or produced by non-natural, synthetic methods. See, *e.g.*, Compounds and Methods for Site Directed Mutagenesis in Eukaryotic Cells, Kmiec, U.S. Pat. No. 5,565,350; *In vivo* Homologous Sequence Targeting in Eukaryotic Cells; Zarling *et al.*, PCT/US93/03868. The isolated nucleic acid may also be produced by the synthetic re-arrangement ("shuffling") of a part or parts of one or more allelic forms of the gene of interest. Likewise, a naturally-occurring nucleic acid (*e.g.*, a promoter) becomes isolated if it is introduced to a different locus of the genome. Nucleic acids which are "isolated," as defined herein, are also referred to as "heterologous" nucleic acids.

[0040] As used herein, the term "marker" refers to a gene encoding a trait or a phenotype which permits the selection of, or the screening for, a plant or plant cell containing the marker.

[0041] As used herein, "nucleic acid" includes reference to a deoxyribonucleotide or ribonucleotide polymer, or chimeras thereof, in either single- or double-stranded form, and unless otherwise limited, encompasses known analogues having the essential nature of natural nucleotides in that they hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (*e.g.*, peptide nucleic acids).

[0042] By "nucleic acid library" is meant a collection of isolated DNA or RNA molecules which comprise and substantially represent the entire transcribed fraction of a genome of a specified organism or of a tissue from that organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology, Vol. 152, Academic Press, Inc., San Diego, Calif. (Berger); Sambrook *et al.*, 1989, Molecular Cloning--A Laboratory Manual, 2nd ed., Vol. 1-3; and Current Protocols in Molecular Biology, F. M. Ausubel *et al.*, Eds., 1994, Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc.

[0043] As used herein "operably linked" includes reference to a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence. Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

[0044] The term "orthologous" as used herein describes a relationship between two or more polynucleotides or proteins. Two polynucleotides or proteins are "orthologous" to one another if they are derived from a common ancestral gene and serve a similar function in different organisms. In general, orthologous polynucleotides or proteins will have similar catalytic functions (when they encode enzymes) or will serve similar structural functions (when they encode proteins or RNA that form part of the ultrastructure of a cell).

[0045] The term "overexpression" is used herein to mean above the normal expression level in the particular tissue, all and/or developmental or temporal stage for said enzyme/expressed protein product. In certain embodiments, overexpression is at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or higher above the normal expression level.

[0046] As used herein, the term "plant" is used in its broadest sense, including, but is not limited to, any species of woody, ornamental or decorative, crop or cereal, fruit or vegetable plant, and algae (*e.g.*, *Chlamydomonas reinhardtii*). Non-limiting examples of plants include plants from the genus *Arabidopsis* or the genus *Oryza*. Other examples include plants from the genuses *Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea*, or *Zinnia*." Plants included in the invention are any plants amenable to transformation techniques, including gymnosperms and angiosperms, both monocotyledons and dicotyledons. Examples of monocotyledonous angiosperms include, but are not limited to, asparagus, field and sweet corn, barley, wheat, rice, sorghum, onion, pearl millet, rye and oats and other cereal grains. Examples of dicotyledonous angiosperms include, but are not limited to tomato, tobacco, cotton, rapeseed, field beans, soybeans, peppers, lettuce, peas, alfalfa, clover, cole crops or *Brassica oleracea* (*e.g.*, cabbage, broccoli, cauliflower, brussel sprouts), radish, carrot, beets, eggplant, spinach, cucumber, squash, melons, cantaloupe, sunflowers and various ornamentals. Examples of woody species include poplar, pine, sequoia, cedar, oak, *etc.* Still other examples of plants include, but are not limited to, wheat, cauliflower, tomato, tobacco, corn, petunia, trees, *etc.* As used herein, the term "cereal crop" is used in its broadest sense. The term includes, but is not limited to, any species of grass, or grain plant (*e.g.*, barley, corn, oats, rice, wild rice, rye, wheat, millet, sorghum, triticale, *etc.*), non-grass plants (*e.g.*, buckwheat flax, legumes or soybeans,

etc.). As used herein, the term "crop" or "crop plant" is used in its broadest sense. The term includes, but is not limited to, any species of plant or algae edible by humans or used as a feed for animals or used, or consumed by humans, or any plant or algae used in industry or commerce. As used herein, the term "plant" also refers to either a whole plant, a plant part, or organs (*e.g.*, leaves, stems, roots, *etc.*), a plant cell, or a group of plant cells, such as plant tissue, plant seeds and progeny of same. Plantlets are also included within the meaning of "plant." The class of plants which can be used in the methods of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants.

[0047] The term "plant cell" as used herein refers to protoplasts, gamete producing cells, and cells which regenerate into whole plants. Plant cell, as used herein, further includes, without limitation, cells obtained from or found in: seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. Plant cells can also be understood to include modified cells, such as protoplasts, obtained from the aforementioned tissues.

[0048] As used herein, "polynucleotide" includes reference to a deoxyribopolynucleotide, ribopolynucleotide, or chimeras or analogs thereof that have the essential nature of a natural deoxy- or ribo-nucleotide in that they hybridize, under stringent hybridization conditions, to substantially the same nucleotide sequence as naturally occurring nucleotides and/or allow translation into the same amino acid(s) as the naturally occurring nucleotide(s). A polynucleotide can be full-length or a subsequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein embraces such chemically-, enzymatically- or metabolically-modified forms of polynucleotides, as well as the chemical forms of

DNA and RNA characteristic of viruses and cells, including among other things, simple and complex cells.

[0049] The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally-occurring amino acid, as well as to naturally-occurring amino acid polymers. The essential nature of such analogues of naturally-occurring amino acids is that, when incorporated into a protein, that protein is specifically reactive to antibodies elicited to the same protein but consisting entirely of naturally occurring amino acids. The terms "polypeptide", "peptide" and "protein" are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation. Further, this invention contemplates the use of both the methionine-containing and the methionine-less amino terminal variants of the protein of the invention.

[0050] As used herein "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells whether or not its origin is a plant cell. Exemplary plant promoters include, but are not limited to, those that are obtained from plants, plant viruses, and bacteria which comprise genes expressed in plant cells such *Agrobacterium* or *Rhizobium*. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, or seeds. Such promoters are referred to as "tissue preferred." Promoters which initiate transcription only in certain tissue are referred to as "tissue specific." A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" or "repressible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may affect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue specific, tissue preferred, cell type specific, and inducible promoters represent the class of "non-constitutive" promoters. A

"constitutive" promoter is a promoter which is active under most environmental conditions.

[0051] As used herein "recombinant" includes reference to a cell or vector that has been modified by the introduction of a heterologous nucleic acid, or to a cell derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell, or exhibit altered expression of native genes, as a result of deliberate human intervention. The term "recombinant" as used herein does not encompass the alteration of the cell or vector by events (*e.g.*, spontaneous mutation, natural transformation, transduction, or transposition) occurring without deliberate human intervention.

[0052] As used herein, a "recombinant expression cassette" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements which permit transcription of a particular nucleic acid in a host cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a nucleic acid to be transcribed, and a promoter.

[0053] The term "regulatory sequence" as used herein refers to a nucleic acid sequence capable of controlling the transcription of an operably associated gene. Therefore, placing a gene under the regulatory control of a promoter or a regulatory element means positioning the gene such that the expression of the gene is controlled by the regulatory sequence(s). Because a microRNA binds to its target, it is a post transcriptional mechanism for regulating levels of mRNA. Thus, an miRNA can also be considered a "regulatory sequence" herein. Not just transcription factors.

[0054] The term "residue" or "amino acid residue" or "amino acid" are used interchangeably herein to refer to an amino acid that is incorporated into a protein, polypeptide, or peptide (collectively "protein"). The amino acid may be a naturally occurring amino acid and, unless otherwise limited, may encompass non-natural analogs of natural amino acids that can function in a similar manner as naturally occurring amino acids.

[0055] The term "tissue-specific promotor" is a polynucleotide sequence that specifically binds to transcription factors expressed primarily or only in such specific tissue.

[0056] The term "selectively hybridizes" includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (*e.g.*, at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least 80% sequence identity, preferably 90% sequence identity, and most preferably 100% sequence identity (*i.e.*, complementary) with each other.

[0057] As used herein, a "stem-loop motif" or a "stem-loop structure," sometimes also referred to as a "hairpin structure," is given its ordinary meaning in the art, *i.e.*, in reference to a single nucleic acid molecule having a secondary structure that includes a double-stranded region (a "stem" portion) composed of two regions of nucleotides (of the same molecule) forming either side of the double-stranded portion, and at least one "loop" region, comprising uncomplemented nucleotides (*i.e.*, a single-stranded region).

[0058] The term "stringent conditions" or "stringent hybridization conditions" includes reference to conditions under which a probe will selectively hybridize to its target sequence, to a detectably greater degree than to other sequences (*e.g.*, at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which are 100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing). Generally, a probe is less than about 1000 nucleotides in length, optionally less than 500 nucleotides in length.

[0059] Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of

destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37°C, and a wash in 1x to 2x SSC (20x SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.5x to 1x SSC at 55 to 60°C Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1x SSC at 60 to 65°C

[0060] Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl, 1984, Anal. Biochem., 138:267-284: T_m=81.5°C+16.6 (log M)+0.41 (%GC)-0.61 (% form)-500/L; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. T_m is reduced by about 1°C for each 1% of mismatching; thus, T_m, hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with ≥90% identity are sought, the T_m can be decreased 10°C Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11,12,13,14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a T_m of less than 45°C (aqueous solution) or 32°C (formamide solution) it is preferred to increase the SSC concentration so that a

higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Tijssen, 1993, Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes, Part I, Chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays", Elsevier, New York; and Current Protocols in Molecular Biology, Chapter 2, Ausubel *et al.*, Eds., 1995, Greene Publishing and Wiley-Interscience, New York. Hybridization and/or wash conditions can be applied for at least 10, 30, 60, 90, 120, or 240 minutes.

[0061] As used herein, "transcription factor" ("TF") includes reference to a protein which interacts with a DNA regulatory element to affect expression of a structural gene or expression of a second regulatory gene. "Transcription factor" may also refer to the DNA encoding said transcription factor protein. The function of a transcription factor may include activation or repression of transcription initiation.

[0062] The term "transfection," as used herein, refers to the introduction of a nucleic acid into a cell. The term "transient transfection,' as used herein, refers to the introduction of a nucleic acid into a cell, wherein the nucleic acids introduced into the transfected cell are not permanently incorporated into the cellular genome.

[0063] As used herein, "transgenic plant" includes reference to a plant which comprises within its genome a heterologous polynucleotide or which lacks, by means of homologous recombination or other methods, a native polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid or lacks a native nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

[0064] The term "underexpression" is used herein to mean below the normal expression level in the particular tissue, all and/or developmental or temporal stage for said enzyme/expressed protein product. In certain embodiments, underexpression is at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or below/lower than the normal expression level.

[0065] As used herein, "vector" includes reference to a nucleic acid used in introduction of a polynucleotide of the present invention into a host cell. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

[0066] The following terms are used to describe the sequence relationships between a polynucleotide/polypeptide of the present invention with a reference polynucleotide/polypeptide: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", and (d) "percentage of sequence identity".

[0067] (a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison with a polynucleotide/polypeptide of the present invention. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

[0068] (b) As used herein, "comparison window" includes reference to a contiguous and specified segment of a polynucleotide/polypeptide sequence, wherein the polynucleotide/polypeptide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide/polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides/amino acids residues in length, and optionally can be 30, 40, 50,100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide/polypeptide sequence, a gap penalty is typically introduced and is subtracted from the number of matches.

[0069] Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, 1981, Adv. Appl. Math. 2: 482; by the homology

alignment algorithm of Needleman and Wunsch, 1970, J. Mol. Biol. 48: 443; by the search for similarity method of Pearson and Lipman, 1988, Proc. Natl. Acad. Sci. 85: 2444; by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, Calif.; GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis., USA; the CLUSTAL program is well described by Higgins and Sharp, 1988, Gene 73: 237-244; Higgins and Sharp, 1989, CABIOS 5: 151-153; Corpet *et al.*, 1988, Nucleic Acids Research 16: 10881-90; Huang *et al.*, 1992, Computer Applications in the Biosciences 8: 155-65; and Pearson *et al.*, 1994, Methods in Molecular Biology 24: 307-331.

[0070] The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, Current Protocols in Molecular Biology, Chapter 19, Ausubel *et al.*, Eds., 1995, Greene Publishing and Wiley-Interscience, New York.

[0071] Software for performing BLAST analyses is publicly available, *e.g.*, through the National Center for Biotechnology Information (world-wide web at ncbi.nlm.nih.gov). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the

cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. USA 89:10915).

[0072] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance.

[0073] BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, 1993, Comput. Chem., 17:149-163) and XNU (Claverie and States, 1993, Comput. Chem., 17:191-201) low-complexity filters can be employed alone or in combination.

[0074] Unless otherwise stated, nucleotide and protein identity/similarity values provided herein are calculated using GAP (GCG Version 10) under default values.

[0075] GAP (Global Alignment Program) can also be used to compare a polynucleotide or polypeptide of the present invention with a reference sequence. GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453,1970) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps. GAP considers all possible alignments and gap positions

and creates the alignment with the largest number of matched bases and the fewest gaps. It allows for the provision of a gap creation penalty and a gap extension penalty in units of matched bases. GAP must make a profit of gap creation penalty number of matches for each gap it inserts. If a gap extension penalty greater than zero is chosen, GAP must, in addition, make a profit for each gap inserted of the length of the gap times the gap extension penalty. Default gap creation penalty values and gap extension penalty values in Version 10 of the Wisconsin Genetics Software Package for protein sequences are 8 and 2, respectively. For nucleotide sequences the default gap creation penalty is 50 while the default gap extension penalty is 3. The gap creation and gap extension penalties can be expressed as an integer selected from the group of integers consisting of from 0 to 100. Thus, for example, the gap creation and gap extension penalties can each independently be: 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60 or greater.

[0076] GAP presents one member of the family of best alignments. There may be many members of this family, but no other member has a better quality. GAP displays four figures of merit for alignments: Quality, Ratio, Identity, and Similarity. The Quality is the metric maximized in order to align the sequences. Ratio is the quality divided by the number of bases in the shorter segment. Percent Identity is the percent of the symbols that actually match. Percent Similarity is the percent of the symbols that are similar. Symbols that are across from gaps are ignored. A similarity is scored when the scoring matrix value for a pair of symbols is greater than or equal to 0.50, the similarity threshold. The scoring matrix used in Version 10 of the Wisconsin Genetics Software Package is BLOSUM62 (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. USA 89:10915).

[0077] Multiple alignment of the sequences can be performed using the CLUSTAL method of alignment (Higgins and Sharp, 1989, CABIOS. 5:151-153) with the default parameters (GAP PENALTY=10, GAP LENGTH PENALTY=10). Default parameters for pairwise alignments using the CLUSTAL method are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5.

[0078] (c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a

specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (*e.g.,* charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, *e.g.*, according to the algorithm of Meyers and Miller, 1988, Computer Applic. Biol. Sci., 4:11-17, *e.g.*, as implemented in the program PC/GENE (Intelligenetics, Mountain View, Calif., USA).

[0079] Polynucleotide sequences having "substantial identity" are those sequences having at least about 50%, 60% sequence identity, generally 70% sequence identity, preferably at least 80%, more preferably at least 90%, and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described above. Preferably sequence identity is determined using the default parameters determined by the program. Substantial identity of amino acid sequences generally means sequence identity of at least 50%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%. Nucleotide sequences are generally substantially identical if the two molecules hybridize to each other under stringent conditions.

[0080] (d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the

identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

[0081] As used herein, the term "transgenic," when used in reference to a plant (*i.e.*, a "transgenic plant") refers to a plant that contains at least one heterologous gene in one or more of its cells, or that lacks at least one native gene, such as by means of homologous recombination, in one or more of its cells.

[0082] As used herein, "substantially complementary," in reference to nucleic acids, refers to sequences of nucleotides (which may be on the same nucleic acid molecule or on different molecules) that are sufficiently complementary to be able to interact with each other in a predictable fashion, for example, producing a generally predictable secondary structure, such as a stem-loop motif. In some cases, two sequences of nucleotides that are substantially complementary may be at least about 75% complementary to each other, and in some cases, are at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99.5%, or 100% complementary to each other. In some cases, two molecules that are sufficiently complementary may have a maximum of 40 mismatches (*e.g.*, where one base of the nucleic acid sequence does not have a complementary partner on the other nucleic acid sequence, for example, due to additions, deletions, substitutions, bulges, *etc.*), and in other cases, the two molecules may have a maximum of 30 mismatches, 20 mismatches, 10 mismatches, or 7 mismatches. In still other cases, the two sufficiently complementary nucleic acid sequences may have a maximum of 0, 1, 2, 3, 4, 5, or 6 mismatches.

[0083] By "variants" is intended substantially similar sequences. For "variant" nucleotide sequences, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the amino acid sequence of the modulator of the invention. Variant nucleotide sequences include synthetically derived sequences, such as those generated, for example, using site-directed mutagenesis. Generally, variants of a particular nucleotide sequence of the invention will have at least about 40%, 50%, 60%, 65%, 70%, generally at least about 75%, 80%, 85%, preferably at least about 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, and more preferably at least about 98%, 99% or more sequence identity to that particular nucleotide sequence as determined by sequence alignment programs described elsewhere herein using default parameters. By "variant" protein is intended a protein derived from the native protein by deletion or addition of one or more amino acids to the N-terminal and/or C-terminal end of the native protein; deletion or addition of one or more amino acids at one or more sites in the native protein; or substitution of one or more amino acids at one or more sites in the native protein. Such variants may result from, for example, genetic polymorphism or human manipulation. Conservative amino acid substitutions will generally result in variants that retain biological function

[0084] As used herein, the term "yield" or "plant yield" refers to increased plant growth, and/or increased biomass. In one embodiment, increased yield results from increased growth rate and increased root size. In another embodiment, increased yield is derived from shoot growth. In still another embodiment, increased yield is derived from fruit growth.

4. DESCRIPTION OF THE FIGURES

[0085] Figure 1. Experimental scheme for TF and signal perturbation (A) and parallel RNA-Seq and ChIP-Seq analysis (B) of bZIP1 primary targets. (A) A GR::TF fusion protein is overexpressed in a protoplast and its location is restricted to the cytoplasm by Hsp90. DEX-treatment, releases the GR::TF from Hsp90 allowing TF entry to nucleus, where the TF binds and regulates its target genes (Bargmann et al., 2013, Molecular Plant 6(3):978; Eklund et al., 2010, Plant Cell 22:349). In the presence of CHX, translation is blocked so that gene expression level changes are caused solely by the TF association with primary targets, and not downstream effectors. (B) Prior to the GR::TF nuclear import, a pre-treatment with a signal (e.g. N) could result in post-translational modifications of the TF and/or transcriptional/post-translational effects on its TF partners (TF2). (C) Experimental design for temporal induction of TF and/or signal followed by identification of primary bZIP1 targets by either Microarray or ChIP-Seq analysis in the *TARGET* cell-based system (Bargmann et al., 2013, Molecular Plant

6(3):978). CHX: cycloheximide; DEX: dexamethasone; N: nitrogen; GR: glucocorticoid receptor.

[0086] Figure 2. Diagram of the pBeaconRFP_GR vector. The pBeaconRFP_GR vector contains a red fluorescent protein (RFP) positive selection cassette and a Gateway recombination cassette that is in frame with the rat glucocorticoid receptor (GR) fusion protein. The plasmid is used to transfect protoplast suspensions, followed by treatment with dexamethasone and/or cycloheximide and cell-sorting of successful transformants for transcriptomic analysis.

[0087] Figure 3. Preliminary analysis and microarray validation. (A) Timecourse qPCR analysis of PER1 and CRU3 induction by DEX in the presence of CHX. (B) The induction of six genes found to be significantly induced by ABI3 activation in the microarray was verified by qPCR analysis of independent transformations. Averages +/- SEM are presented, ns-not significant, **p<0.01, ***p<0.001 t-test DEX-treatment n=3.

[0088] Figure 4. Promoter analysis of genes directly up-regulated by ABI3. (A) Spatial representation of RY-repeat, ABRE , G-box and bZIP-core CREs in the promoters of the 186 direct ABI3 up-regulated genes. Genes were ordered by fold induction. (B) Relative binding-site density distribution for the CREs in A 1000 bp upstream of the transcription start site in the 186 direct up-regulated genes. (C) Statistical overrepresentation of CREs in direct up-regulated genes. A sliding window of 30 genes was applied to calculate significance according to a hypergeometric test. Black dotted line indicates log fold change of the 186 genes. (D) The ABRE, G-box and bZIP-core elements.

[0089] Figure 5. qPCR quantification of CRU3 transcript levels in protoplasts transformed with pBeaconRFP_GR-ABI3 or an empty vector control and treated with DEX and/or CHX. Averages +/-SEM are presented, ns-not significant, *p<0.05, ***p<0.001 t-test DEX-treatment n=3.

[0090] Figure 6. qPCR quantification of PER1 transcript levels in protoplasts transformed with pBeaconRFP_GR-ABI3 or an empty vector control and treated with DEX and/or CHX. Averages +/-SEM are presented, ns-not significant, *p<0.05, ***p<0.001 t-test DEX-treatment n=3. Figure 6. Proposed model of the interaction between the *Arabidopsis* circadian clock and N-assimilatory pathway. Arrows indicate

influences that affect the function of the two processes. Black arrow: Clock function would affect N-assimilation. This influence is at least partly due to the direct regulatory role of CCA1 on N-assimilation. Grey arrow: N-assimilation would influence clock function through downstream metabolites such as Glu, Gln and possibly other N-metabolites.

[0091] Figure 7. The intersection of 186 genes identified by *TARGET* as directly up-regulated by ABI3 and genes identified by previous studies as direct up-regulated targets of ABI3 (98 genes;), up-regulated targets of VP1 (51 genes) and ABI5 (59 genes).

[0092] Figure 8. Network model of putative ABI3 connections to its direct up-regulated target genes via the RY-repeat motif (CATGCA) and through interaction with ABRE binding factors (ABFs) and ABRE (ACGTGKC) or the more degenerate G-box (CACGTG) and bZIP core (ACGTG) elements. Target genes (circles) are sized according to their strength of induction.

[0093] Figure 9. Weight matrix representation of the ABRE-like (CACGTGKC) motif retrieved by the MotifSampler and MEME algorithms from the 1 kb upstream of the transcription start sites of the top fifty direct up-regulated ABI3 targets, Ze=7.19 and Ze=7.11, respectively.

[0094] Figure 10. Identification of primary targets of bZIP1 by *either* Microarray *or* ChIP-Seq and integration of results. (A) Bioinformatics pipeline used to analyze the transcriptome data for transcriptionally regulated genes and the ChIP-Seq data for bZIP1-bound genes. Data from both sources were then integrated to decipher the binding and regulation dynamics. (B) Identification of primary targets regulated by bZIP1 in the presence of cycloheximide (to block secondary targets) and (C) their associated cis-regulatory motifs. (D) Identification of bZIP1-bound genes by ChIP-Seq (E) and their associated cis-regulatory motifs.

[0095] Figure 11. Three distinct classes of bZIP1 primary targets identified by integration of microarray and ChIP-SEQ data (A) TF primary targets identified by *either* bZIP1-induced regulation in the presence of CHX (microarray) *or* bZIP1 binding (ChIP-SEQ) led to the identification of three distinct classes of bZIP1 primary targets: (I) "Poised" TF-bound but not regulated, (II) "Active" TF-bound and regulated, and (III) "Transient" TF-regulated but no binding, which can further be divided into subclasses

based on the direction of regulation. Note that 187 bZIP1-bound TF-targets are not on the ATH1 microarray. The over-represented GO terms (FDR <0.01) for each subclass are listed. The significance of overlap with the N-responsive genes, or genes regulated by N*bZIP1 interaction was calculated for each subclass by hypergeometric distribution. (B) Comparison of the subclasses with previous reported bZIP1 regulated genes *in planta* (Kang et al., 2010, Molecular Plant 3:361), steady-state N-regulated genes (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939), and early/transient N-regulated genes (Krouk et al., 2010, Genome Biology 11:R123). (C) Enrichment of mRNA of different half-lives (Chiba et al., 2013, Plant & cell physiology. 54:180) in Class II and Class III of bZIP1 primary targets (filtered to only contain genes that are regulated by DEX in the presence and absence of CHX). The number of genes overlapping in each comparison is listed and the significance of the overlap is noted. Any overlap significance < 0.01 is highlighted.

[0096] Figure 12. A model for three modes of temporal TF Action of bZIP1 on primary target genes: "poised", "active" and "transient". This model illustrates temporal modes of action of bZIP1 with the three different classes of primary gene targets- I "poised", II "active", and III "transient" (A) and significantly over-represented cis-element motifs in each class (B). The significance of the over-representation of known bZIP binding motifs (hybrid ACGT box [ACG]ACGT[GC] (Kang et al., 2010, Molecular Plant 3:361) and GCN4 binding motif (Onodera et al., 2001, Journal of Biological Chemistry 276:14139)) are listed. The significance of specific cis-motifs enriched in each subclass, compared to other classes, is shown as a heat-map.

[0097] Figure 13. Heatmap showing the expression profiles of nitrogen (N)-responsive genes in the *TARGET* cell-based system (Bargmann et al., 2013, Molecular Plant 6(3):978) identified by microarray. The GO terms over-represented (FDR adjusted pval<0.05) were identified for the N up-regulated and N down-regulated genes.

[0098] Figure 14. Genes regulated in response to DEX treatment (i.e. DEX-induced TF nuclear import) (FDR<0.05) and with a significant N*DEX interaction (pval<0.01) from ANOVA analysis. (A) Heatmap showing four distinct clusters were observed and their significantly enriched GO terms are listed. (B) Gene regulatory network constructed

from the genes in (A) and bZIP1 using Multinetwork feature in VirtualPlant (Katari et al., 2010, Plant Physiology 152:500).

[0099] Figure 15. bZIP1 targets identified in this study validate the predicted bZIP1 targets based on network analysis of *in planta* N-treatment transcriptome data (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939). 27 genes were predicted to be the targets of bZIP1 of which 14 were confirmed by this study.

[00100] The comparison of the genes of the 5 subclasses with (A) DEX regulated genes in the absence of CHX and (B) previously reported Carbon (C)- and Light (L)-regulated gene lists identified from roots and shoots (Krouk et al., 2009, PLoS Computational Biology 5:e1000326). The number of genes overlapping in each comparison is listed and the significance of the overlap noted. A significance of overlap < 0.01 is highlighted.

[00101] Figure 17. Cis-regulatory motif analysis of the subclasses of bZIP1 target genes. The significance of over-representation of known cis-regulatory motifs were calculated for each subclass, and if the significance in at least one subclass is smaller than 0.01, the motif is listed and significance shown as a heatmap (A). From this collection of significant motifs, relatively enriched motifs in each subclass were selected by the pattern match algorithm PTM in Mev (B). The motifs enriched in the subgroups were also identified by PTM for the following subgroups: activated subgroup, repressed subgroup, bound and regulated subgroup, and no binding but regulated subgroup.

[00102] Figure 18. Enrichment of mRNA of different half-lives (34) in Class II and Class III of bZIP1 primary target genes. The Class II and Class III genes here are filtered to only contain genes that are also regulated by DEX in the absence of CHX. Number of genes overlapping in each comparison is listed and the significance of the overlap noted. A significance of overlap < 0.01 is highlighted.

[00103] Figure 19. Schematic diagram of the data mining approach used in this study. Briefly, O. *sativa* (rice) and *A. thaliana* plants were grown for 12 days before treatment with nitrogen. Genome-wide analysis using Affymetrix chips has been used in order to quantify mRNA levels. Modeling of microarray data, using ANOVA and ortholog and network analysis (detailed in Methods), were used to identify a core translational network.

[00104] Figure 20. Number of N-responsive genes in *O. sativa* and *A. thaliana* with ortholog information in the other species (*E-value cutoff $1e^{-20}$).

[00105] Figure 21. Flowchart of N-regulated rice core correlated network analysis process.

[00106] Figure 22. NutriNet Modules: Constructing maize N-regulatory networks exploiting Arabidopsis Network Knowledge.

[00107] Figure 23. A NutriNet Module: Core N-regulatory module conserved between maize and Arabidopsis includes previously validated transcription factor hubs (CCA1, GLK1, and bZIP) (Gutierrez et al., 2008, Proc Natl Acad Sci USA 105(12):4939; Baulcombe, 2010, Science 327(5967):761).

[00108] Figures 24 A-D. Experimental scheme for TF (A) and N-signal perturbation (B), and parallel RNA-Seq and ChIP-Seq analysis (C & D) of bZIP1 primary targets. (A) A GR::TF fusion protein is overexpressed in protoplasts and its location is restricted to the cytoplasm by Hsp90. DEX-treatment releases the GR::TF from Hsp90 allowing TF entry to the nucleus, where the TF binds to and regulates its target genes. CHX blocks translation. Thus, when DEX-induced TF import is performed in the presence of CHX, changes in transcript levels are attributed to the direct interaction of the target with the TF of interest. (B) Prior to DEX-induction of GR::TF nuclear import, pre-treatment with a signal (e.g. N-nutrient signal) could result in posttranslational modifications of the TF and/or transcriptional/post-translational effects on its TF partners (e.g. TF2). Genes whose response to TF-induced regulation (by DEX) is altered by CHX treatment were removed from the study to eliminate potential side effects of CHX. (C) Experimental design for identification of primary bZIP1 targets by either Microarray or ChIP-Seq analysis in the cell-based *TARGET* system (11, 26). CHX: cycloheximide; DEX: dexamethasone; N: nitrogen; GR: glucocorticoid receptor. (D) Bioinformatics pipeline to identify bZIP1 primary targets based on transcriptional response or TF binding. bZIP1-regulated genes were identified by ATH1 arrays. bZIP1-bound genes were identified by ChIP-Seq analysis. The integrated datasets were analyzed for the functional significance of classes of genes grouped based on TF-binding and/or TF-regulation.

[00109] Figure 25. Nitrogen-responsive genes in the cell-based TARGET system. A heat map showing the expression profiles of 328 nitrogen (N)-responsive genes in the

TARGET cell-based system as identified by microarray in this study. The GO terms over-represented (FDR adjusted p-val<0.05) were identified for the genes up-regulated or down-regulated in response to the N-signal perturbation.

[00110] Figure 26. Validation of N-response in TARGET system. The 328 N-responsive genes in the cell-based TARGET system show significant overlaps with previously reported N-response gene in roots of whole plants and in seedlings. The significance of overlap between any two of these N-responsive sets is determined by the Genesect tool inVirtualPlant Platform (www.virtualplant.org).

[00111] Figures 27 A-D. Primary targets of bZIP1 are identified by either TF-activation or TF-binding. (A) Cluster analysis of bZIP1 primary target genes identified by their upregulation or down-regulation by DEX-induced bZIP1 nuclear import in Arabidopsis root protoplasts sequentially treated with inorganic N, CHX and DEX. bZIP motifs and other cismotifs are significantly over-represented in the promoters of bZIP1 primary target genes identified by transcriptional response (B), or by bZIP1 binding (D). (C) Examples of primary targets bound transiently by bZIP1 based on time-course ChIP-Seq.

[00112] Figure 28. Genes influenced by a significant N-signal x bZIP1 interaction in the cell-based TARGET system. Genes regulated in response to DEX-induced bZIP1 nuclear import (FDR<0.05) and with a significant N-signal*bZIP1 interaction (p-val<0.01) from ANOVA analysis. Heat map showing four distinct clusters of genes regulated by a N-signal x bZIP1 interaction. Note that two of the "early response" genes shown to bind transiently to bZIP1 (NLP3 and LBD39, see Fig. 29C), are in cluster 1 of the genes regulated by a N-signal x bZIP1 interaction.

[00113] Figures 29 A-D. Class III transient targets of bZIP1 are uniquely associated with rapid N signaling. (A) Primary bZIP1 targets identified by *either* bZIP1-induced regulation *or* bZIP1-binding assayed in the same root protoplasts samples. Intersection of these datasets revealed three distinct classes of primary targets: (Class I) "Poised", TF-bound but not regulated, (Class II) "Stable", TF-bound and regulated, and (Class III) "Transient", TF-regulated but no detectable binding. Classes II and III are subdivided into activated or repressed, with their associated over-represented GO terms (FDR <0.01) listed. (B) bZIP1 primary targets detected in protoplasts were compared with bZIP1

regulated genes *in planta*. The size of overlap is listed and significance is indicated by asterisks (highlight: p-val<0.001)). (C) bZIP1 primary targets detected in protoplasts were compared with and N-regulated genes in plants. The size of overlap is listed and significance is indicated by asterisks (highlight: p-val<0.001)). Class III "transient" targets are uniquely enriched in genes related to rapid N-signaling. (D) Class IIIA target genes (NLP3 and NRT2.1) show transient bZIP1 binding at 1 and 5 minutes after nuclear import of bZIP1, but not at later time-points (30 and 60 min).

[00114] Figure 30. Class III bZIP1 transient targets are specifically enriched in co-inherited *cis*-motif elements. The significance of the over-representation of the known bZIP binding motifs hybrid ACGT box, and GCN4 binding motif, are listed for each class of bZIP1 primary targets. In addition to these bZIP binding sites, the significance of enrichment of co-inherited *cis*-regulatory motifs is shown as a heat-map specific to each subclass.

[00115] Figure 31. Over-represented GO terms in each of the bZIP1 target classes. The set of genes from each class of bZIP1 targets were analyzed for over-representation of GO terms using the BioMaps feature of VirtualPlant (www.virtualplant.org). All classes of bZIP1 targets have an over-representation of GO terms related to "Stress" and "Stimulus". When sub-divided by direction of regulation, Class IIA loses all significant GO terms. In addition to the stress terms, Class I is over-represented for genes responding to "biotic stress" and "divalent ion transport". Class IIIA shows specific enrichment of GO terms for "Amino acid metabolism," hence showing an enrichment of genes related to the N-signal. Class IIIB has specific enrichment of genes related to cell death and phosphorus metabolism.

[00116] Figure 32. A network of biological processes represented by Class III transient bZIP1 targets. The set of genes from Class III "transient" bZIP1 targets were analyzed for over-representation of GO terms using the Bingo plugin in Cytoscape (Smoot et al., 2011, *Bioinformatics* 27(3):431-432). In addition to terms related to "Stress" and "Stimulus" which are found in all 3 classes of bZIP1 targets, the Class III transient targets also shows class-specific enrichment of GO terms both for "nitrogen metabolism" and the "regulation of nitrogen compound metabolism", hence showing an enrichment of genes

related to the N-signal. Class III transient targets also show overrepresentation of genes involved in "defense response", "phosphorylation" and "regulation of metabolism."

[00117] Figure 33. bZIP1 as a pioneer TF for N-uptake/assimilation pathway genes. Global analysis of bZIP1 targets reveals that it regulates multiple genes encoding for the Nuptake/assimilation pathway. Multiple genes encoding nitrate transporters and isoenzymes in the N-assimilation pathway are represented by hexagonal nodes. The nodes targeted by bZIP1 are connected with larger arrows. Thickness of the arrow is proportional to the number of genes in that node that are targeted by bZIP1. The IDs of the targeted genes are listed adjacent to the node. This pathway overview suggests that bZIP1 is a master regulator of the N-assimilation pathway. The pathway was constructed in Cytoscape (www.cytoscape.org) based on KEGG annotation (www.genome.jp/kegg/) . Node abbreviations: NRT: Nitrate transporters; AMT: Ammonia transporters; GDH: Glutamate dehydrogenases; GOGAT: Glutamate synthases; GS: Glutamine synthetases; ASN: Asparagine synthetases.

[00118] Figure 34. A "Hit-and-Run" transcription model enables bZIP1 to rapidly and catalytically activate genes in response to a N-signal. The transient mode-of-action for Class III bZIP1 targets follows a classic model for "hit-and-run" transcription. In this model, transient interactions of bZIP1 with Class III targets (the "hit"), lead to recruitment of the transcription machinery and possibly other TFs. Next, the transient nature of the bZIP1-target interaction (the "run") enables bZIP1 to catalytically activate a large set of rapidly induced genes (e.g. target 2 …target *n*) biologically relevant to rapid transduction of the N-signal.

[00119] Figures 35 A-D. 4sU RNA tagging. (A) Dot blot showing that protoplasts are able to use 4sU for RNA synthesis in 20min after the addition of 4sU. (B) Overlap of the actively transcribed genes regulated by bZIP1 (rows) with the three classes of bZIP1 targets (columns). The size of the overlap of two gene sets (labeled by the row and the column) was indicated by the numbers. The significance of overlap was indicated as: **: $p<0.01$; ***: $p<0.001$ (shade). (C). Time-series ChIP-seq showing the transient binding of bZIP1 to NLP3 at 1-5 min after nuclear import of bZIP1. (D) 4sU tagging showing that NLP3 is transcribed due to bZIP1 at both 20min and 5hr after nuclear import of bZIP1.

[00120] Figure 36. Transient bZIP1 targets detected in TARGET cell-based system (inner circle) are predicted to regulate secondary targets of TF1 identified in planta (outer circle).

[00121] Figure 37. The Network Walking Pipeline. Network inference links transient TF2 targets of TF1, detected only in the cell-based TARGET system, to secondary TF targets (gene Z) detected only by in planta TF1 perturbation.

[00122] Figures 38 A-B. bZIP1 acts in a Feed Forward Loop (FFL) to regulate expression of NRT2.1, the major nitrate transporter controlling the high-affinity N-uptake system. (A). bZIP1 regulates NRT2.1 directly and through a repressor (LBD38) and an activator (LBD39) to form both and Incoherent FFL and a Coherent FFL. (B). bZIP1 quickly activates NRT2.1 through the "response accelerator" I1-FFL mechanism and sustains expression via the "persistence detector" C1-FFL mechanism.

[00123] Figures 39 A-C. Network Walking links transient TF targets detected in cells to downstream effector genes in planta. (A). Transient TF2 targets of bZIP1 detected specifically in the cell-based *TARGET* system (inner ring TFs) are inferred using DFG to regulate secondary bZIP1 targets detected *in planta* (outer ring genes) including N-assimilation targets. (B). bZIP1 forms multiple Feed-Forward loops through the transient TF2 targets (LBD38 and LBD39) to regulate a high affinity nitrate transporter, NRT2.1. (C). A similar Network Walk for NLP7, a well-known N-response regulator predicts that TF2 targets identified in *TARGET* system (inner ring triangles), are intermediates that regulate NLP7 effector genes *in planta* (outer ring) generalizing the discoveries for bZIP1.

[00124] Figure 40. "Network Walking" Pipeline links transient TFs in cells to downstream targets in plants. Perturb "Catalyst TF1" in cells to identify transient targets (Step 1) and link to secondary *in planta* targets by dynamic network inference (Step 2). Perturb transient TF2s in *TARGET* to identify their primary targets (Step 3) and repeat network inference to identify fine-scale network structure (Step 4) in an iterative cycle. Finally discover FFLs critical to N-signaling (Step 5).

[00125] Figures 41 A-B. "Catalyst TFs" provide secondary inputs to a primary N-signal. (A). bZIP1 provides the energy/carbon status input to the N-response GRN by regulating early and transient TF2s (NLP3, LBD38,39) implicated in N-signaling. (B).

New catalyst TFs (CRF3 and HRS1) predicted to regulate many N-assimilation genes, potentially integrate hormonal and macronutrient input to N-response. Targets of catalyst TFs and TF2's will be validated in the cell-based *TARGET* system and *in planta*.

[00126] Figure 42. A schematic diagram of the experimental and data mining approach used in Example 9. Briefly, *O. sativa* (rice) and *A. thaliana* plants were grown for 12 days before a 2 hr treatment with 1xN vs. KCl control. Genome-wide analysis using Affymetrix chips was used in order to quantify mRNA levels. Modeling of microarray data, using ANOVA, homology/orthology and network analysis, were used to identify a core translational N-regulatory network shared between rice and Arabidopsis.

[00127] Figure 43. The workflow of the network analysis of N-regulated genes differentially expressed in rice resulting in "Rice-Arabidopsis N-regulatory Network (RANN-Union)". The input was 451 rice N-regulated genes. In each of the three steps, rice and Arabidopsis data were introduced in order to identify the RANN-Union network, which includes N-regulated genes and network modules conserved between rice and Arabidopsis.

[00128] Figure 44. Supernode network analysis created from the 182 genes of "Rice-Arabidopsis N-regulatory Network" (RANN-Union). Individual nodes were clustered based on PlantCyc pathways and TF families classification to form supernodes. Genes which do not belong to either of the two classifications are not shown. Triangles represent TFs families and squares represent PlantCyc pathways. The size of the nodes is proportional to the number of genes within that particular category (from 1 to 5). Nodes are connected by TF:target (solid lines = predicted negative correlation; dashed lines = predicted positive correlation) and predicted protein-protein interactions (double dashed lines). All nodes are present in the "Rice-Arabidopsis N-regulatory Network" (RANN-BLAST) supernode network. Nodes circled in thick grey lines are also present in the "Rice-Arabidopsis N-regulatory Network" (RANN-OrthoMCL) supernode network.

[00129] Figure 45. Rice N-regulated gene lists compared using the Sungear tool (Poultney et al., 2007) housed in Virtual Plant (www.virtualplant.org). The polygon shows the four lists of N-regulated genes at the vertices. The circles inside the polygon (vessels) represent the list of genes that are shared by the anchors (gene lists), as indicated by the arrows around the vessels with the number of shared genes in

parenthesis. The area of each vessel is proportional the number of genes associated with that vessel.

[00130] Figure 46. Quantification of mRNA levels of *O. sativa* N-regulated genes. Transcript levels were determined by RT-qPCR and are shown as relative to expression of a housekeeping rice actin gene (LOC_Os10g36650). Values are the mean ±SE from three biological replicates. Asterisks indicate significant differences between control (N-) and treatment (N+) for each tissue according to ANOVA analysis ($p<0.05$).

[00131] Figure 47. Arabidopsis N-regulated gene lists compared using the Sungear tool (Poultney et al., 2007) housed in Virtual Plant (www.virtualplant.org). The polygon shows the four lists of N-regulated genes at the vertices. The circles inside the polygon (vessels) represent the list of genes that are shared by the anchors (gene lists), as indicated by the arrows around the vessels with the number of shared genes in parenthesis. The area of each vessel is proportional the number of genes associated with that vessel.

[00132] Figure 48. Quantification of mRNA levels of *A. thaliana* N-regulated genes. Transcript levels were determined by RT-qPCR and are shown as relative to expression of a housekeeping Clathrin gene (At4g24550). Values are the mean ±SE from three biological replicates. Asterisks indicate significant differences between control (N-) and treatment (N+) for each tissue according to ANOVA analysis ($p<0.05$).

[00133] Figure 49. Arabidopsis and rice HRS1/HHO transcription factor family phylogenetic tree built by ClustalW alignment and maximum likelihood method. The bootstrap values displayed were calculated based on 500 replications (MEGA6). N-regulated genes are indicated under the shaded rectangles (solid circle for rice genes and open circle for Arabidopsis genes). Genes identified as homologs or orthologs based on BLAST or OrthoMCL respectively, are indicated with a check mark.

[00134] Figure 50. Arabidopsis and rice TGA transcription factor family phylogenetic tree built by ClustalW alignment and maximum likelihood method. The bootstrap values displayed were calculated based on 500 replications (MEGA6). N-regulated genes are indicated by the shaded rectangles (solid circle for rice genes and open circle for Arabidopsis genes). Genes identified as homologs or orthologs based on BLAST or OrthoMCL, respectively are indicated with a check mark.

[00135] Figure 51. The workflow of the analysis of N-regulated genes differentially expressed in rice resulting in "Arabidopsis-Rice N-regulatory Network (ARNN-Union)". The input was 1417 Arabidopsis N-regulated genes. In each of the three steps shown, rice and Arabidopsis data were introduced in order to identify the Arabidopsis core translational network, which includes N-regulated genes and network modules conserved between rice and Arabidopsis.

[00136] Figure 52. Phylogenetic relationship of Arabidopsis (Atb), Rice (Os) and Maize (Zmb) bZIP genes. Based on this analysis, the Maize and Rice orthologs of Arabidopsis bZIP1 were identified.

[00137] Figure 53. Schematic representation of the gene structure of HHO5 and the position of the T-DNA insertion for each mutant line. CS876991 mutant has a T-DNA insertion in exon 5 of the HHO5 gene of Arabidopsis. SALK_077802 mutant has a T-DNA insertion in exon 1 of the HHO5 gene of Arabidopsis.

[00138] Figures 54 A-E. Expression of HHO5 and targets of HHO5 in hho5 mutant plants. (A). Bar graph showing that mRNA for HHO5 (At4g37180) is absent in the hho5 mutant plants (CS876991) as compared to wild-type plants (Col0). (B)-(D). Bar graphs showing that the expression of targets of HHO5 predicted by the N-regulatory network (NIA1, NiR and GLT1) are significantly reduced in the *hho5* mutant plants as compared to wild-type plants (Col0). Expression levels of tested genes were normalized to expression levels of the housekeeping actin genes (At3g18780/At1g49240 (ACT2/8). Values are the mean ±SE from three biological replicates. Asterisks denote significant difference between Col0 and hho5 mutant line according to 1 way-ANOVA (**$p<0.001$, *$p<0.05$). (E). Predicted HHO5 direct targets genes. Network of predicted HHO5 direct targets genes nodes are connected with long arrows indicating positive correlation among TF-target expression data and the presence of HHO cis-motif in the promoter of their putative targets. Network visualization was created using Cytoscape (v2.8.3) software (Shannon et al., 2003, Genome Research 13: 2498–504). NIA1, Nitrate reductase; NiR, Nitrite reductase; GLN, Glutamine synthetase; GLT1, Glutamate synthase.

[00139] Figure 55. Nitrogen treatments of Col0 (wild type) and *hho5* mutant (CS876991) plants. Seeds were germinated and grown on vertical plates on media

containing increasing amounts of Nitrogen vs. KCl control. Primary root length was measured every 3 days.

[00140] Figures 56 A-B. Arabidopsis *hho5* mutant plants (CS876691) in the At4g37180 (HHO5) gene utilize NO_3 less efficiently compared to Col-0 (wild-type) plants. (A). Primary root growth over time of Arabidopsis plants grew on MS supplemented with 0.1, 1 or 10 mM KNO_3. Control plants were grown on MS supplemented with 0.1, 1 or 10 mM KCl. Primary root length was measured every three days. (B). Primary root length of wild-type and *hho5* mutant plants at the end of the experiment (day 10). Values are the mean ±SE from three biological replicates. Asterisks denote statistical differences between genotypes according to 1 way-ANOVA (*$p<0.05$, **$p<0.01$).

[00141] Figures 57 A-B. Arabidopsis *hho5* mutant plants (CS876691) in the At4g37180 (HHO5) gene utilize NH_4NO_3 less efficiently compared to Col-0 (wild-type) plants. (A). Primary root growth over time of Arabidopsis plants (hho5 vs wild-type Col-0) grown on MS supplemented with 0.1, 1 or 10 mM NH_4NO_3. Control plants were grown on MS supplemented with 0.1, 1 or 10 mM KCl. Primary root length was measured every three days. (B). Primary root length of wild-type and *hho5* mutant plants at the end of the experiment (day 18). Asterisks denote statistical differences between genotypes based on 1 way-ANOVA (*$p<0.05$, **$p<0.01$, ***$p<0.0001$).

[00142] Figure 58. *hho5* mutant seeds have less Nitrogen content compared to Col0. Nitrogen assimilation was estimated comparing total N content in Col0 (wild-type) and *hho5* mutant seeds by the Kjeldahl method and expressed as mg N 100 mg^{-1} dry weight (performed by Laboratorio de Análisis Clínicos y Biología Molecular, Laboratorios Fox (Venado Tuerto, Santa Fe, Argentina)). Asterisk denotes statistical differences between genotypes based on 1 way-ANOVA ($p<0.003$). Values are the mean ±SE from two biological replicates.

[00143] Figure 59. Phylogenetic tree built by Mafft alignment and parsimony method. N-regulated genes in Arabidopsis and Rice are boxed (solid box for rice genes and dashed box for Arabidopsis genes). This HHO5 ortholog includes 104 genes across 33 plant genomes.

5. DETAILED DESCRIPTION

[00144] The present invention involves plant genes that are regulated by transcription factors that control the gene network response to an environmental perturbation or signal (*e.g.*, nitrogen, water, sunlight, oxygen, temperature). These genes respond rapidly to their environment, but surprisingly, there is no evidence of direct transcription factor interaction. More particularly, the large class of genes described herein (and exemplified in Tables 1, 2, 19, 20, and 23) respond to the perturbation of a regulatory transcription factor and the signal it transduces, but in fact are *not* stably bound to the transcription factor, and yet are most relevant to the signal induced *in vivo* – in other words, they represent members of the "dark matter" of metabolic regulatory circuits. In some embodiments, these "response genes" are transgenically manipulated so that their respective gene products are either overexpressed or underexpressed in a plant in order to confer a desired phenotype. In other embodiments, the genes encoding the transcription factors regulating these "response genes" are transgenically manipulated so that their respective gene products are either overexpressed or underexpressed in a plant in order to confer a desired phenotype. In a particular embodiment, the desired phenotype is increased nitrogen usage, which may be desired to enhance plant growth. In another embodiment, the desired phenotype is increased nitrogen storage, which may be desired to enhance the storage of nitrogen in seeds of seed crops. In yet other embodiments, the desired phenotype is increased nitrogen-assimilation capacity.

[00145] In certain embodiments, the transgenically manipulated response gene is one or more of the following (also listed in Tables 1 and 2): At3g28510, At1g73260, At1g22400, At1g80460, At1g05570, At5g22570, At5g65110, At1g24440, At5g04310, At3g16150, At4g13430, At1g08090, At5g57655, At1g62660, At3g14050, At5g18670, At1g15380, At5g56870, At2g43400, At3g28510, At1g73260, At1g22400, At1g80460, At1g05570, At5g22570, At5g65110, At1g24440, At5g04310, At3g16150, At4g13430, At1g08090, At5g57655, At1g62660, At3g14050, At5g18670, At1g15380, At5g56870, At2g43400, At3g28510, At1g73260, At1g22400, At1g80460, At1g05570, At5g22570, At5g65110, At1g24440, At5g04310, At3g16150, At4g13430, At1g08090, At5g57655, At1g62660, At3g14050, At5g18670, At1g15380, At5g56870, At2g43400, At3g28510, At1g73260, At1g22400, At1g80460, At1g05570, At5g22570, At5g65110, At1g24440,

At5g04310, At3g16150, At4g13430, At1g08090, At5g57655, At1g62660, At3g14050, At5g18670, At1g15380, At5g56870, or At2g43400.

[00146] In certain embodiments, the transgenically manipulated TF is one or more of the following (also listed in Table 3): At1g01060, At1g01720, At1g13300, At1g15100, At1g22070, At1g25550, At1g25560, At1g29160, At1g43160, At1g51700, At1g51950, At1g53910, At1g66140, At1g68670, At1g68840, At1g74660, At1g74840, At1g75390, At1g77450, At1g80840, At2g04880, At2g20570, At2g22430, At2g22850, At2g24570, At2g25000, At2g28510, At2g28550, At2g30250, At2g33710, At2g38470, At2g46830, At3g01560, At3g04070, At3g06590, At3g20770, At3g25790, At3g46130, At3g47620, At3g51920, At3g54620, At3g60490, At3g61150, At3g61890, At3g62420, At4g17490, At4g17500, At4g24240, At4g27410, At4g31800, At4g34590, At4g36540, At4g37180, At4g37260, At4g37610, At4g37730, At5g05410, At5g06800, At5G10030, At5g13080, At5g14540, At5g24800, At5g39610, At5g44190, At5g47230, At5g48655, At5g49450, At5g49520, At5g56270, At5g60850, At5g63790, At5G65210, or At5g65640.

[00147] HHO5 that was identified as a hit and run transciption factor by the cell based TARGET assay described herein (see Table 3). HHO5 was also unexpectedly identified as a gene involved in nitrogen response in a cross-species study describd herein that identified N-regulated genes conserved across Arabidopsis an Rice (see Example 9). It was hypothesized that HHO5 is a key TF regulating N-assimilation and Nitrogen Use Efficiency (NUE) in plants. It was subsequently shown, as described in Example 10 herein, that Arabidopsis hho5 mutant plants are defective in N-assimilation and NUE. These experimental findings for HHO5 confirm that the TARGET assay and the N-regulatory networks conserved between Arabidopsis and Rice can be used to identify TFs of importance to nitrogen regulation and to accurately predict their network target. In particular, these findings indicate that transgenic plants with ectopic expression of HHO5, an ortholog, or homologous protein may have increased nitrogen use efficiency.

[00148] Provided herein are transgenic plants that ectopically express genes that increase the nitrogen use efficiency (NUE) of the plants. In certain embodiments, the transgenic plants increase NUE by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% as compared to wild-type plants or a control (e.g., a corresponding plant of the same type

that has not been engineered to ectopically express a gene that increases NUE). In certain embodiments, the transgenic plant of the present invention contains a heterologous gene construct comprising a polynucleotide encoding HHO5 and/or WRKY28, wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

[00149] In certain embodiments, a transgenic plant of the invention contains a heterologous gene construct comprising a polynucleotide encoding a polypeptide having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or higher amino acid sequence identity to a polypeptide encoded by one or more transgenes or transcription factor genes, specified herein. In certain embodiments, a transgenic plant of the invention contains a heterologous gene construct comprising a polynucleotide encoding a polypeptide having at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or higher amino acid sequence identity to HHO5 and/or WRKY28.

[00150] In certain embodiments, a transgenic plant of the invention contains a nucleic acid construct that is a gene targeting vector which replaces a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence as described, *e.g.*, in International Publication Nos. WO 94/12650 and WO 01/68882, which are incorporated by reference herein in their entireties. In certain embodiments, a transgenic plant can be engineered to increase production of endogenous HHO5 and/or WRKY28 by, *e.g.*, altering the regulatory region of the endogenous HHO5 and/or WRKY28 genes. In certain embodiments, a transgenic plant can be engineered to increase production of endogenous transcription factors by, *e.g.*, altering the regulatory region of the endogenous transcription factor genes.

[00151] In certain embodiments, the transgenic plant of the present invention ectopically expresses one or more transcription factor genes conserved in Arabidopsis and Maize, wherein said one or more transcription factor genes comprises a polynucleotide that encodes AT5G44190, AT2G20570, AT1G01060, AT2G46830, AT5G24800, AT2G22430, AT1G68840, AT1G53910, AT1G80840, AT3G04070, AT1G77450, AT1G01720, AT3G01560, AT2G38470, AT3G60030, and/or AT5G49450, and wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

[00152] In certain embodiments, the transgenic plant of the present invention ectopically expresses one or more transcription factor genes conserved in Arabidopsis and Maize, wherein said one or more transcription factor genes comprises a polynucleotide that encodes GRMZM2G026833, GRMZM2G087804, GRMZM2G409974, GRMZM2G026833, GRMZM2G087804, GRMZM2G474769, GRMZM2G145041, GRMZM2G181030, GRMZM2G014902, GRMZM2G170148, GRMZM2G103647, GRMZM2G098904, GRMZM2G122076, GRMZM2G041127, GRMZM2G018336, GRMZM2G110333, GRMZM2G148333, GRMZM2G120320, GRMZM2G176677, GRMZM2G031001, GRMZM2G123667, GRMZM2G054252, GRMZM2G167018, GRMZM2G127379, GRMZM2G180328, GRMZM2G159500, GRMZM2G104400, GRMZM2G025215, GRMZM2G012724, GRMZM2G054125, GRMZM2G169270, GRMZM2G081127, GRMZM2G133646, GRMZM2G101499, GRMZM2G093020, GRMZM2G361611, GRMZM2G444748, and/or GRMZM2G092137, and wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

[00153] In certain embodiments, the transgenically manipulated plant is a species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable. In other embodiments, the plant is a species of one of the following genuses: *Acorus, Aegilops, Allium, Amborella, Antirrhimum, Apium, Arabidopsis, Arachis, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea, or Zinnia.*

[00154] In other embodiments, the transgenically manipulated plant is one of the following species: *Citrus clementina, Citrus sinensis, Linum usitatissimum, Populus trichocarpa, Ricinus communis, Manihot esculenta, Cucumis sativus, Glycine max, Phaseolus vulgaris, Medicago truncatula, Malus domestica, Prunus persica, Fragaria vesca, Gossypium raimondii, Carica papaya, Eucalyptus grandis, Vitis vinifera, Solanum*

tuberosum, Solanum lycopersicum, Arabidopsis thaliana, Arabidopsis lyrata, Capsella rubella, Brassica rapa, Medicago truncatula, Gossypium raimondii, Theobroma cacao, Eucalyptus grandis, Malus domestica, Brassica rapa, Thellungiella halophila, Setaria italica, Sorghum bicolor, Zea mays, Oryza sativa, Brachypodium disctachyon, Manihot esculenta, Eucalyptus grandis, or Physcomitrella patens.

[00155] The invention is based, in part, on the development of a rapid technique named "TARGET" that uses transient expression of a glucocorticoid receptor (GR)-tagged TF in protoplasts to study the genome-wide effects of TF activation. In some embodiments, the *TARGET* system can retrieve information on direct target genes in less than two weeks time. Multiple experimental designs exist for use of the *TARGET* system, as shown in Figure 1. In some embodiments, the present invention is directed to a method for identifying target genes of a transcription factor comprising: (i) transfecting host cells with an isolated nucleic acid molecule that encodes (a) a chimeric protein comprising a transcription factor fused to a domain comprising an inducible cellular localization signal; and (b) an independently expressed selectable marker; (ii) detecting host cells that express the selectable marker; (iii) contacting the host cells that express the selectable marker with an agent that induces localization (*e.g.* counters sequestration in the cytoplasm and/or targets to the nucleus, mitochondria, or chloroplasts) of the chimeric protein; and (iv) detecting the level of mRNA expressed in the host cells; wherein an alteration in the level of the mRNA expressed in the host cells that have nuclear localization of the chimeric protein compared to the level of the mRNA expressed in the host cells that do not have nuclear localization of the chimeric protein indicates the identification of target genes of the transcription factor.

[00156] In certain embodiments, the method of the present invention further comprises identifying direct target genes of the transcription factor comprising: (v) contacting the host cells with cyclohexamide; and (vi) detecting the level of mRNA expressed in the host cells; wherein an alteration in the level of the mRNA expressed in the host cells treated with cyclohexamide compared to the level of the mRNA expressed in the host cells not treated with cyclohexamide indicates the identification of direct target genes of the transcription factor.

[00157] In some embodiments, the nucleic acid molecule utilized in the methods of the invention is a DNA plasmid. In some embodiments, the domain comprising an inducible cellular localization signal encoded by the nucleic acid molecule used in the method of the invention is glucocorticoid receptor and the agent that allows for nuclear localization of the chimeric protein is dexamethasone. Dexamethasone prevents sequestration of the GR-TF fusion in the cytoplasm, allowing for localization to the nucleus. In some embodiments, the cellular localization signal encoded by the nucleic acid molecule allows for localization to the chloroplast or mitochondria upon treatment with the inducing agent.

[00158] In one embodiment, a) an isolated nucleic acid encoding a GR-TF fusion construct and an independently expressed selectable marker (*e.g.* a fluorescent protein such as RFP) is transiently transfected into plant protoplasts; b) treatment of the protoplasts with dexamethasone releases the GR-TF fusion from sequestration in the cytoplasm, allowing the TF to reach target genes; c) protoplasts that have been transiently transfected are identified by means of the detectable signal gene (*e.g.* by fluorescence activated cell sorting (FACS) to determine the presence of a fluorescent protein such as RFP); d) mRNA transcripts are measured from the transiently transfected protoplasts through use of a microarray analysis.

[00159] In some embodiments, the protoplasts are optionally exposed to an environmental signal, such as nitrogen, before treatment with dexamethasone, allowing for the measurement of transcription factor activity in response to the signal. In some embodiments, protoplasts may optionally be treated with cyclohexamide prior to or concurrently with dexamethasone treatment, which blocks translation, allowing for the distinction of primary target genes, which are still expressed in the presence of cyclohexamide, from secondary target genes, which are not expressed in the presence of cyclohexamide. In some embodiments, TF binding to response genes in transiently transfected protoplasts may optionally be analyzed using ChIP-Seq. In some embodiments, ChIP-Seq or microarray analysis is performed at differing time points after an environmental signal in order to determine temporal changes in TF binding or gene expression.

[00160] In certain embodiments, gene networks are identified that are regulated by TFs which demonstrate only transient association with a target gene. The identified TFs that regulate a target gene but are only transiently associated with that target gene can be referred to as "touch and go" or "hit and run" TFs. Touch and go (hit and run) TFs are implicated when (i) one or more particular gene transcript levels are perturbed when the TF-fusion construct is transiently expressed and released from sequestration in the cytoplasm, and (ii) stable binding to the gene or genes is not detected by ChIP SEQ analysis. In some embodiments, these touch and go (hit and run) TFs regulate genes that control responsiveness to an environmental signal, perturbation, or cue. The identified genes targeted by these transiently-associating TFs in response to an environmental signal, perturbation, or cue can be referred to as "response genes." "Response genes" are implicated when, in the presence of an environmental signal, perturbation, or cue, "touch and go" (hit and run) TFs perturb the levels of one or more particular gene transcript yet do not stably bind the gene as measured by ChIP-Seq analysis. The identification of a particular response gene or set of genes may vary with time after the protoplast is exposed to the environmental signal, perturbation, or cue.

[00161] The present invention uses nucleic acid molecules, compositions and methods for determining the target genes of transcription factors and the structure of gene regulatory networks (GRN) by transiently expressing transcription factors of interest in host cells, such as protoplasts. The protoplasts can be isolated and utilized from virtually any plant genus and species in the methods of the invention so that target genes and gene regulatory networks in poorly characterized plant genus and species can be studied. The methods of the invention allow for cross-species studies in order to analyze evolutionary conserved networks using genes from a poorly characterized plant genus or species in a better characterized model genus, such as *Arabidopsis,* which has a fully sequenced genome and has microarray chip data available. By providing the ability to do reciprocal cross species genetic network comparisons, the *TARGET* technique allows for the determination of what is evolutionary conserved and therefore likely the most important elements of transcription factor networks.

[00162] In some embodiments, the selectable marker encoded by the nucleic acid molecule used in the method of the invention is a fluorescent selection marker. A

fluorescent selection marker that can be used in the method of the invention includes, but is not limited to, green fluorescent protein, yellow fluorescent protein, red fluorescent protein, cyan fluorescent protein, or blue fluorescent protein. In a specific embodiment, the fluorescent selection marker used in the method of the invention is red fluorescent protein. In certain embodiments, the step of detecting host cells that express the selectable marker is performed by Fluorescence Activated Cell Sorting ("FACS").

[00163] In a specific embodiment, the nucleic acid molecule utilized in the methods of the invention is DNA plasmid pBeaconRFP_GR, which comprises the nucleotide sequence of SEQ ID NO: 1.

[00164] In certain embodiments, the host cell utilized in the methods of the present invention are transiently transfected with the nucleic acid molecules of the invention. In some embodiments, the host cell utilized in the methods of the present invention is a plant protoplast. In particular embodiments, the plant protoplast is derived from one of the following genuses: Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arabidopsis, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea, or Zinnia. In some embodiments, the host cell is derived from a genus that is different from the genus from which the transcription factor is derived from. For example, the host cell is a plant protoplast derived from the genus *Arabidopsis* and the transcription factor is derived from the genus *Zea*.

5.1. RESPONSE GENES AND TRANSCRIPTION FACTORS

[00165] The tables below list transcription factors and response genes for which expression may be modified in transgenic plants to produce desired phenotypes. In Section 5.2, methods for the production of transgenic plants with modified expression of one or more of these genes are enumerated.

[00166] Table 1 shows 20 genes that are (1) ClassIIIA, i.e. no TF binding but TF-activated and (2) transiently upregulated by N. These genes are examples of "response" genes. Table 2 shows 14 genes that are (1) ClassIIIA, i.e. no binding but activated and (2) early (9-20 min) upregulated by N. These are also "response" genes. Table 3 lists "touch and go" ("hit and run") transcription factors that may be utilized with the *TARGET* system to discover more response genes, which may be modified in transgenic plants to create a desired phenotype. Likewise, the transcription factor genes listed in Table 3 may themselves be modified in transgenic plants to create a desired phenotype.

TABLE 1

PUB LOCUS	*ANNOTATION*
At3g28510	P-loop containing nucleoside triphosphate hydrolases superfamily protein
At1g73260	ATKTI1, KTI1, kunitz trypsin inhibitor 1
At1g22400	ATUGT85A1, UGT85A1, UDP-Glycosyltransferase superfamily protein
At1g80460	GLI1, NHO1, Actin-like ATPase superfamily protein
At1g05570	ATGSL06, ATGSL6, CALS1, GSL06, GSL6, callose synthase 1
At5g22570	ATWRKY38, WRKY38, WRKY DNA-binding protein 38
At5g65110	ACX2, ATACX2, acyl-CoA oxidase 2
At1g24440	RING/U-box superfamily protein
At5g04310	Pectin lyase-like superfamily protein
At3g16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases superfamily protein)
At4g13430	ATLEUC1, IIL1, isopropyl malate isomerase large subunit 1
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1
At5g57655	xylose isomerase family protein
At1g62660	Glycosyl hydrolases family 32 protein
At3g14050	AT-RSH2, ATRSH2, RSH2, RELA/SPOT homolog 2
At5g18670	BAM9, BMY3, beta-amylase 3
At1g15380	Lactoylglutathione lyase / glyoxalase I family protein
At5g56870	BGAL4, beta-galactosidase 4
At2g43400	ETFQO, electron-transfer flavoprotein:ubiquinone oxidoreductase

TABLE 2

PUB LOCUS	*ANNOTATION*

At1g62660:	Glycosyl hydrolases family 32 protein
At3g49940:	LBD38, LOB domain-containing protein 38
At5g10210:	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).
At1g07150:	MAPKKK13, mitogen-activated protein kinase kinase kinase 13
At3g20320:	TGD2, trigalactosyldiacylglycerol2
At2g43400:	ETFQO, electron-transfer flavoprotein:ubiquinone oxidoreductase
At1g22400:	ATUGT85A1, UGT85A1, UDP-Glycosyltransferase superfamily protein
At1g05570:	ATGSL06, ATGSL6, CALS1, GSL06, GSL6, callose synthase 1
At4g38490:	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).
At4g37540:	LBD39, LOB domain-containing protein 39
At5g65110:	ACX2, ATACX2, acyl-CoA oxidase 2
At5g04310:	Pectin lyase-like superfamily protein
At4g39780:	Integrase-type DNA-binding superfamily protein
At5g51550:	EXL3, EXORDIUM like 3

TABLE 3

PUB LOCUS	*Name/Symbol*	*Annotation*
At1g01060	myb-related transcription factor (LHY)	LHY encodes a myb-related putative transcription factor involved in circadian rhythm along with another myb transcription factor CCA1
At1g01720	putative transcriptional activator with NAC domain (ANAC002)	Belongs to a large family of putative transcriptional activators with NAC domain. Transcript level increases in response to wounding and abscisic acid. ATAF1 attentuates ABA signaling and sythesis. Mutants are hyposensitive to ABA
At1g13300	HRS1	Overexpression confers hypersensitivity to low phosphate-elicited inhibition of primary root growth
At1g15100	Ring-H2 finger A2A (RHA2A)	Encodes a putative RING-H2 finger protein RHA2a.
At1g22070	bZIP1 family transcription factor	Encodes a transcription factor. Like other TGAla-

	(TGA3)	related factors, TGA3 has a highly conserved bZIP region and exhibits similar DNA-binding properties.
At1g25550	HHO3	myb-like transcription factor family protein
At1g25560	putative AP2-domain containing transcription factor (TEM1)	Encodes a member of the RAV transcription factor family that contains AP2 and B3 binding domains. Involved in the regulation of flowering under long days. Loss of function results in early flowering. Overexpression causes late flowering and repression of expression of FT. TBDvel transcriptional regulator involved in ethylene signaling. Promoter bound by EIN3. EDF1 in turn, binds to promoter elements in ethylene responsive genes.
At1g29160	Dof-type zinc finger domain-containing protein	
At1g43160	AP2 domain-containing protein RAP2.6 (RAP2.6)	encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family (RAP2.6). The protein contains one AP2 domain
At1g51700	Dof-type zinc finger domain-containing protein (ADOF1)	Encodes dof zinc finger protein (adof1).
At1g51950	IAA18, indole-3-acetic acid inducible 18	Auxin responsive
At1g53910	AP2 domain-containing protein RAP2.12 (RAP2.12)	Encodes a member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family (RAP2.12). The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12. Involved in oxygen sensing.
At1g66140	zinc finger protein 4 transcription factor (ZFP4)	
At1g68670	HHO2	myb-like transcription factor family protein
At1g68840	regulator of ATPase of the vacuolar membrane (RAV2)	Rav2 is part of a complex that has been named `regulator of the (H+)-ATPase of the vacuolar and endosomal membranes' (RAVE)
At1g74660	Mini zinc finger 1 transcription factor (MIF1)	
At1g74840	MYB	Homeodomain-like superfamily protein

At1g75390	AtbZIP44, bZIP44, basic leucine-zipper 44	
At1g77450	NAC45	NAC domain containing protein 32 (NAC032); FUNCTIONS IN: sequence-specific DNA binding transcription factor activity; INVOLVED IN: multicellular organismal development, regulation of transcription
At1g80840	WRKY40	Pathogen-induced transcription factor. Binds W-box sequences in vitro. Forms protein complexes with itself and with WRKY40 and WRKY60. Coexpression with WRKY18 or WRKY60 made plants more susceptible to both P. syringae and B. cinerea.
At2g04880	WRKY1	Encodes WRKY1, a member of the WRKY transcription factors in plants involved in disease resistance, abiotic stress, senescence as well as in some developmental processes. WRKY1 is involved in the salicylic acid signaling pathway. The crystal structure of the WRKY1 C-terminal domain revealed a zinc-binding site and identified the DNA-binding residues of WRKY1.
At2g20570	golden2-like transcription factor (GLK1)	Encodes GLK1, Golden2-like 1, one of a pair of partially redundant nuclear transcription factors that regulate chloroplast development in a cell-autonomous manner. GLK2, Golden2-like 2, is encoded by At5g44190. GLK1 and GLK2 regulate the expression of the photosynthetic apparatus.
At2g22430	ATHB6	Encodes a homeodomain leucine zipper class I (HD-Zip I) protein that is a target of the protein phosphatase ABI1 and regulates hormone responses in Arabidopsis.
At2g22850	AtbZIP6, bZIP6, basic leucine-zipper 6	
At2g24570	WRKY17	
At2g25000	WRKY60	Pathogen-induced transcription factor. Forms protein complexes with itself and with WRKY40
At2g28510	Dof-type zinc finger domain containing protein	Dof-type zinc finger DNA-binding family protein

At2g28550	RAP2.7/TOE1	related to AP2.7 (RAP2.7)
At2g30250	WRKY25	member of WRKY Transcription Factor; Group I. Located in nucleus. Involved in response to various abiotic stresses - especially salt stress
At2g33710	AP2-33	encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain
At2g38470	WRKY33	Member of the plant WRKY transcription factor family. Regulates the antagonistic relationship between defense pathways mediating responses to P. syringae and necrotrophic fungal pathogens. Located in nucleus. Involved in response to various abiotic stresses - especially salt stress.
At2g46830	myb-related transcription factor (CCA1)	Encodes a transcriptional repressor that performs overlapping functions with LHY in a regulatory feedback loop that is closely associated with the circadian oscillator of Arabidopsis.
At3g01560	TTF1	Ubiquitin-associated/translation elongation factor EF1B, N-terminal
At3g04070	NAC transcription factor family (ANAC047)	NAC domain containing protein 47 (NAC047); FUNCTIONS IN: sequence-specific DNA binding transcription factor activity; INVOLVED IN: multicellular organismal development, regulation of transcription
At3g06590	Basic helix-loop-helix (bHLH) DNA binding superfamily protein	
At3g20770	EIN3	Encodes EIN3 (ethylene-insensitive3), a nuclear transcription factor that initiates downstream transcriptional cascades for ethylene responses.
At3g25790	HHO1	myb-like transcription factor family protein
At3g46130	ATMYB48, ATMYB48-1, ATMYB48-2, ATMYB48-3, MYB48, myb domain protein 48	
At3g47620	AtTCP14, TCP14, TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14	
At3g51920	Calmodulin-like protein 9 (CAM9)	encodes a divergent member of calmodulin, which is

		an EF-hand family of Ca2+-binding proteins.
At3g54620	bZIP25	
At3g60490	Integrase-type DNA-binding superfamily protein	
At3g61150	HBZIP	Encodes a homeobox-leucine zipper family protein belonging to the HD-ZIP IV family.
At3g61890	ATHB12	Encodes a homeodomain leucine zipper class I (HD-Zip I) protein. Loss of function mutant has abnormally shaped leaves and stems.
At3g62420	bZIP53	Encodes a group-S bZIP transcription factor. Forms heterodimers with group-C bZIP transcription factors. The heterodimers bind to the ACTCAT cis-element of proline dehydrogenase gene.
At4g17490	ethylene-responsive element binding factor 6 (ERF6)	Encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ATERF-6). The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5. It is involved in the response to reactive oxygen species and light stress.
At4g17500	ethylene-responsive element-binding protein 1 (ERF1)	Encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ATERF-1). The protein contains one AP2 domain.
At4g24240	WRKY7	Encodes a Ca-dependent calmodulin binding protein. Sequence similarity to the WRKY transcription factor gene family.
At4g27410	NAC transcription factor family (RD26)	Encodes a NAC transcription factor induced in response to dessication. It is localized to the nucleus and acts as a transcriptional activator in ABA-mediated dehydration response.
At4g31800	WRKY18	Pathogen-induced transcription factor. Binds W-box sequences in vitro. Forms protein complexes with itself and with WRKY40 and WRKY60
At4g34590	ATB2, AtbZIP11, BZIP11, GBF6, G-box binding factor 6	
At4g36540	BEE2, BR enhanced expression 2	

At4g37180	HHO5	
At4g37260	myb family transcription factor (MYB73)	Member of the R2R3 factor gene family.
At4g37610	BT5	BTB and TAZ domain protein. Located in cytoplasm and expressed in fruit, flower and leaves.
At4g37730	AtbZIP7, bZIP7, basic leucine-zipper 7	
At5g05410	DRE-binding protein 2A (DREB2A)	Encodes a transcription factor that specifically binds to DRE/CRT cis elements (responsive to drought and low-temperature stress). Belongs to the DREB subfamily A-2 of ERF/AP2 transcription factor family (DREB2A)
At5g06800	myb-like HTH transcriptional regulator family protein	
At5G10030	TGA4	
At5g13080	ATWRKY75, WRKY75, WRKY DNA-binding protein 75	
At5g14540	TTF2	proline-rich family protein contains proline rich extensin domains
At5g24800	bZIP1 transcription factor family protein (bZIP9)	Encodes bZIP protein BZO2H2.
At5g39610	NAC6	Encodes a NAC-domain transcription factor. Positively regulates aging-induced cell death and senescence in leaves. This gene is upregulated in response to salt stress in wildtype as well as NTHK1 transgenic lines although in the latter case the induction was drastically reduced
At5g44190	myb family transcription factor (GLK2)	Encodes GLK2, Golden2-like 2, one of a pair of partially redundant nuclear transcription factors that regulate chloroplast development in a cell-autonomous manner. GLK1, Golden2-like 1, is encoded by At2g20570. GLK1 and GLK2 regulate the expression of the photosynthetic apparatus.
At5g47230	AP2-6	encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ATERF-5). The protein contains one AP2 domain

At5g48655	C3HC4 RING	RING/U-box superfamily protein
At5g49450	bZIP1 transcription factor family protein (bZIP1)	Encodes a transcription activator is a positive regulator of plant tolerance to salt, osmotic and drought stresses.
At5g49520	ATWRKY48, WRKY48, WRKY DNA-binding protein 48	
At5g56270	ATWRKY2, WRKY2, WRKY DNA-binding protein 2	
At5g60850	Dof-type zinc finger domain containing protein (OBF4)	Encodes a zinc finger protein.
At5g63790	NAC transcription factor family (ANAC102)	Encodes a member of the NAC family of transcription factors. ANAC102 appears to have a role in mediating response to low oxygen stress (hypoxia) in germinating seedlings.
At5G65210	TGA1	
At5g65640	BHLH093	beta HLH protein 93 (bHLH093)

5.2. TRANSGENIC PLANTS

5.2.1. Modulation of Gene Expression

[00167] The methods of the invention involve modulation of the expression of one, two, three or more target nucleotide sequences (i.e., target genes) in a host cell, such as a plant protoplast. That is, the expression of a target nucleotide sequence of interest may be increased or decreased.

[00168] The target nucleotide sequences may be endogenous or exogenous in origin. By "modulate expression of a target gene" is intended that the expression of the target gene is increased or decreased relative to the expression level in a host cell that has not been altered by the methods described herein.

[00169] By "increased or over expression" is intended that expression of the target nucleotide sequence is increased over expression observed in conventional transgenic lines for heterologous genes and over endogenous levels of expression for homologous genes. Heterologous or exogenous genes comprise genes that do not occur in the host cell of interest in its native state. Homologous or endogenous genes are those that are

natively present in the plant genome. Generally, expression of the target sequence is substantially increased. That is expression is increased at least about 25%-50%, preferably about 50%-100%, more preferably about 100%, 200% and greater.

[00170] By "decreased expression" or "underexpression" it is intended that expression of the target nucleotide sequence is decreased below expression observed in conventional transgenic lines for heterologous genes and below endogenous levels of expression for homologous genes. Generally, expression of the target nucleotide sequence of interest is substantially decreased. That is expression is decreased at least about 25%-50%, preferably about 50%-100%, more preferably about 100%, 200% and greater.

[00171] Expression levels may be assessed by determining the level of a gene product by any method known in the art including, but not limited to determining the levels of the RNA and protein encoded by a particular target gene. For genes that encode proteins, expression levels may determined, for example, by quantifying the amount of the protein present in plant cells, or in a plant or any portion thereof. Alternatively, it desired target gene encodes a protein that has a known measurable activity, then activity levels may be measured to assess expression levels.

5.2.2. Transfection

[00172] Any method or delivery system may be used for the delivery and/or transfection of the nucleic acid vectors encoding any of the genes of interest of the present invention in the host cell, e.g., plant protoplast. The vectors may be delivered to the host cell either alone, or in combination with other agents. Transient expression systems may also be used. Homologous recombination may also be used.

[00173] Transfection may be accomplished by a wide variety of means, as is known to those of ordinary skill in the art. Such methods include, but are not limited to, Agrobacterium-mediated transformation (*e.g.*, Komari *et al.*, 1998, Curr. Opin. Plant Biol., 1:161), particle bombardment mediated transformation (*e.g.*, Finer *et al.*, 1999, Curr. Top. Microbiol. Immunol., 240:59), protoplast electroporation (*e.g.*, Bates, 1999, Methods Mol. Biol., 111:359), viral infection (*e.g.*, Porta and Lomonossoff, 1996, Mol. Biotechnol. 5:209), microinjection, and liposome injection. Other exemplary delivery systems that can be used to facilitate uptake by a cell of the nucleic acid include calcium

phosphate and other chemical mediators of intracellular transport, microinjection compositions, and homologous recombination compositions (*e.g.*, for integrating a gene into a preselected location within the chromosome of the cell). Alternative methods may involve, for example, the use of liposomes, electroporation, or chemicals that increase free (or "naked") DNA uptake, transformation using viruses or pollen and the use of microprojection. Standard molecular biology techniques are common in the art (*e.g.*, Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, New York).

[00174] One of skill in the art will be able to select an appropriate vector for introducing the encoding nucleic acid sequence in a relatively intact state. Thus, any vector which will produce a host cell, e.g., plant protoplast, carrying the introduced encoding nucleic acid should be sufficient. The selection of the vector, or whether to use a vector, is typically guided by the method of transformation selected.

[00175] The transformation of plants cells in accordance with the invention may be carried out in essentially any of the various ways known to those skilled in the art of plant molecular biology. (See, for example, Methods of Enzymology, Vol. 153, 1987, Wu and Grossman, Eds., Academic Press, incorporated herein by reference).

[00176] Plant cells can comprise two or more nucleotide sequence constructs. Any means for producing a plant cell, e.g., protoplast, comprising the nucleotide sequence constructs described herein are encompassed by the present invention. For example, a nucleotide sequence encoding the modulator can be used to transform a plant cell at the same time as the nucleotide sequence encoding the precursor RNA. The nucleotide sequence encoding the precursor mRNA can be introduced into a plant cell that has already been transformed with the modulator nucleotide sequence. Likewise, viral vectors may be used to express gene products by various methods generally known in the art. Suitable plant viral vectors for expressing genes should be self-replicating, capable of systemic infection in a host, and stable. Additionally, the viruses should be capable of containing the nucleic acid sequences that are foreign to the native virus forming the vector.

[00177] Homologous recombination may be used as a method of gene inactivation.

[00178] The particular choice of a transformation technology will be determined by its efficiency to transform certain plant species as well as the experience and preference of the person practicing the invention with a particular methodology of choice. It will be apparent to the skilled person that the particular choice of a transformation system to introduce nucleic acid into plant cells is not essential to or a limitation of the invention, nor is the choice of technique for plant regeneration.

[00179] **Agrobacterium**. The nucleic acid sequences utilized in the present invention can be introduced into plant cells using Ti plasmids of *Agrobacterium tumefaciens* (*A. tumefaciens*), root-inducing (Ri) plasmids of *Agrobacterium rhizogenes* (*A. rhizogenes*), and plant virus vectors. For reviews of such techniques see, for example, Weissbach & Weissbach, 1988, Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey, 1988, Plant Molecular Biology, 2d Ed., Blackie, London, Ch. 7-9, and Horsch *et al.*, 1985, Science, 227:1229.

[00180] In using an *A. tumefaciens* culture as a transformation vehicle, it is most advantageous to use a non-oncogenic strain of *Agrobacterium* as the vector carrier so that normal non-oncogenic differentiation of the transformed tissues is possible. It is also preferred that the *Agrobacterium* harbor a binary Ti plasmid system. Such a binary system comprises 1) a first Ti plasmid having a virulence region essential for the introduction of transfer DNA (T-DNA) into plants, and 2) a chimeric plasmid. The chimeric plasmid contains at least one border region of the T-DNA region of a wild-type Ti plasmid flanking the nucleic acid to be transferred. Binary Ti plasmid systems have been shown effective in the transformation of plant cells (De Framond, Biotechnology, 1983, 1:262; Hoekema *et al.*, 1983, Nature, 303:179). Such a binary system is preferred because it does not require integration into the Ti plasmid of *A. tumefaciens*, which is an older methodology.

[00181] In some embodiments, a disarmed Ti-plasmid vector carried by *Agrobacterium* exploits its natural gene transferability (EP-A-270355, EP-A-01 16718, Townsend *et al.*, 1984, NAR, 12:8711, U.S. Pat. No. 5,563,055).

[00182] Methods involving the use of *Agrobacterium* in transformation according to the present invention include, but are not limited to: 1) co-cultivation of *Agrobacterium*

with cultured isolated protoplasts; 2) transformation of plant cells or tissues with *Agrobacterium*; or 3) transformation of seeds, apices or meristems with *Agrobacterium*.

[00183] In addition, gene transfer can be accomplished by in planta transformation by *Agrobacterium*, as described by Bechtold *et al.*, (C.R. Acad. Sci. Paris, 1993, 316:1194). This approach is based on the vacuum infiltration of a suspension of *Agrobacterium* cells.

[00184] In certain embodiments, nucleic acid molecue is introduced into plant cells by infecting such plant cells, an explant, a meristem or a seed, with transformed *A. tumefaciens* as described above. Under appropriate conditions known in the art, the transformed plant cells are grown to form shoots, roots, and develop further into plants.

[00185] Other methods described herein, such as microprojectile bombardment, electroporation and direct DNA uptake can be used where *Agrobacterium* is inefficient or ineffective. Alternatively, a combination of different techniques may be employed to enhance the efficiency of the transformation process, *e.g.*, bombardment with *Agrobacterium*-coated microparticles (EP-A-486234) or microprojectile bombardment to induce wounding followed by co-cultivation with *Agrobacterium* (EP-A-486233).

[00186] **CaMV**. In some embodiments, cauliflower mosaic virus (CaMV) is used as a vector for introducing a desired nucleic acid into plant cells (U.S. Pat. No. 4,407,956). CaMV viral DNA genome can be inserted into a parent bacterial plasmid creating a recombinant DNA molecule which can be propagated in bacteria. After cloning, the recombinant plasmid again can be cloned and further modified by introduction of the desired nucleic acid sequence. The modified viral portion of the recombinant plasmid can then be excised from the parent bacterial plasmid, and used to inoculate the plant cells or plants.

[00187] **Mechanical and Chemical Means**. In some embodiments, a nucleic acid molecule of the invention is introduced into a plant cell using mechanical or chemical means. Exemplary mechanical and chemical means are provided below.

[00188] As used herein, the term "contacting" refers to any means of introducing a nucleic acid molecule into a plant cell, including chemical and physical means as described above. Preferably, contacting refers to introducing the nucleic acid or vector containing the nucleic acid into plant cells (including an explant, a meristem or a seed), via A. tumefaciens transformed with the nucleic acid molecule.

[00189] **Microinjection**. In one embodiment, the nucleic acid molecule can be mechanically transferred into the plant cell by microinjection using a micropipette. See, *e.g.*, WO 92/09696, WO 94/00583, EP 331083, EP 175966, Green *et al.*, 1987, Plant Tissue and Cell Culture, Academic Press, Crossway *et al.*, 1986, Biotechniques 4:320-334.

[00190] **PEG.** In other embodiment, the nucleic acid can also be transferred into the plant cell by using polyethylene glycol (PEG)which forms a precipitation complex with genetic material that is taken up by the cell.

[00191] **Electroporation.** Electroporation can be used, in another set of embodiments, to deliver a nucleic acid to the cell (see, *e.g.*, Fromm *et al.*, 1985, PNA5, 82:5824). "Electroporation," as used herein, is the application of electricity to a cell, such as a plant protoplast, in such a way as to cause delivery of a nucleic acid into the cell without killing the cell. Typically, electroporation includes the application of one or more electrical voltage "pulses" having relatively short durations (usually less than 1 second, and often on the scale of milliseconds or microseconds) to a media containing the cells. The electrical pulses typically facilitate the non-lethal transport of extracellular nucleic acids into the cells. The exact electroporation protocols (such as the number of pulses, duration of pulses, pulse waveforms, *etc.*), will depend on factors such as the cell type, the cell media, the number of cells, the substance(s) to be delivered, *etc.*, and can be determined by those of ordinary skill in the art. Electroporation is discussed in greater detail in, *e.g.,* EP 290395, WO 8706614, Riggs *et al.*, 1986, Proc. Natl. Acad. Sci. USA 83:5602-5606; D'Halluin *et al.*, 1992, Plant Cell 4:1495-1505). Other forms of direct DNA uptake can also be used in the methods provided herein, such as those discussed in, *e.g.,* DE 4005152, WO 9012096, U.S. Pat. No. 4,684,611, Paszkowski *et al.*, 1984, EMBO J. 3:2717-2722.

[00192] **Ballistic and Particle Bombardment.** Another method for introducing a nucleic acid molecule is high velocity ballistic penetration by small particles with the nucleic acid to be introduced contained either within the matrix of such particles, or on the surface thereof (Klein *et al.*, 1987, Nature 327:70). Genetic material can be introduced into a cell using particle gun ("gene gun") technology, also called microprojectile or microparticle bombardment. In this method, small, high-density

particles (microprojectiles) are accelerated to high velocity in conjunction with a larger, powder-fired macroprojectile in a particle gun apparatus. The microprojectiles have sufficient momentum to penetrate cell walls and membranes, and can carry RNA or other nucleic acids into the interiors of bombarded cells. It has been demonstrated that such microprojectiles can enter cells without causing death of the cells, and that they can effectively deliver foreign genetic material into intact tissue. Bombardment transformation methods are also described in Sanford *et al.* (Techniques 3:3-16, 1991) and Klein *et al.* (Bio/Techniques 10:286, 1992). Although, typically only a single introduction of a new nucleic acid sequence(s) is required, this method particularly provides for multiple introductions.

[00193] Particle or microprojectile bombardment are discussed in greater detail in, *e.g.,* the following references: U.S. Pat. No. 5,100,792, EP-A-444882, EP-A-434616; Sanford *et al.*, U.S. Pat. No. 4,945,050; Tomes *et al.*, 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in Plant Cell, Tissue, and Organ Culture: Fundamental Methods, ed. Gamborg and Phillips (Springer-Verlag, Berlin); and McCabe *et al.*, 1988, Biotechnology 6:923-926.

[00194] **Colloidal Dispersion.** In other embodiments, a colloidal dispersion system may be used to facilitate delivery of a nucleic acid into the cell. As used herein, a "colloidal dispersion system" refers to a natural or synthetic molecule, other than those derived from bacteriological or viral sources, capable of delivering to and releasing the nucleic acid to the cell. Colloidal dispersion systems include, but are not limited to, macromolecular complexes, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. One example of a colloidal dispersion system is a liposome. Liposomes are artificial membrane vessels. It has been shown that large unilamellar vessels ("LUV"), which-range in size from 0.2 to 4.0 microns, can encapsulate large macromolecules within the aqueous interior and these macromolecules can be delivered to cells in a biologically active form (*e.g.*, Fraley *et al.*, 1981, Trends Biochem. Sci., 6:77).

[00195] **Lipids.** Lipid formulations for the transfection and/or intracellular delivery of nucleic acids are commercially available, for instance, from QIAGEN, for example as EFFECTENE® (a non-liposomal lipid with a special DNA condensing enhancer) and

SUPER-FECT® (a novel acting dendrimeric technology) as well as Gibco BRL, for example, as LIPOFECTIN® and LIPOFECTACE®, which are formed of cationic lipids such as N-[1-(2,3-dioleyloxy)-propyl]-N,N,N-trimethylammonium chloride ("DOTMA") and dimethyl dioctadecylammonium bromide ("DDAB"). Liposomes are well known in the art and have been widely described in the literature, for example, in Gregoriadis, G., 1985, Trends in Biotechnology 3:235-241; Freeman *et al.*, 1984, Plant Cell Physiol. 29:1353).

[00196] **Other Methods.** In addition to the above, other physical methods for the transformation of plant cells are reviewed in the following and can be used in the methods provided herein. Oard , 1991, Biotech. Adv. 9:1-11. See generally, Weissinger *et al.*, 1988, sAnn. Rev. Genet. 22:421-477; Sanford *et al.*, 1987, Particulate Science and Technology 5:27-37; Christou *et al.*, 1988, Plant Physiol. 87:671-674; McCabe *et al.*, 1988, Bio/Technology 6:923-926; Finer and McMullen, 1991, *In vitro* Cell Dev. Biol. 27P:175-182; Singh *et al.*, 1998, Theor. Appl. Genet. 96:319-324; Datta *et al.*, 1990, Biotechnology 8:736-740; Klein *et al.*, 1988, Proc. Natl. Acad. Sci. USA 85:4305-4309; Klein *et al.*, 1988, Biotechnology 6:559-563; Tomes, U.S. Pat. No. 5,240,855; Buising *et al.*, U.S. Pat. Nos. 5,322,783 and 5,324,646; Klein *et al.*, 1988, Plant Physiol. 91:440-444; Fromm *et al.*, 1990, Biotechnology 8:833-839; Hooykaas-Van Slogteren *et al.*, 1984, Nature (London) 311:763-764; Bytebier *et al.*, 1987, Proc. Natl. Acad. Sci. USA 84:5345-5349; De Wet *et al.*, 1985, The Experimental Manipulation of Ovule Tissues, ed. Chapman *et al.* (Longman, N.Y.), pp. 197-209; Kaeppler *et al.*, 1990, Plant Cell Reports 9:415-418 and Kaeppler *et al.*, 1992, Theor. Appl. Genet. 84:560-566; Li *et al.*, 1993, Plant Cell Reports 12:250-255 and Christou and Ford, 1995, Annals of Botany 75:407-413; Osjoda *et al.*, 1996, Nature Biotechnology 14:745-750; all of which are herein incorporated by reference.

5.2.3. Nucleic Acid Constructs

[00197] The nucleic acid molecules of the invention may be provided in nucleotide sequence constructs or expression cassettes for expression in the plant cell of interest. The cassette will include 5' and 3' regulatory sequences operably linked to an encoding nucleotide sequence of the invention.

[00198] The expression cassette may additionally contain at least one additional gene to be co-transformed into the organism. Alternatively, the additional gene(s) can be provided on multiple expression cassettes.

[00199] In certain embodiments, an expression cassette can be used with a plurality of restriction sites for insertion of the sequences of the invention to be under the transcriptional regulation of the regulatory regions. The expression cassette can additionally contain selectable marker genes (see below).

[00200] The expression cassette will generally include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of the invention, and a transcriptional and translational termination region functional in plants. The transcriptional initiation region, the promoter, may be native or analogous or foreign or heterologous to the plant host. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. By "foreign" is intended that the transcriptional initiation region is not found in the native plant into which the transcriptional initiation region is introduced. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

[00201] The termination region may be native with the transcriptional initiation region, may be native with the operably linked DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.*, 1991, Mol. Gen. Genet. 262:141-144; Proudfoot, 1991, Cell 64:671-674; Sanfacon *et al.*, 1991, Genes Dev. 5:141-149; Mogen *et al.*, 1990, Plant Cell 2:1261-1272; Munroe *et al.*, 1990, Gene 91:151-158; Ballas *et al.*, 1989, Nucleic Acids Res. 17:7891-7903; and Joshi *et al.*, 1987, Nucleic Acid Res. 15:9627-9639.

[00202] In some embodiments, a nucleic acid can be delivered to the cell in a vector. As used herein, a "vector" is any vehicle capable of facilitating the transfer of the nucleic acid to the cell such that the nucleic acid can be processed and/or expressed in the cell. The vector may transport the nucleic acid to the cells with reduced degradation, relative to the extent of degradation that would result in the absence of the vector. The vector

optionally includes gene expression sequences or other components (such as promoters and other regulatory elements) able to enhance expression of the nucleic acid within the cell. The invention also encompasses the cells transfected with these vectors, including those cells previously described.

[00203] To commence a transformation process in certain embodiments, it is first necessary to construct a suitable vector and properly introduce it into the plant cell. Vector(s) employed in the present invention for transformation of a plant cell include an encoding nucleic acid sequence operably associated with a promoter, such as a leaf-specific promoter. Details of the construction of vectors utilized herein are known to those skilled in the art of plant genetic engineering.

[00204] In general, vectors useful in the invention include, but are not limited to, plasmids, phagemids, viruses, other vehicles derived from viral or bacterial sources that have been manipulated by the insertion or incorporation of the nucleotide sequences (or precursor nucleotide sequences) of the invention. Viral vectors useful in certain embodiments include, but are not limited to, nucleic acid sequences from the following viruses: retroviruses; adenovirus, or other adeno-associated viruses; mosaic viruses such as tobamoviruses; potyviruses, nepoviruses, and RNA viruses such as retroviruses. One can readily employ other vectors not named but known to the art. Some viral vectors can be based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the nucleotide sequence of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA.

[00205] Genetically altered retroviral expression vectors can have general utility for the high-efficiency transduction of nucleic acids. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the cells with viral particles) are well known to those of ordinary skill in the art. Examples of standard protocols can be found in Kriegler, M., 1990, Gene Transfer and Expression, A Laboratory Manual, W.H.

Freeman Co., New York, or Murry, E. J. Ed., 1991, Methods in Molecular Biology, Vol. 7, Humana Press, Inc., Cliffton, N.J.

[00206] Another-example of a virus for certain applications is the adeno-associated virus, which is a double-stranded DNA virus. The adeno-associated virus can be engineered to be replication-deficient and is capable of infecting a wide range of-cell types and species. The adeno-associated virus further has advantages, such as heat and lipid solvent stability; high transduction frequencies in cells of diverse lineages; and/or lack of superinfection inhibition, which may allow multiple series of transductions.

[00207] Another vector suitable for use with the method provided herein is a plasmid vector. Plasmid vectors, have been extensively described in the art and are well-known to those of skill in the art. See, *e.g.*, Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press. These plasmids may have a promoter compatible with the host cell, and the plasmids can express a peptide from a gene operatively encoded within the plasmid. Some commonly used plasmids include pBR322, pUC18, pUC19, pRC/CMV, SV40, and pBlueScript. Other plasmids are well-known to those of ordinary skill in the art. Additionally, plasmids may be custom-designed, for example, using restriction enzymes and ligation reactions, to remove and add specific fragments of DNA or other nucleic acids, as necessary. The present invention also includes vectors for producing nucleic acids or precursor nucleic acids containing a desired nucleotide sequence (which can, for instance, then be cleaved or otherwise processed within the cell to produce a precursor miRNA). These vectors may include a sequence encoding a nucleic acid and an *in vivo* expression element, as further described below. In some cases, the *in vivo* expression element includes at least one promoter.

[00208] Where appropriate, the gene(s) for enhanced expression may be optimized for expression in the transformed plant. That is, the genes can be synthesized using plant-preferred codons corresponding to the plant of interest. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Pat. Nos. 5,380,831, and 5,436,391, and Murray *et al.*, 1989, Nucleic Acids Res. 17:477-498.

[00209] Additional sequence modifications are known to enhance gene expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation

signals, exon-intron splice site signals, transposon-like repeats, and other such well-characterized sequences that may be deleterious to gene expression. The G-C content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. When desired, the sequence is modified to avoid predicted hairpin secondary mRNA structures. However, it is recognized that in the case of nucleotide sequences encoding the miRNA precursors, one or more hairpin and other secondary structures may be desired for proper processing of the precursor into an mature miRNA and/or for the functional activity of the miRNA in gene silencing.

[00210] The expression cassettes can additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region) (Elroy-Stein *et al.*, 1989, PNAS USA 86:6126-6130); potyvirus leaders, for example, TEV leader (Tobacco Etch Virus) (Allison *et al.*, 1986); MDMV leader (Maize Dwarf Mosaic Virus); Virology 154:9-20), and human immunoglobulin heavy-chain binding protein (BiP), (Macejak *et al.*, 1991, Nature 353:90-94); untranslated leader from the coat protein miRNA of alfalfa mosaic virus (AMV RNA 4) (Jobling *et al.*, 1987, Nature 325:622-625); tobacco mosaic virus leader (TMV) (Gallie *et al.*, 1989, Molecular Biology of RNA, ed. Cech (Liss, New York), pp. 237-256); and maize chlorotic mottle virus leader (MCMV) (Lommel *et al.*, 1991, Virology 81:382-385). See also, Della-Cioppa *et al.*, 1987, Plant Physiol. 84:965-968.

[00211] In preparing the expression cassette, the various DNA fragments can be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers can be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, *e.g.*, transitions and transversions, may be involved.

5.2.4. Host Cells

[00212] Provided herein are host cells that contain a vector, e.g., a DNA plasmid and support the replication and/or expression of the vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, plant, insect, amphibian, or mammalian cells. In some embodiments, host cells are monocotyledonous or dicotyledonous plant cells. In other embodiments monocotyledonous host cell is a maize host cell. In certain embodiments, the host cell utilized in the methods of the present invention are transiently transfected with the nucleic acid molecules of the invention.

[00213] In preferred embodiments, the host cell utilized in the methods of the present invention is a plant protoplast. Plant protoplasts are plant cells that had their entire plant cell wall enzymatically removed prior to the introduction of the molecule of interest. The complete removal of the cell wall disrupts the connection between cells producing a homogenous suspension of individualized cells which allows more uniform and large scale transfection experiments. This comprises, but is not restricted to protoplast fusion, electroporation, liposome-mediated transfection, and polyethylene glycol-mediated transfection. Protoplast preparation is therefore a very reliable and inexpensive method to produce millions of cells.

[00214] In particular embodiments, the plant protoplast is derived from one of the following genuses: Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arabidopsis, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea, or Zinnia. In some embodiments, the host cell is derived from a genus that is different from the genus from which the transcription factor is derived from. For example, the host cell is a plant protoplast derived from the genus *Arabidopsis* and the transcription factor is derived from the genus *Zea*.

[00215] Also provided herein are plant cells having the nucleotide sequence constructs of the invention. A further aspect of the present invention provides a method of making

such a plant cell involving introduction of a vector including the construct into a plant cell. For integration of the construct into the plant genome, such introduction will be followed by recombination between the vector and the plant cell genome to introduce the sequence of nucleotides into the genome. RNA encoded by the introduced nucleic acid construct may then be transcribed in the cell and descendants thereof, including cells in plants regenerated from transformed material. A gene stably incorporated into the genome of a plant is passed from generation to generation to descendants of the plant, so such descendants should show the desired phenotype.

[00216] Optionally, germ line cells may be used in the methods described herein rather than, or in addition to, somatic cells. The term "germ line cells" refers to cells in the plant organism which can trace their eventual cell lineage to either the male or female reproductive cell of the plant. Other cells, referred to as "somatic cells" are cells which give rise to leaves, roots and vascular elements which, although important to the plant, do not directly give rise to gamete cells. Somatic cells, however, also may be used. With regard to callus and suspension cells which have somatic embryogenesis, many or most of the cells in the culture have the potential capacity to give rise to an adult plant. If the plant originates from single cells or a small number of cells from the embryogenic callus or suspension culture, the cells in the callus and suspension can therefore be referred to as germ cells. In the case of immature embryos which are prepared for treatment by the methods described herein, certain cells in the apical meristem region of the plant have been shown to produce a cell lineage which eventually gives rise to the female and male reproductive organs. With many or most species, the apical meristem is generally regarded as giving rise to the lineage that eventually will give rise to the gamete cells. An example of a non-gamete cell in an embryo would be the first leaf primordia in corn which is destined to give rise only to the first leaf and none of the reproductive structures.

5.2.5. Promoters and Other Regulatory Sequences

[00217] In the broad method of the invention, the nucleic acid molecule of the invention is operably linked with a promoter. It may be desirable to introduce more than one copy of a polynucleotide into a plant cell for enhanced expression.

[00218] In general, promoters are found positioned 5' (upstream) of the genes that they control. Thus, in the construction of promoter gene combinations, the promoter is preferably positioned upstream of the gene and at a distance from the transcription start site that approximates the distance between the promoter and the gene it controls in the natural setting. As is known in the art, some variation in this distance can be tolerated without loss of promoter function. Similarly, the preferred positioning of a regulatory element, such as an enhancer, with respect to a heterologous gene placed under its control reflects its natural position relative to the structural gene it naturally regulates.

[00219] Thus, the nucleic acid, in one embodiment, is operably linked to a gene expression sequence, which directs the expression of the nucleic acid within the cell. A "gene expression sequence," as used herein, is any regulatory nucleotide sequence, such as a promoter sequence or promoter-enhancer combination, which facilitates the efficient transcription and translation of the nucleotide sequence to which it is operably linked. The gene expression sequence may, for example, be a eukaryotic promoter or a viral promoter, such as a constitutive or inducible promoter. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription, for instance, as discussed in Maniatis *et al.*, 1987, Science 236:1237. Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in plant, yeast, insect and mammalian cells and viruses (analogous control elements, *i.e.*, promoters, are also found in prokaryotes). In some embodiments, the nucleic acid is linked to a gene expression sequence which permits expression of the nucleic acid in a plant cell. A sequence which permits expression of the nucleic acid in a plant cell is one which is selectively active in the particular plant cell and thereby causes the expression of the nucleic acid in these cells. Those of ordinary skill in the art will be able to easily identify promoters that are capable of expressing a nucleic acid in a cell based on the type of plant cell.

[00220] A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. Generally, the nucleotide sequence and the modulator sequences can be combined with promoters of choice to alter gene expression if the target sequences in the tissue or organ of choice. Thus, the nucleotide sequence or modulator nucleotide sequence can be combined with

constitutive, tissue-preferred, inducible, developmental, or other promoters for expression in plants depending upon the desired outcome.

[00221] The selection of a particular promoter and enhancer depends on what cell type is to be used and the mode of delivery. For example, a wide variety of promoters have been isolated from plants and animals, which are functional not only in the cellular source of the promoter, but also in numerous other plant species. There are also other promoters (*e.g.*, viral and Ti-plasmid) which can be used. For example, these promoters include promoters from the Ti-plasmid, such as the octopine synthase promoter, the nopaline synthase promoter, the mannopine synthase promoter, and promoters from other open reading frames in the T-DNA, such as ORF7, *etc*. Promoters isolated from plant viruses include the 35S promoter from cauliflower mosaic virus. Promoters that have been isolated and reported for use in plants include ribulose-1,3-biphosphate carboxylase small subunit promoter, phaseolin promoter, *etc.* Thus, a variety of promoters and regulatory elements may be used in the expression vectors of the present invention.

[00222] Promoters useful in the compositions and methods provided herein include both natural constitutive and inducible promoters as well as engineered promoters. The CaMV promoters are examples of constitutive promoters. Other constitutive mammalian promoters include, but are not limited to, polymerase promoters as well as the promoters for the following genes: hypoxanthine phosphoribosyl transferase ("HPTR"), adenosine deaminase, pyruvate kinase, and alpha-actin.

[00223] Promoters useful as expression elements of the invention also include inducible promoters. Inducible promoters are expressed in the presence of an inducing agent. For example, a metallothionein promoter can be induced to promote transcription in the presence of certain metal ions. Other inducible promoters are known to those of ordinary skill in the art. The *in vivo* expression element can include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription, and can optionally include enhancer sequences or upstream activator sequences.

[00224] For example, in some embodiments an inducible promoter is used to allow control of nucleic acid expression through the presentation of external stimuli (*e.g.*, environmentally inducible promoters), as discussed below. Thus, the timing and amount

of nucleic acid expression can be controlled in some cases. Non-limiting examples of expression systems, promoters, inducible promoters, environmentally inducible promoters, and enhancers are well known to those of ordinary skill in the art. Examples include those described in International Patent Application Publications WO 00/12714, WO 00/11175, WO 00/12713, WO 00/03012, WO 00/03017, WO 00/01832, WO 99/50428, WO 99/46976 and U.S. Pat. Nos. 6,028,250, 5,959,176, 5,907,086, 5,898,096, 5,824,857, 5,744,334, 5,689,044, and 5,612,472. A general descriptions of plant expression vectors and reporter genes can also be found in Gruber *et al.*, 1993, "Vectors for Plant Transformation," in Methods in Plant Molecular Biology & Biotechnology, Glich *et al.*, Eds., p. 89-119, CRC Press.

[00225] For plant expression vectors, viral promoters that can be used in certain embodiments include the 35S RNA and 19S RNA promoters of CaMV (Brisson *et al.*, Nature, 1984, 310:511; Odell *et al.*, Nature, 1985, 313:810); the full-length transcript promoter from Figwort Mosaic Virus (FMV) (Gowda *et al.*, 1989, J. Cell Biochem., 13D: 301) and the coat protein promoter to TMV (Takamatsu *et al.*, 1987, EMBO J. 6:307). Alternatively, plant promoters such as the light-inducible promoter from the small subunit of ribulose bis-phosphate carboxylase (ssRUBISCO) (Coruzzi *et al.*, 1984, EMBO J., 3:1671; Broglie *et al.*, 1984, Science, 224:838); mannopine synthase promoter (Velten *et al.*, 1984, EMBO J., 3:2723) nopaline synthase (NOS) and octopine synthase (OCS) promoters (carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*) or heat shock promoters, *e.g.*, soybean hsp17.5-E or hsp17.3-B (Gurley *et al.*, 1986, Mol. Cell. Biol., 6:559; Severin *et al.*, 1990, Plant Mol. Biol., 15:827) may be used. Exemplary viral promoters which function constitutively in eukaryotic cells include, for example, promoters from the simian virus, papilloma virus, adenovirus, human immunodeficiency virus, Rous sarcoma virus, cytomegalovirus, the long terminal repeats of Moloney leukemia virus and other retroviruses, and the thymidine kinase promoter of herpes simplex virus. Other constitutive promoters are known to those of ordinary skill in the art.

[00226] To be most useful, an inducible promoter should 1) provide low expression in the absence of the inducer; 2) provide high expression in the presence of the inducer; 3) use an induction scheme that does not interfere with the normal physiology of the plant;

and 4) have no effect on the expression of other genes. Examples of inducible promoters useful in plants include those induced by chemical means, such as the yeast metallothionein promoter which is activated by copper ions (Mett *et al.*, Proc. Natl. Acad. Sci., U.S.A., 90:4567, 1993); In2-1 and In2-2 regulator sequences which are activated by substituted benzenesulfonamides, *e.g.*, herbicide safeners (Hershey *et al.*, Plant Mol. Biol., 17:679, 1991); and the GRE regulatory sequences which are induced by glucocorticoids (Schena *et al.*, Proc. Natl. Acad Sci., U.S.A., 88:10421, 1991). Other promoters, both constitutive and inducible will be known to those of skill in the art.

[00227] A number of inducible promoters are known in the art. For resistance genes, a pathogen-inducible promoter can be utilized. Such promoters include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; *e.g.*, PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, *etc.* See, for example, Redolfi *et al.*, 1983, Neth. J. Plant Pathol. 89:245-254; Uknes *et al.*, 1992, Plant Cell 4:645-656; and Van Loon, 1985, Plant Mol. Virol. 4:111-116. Of particular interest are promoters that are expressed locally at or near the site of pathogen infection. See, for example, Marineau *et al.*, 1987, Plant Mol. Biol. 9:335-342; Matton *et al.*, 1989, Molecular Plant-Microbe Interactions 2:325-331; Somsisch *et al.*, 1986, Proc. Natl. Acad. Sci. USA 83:2427-2430; Somsisch *et al.*, 1988, Mol. Gen. Genet. 2:93-98; and Yang, 1996, Proc. Natl. Acad. Sci. USA 93:14972-14977. See also, Chen *et al.*, 1996, Plant J. 10:955-966; Zhang *et al.*, 1994, Proc. Natl. Acad. Sci. USA 91:2507-2511; Warner *et al.*, 1993, Plant J. 3:191-201; Siebertz *et al.*, 1989, Plant Cell 1:961-968; U.S. Pat. No. 5,750,386; Cordero *et al.*, 1992, Physiol. Mol. Plant Path. 41:189-200; and the references cited therein.

[00228] Additionally, as pathogens find entry into plants through wounds or insect damage, a wound-inducible promoter may be used in the DNA constructs of the invention. Such wound-inducible promoters include potato proteinase inhibitor (pin II) gene (Ryan, 1990, Ann. Rev. Phytopath. 28:425-449; Duan *et al.*, 1996, Nature Biotechnology 14:494-498); wun1 and wun2, U.S. Pat. No. 5,428,148; win1 and win2 (Stanford *et al.*, 1989, Mol. Gen. Genet. 215:200-208); systemin (McGurl *et al.*, 1992, Science 225:1570-1573); WIPI (Rohmeier *et al.*, 1993, Plant Mol. Biol. 22:783-792;

Eckelkamp *et al.*, 1993, FEBS Letters 323:73-76); MPI gene (Corderok *et al.*, 1994, Plant J. 6(2):141-150); and the like. Such references are herein incorporated by reference.

[00229] Chemical-regulated promoters can be used to modulate the expression of a gene in a plant through the application of an exogenous chemical regulator. Depending upon the objective, the promoter may be a chemical-inducible promoter, where application of the chemical induces gene expression, or a chemical-repressible promoter, where application of the chemical represses gene expression. Chemical-inducible promoters are known in the art and include, but are not limited to, the maize In2-2 promoter, which is activated by benzenesulfonamide herbicide safeners, the maize GST promoter, which is activated by hydrophobic electrophilic compounds that are used as pre-emergent herbicides, and the tobacco PR-1 a promoter, which is activated by salicylic acid. Other chemical-regulated promoters of interest include steroid-responsive promoters (see, for example, the glucocorticoid-inducible promoter in Schena *et al.*, 1991, Proc. Natl. Acad. Sci. USA 88:10421-10425 and McNellis *et al.*, 1998, Plant J. 14(2):247-257) and tetramiR167e-inducible and tetramiR167e-repressible promoters (see, for example, Gatz *et al.*, 1991, Mol. Gen. Genet. 227:229-237, and U.S. Pat. Nos. 5,814,618 and 5,789,156), herein incorporated by reference.

[00230] Where enhanced expression in particular tissues is desired, tissue-preferred promoters can be utilized. Tissue-preferred promoters include those described by Yamamoto *et al.*, 1997, Plant J. 12(2):255-265; Kawamata *et al.*, 1997, Plant Cell Physiol. 38(7):792-803; Hansen *et al.*, 1997, Mol. Gen Genet. 254(3):337-343; Russell *et al.*, 1997, Transgenic Res. 6(2):157-168; Rinehart *et al.*, 1996, Plant Physiol. 112(3):1331-1341; Van Camp *et al.*, 1996, Plant Physiol. 112(2):525-535; Canevascini *et al.*, 1996, Plant Physiol. 12(2):513-524; Yamamoto *et al.*, 1994, Plant Cell Physiol. 35(5):773-778; Lam, 1994, Results Probl. Cell Differ. 20:181-196; Orozco *et al.*, 1993, Plant Mol. Biol. 23(6): 1129-1138; Matsuoka *et al.*, 1993, Proc Natl. Acad. Sci. USA 90(20):9586-9590; and Guevara-Garcia *et al.*, 1993, Plant J 4(3):495-505.

[00231] The particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of structural gene product in the plant cell to cause upregulation of genes as compared to wild type. The promoters used in the vector constructs of the present invention may be modified, if desired, to

affect their control characteristics. In certain embodiments, chimeric promoters can be used.

[00232] There are promoters known which limit expression to particular plant parts or in response to particular stimuli. One skilled in the art will know of many such plant part-specific promoters which would be useful in the present invention. In certain embodiments, to provide pericycle-specific expression, any of a number of promoters from genes in *Arabidopsis* can be used. In some embodiments, the promoter from one (or more) of the following genes may be used: (i) At1g11080, (ii) At3g60160, (iii) At1g24575, (iv) At3g45160, or (v) At1g23130. In specific embodiments, (vi) promoter elements from the GFP-marker line used in Gifford *et al.* (in preparation) will be used (see also, Bonke *et al.*, 2003, Nature 426, 181-6; Tian *et al.*, 2004, Plant Physiol 135, 25-38). Several of the predicted genes have a number of potential orthologs in rice and poplar and thus are predicted that they will be applicable for use in crop species; (i) Os04g44410, Os10g39560, Os06g51370, Os02g42310, Os01g22980, Os05g06660, and Poptr1#568263, Poptr1#555534, Poptr1#365170; (ii) Os04g49900, Os04g49890, Os01g67580, and Poptr1#87573, Poptr1#80582, Poptr1#565079, Poptr1#99223.

[00233] Promoters used in the nucleic acid constructs of the present invention can be modified, if desired, to affect their control characteristics. For example, the CaMV 35S promoter may be ligated to the portion of the ssRUBISCO gene that represses the expression of ssRUBISCO in the absence of light, to create a promoter which is active in leaves but not in roots. The resulting chimeric promoter may be used as described herein. For purposes of this description, the phrase "CaMV 35S" promoter thus includes variations of CaMV 35S promoter, *e.g.*, promoters derived by means of ligation with operator regions, random or controlled mutagenesis, *etc*. Furthermore, the promoters may be altered to contain multiple "enhancer sequences" to assist in elevating gene expression.

[00234] An efficient plant promoter that may be used in specific embodiments is an "overproducing" or "overexpressing" plant promoter. Overexpressing plant promoters that can be used in the compositions and methods provided herein include the promoter of the small sub-unit ("ss") of the ribulose-1,5-biphosphate carboxylase from soybean (*e.g.*, Berry-Lowe *et al.*, 1982, J. Molecular & App. Genet., 1:483), and the promoter of

the chorophyll a-b binding protein. These two promoters are known to be light-induced in eukaryotic plant cells. For example, see Cashmore, Genetic Engineering of plants: An Agricultural Perspective, p. 29-38; Coruzzi *et al.*, 1983, J. Biol. Chem., 258:1399; and Dunsmuir *et al.*, 1983, J. Molecular & App. Genet., 2:285.

[00235] The promoters and control elements of, *e.g.,* SUCS (root nodules; broadbean; Kuster *et al.*, 1993, Mol Plant Microbe Interact 6:507-14) for roots can be used in compositions and methods provided herein to confer tissue specificity.

[00236] In certain embodiment, two promoter elements can be used in combination, such as, for example, (i) an inducible element responsive to a treatment that can be provided to the plant prior to N-fertilizer treatment, and (ii) a plant tissue-specific expression element to drive expression in the specific tissue alone.

[00237] Any promoter of other expression element described herein or known in the art may be used either alone or in combination with any other promoter or other expression element described herein or known in the art. For example, promoter elements that confer tissue specific expression of a gene can be used with other promoter elements conferring constitutive or inducible expression.

5.2.6. Isolating Related Promoter Sequences

[00238] Promoter and promoter control elements that are related to those described in herein can also be used in the compositions and methods provided herein. Such related sequence can be isolated utilizing (a) nucleotide sequence identity; (b) coding sequence identity of related, orthologous genes; or (c) common function or gene products.

[00239] Relatives can include both naturally occurring promoters and non-natural promoter sequences. Non-natural related promoters include nucleotide substitutions, insertions or deletions of naturally-occurring promoter sequences that do not substantially affect transcription modulation activity. For example, the binding of relevant DNA binding proteins can still occur with the non-natural promoter sequences and promoter control elements of the present invention.

[00240] According to current knowledge, promoter sequences and promoter control elements exist as functionally important regions, such as protein binding sites, and spacer regions. These spacer regions are apparently required for proper positioning of the protein binding sites. Thus, nucleotide substitutions, insertions and deletions can be tolerated in these spacer regions to a certain degree without loss of function.

[00241] In contrast, less variation is permissible in the functionally important regions, since changes in the sequence can interfere with protein binding. Nonetheless, some variation in the functionally important regions is permissible so long as function is conserved.

[00242] The effects of substitutions, insertions and deletions to the promoter sequences or promoter control elements may be to increase or decrease the binding of relevant DNA binding proteins to modulate transcript levels of a polynucleotide to be transcribed. Effects may include tissue-specific or condition-specific modulation of transcript levels of the polypeptide to be transcribed. Polynucleotides representing changes to the nucleotide sequence of the DNA-protein contact region by insertion of additional nucleotides, changes to identity of relevant nucleotides, including use of chemically-modified bases, or deletion of one or more nucleotides are considered encompassed by the present invention.

[00243] Typically, related promoters exhibit at least 80% sequence identity, preferably at least 85%, more preferably at least 90%, and most preferably at least 95%, even more preferably, at least 96%, at least 97%, at least 98% or at least 99% sequence identity. Such sequence identity can be calculated by the algorithms and computers programs described above.

[00244] Usually, such sequence identity is exhibited in an alignment region that is at least 75% of the length of a sequence or corresponding full-length sequence of a promoter described herein; more usually at least 80%; more usually, at least 85%, more usually at least 90%, and most usually at least 95%, even more usually, at least 96%, at least 97%, at least 98% or at least 99% of the length of a sequence of a promoter described herein.

[00245] The percentage of the alignment length is calculated by counting the number of residues of the sequence in region of strongest alignment, *e.g.*, a continuous region of

the sequence that contains the greatest number of residues that are identical to the residues between two sequences that are being aligned. The number of residues in the region of strongest alignment is divided by the total residue length of a sequence of a promoter described herein. These related promoters may exhibit similar preferential transcription as those promoters described herein.

[00246] In certain embodiments, a promoter, such as a leaf-preferred or leaf-specific promoter, can be identified by sequence homology or sequence identity to any root specific promoter identified herein. In other embodiments, orthologous genes identified herein as leaf-specific genes (*e.g.*, the same gene or different gene that if functionally equivalent) for a given species can be identified and the associated promoter can also be used in the compositions and methods provided herein. For example, using high, medium or low stringency conditions, standard promoter rules can be used to identify other useful promoters from orthologous genes for use in the compositions and methods provided herein. In specific embodiments, the orthologous gene is a gene expressed only or primarily in the root, such as pericycle cells.

[00247] Polynucleotides can be tested for activity by cloning the sequence into an appropriate vector, transforming plants with the construct and assaying for marker gene expression. Recombinant DNA constructs can be prepared, which comprise the polynucleotide sequences of the invention inserted into a vector suitable for transformation of plant cells. The construct can be made using standard recombinant DNA techniques (Sambrook *et al.*, 1989) and can be introduced to the species of interest by *Agrobacterium*-mediated transformation or by other means of transformation as referenced below.

[00248] The vector backbone can be any of those typical in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs and PACs and vectors of the sort described by (a) BAC: Shizuya *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89: 8794-8797; Hamilton *et al.*, 1996, Proc. Natl. Acad. Sci. USA 93: 9975-9979; (b) YAC: Burke *et al.*, 1987, Science 236:806-812; (c) PAC: Stemberg N. *et al.*, 1990, Proc Natl Acad Sci USA. January; 87(1):103-7; (d) Bacteria-Yeast Shuttle Vectors: Bradshaw *et al.*, 1995, Nucl Acids Res 23: 4850-4856; (e) Lambda Phage Vectors: Replacement Vector, *e.g.*, Frischauf *et al.*, 1983, J. Mol. Biol. 170: 827-842; or Insertion vector, *e.g.*, Huynh *et al.*,

1985, In: Glover N M (ed) DNA Cloning: A practical Approach, Vol. 1 Oxford: IRL Press; T-DNA gene fusion vectors: Walden *et al.*, 1990, Mol Cell Biol 1: 175-194; and (g) Plasmid vectors: Sambrook *et al.*, *infra.*

[00249] Typically, the construct comprises a vector containing a sequence of the present invention operationally linked to any marker gene. The polynucleotide was identified as a promoter by the expression of the marker gene. Although many marker genes can be used, Green Fluorescent Protein (GFP) is preferred. The vector may also comprise a marker gene that confers a selectable phenotype on plant cells. The marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or phosphinotricin (see below). Vectors can also include origins of replication, scaffold attachment regions (SARs), markers, homologous sequences, introns, *etc*.

5.2.7. Cell-Type Preferential Transcription

[00250] Specific promoters may be used in the compositions and methods provided herein. As used herein, "specific promoters" refers to a subset of promoters that have a high preference for modulating transcript levels in a specific tissue or organ or cell and/or at a specific time during development of an organism. By "high preference" is meant at least 3-fold, preferably 5-fold, more preferably at least 10-fold still more preferably at least 20-fold, 50-fold or 100-fold increase in transcript levels under the specific condition over the transcription under any other reference condition considered. Typical examples of temporal and/or tissue or organ specific promoters of plant origin that can be used in the compositions and methods of the present invention, inlcude RCc2 and RCc3, promoters that direct root-specific gene transcription in rice (Xu *et al.*, 1995, Plant Mol. Biol. 27:237 and TobRB27, a root-specific promoter from tobacco (Yamamoto *et al.*, 1991, Plant Cell 3:371). Examples of tissue-specific promoters under developmental control include promoters that initiate transcription only in certain tissues or organs, such as roots

[00251] "Preferential transcription" is defined as transcription that occurs in a particular pattern of cell types or developmental times or in response to specific stimuli or

combination thereof. Non-limitative examples of preferential transcription include: high transcript levels of a desired sequence in root tissues; detectable transcript levels of a desired sequence in certain cell types during embryogenesis; and low transcript levels of a desired sequence under drought conditions. Such preferential transcription can be determined by measuring initiation, rate, and/or levels of transcription.

[00252] Typically, promoter or control elements, which provide preferential transcription in cells, tissues, or organs of a root, produce transcript levels that are statistically significant as compared to other cells, organs or tissues. For preferential up-regulation of transcription, promoter and control elements produce transcript levels that are above background of the assay.

5.2.8. Selection and Identification of Transfected Host Cells

[00253] The method of the present invention comprises detecting host cells that express a selectable marker. In certain embodiments, the step of detecting host cells that express the selectable marker is performed by Fluorescence Activated Cell Sorting (FACS) in the methods of the present invention. Fluorescence activated cell sorting (FACS) is a well-known method for separating particles, including cells, based on the fluorescent properties of the particles (see, e.g., Kamarch, 1987, Methods Enzymol, 151:150-165). Laser excitation of fluorescent moieties in the individual particles results in a small electrical charge allowing electromagnetic separation of positive and negative particles from a mixture. In one embodiment, cell surface marker-specific antibodies or ligands are labeled with distinct fluorescent labels. Cells are processed through the cell sorter, allowing separation of cells based on their ability to bind to the antibodies used. FACS sorted particles may be directly deposited into individual wells of 96-well or 384-well plates to facilitate separation and cloning.

[00254] Also, desired plants may be obtained by engineering the disclosed gene constructs into a variety of plant cell types, including but not limited to, protoplasts, tissue culture cells, tissue and organ explants, pollens, embryos as well as whole plants. In an embodiment of the present invention, the engineered plant material is selected or screened for transformants (those that have incorporated or integrated the introduced gene construct(s)) following the approaches and methods described below. An isolated

transformant may then be regenerated into a plant. Alternatively, the engineered plant material may be regenerated into a plant or plantlet before subjecting the derived plant or plantlet to selection or screening for the marker gene traits. Procedures for regenerating plants from plant cells, tissues or organs, either before or after selecting or screening for marker gene(s), are well known to those skilled in the art.

[00255] A transformed plant cell, callus, tissue or plant may be identified and isolated by selecting or screening the engineered plant material for traits encoded by the marker genes present on the transforming DNA. For instance, selection may be performed by growing the engineered plant material on media containing inhibitory amount of the antibiotic or herbicide to which the transforming gene construct confers resistance. Further, transformed plants and plant cells may also be identified by screening for the activities of any visible marker genes (*e.g.*, the β-glucuronidase, luciferase, B or C1 genes) that may be present on the recombinant nucleic acid constructs of the present invention. Such selection and screening methodologies are well known to those skilled in the art.

[00256] Physical and biochemical methods also may be also to identify plant or plant cell transformants containing the gene constructs of the present invention. These methods include but are not limited to: 1) Southern analysis or PCR amplification for detecting and determining the structure of the recombinant DNA insert; 2) Northern blot, S1 RNase protection, primer-extension or reverse transcriptase-PCR amplification for detecting and examining RNA transcripts of the gene constructs; 3) enzymatic assays for detecting enzyme or ribozyme activity, where such gene products are encoded by the gene construct; 4) protein gel electrophoresis, Western blot techniques, immunoprecipitation, or enzyme-linked immunoassays, where the gene construct products are proteins. Additional techniques, such as in situ hybridization, enzyme staining, and immunostaining, also may be used to detect the presence or expression of the recombinant construct in specific plant organs and tissues. The methods for doing all these assays are well known to those skilled in the art.

5.2.9. Plant Regeneration

[00257] Following transformation, a plant may be regenerated, *e.g.*, from single cells, callus tissue or leaf discs, as is standard in the art. Almost any plant can be entirely regenerated from cells, tissues, and organs of the plant. Available techniques are reviewed in Vasil *et al.*, 1984, in Cell Culture and Somatic Cell Genetics of Plants, Vols. I, II, and III, Laboratory Procedures and Their Applications (Academic Press); and Weissbach *et al.*, 1989, Methods For Plant Mol. Biol.

[00258] The transformed plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved.

[00259] Normally, a plant cell is regenerated to obtain a whole plant from the transformation process. The term "growing" or "regeneration" as used herein means growing a whole plant from a plant cell, a group of plant cells, a plant part (including seeds), or a plant piece (*e.g.*, from a protoplast, callus, or tissue part).

[00260] Regeneration from protoplasts varies from species to species of plants, but generally a suspension of protoplasts is first made. In certain species, embryo formation can then be induced from the protoplast suspension. The culture media will generally contain various amino acids and hormones, necessary for growth and regeneration. Examples of hormones utilized include auxins and cytokinins. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these variables are controlled, regeneration is reproducible.

[00261] Regeneration also occurs from plant callus, explants, organs or parts. Transformation can be performed in the context of organ or plant part regeneration (see Methods in Enzymology, Vol. 118 and Klee *et al.*, Annual Review of Plant Physiology, 38:467, 1987). Utilizing the leaf disk-transformation-regeneration method of Horsch *et al.*, Science, 227:1229, 1985, disks are cultured on selective media, followed by shoot formation in about 2-4 weeks. Shoots that develop are excised from calli and transplanted to appropriate root-inducing selective medium. Rooted plantlets are

transplanted to soil as soon as possible after roots appear. The plantlets can be repotted as required, until reaching maturity.

[00262] In vegetatively propagated crops, the mature transgenic plants are propagated by utilizing cuttings or tissue culture techniques to produce multiple identical plants. Selection of desirable transgenics is made and new varieties are obtained and propagated vegetatively for commercial use.

[00263] In seed propagated crops, mature transgenic plants can be self crossed to produce a homozygous inbred plant. The resulting inbred plant produces seed containing the newly introduced foreign gene(s). These seeds can be grown to produce plants that would produce the selected phenotype, *e.g.*, increased lateral root growth, uptake of nutrients, overall plant growth and/or vegetative or reproductive yields.

[00264] Parts obtained from the regenerated plant, such as flowers, seeds, leaves, branches, fruit, and the like are included in the invention, provided that these parts comprise cells comprising the isolated nucleic acid of the present invention. Progeny and variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced nucleic acid sequences. Transgenic plants expressing the selectable marker can be screened for transmission of the nucleic acid of the present invention by, for example, standard immunoblot and DNA detection techniques. Transgenic lines are also typically evaluated on levels of expression of the heterologous nucleic acid. Expression at the RNA level can be determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis can be employed and include PCR amplification assays using oligonucleotide primers designed to amplify only the heterologous RNA templates and solution hybridization assays using heterologous nucleic acid-specific probes. The RNA-positive plants can then analyzed for protein expression by Western immunoblot analysis using the specifically reactive antibodies of the present invention. In addition, in situ hybridization and immunocytochemistry according to standard protocols can be done using heterologous nucleic acid specific polynucleotide probes and antibodies, respectively, to localize sites of expression within transgenic tissue. Generally, a number of transgenic lines are usually screened for the incorporated nucleic acid to identify and select plants with the most appropriate expression profiles.

[00265] A preferred embodiment is a transgenic plant that is homozygous for the added heterologous nucleic acid; *i.e.*, a transgenic plant that contains two added nucleic acid sequences, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) a heterozygous transgenic plant that contains a single added heterologous nucleic acid, germinating some of the seed produced and analyzing the resulting plants produced for altered expression of a polynucleotide of the present invention relative to a control plant (*i.e.*, native, non-transgenic). Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated.

[00266] Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype. Such regeneration techniques often rely on manipulation of certain phytohormones in a tissue culture growth medium. For transformation and regeneration of maize see, Gordon-Kamm *et al.*, 1990, The Plant Cell, 2:603-618.

[00267] Plants cells transformed with a plant expression vector can be regenerated, *e.g.*, from single cells, callus tissue or leaf discs according to standard plant tissue culture techniques. It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant. Plant regeneration from cultured protoplasts is described in Evans *et al.*, 1983, Protoplasts Isolation and Culture, Handbook of Plant Cell Culture, Macmillan Publishing Company, New York, pp. 124-176; and Binding, Regeneration of Plants, Plant Protoplasts, 1985, CRC Press, Boca Raton, pp. 21-73.

[00268] The regeneration of plants containing the foreign gene introduced by *Agrobacterium* from leaf explants can be achieved as described by Horsch *et al.*, 1985, Science, 227:1229-1231. In this procedure, transformants are grown in the presence of a selection agent and in a medium that induces the regeneration of shoots in the plant species being transformed as described by Fraley *et al.*, 1983, Proc. Natl. Acad. Sci. (U.S.A.), 80:4803. This procedure typically produces shoots within two to four weeks and these transformant shoots are then transferred to an appropriate root-inducing medium containing the selective agent and an antibiotic to prevent bacterial growth. Transgenic plants of the present invention may be fertile or sterile.

[00269] The regeneration of plants from either single plant protoplasts or various explants is well known in the art. See, for example, Methods for Plant Molecular Biology, A. Weissbach and H. Weissbach, eds., 1988, Academic Press, Inc., San Diego, Calif.. This regeneration and growth process includes the steps of selection of transformant cells and shoots, rooting the transformant shoots and growth of the plantlets in soil. For maize cell culture and regeneration see generally, The Maize Handbook, Freeling and Walbot, Eds., 1994, Springer, New York 1994; Corn and Corn Improvement, 3rd edition, Sprague and Dudley Eds., 1988, American Society of Agronomy, Madison, Wis.

5.2.10. Plants

[00270] The present invention also provides a plant comprising a plant cell as disclosed. Transformed seeds and plant parts are also encompassed.

[00271] In addition to a plant, the present invention provides any clone of such a plant, seed, selfed or hybrid progeny and descendants, and any part of any of these, such as cuttings, seed. The invention provides any plant propagule, that is any part which may be used in reproduction or propagation, sexual or asexual, including cuttings, seed and so on. Also encompassed by the invention is a plant which is a sexually or asexually propagated off-spring, clone or descendant of such a plant, or any part or propagule of said plant, off-spring, clone or descendant. Plant extracts and derivatives are also provided.

[00272] Any species of woody, ornamental or decorative, crop or cereal, fruit or vegetable plant, and algae (*e.g.*, *Chlamydomonas reinhardtii*) may be used in the compositions and methods provided herein. Non-limiting examples of plants include plants from the genus *Arabidopsis* or the genus *Oryza*. Other examples include plants from the genuses *Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum,*

Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea, or *Zinnia*.

[00273] Plants included in the invention are any plants amenable to transformation techniques, including gymnosperms and angiosperms, both monocotyledons and dicotyledons.

[00274] Examples of monocotyledonous angiosperms include, but are not limited to, asparagus, field and sweet corn, barley, wheat, rice, sorghum, onion, pearl millet, rye and oats and other cereal grains.

[00275] Examples of dicotyledonous angiosperms include, but are not limited to tomato, tobacco, cotton, rapeseed, field beans, soybeans, peppers, lettuce, peas, alfalfa, clover, cole crops or Brassica oleracea (*e.g.*, cabbage, broccoli, cauliflower, brussel sprouts), radish, carrot, beets, eggplant, spinach, cucumber, squash, melons, cantaloupe, sunflowers and various ornamentals.

[00276] Examples of woody species include poplar, pine, sequoia, cedar, oak, *etc.*

[00277] Still other examples of plants include, but are not limited to, wheat, cauliflower, tomato, tobacco, corn, petunia, trees, *etc.*

[00278] In certain embodiments, plants of the present invention are crop plants (for example, cereals and pulses, maize, wheat, potatoes, tapioca, rice, sorghum, millet, cassaya, barley, pea, and other root, tuber, or seed crops. Exemplary cereal crops used in the compositions and methods of the invention include, but are not limited to, any species of grass, or grain plant (*e.g.*, barley, corn, oats, rice, wild rice, rye, wheat, millet, sorghum, triticale, *etc.*), non-grass plants (*e.g.*, buckwheat flax, legumes or soybeans, *etc.*). Grain plants that provide seeds of interest include oil-seed plants and leguminous plants. Other seeds of interest include grain seeds, such as corn, wheat, barley, rice, sorghum, rye, *etc.* Oil seed plants include cotton, soybean, safflower, sunflower, Brassica, maize, alfalfa, palm, coconut, *etc.* Other important seed crops are oil-seed rape, sugar beet, maize, sunflower, soybean, and sorghum. Leguminous plants include beans and peas. Beans include guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, *etc.*

[00279] Horticultural plants to which the present invention may be applied may include lettuce, endive, and vegetable brassicas including cabbage, broccoli, and

cauliflower, and carnations and geraniums. The present invention may also be applied to tobacco, cucurbits, carrot, strawberry, sunflower, tomato, pepper, chrysanthemum, poplar, eucalyptus, and pine.

[00280] The present invention may be used for transformation of other plant species, including, but not limited to, corn (*Zea mays*), canola (*Brassica napus, Brassica rapa ssp.*), alfalfa (Medicago sativa), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor, Sorghum vulgare*), sunflower (*Helianthus annuus*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum, Nicotiana benthamiana*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassaya (*Manihot esculenta*), coffee (*Coffea spp.*), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus spp.*), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa spp.*), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), oats, barley, *Arabidopsis* spp., vegetables, ornamentals, and conifers.

5.2.11. Cultivation

[00281] Methods of cultivation of plants are well known in the art. For example, for the cultivation of wheat see Alcoz *et al.*, 1993, Agronomy Journal 85:1198-1203; Rao and Dao, 1992, J. Am. Soc. Agronomy 84:1028-1032; Howard and Lessman, 1991, Agronomy Journal 83:208-211; for the cultivation of corn see Tollenear *et al.*, 1993, Agronomy Journal 85:251-255; Straw *et al.*, Tennessee Farm and Home Science: Progress Report, Spring 1993, 166:20-24; Miles, S. R., 1934, J. Am. Soc. Agronomy 26:129-137; Dara *et al.*, 1992, J. Am. Soc. Agronomy 84:1006-1010; Binford *et al.*, 1992, Agronomy Journal 84:53-59; for the cultivation of soybean see Chen *et al.*, 1992, Canadian Journal of Plant Science 72:1049-1056; Wallace *et al.*, 1990, Journal of Plant Nutrition 13:1523-1537; for the cultivation of rice see Oritani and Yoshida, 1984, Japanese Journal of Crop Science 53:204-212; for the cultivation of linseed see Diepenbrock and Porksen, 1992, Industrial Crops and Products 1:165-173; for the

cultivation of tomato see Grubinger *et al.*, 1993, Journal of the American Society for Horticultural Science 118:212-216; Cerne, M., 1990, Acta Horticulture 277:179-182; for the cultivation of pineapple see Magistad *et al.*, 1932, J. Am. Soc. Agronomy 24:610-622; Asoegwu, S. N., 1988, Fertilizer Research 15:203-210; Asoegwu, S. N., 1987, Fruits 42:505-509; for the cultivation of lettuce see Richardson and Hardgrave, 1992, Journal of the Science of Food and Agriculture 59:345-349; for the cultivation of mint see Munsi, P. S., 1992, Acta Horticulturae 306:436-443; for the cultivation of camomile see L*etc*hamo, W., 1992, Acta Horticulturae 306:375-384; for the cultivation of tobacco see Sisson *et al.*, 1991, Crop Science 31:1615-1620; for the cultivation of potato see Porter and Sisson, 1991, American Potato Journal, 68:493-505; for the cultivation of brassica crops see Rahn *et al.*, 1992, Conference "Proceedings, second congress of the European Society for Agronomy"Warwick Univ., p.424-425; for the cultivation of banana see Hegde and Srinivas, 1991, Tropical Agriculture 68:331-334; Langenegger and Smith, 1988, Fruits 43:639-643; for the cultivation of strawberries see Human and Kotze, 1990, Communications in Soil Science and Plant Analysis 21:771-782; for the cultivation of songhum see Mahalle and Seth, 1989, Indian Journal of Agricultural Sciences 59:395-397; for the cultivation of plantain see Anjorin and Obigbesan, 1985, Conference "International Cooperation for Effective Plantain and Banana Research" Proceedings of the third meeting. Abidjan, Ivory Coast, p. 115-117; for the cultivation of sugar cane see Yadav, R. L., 1986, Fertiliser News 31:17-22; Yadav and Sharma, 1983, Indian Journal of Agricultural Sciences 53:38-43; for the cultivation of sugar beet see Draycott *et al.*, 1983, Conference "Symposium Nitrogen and Sugar Beet" International Institute for Sugar Beet Research--Brussels Belgium, p. 293-303. See also Goh and Haynes, 1986, "Nitrogen and Agronomic Practice" in Mineral Nitrogen in the Plant-Soil System, Academic Press, Inc., Orlando, Fla., p. 379-468; Engelstad, O. P., 1985, Fertilizer Technology and Use, Third Edition, Soil Science Society of America, p.633; Yadav and Sharmna, 1983, Indian Journal of Agricultural Sciences, 53:3-43.

5.2.12. Products of Transgenic Plants

[00282] Engineered plants exhibiting the desired physiological and/or agronomic changes can be used directly in agricultural production.

[00283] Thus, provided herein are products derived from the transgenic plants or methods of producing transgenic plants provided herein. In certain embodiments, the products are commercial products. Some non-limiting example include genetically engineered trees for *e.g.,* the production of pulp, paper, paper products or lumber; tobacco, *e.g.,* for the production of cigarettes, cigars, or chewing tobacco; crops, *e.g.,* for the production of fruits, vegetables and other food, including grains, *e.g.,* for the production of wheat, bread, flour, rice, corn; and canola, sunflower, *e.g.*, for the production of oils or biofuels.

[00284] In certain embodiments, commercial products are derived from a genetically engineered (*e.g.,* comprising overexpression of *GLK1* in the vegetative tissues of the plant) species of woody, ornamental or decorative, crop or cereal, fruit or vegetable plant, and algae (*e.g.*, *Chlamydomonas reinhardtii*), which may be used in the compositions and methods provided herein. Non-limiting examples of plants include plants from the genus *Arabidopsis* or the genus *Oryza*. Other examples include plants from the genuses *Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea*, or *Zinnia*.

[00285] In some embodiments, commercial products are derived from a genetically engineered gymnosperms and angiosperms, both monocotyledons and dicotyledons. Examples of monocotyledonous angiosperms include, but are not limited to, asparagus, field and sweet corn, barley, wheat, rice, sorghum, onion, pearl millet, rye and oats and other cereal grains. Examples of dicotyledonous angiosperms include, but are not limited to tomato, tobacco, cotton, rapeseed, field beans, soybeans, peppers, lettuce, peas, alfalfa, clover, cole crops or Brassica oleracea (*e.g.*, cabbage, broccoli, cauliflower, brussel sprouts), radish, carrot, beets, eggplant, spinach, cucumber, squash, melons, cantaloupe, sunflowers and various ornamentals.

[00286] In certain embodiments, commercial products are derived from a genetically engineered woody species, such as poplar, pine, sequoia, cedar, oak, *etc.*

[00287] In other embodiments, commercial products are derived from a genetically engineered plant including, but are not limited to, wheat, cauliflower, tomato, tobacco, corn, petunia, trees, *etc.*

[00288] In certain embodiments, commercial products are derived from a genetically engineered crop plants, for example, cereals and pulses, maize, wheat, potatoes, tapioca, rice, sorghum, millet, cassaya, barley, pea, and other root, tuber, or seed crops. In one embodiment, commercial products are derived from a genetically engineered cereal crops, including, but are not limited to, any species of grass, or grain plant (*e.g.*, barley, corn, oats, rice, wild rice, rye, wheat, millet, sorghum, triticale, *etc.*), non-grass plants (*e.g.*, buckwheat flax, legumes or soybeans, *etc.*). In another embodiments, commercial products are derived from a genetically engineered grain plants that provide seeds of interest, oil-seed plants and leguminous plants. In other embodiments, commercial products are derived from a genetically engineered grain seed plants, such as corn, wheat, barley, rice, sorghum, rye, *etc.* In yet other embodiments, commercial products are derived from a genetically engineered oil seed plants, such as cotton, soybean, safflower, sunflower, Brassica, maize, alfalfa, palm, coconut, *etc.* In certain embodiments, commercial products are derived from a genetically engineered oil-seed rape, sugar beet, maize, sunflower, soybean, or sorghum. In some embodiments, commercial products are derived from a genetically engineered leguminous plants, such as beans and peas (*e.g.*, guar, locust bean, fenugreek, soybean, garden beans, cowpea, mungbean, lima bean, fava bean, lentils, chickpea, *etc.*)

[00289] In certain embodiments, commercial products are derived from a genetically engineered horticultural plant of the present invention, such as lettuce, endive, and vegetable brassicas including cabbage, broccoli, and cauliflower, and carnations and geraniums; tomato, tobacco, cucurbits, carrot, strawberry, sunflower, tomato, pepper, chrysanthemum, poplar, eucalyptus, and pine.

[00290] In still other embodiments, commercial products are derived from a genetically engineered corn (*Zea mays*), canola (*Brassica napus, Brassica rapa ssp.*), alfalfa (Medicago sativa), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum*

bicolor, Sorghum vulgare), sunflower (*Helianthus annuus*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum, Nicotiana benthamiana*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium hirsutum*), sweet potato (*Ipomoea batatus*), cassaya (*Manihot esculenta*), coffee (*Coffea spp.*), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus spp.*), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa spp.*), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), oats, barley, *Arabidopsis* spp., vegetables, ornamentals, and conifers.

5.3. COMPONENTS OF THE TARGET SYSTEM

[00291] The *TARGET* system utilizes a nucleic acid encoding a chimeric protein comprising a transcription factor fused to a domain comprising an inducible cellular localization signal and an independently expressed selectable marker. Nucleic acids for use with the target system may be plasmids or other appropriate nucleic acid constructs as described in Section 5.2.3. The *TARGET* system also comprises methods of measuring mRNA expression levels and may additionally comprise methods of detecting TF binding to gene targets.

5.3.1. Transcription Factors

[00292] The transcription factor component chimeric protein encoded by the nucleic acid constuct may be, but is not limitied to, one of those listed in Table 3. The transcription factor used is not limited to nuclear transcription factors, but may also include proteins that modulate mitochondrial or chloroplast gene expression.

5.3.2. Localization Signals and Inducing Agents

[00293] The glucorticoid receptor (GR) may be used as the inducible cellular localization signal in the chimeric protein encoded by the nucleic acid construct. In the case of the a TF-GR chimeric protein, dexamethasone may be used as the inducing agent.

Alternately, another glucocorticoid may be used instead of dexamethasone. Treatement with dexamethasone releases the glucocorticoid receptor from sequestration in the cytoplasm, allowing the TF-GR fusion protein to access its target genes (*e.g.*, in the nucleus). The GR is not the only such inducible cellular localization signal that may be used in this method. Any receptor component or other protein known in the art that is capable of being released from sequestration or otherwise re-localized to the destination of the transcription factor component by treatment of the protoplasts with an inducing agent may potentially be used in the *TARGET* system.

5.3.3. Expression System and Selectable Markers

[00294] Using any gene transfer technique, such as the above-listed techniques (of Section 5.2), an expression vector harboring the nucleic acid may be transformed into a cell to achieve temporary or prolonged expression. Any suitable expression system may be used, so long as it is capable of undergoing transformation and expressing of the precursor nucleic acid in the cell. In one embodiment, a pET vector (Novagen, Madison, Wis.), or a pBI vector (Clontech, Palo Alto, Calif.) is used as the expression vector. In some embodiments an expression vector further encoding a green fluorescent protein ("GFP") is used to allow simple selection of transfected cells and to monitor expression levels. Non-limiting examples of such vectors include Clontech's "Living Colors Vectors" pEYFP and pEYFP-C.

[00295] The recombinant construct of the present invention may include a selectable marker for propagation of the construct. For example, a construct to be propagated in bacteria preferably contains an antibiotic resistance gene, such as one that confers resistance to kanamycin, tetracycline, streptomycin, or chloramphenicol. Suitable vectors for propagating the construct include plasmids, cosmids, bacteriophages or viruses, to name but a few.

[00296] In some embodiments, the selectable marker encoded by the nucleic acid molecule used in the method of the invention is a fluorescent selection marker. A fluorescent selection marker that can be used in the method of the invention includes, but is not limited to, green fluorescent protein, yellow fluorescent protein, red fluorescent protein, cyan fluorescent protein, or blue fluorescent protein. In a specific embodiment,

the fluorescent selection marker used in the method of the invention is red fluorescent protein. In certain embodiments, the step of detecting host cells that express the selectable marker is performed by Fluorescence Activated Cell Sorting (FACS). Any selectable marker known in the art that may be encoded in the nucleic acid construct and which is selectable using a cell sorting or other selection technique may be used to identify those cells that have expressed the nucleic acid construct containing the chimeric protein.

[00297] In addition, the recombinant constructs may include plant-expressible selectable or screenable marker genes for isolating, identifying or tracking of plant cells transformed by these constructs. Selectable markers include, but are not limited to, genes that confer antibiotic resistances (*e.g.*, resistance to kanamycin or hygromycin) or herbicide resistance (*e.g.*, resistance to sulfonylurea, phosphinothricin, or glyphosate). Screenable markers include, but are not limited to, the genes encoding .beta.-glucuronidase (Jefferson, 1987, Plant Molec Biol. Rep 5:387-405), luciferase (Ow *et al.*, 1986, Science 234:856-859), B and C1 gene products that regulate anthocyanin pigment production (Goff *et al.*, 1990, EMBO J 9:2517-2522).

[00298] In some cases, a selectable marker may be included with the nucleic acid being delivered to the cell. A selectable marker may refer to the use of a gene that encodes an enzymatic or other detectable activity (*e.g.*, luminescence or fluorescence) that confers the ability to distinguish cells expressing the nucleic acid construct from those that do not. A selectable marker may confer resistance to an antibiotic or drug upon the cell in which the selectable marker is expressed. Selectable markers may be "dominant" in some cases; a dominant selectable marker encodes an enzymatic or other activity (*e.g.*, luminescence or fluorescence) that can be detected in any cell or cell line.

[00299] In some embodiments, the marker gene is an antibiotic resistance gene whereby the appropriate antibiotic can be used to select for transformed cells from among cells that are not transformed. Examples of suitable selectable markers include adenosine deaminase, dihydrofolate reductase, hygromycin-B-phosphotransferase, thymidine kinase, xanthine-guanine phospho-ribosyltransferase and amino-glycoside 3'-O-phosphotransferase II. Other suitable markers will be known to those of skill in the art.

5.3.4. Detecting the Level of mRNA Expressed in Host Cells

[00300] The methods of the present invention comprise a step of detecting the level of mRNA expressed in the host cells of the invention.

[00301] In some embodiments, the level of mRNA expressed in host cells is determined by quantitative real-time PCR (qPCR), a method for DNA amplification in which fluorescent dyes are used to detect the amount of PCR product after each PCR cycle. (Higuchi et al., 1992; Simultaneous amplification and detection of specific DNA-sequences. Bio-Technology 10(4), 413-417].). The qPCR method has become the tool of choice for many scientists because of method's dynamic range, accuracy, high sensitivity, specificity and speed. Quantitative PCR is carried out in a thermal cycler with the capacity to illuminate each sample with a beam of light of a specified wavelength and detect the fluorescence emitted by the excited fluorochrome. The thermal cycler is also able to rapidly heat and chill samples thereby taking advantage of the physicochemical properties of the nucleic acids and DNA polymerase.

[00302] In some embodiments, the level of mRNA expressed in host cells is determined by high high throughput sequencing (Next-generation sequencing ; also 'Next-gen sequencing' or NGS). = NGS methods are highly parallelized processes that enable the sequencing of thousands to millions of molecules at once. Popular NGS methods include pyrosequencing developed by 454 Life Sciences (now Roche), which makes use of luciferase to read out signals as individual nucleotides are added to DNA templates, Illumina sequencing that uses reversible dye-terminator techniques that adds a single nucleotide to the DNA template in each cycle and SOLiD sequencing by Life Technologies that sequences by preferential ligation of fixed-length oligonucleotides.

[00303] In some embodiments, the level of mRNA expressed in host cells is determined by gene microarrays. A microarray works by exploiting the ability of a given mRNA molecule to bind specifically to, or hybridize to, the DNA template from which it originated. By using an array containing many DNA samples, it can be determined in a single experiment, the expression levels of hundreds or thousands of genes within a cell by measuring the amount of mRNA bound to each site on the array. With the aid of a computer, the amount of mRNA bound to the spots on the microarray is precisely measured, generating a profile of gene expression in the cell.

5.3.5. Detecting TF Binding to Gene Targets

[00304] In some embodiments, the method comprises detection of the level of TF binding to gene targets by ChIP-Seq analysis. ChIP-Seq analysis utilizes chromatin immunoprecipitation in parallel with DNA sequencing to map the binding sites of a TF or other protein of interest. First, protein interactions with chromatin are cross-linked and fragmented. Then, immunoprecipitation is used to isolate the TF with bound chromatin/DNA. The associated chromatin/DNA fragments are sequenced to determine the gene location of protein binding. Other assays known in the art may be used to detect the location of TF binding to genomic regions of DNA.

[00305] In some embodiments, the yeast one hybrid method may be used. The yeast one hybrid method detects protein-DNA interactions, and may be adapted for use in plants. The DNA binding domains unveiled by ChIP-Seq may be cloned upstream of a reporter gene in a vector or may be introduced into the plant genome by homologous recombination, which allows the transcription factor to interact with the DNA element in a natural environment. A fusion protein containing a constitutive TF activation domain and the DNA binding domain of the TF of interest may then be expressed, and the interaction of the binding domain with the DNA will be detected by reporter gene expression. The yeast one hybrid method can thus be used in some embodiments as a way to interrogate the relationship between binding and activation, as only the binding domain of the TF of interest is used in the fusion protein in the heterologous system.

5.3.6. Identifying Conserved Connections Across Species

[00306] In some embodiments, gene networks conserved between Arabidopsis (or another model species) and a species of interest may be determined by a data mining approach. In this approach, Arabidopsis plants are grown under the same conditions as plants from another species of interest, including perturbation of environmental signals (*e.g.* nitrogen). RNA is then extracted from the roots and shoots of the plants, and cDNA synthesized from the extracted RNA. A microarray analysis and filtering approach may be used to determine the genes of each species regulated by the environmental signal when compared with control conditions. An ortholog analysis may then determine the

genes orthologous between the two species. Data integration and network analysis then allows for the determination of a core translational network. In some embodiments, the response genes in a species of plant for which a protoplast system is not feasible may be discovered by using such a data mining approach, as described, in combination with the *TARGET* system for Arabidopsis or another species used as a model.

6. EXAMPLE 1

6.1. INTRODUCTION

[00307] A rapid technique to study the genome-wide effects of TF activation in protoplasts that uses transient expression of a glucocorticoid receptor (GR)-tagged TF has been developed in the present invention. This system can be used to rapidly retrieve information on direct target genes in less than two week's time. As a proof-of-principle candidate, the well-studied transcription factor, Abscicic acid insensitive 3 (ABI3; Koornneef et al., 1989, Plant physiology, 90:463-469; Mönke et al., 2012, Nucleic acids research 40:8240-8254) was used. The *de novo* identification of the abscisic acid response element (ABRE) and a majority of the previously classified direct targets was established by use of this method. This technique was named *TARGET*, for *Transient Assay Reporting Genome-wide Effects of Transcription factors*.

[00308] Technically, plant protoplasts are transfected with a plasmid (pBeaconRFP_GR) that expresses the TF-of-interest fused to GR, which allows the controlled entry of the chimeric GR-TF into the nucleus by addition of the GR-ligand dexamethasone (DEX; Schena and Yamamoto, 1988, Science 241:965-967). In addition, the vector contains a separate expression cassette with a positive fluorescent selection marker (red fluorescent protein; RFP) which enables fluorescence activated cell sorting (FACS) of successfully transformed protoplasts (see Figure 2; Bargmann and Birnbaum, 2009, Plant physiology 149:1231-1239). This purification step allows reliable qPCR or transcriptomic analysis of multiple independent transfections, which would otherwise be hampered by the presence of a population of untransformed cells that varies from experiment to experiment. Lastly, the effect of target gene induction by DEX treatment is measured in the presence or absence of the translation inhibitor

cycloheximide (CHX), allowing for the distinction of direct and indirect target genes of the TF under study. pBeaconRFP_GR-ABI3 was used to transfect protoplasts prepared from the roots of Arabidopsis seedlings, where ABI3, known largely for its role in seed development, has also been shown to be involved in development (Brady et al., 2003, The Plant journal : for cell and molecular biology 34:67-75).

6.2. MATERIALS AND METHODS

[00309] Plant materials and treatment. Wild-type *Arabidopsis thaliana* seed (Col-0, Arabidopsis Biological Resource Center) was sterilized by 5 min incubation with 96% ethanol followed by 20 min incubation with 50% household bleach and rinsing with sterile water. Seeds were plated on square 10x10 cm plates (Fisher Scientific) with MS-agar (2.2 g/l Murashige and Skoog Salts [Sigma-Aldrich], 1% [w/v] sucrose, 1% [w/v] agar, 0.5 g/l MES hydrate [Sigma-Aldrich], pH 5.7 with KOH) on top of a sterile nylon mesh (NITEX 03-100/47, Sefar filtration Inc.) to facilitate harvesting of the roots. Seeds were plated in two dense rows. Plates were vernalized for 2 days at 4° C in the dark and placed vertically in an Advanced Intellus environmental controller (Percival) set to 35 $\mu mol/m_2*sec_{-1}$ and 22° C with an 18h-light/6h-dark regime.

[00310] Vector construction. pBeaconRFP_GR was constructed by PCR amplification of the glucocorticoid receptor from pJCGLOX (Joubes et al., 2004, The Plant Journal 37: 889-896) with primers GR-F and GR-R, both with an SpeI restriction site, using Phusion polymerase (New England Biolabs). The PCR product was ligated into the SpeI site upstream of the GATEWAY (Invitrogen) cassette in pBeaconRFP (Bargmann and Birnbaum, 2009; Plant physiology 149:1231-1239). The orientation of the insert was checked by PCR. The pBeaconRFP_GR vector (as well as the pMON999_mRFP control vector, containing only 35S::mRFP) will be made available through the VIB website: http://gateway.psb.ugent.be/.

[00311] ABI3 cDNA was PCR amplified with primers ABI3_AttB1 and ABI3_AttB2, and subsequently re-amplified with primers AttB1 and AttB2 using Phusion polymerase. The PCR product was recombined into pDONR221 using BP clonase and subsequently shuttled into pBeaconRFP_GR with LR clonase (Invitrogen).

[00312] Protoplast preparation, transfection, treatment and cell sorting. Protoplast were prepared, transfected and sorted as described in Bargmann and

Birnbaum, 2009; Plant physiology 149:1231-1239; and Bargmann and Birnbaum, 2010, JoVE. Briefly, roots of 10-day-old seedling were harvested and treated with cell wall digesting enzymes (Cellulase and Macerozyme; Yakult, Japan) for 3 hours. Cells were filtered, washed and 106 cells were transfected with a polyethylene glycol treatment using 50 μg of plasmid DNA and incubated at room temperature overnight. Protoplast suspensions were pretreated with 35 μM cycloheximide (CHX; Sigma-Aldrich) for 30 min, after which 10 μM dexamethasone (DEX; Sigma-Aldrich) was added and cells were incubated at room temperature. Controls were treated with solvent alone. A 10 mM DEX stock was dissolved in ethanol and a 50 mM CHX stock was dissolved in dimethylsulfoxide, both were stored at -20° C. All transfections and treatments were performed in triplicate. Treated protoplasts suspensions were sorted with a FACSAria (BD Biosciences), using 488 nm excitation and measuring emission at 530/30 nm for green fluorescence and 610/20 nm for red fluorescence. RFP-positive cells were sorted directly into RNA extraction buffer. Twenty thousand RFPpositive cells (+/- 10% of sorted events were RFP-positive under these experimental conditions) were then isolated by FACS and RNA was extracted for transcript analysis by qPCR.

[00313] A temporal qPCR analysis of *PER1* and *CRU3* induction by DEX in the presence of CHX was performed after a 1-hour, 5-hour and overnight (16-hour) incubation (see Figure 3A). Results indicated that, although induction could be seen as early as 1 hour after the addition of DEX for *CRU3*, the expression of both *PER1* and *CRU3* continued to increase after 5 and 16 hours (see Figure 3A). In order to achieve a large fold-change in expression between control and treatment, microarray analysis was performed after an overnight treatment.

[00314] **qPCR and microarray analysis.** RNA was extracted using an RNeasy Micro Kit with RNase-free DNase Set according to the manufacturer's instructions (QIAGEN). RNA was quantified with a Bioanalyzer (Agilent Technologies). Gene expression was determined by quantitative real-time PCR (LightCycler; Roche Diagnostics) using gene-specific primers and LightCycler FastStart DNA Master SYBR Green (Roche Diagnostics). Expression levels of tested genes were normalized to expression levels of the*ACT2/8* and *CLATHRIN* genes as described in (Krouk et al., 2006 Plant Physiol 142:1075-1086). For microarray analysis, RNA was amplified and labeled

with WT-Ovation Pico RNA Amplification System and FL-Ovation cDNA Biotin Module V2, respectively (NuGEN). The labeled cDNA was hybridized, washed and stained on an ATH-121501 Arabidopsis full genome microarray using a Hybridization Control Kit, a GeneChip Hybridization, Wash, and Stain Kit, a GeneChip Fluidics Station 450 and a GeneChip Scanner (Affymetrix). The microarray data reported in this paper have been deposited in the Gene Expression Omnibus (GEO, http://www.ncbi.nlm.nih.gov/geo/) database, (accession # GSE33344). Raw microarray data was normalized using MAS5.0 (scaling factor of 250, Flexarray; http://www.gqinnovationcenter.com/services/bioinformatics/flexarray/index.aspx?l=e). Data was logged prior to running a Tukey *post hoc* test on the significance coefficients of a two way ANOVA carried out on CHX versus DEX treatment (in-house [R] script) for differential responses to DEX with or without CHX on non-ambiguous probesets . Heatmaps were created using Multiple Experiment Viewer software (TIGR; http://www.tm4.org/mev/). For the overlap analysis with previously identified targets of ABI3 (Mönke et al., 2012, Nucleic acids research 40:8240-8254), VP1 (Suzuki et al., 2003, Plant physiology 132:1664-1677) and ABI5 (Reeves et al., 2011, Plant molecular biology, 75:347-363), distance between non-parametric distributions (one from the overlap of sampled input gene sets and one from two randomly sampled sets of genes represented on the ATH1 array) was calculated using the genesect [R] script (Krouk et al., 2010, Genome biology 11:R123). For the overlap with VP1 targets, the background consisted of genes represented on both the ATH1- and the 8k AG array [Affymetrix] used by Suzuki and co-workers.

[00315] GO-term and promoter analysis. GO-term analysis was performed online using the BioMaps function on the VirtualPlant website (www.virtualplant.org) with a default corrected p-value cutoff on the Fisher exact test of $p<10-3$ (Katari et al., 2010; Plant Physiology, 152:500-515). To determine enrichment of known promoter motifs, the number of 1 kb upstream promoters, out of the top fifty ABI3 up-regulated genes, having one or more of the motifs described in the PLACE database was counted (http://www.dna.affrc.go.jp/PLACE/). p-values were generated using hypergeometric distribution, and values were FDR corrected using an FDR q-value cutoff of 0.01.promoter element enrichment analysis was performed using [R] (http://www.r-

project.org/). For the sliding window analysis for promoter element enrichment (see Figure 4), significance was calculated using the hypergeometric test, comparing the number of motif occurrences in a 30-gene window to the number expected by chance, which was derived from the propensity of the motif in the promoters of all genes nonambiguously represented on the ATH1 chips. The search for recurring promoter motifs was performed using the Cistome website (http://bar.utoronto.ca/cistome/cgibin/BAR_Cistome.cgi). Motif Sampler and MEME were used to look for recurring 8-mer motifs in the 1000 bp upstream of the top fifty direct up-regulated genes with the following significance parameters: Ze cutoff 3.0, functional depth cutoff 0.35, proportion of genes the motif should be found in 0.5.

6.3. RESULTS

[00316] As a first test of the *TARGET* system, the expression of known direct ABI3 targets *PER1* and *CRU3* were assayed by qPCR. Compared to control gene expression, both *PER1* and *CRU3* showed significant induction of transcript levels upon DEX treatment in the ABI3-GR transfected protoplasts in the presence of CHX (**Figures 5 and 6**). *PER1* and *CRU3* expression in protoplasts transformed with an empty vector control showed no significant induction by DEX treatment (**Figure 5 and 6**). Significant induction of *CRU3* expression could only be measured when CHX was present, indicating that the effects of CHX may in some cases facilitate ABI3 function. Enhancement of ABA signaling output by protein synthesis inhibitors, that could explain this phenomenon, has been noted before by independent studies (Reeves et al., 2011, Plant molecular biology 75:347-363).. For the transcriptomic analysis, using ATH1 Genome Array chips, a two-way analysis of variance (ANOVA) was performed, followed by a Tukey *post hoc* test to identify genes whose expression is differentially regulated in response to DEX treatment in the absence or presence of CHX ($p<0.05$, fold change>1.5). Genes found to be significantly regulated by DEX treatment in the empty vector control were omitted from further analysis. This analysis yielded a total of 668 unique genes whose expression was affected by DEX-induced nuclear localization of ABI3; 227 regulated genes without CHX and 458 regulated genes with CHX (microarray results were validated by qPCR). There was just a 17-gene overlap with and without

CHX, reiterating that (as was seen for *CRU3* in preliminary qPCR analysis) there are many genes whose response to GR-ABI3 was facilitated by the presence of the protein synthesis inhibitor CHX. The 210 genes regulated only in the absence of CHX were categorized as putative indirect targets of ABI3, whereas the 458 genes regulated in the presence of CHX (186 induced and 272 repressed genes) were designated as putative direct targets of ABI3.

[00317] The list of 186 putative direct up-regulated genes was highly significantly enriched for genes previously identified as direct targets of ABI3 in whole plant studies (Ze=54.3), as well as targets of the maize homolog VIVIPAROUS1 (Ze=20.8) and co-regulator ABI5 (Ze=20.9) (**Figures 7 and 8**; (Mönke et al., 2012, Nucleic acids research 40:8240-8254; Reeves et al., 2011, Plant molecular biology 75:347-363; Suzuki et al., 2003, Plant physiology 132:1664-1677). These substantial intersections indicate that the activation of ABI3 in protoplasts reflects the effects attributed to this transcriptional regulator in *in planta* studies. The list also showed a significant overrepresentation of GO-terms, including response to ABA, response to water deprivation, lipid storage and embryo development (no significant overlap or enrichments were found in the lists of indirect targets or direct down-regulated targets). Furthermore, promoter analysis of the fifty most strongly induced direct up-regulated genes found significant enrichment of previously identified ABRE-like elements and the RY-repeat motif (**Figure 8**). *De novo* searches for recurring motifs within these promoters (using two independent algorithms, *MEME* and *MotifSampler*) yielded the recovery of the CACGTGKC ABRE (**Figure 9).** These results show the *TARGET* system can be used successfully to investigate TF function in protoplasts with significance to whole plants.

6.4. DISCUSSION

[00318] One advantage of the *TARGET* system lies in the speed at which identification of genome-wide TF targets can be performed. A candidate TF can now be scrutinized for its target genes in a genome in a matter of weeks rather than the months required for the generation of stable transgenic plant lines. The *TARGET* transient transformation system can also be used purely as a verification of specific TF-target interactions by qPCR, much as yeast-one-hybrid (Y1H) assays are often used, but now in the context of endogenous gene activation in plant cells rather than promoter binding in a yeast strain. The *TARGET*

approach brings the convenience of microbiological systems like Y1H to the genome-wide transcriptomic capabilities of *in planta* studies. Another advantage of the use of protoplast transformation in the *TARGET* system is that it can be done in a wide range of species where the generation of transgenic plant lines is either impossible or problematic and more time-consuming (Sheen et al., 2001, Plant physiology 127:1466-1475). The *TARGET* system combined with RNA sequencing, can enable rapid and systematic assessment of TF function in numerous plant species, for example in important crop model species.

[00319] This system is not a replacement for in-depth studies using transcriptional- and chromatin immuno-precipitation (ChIP) analyses in transgenic plants. Rather, *TARGET* is rapid tool for GRN investigations that may have uses in particular circumstances. There are considerations associated with the use of this system. On its own, a genome-wide analysis will yield results that contain false-positives and false-negatives. Identification of direct regulated genes by *TARGET* is therefore not unequivocal, additional assays for direct TF-target interaction (*e.g.* ChIP, Y1H, gel shift assays) are required for definitive identification of TF targets. The functionality of the chimeric GR-TF is not tested in this system, other than by the substance of the results. CHX treatment by itself may have effects on transcription that influence the DEX effect on certain direct target genes. Lastly, the cellular dissociation procedure itself may induce gene expression responses that could conceal the effects of TF activation. One can envisage two ways of using the *TARGET* system; either in combination with other techniques to get high confidence target lists for a particular TF, or as a high-throughput analysis of numerous TFs in a given GRN to get a broad view of putative interactions.

[00320] Overall, the results presented here demonstrate that *TARGET* represents a novel and rapid transient system for TF investigation that can be used to help map GRN. Important indications of TF operation, such as direct target genes, biological function by GO-term associations and *cis*-regulatory elements involved in its action, can be obtained in a rapid and straightforward manner. The proof-of-principle analysis with ABI3 offers a new dataset of transcripts affected by this TF, adding to the understanding of the downstream significance of this central regulator.

[00321] The pBeaconRFP_GR vector will be made available through the VIB website (http://gateway.psb.ugent.be/).

7. EXAMPLE 2

7.1. INTRODUCTION

[00322] Evidence for temporal, signal induced TF-target associations that involve the rapid and transient induction of genes related to the signal has been developed in the present invention. This discovery was enabled by a combination of conceptual and technical advances in a cell-based system, which enabled overexpression of a specific TF of interest and temporal induction of its nuclear localization. By temporally inducing TF nuclear localization using dexamethasone (DEX) in the presence of cycloheximide (CHX) to block translation, identification of the primary targets of a TF of interest was possible, based on *either* TF-regulation *or* TF-binding assayed in the same samples, exposed to a signal. Moreover, the perturbation of both the TF *and* the signal it transduces uncovered three distinct TF modes-of-action, "poised", "active" and "transient", the latter encompassing signal-dependent, transient TF-target associations. This discovery was made for bZIP1 (BASIC LEUCINE ZIPPER 1), a TF implicated as an integrator of cellular and metabolic signaling in Arabidopsis and shared in other eukayrotes (Weltmeier et al., 2008, Plant Molecular Biology 69:107; Sun et al., 2011, Journal of Plant Research 125:429; Baena-Gonzalez et al., 2007, Nature 448:938; Kietrich et al., 2011, The Plant Cell 23:381; Kang et al., 2010, Molecular Plant 3:361; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A., 105:4939; Obertello et al., 2010, BMC systems biology 4:111). The discovery of this new *class of* "transient", signal-induced TF-target interactions opens a window into TF network dynamics that has been missed in previous TF studies in plants and animals. The inclusion of such context-dependent TF-target interactions in GRNs, will improve the predictive capability of GRN models to generate hypotheses that will direct future experimental efforts in living systems.

7.2. MATERIALS AND METHODS

[00323] Plant Materials and DNA Constructs. Wild-type *Arabidopsis thaliana* seeds [Columbia ecotype (Col-0)] were vapor-phase sterilized, vernalized for 3 days, then 1 ml of seeds were sown on 24 agar plates containing MS [2.2 g/l custom made Murashige and Skoog salts without N or sucrose [Sigma-Aldrich]; 1% [w/v] sucrose; 0.5 g/l MES hydrate [Sigma-Aldrich]; 1 mM KNO_3; 2% [w/v] agar; pH 5.7 with HCl]. Plants were grown vertically in an Intellus environment controller [Percival Scientific, Perry, IA] set to 35 μmol $m^{-2}s^{-1}$ and 16h-light/8h-dark regime at constant 22°C. bZIP1 [At5g49450] cDNA in pENTR was obtained from the REGIA collection (Paz-Ares et al., 2002, Comparative and functional genomics 3:102) and was then cloned into the destination vector pBeaconRFP_GR (Bargmann et al., 2013, Molecular Plant 6(3):978) by LR recombination [Life Technologies].

[00324] Protoplast Preparation, Transfection, Treatment and Cell Sorting. Protoplasts were prepared, transfected and sorted as previously described (Bargmann et al., 2013, Molecular Plant 6(3):978; Yoo et al., 2007, Nature Protocols 2:1565; Bargmann et al., 2009, Plant physiology 149:1231). Briefly, roots of 10-day-old seedlings were harvested and treated with cell wall digesting enzymes [Cellulase and Macerozyme; Yakult, Japan] for 4 h. Cells were filtered and washed then transfected with 40 μg of pBeaconRFP_GR::bZIP1 plasmid DNA per 1 x 10^6 cells facilitated by polyethylene glycol treatment [PEG; Fluka 81242] for 25 minutes (Bargmann et al., 2013, Molecular Plant 6(3):978). Cells were washed drop-wise, concentrated by centrifugation, then resuspended in wash solution for overnight incubation at room temperature. Protoplast suspensions were treated sequentially with a N-signal treatment of either a 20 mM KNO_3 and 20 mM NH_4NO_3 solution [N] or 20 mM KCl [control] for 2 h, either cycloheximide [CHX] [35 μM in DMSO; Sigma-Aldrich] or solvent alone as mock for 20 min, and then with either dexamethasone [DEX] [10 μM in EtOH; Sigma-Aldrich] or solvent alone as mock for 4 h at room temperature. Treated protoplast suspensions were sorted as in (Bargmann et al., 2009, Plant physiology 149:1231): approximately 10,000 RFP-positive cells were sorted directly into RLT buffer [QIAGEN].

[00325] RNA Extraction And Microarray. RNA was extracted from protoplasts [6 replicates: 3 treatment replicates and 2 biological replicates] using an RNeasy Micro Kit with RNase-free DNaseI Set [QIAGEN] and quantified on a Bioanalyzer RNA Pico Chip

[Agilent Technologies]. RNA was then converted into cDNA, amplified and labeled with Ovation Pico WTA System V2 [NuGEN] and Encore Biotin Module [NuGEN], respectively. The labeled cDNA was hybridized, washed and stained on an ATH1-121501 Arabidopsis Genome Array [Affymetrix] using a Hybridization Control Kit [Affymetrix], a GeneChip Hybridization, Wash, and Stain Kit [Affymetrix], a GeneChip Fluidics Station 450 and a GeneChip Scanner [Affymetrix].

[00326] Analysis of microarray data with CHX treatment: Microarray intensities were normalized using the GCRMA [http://www.bioconductor.org/packages/2.11/bioc/html/gcrma.html] package. Differentially expressed genes were then determined by a 3-way ANOVA with N, DEX and biological replicates as factors. The raw p-value from ANOVA was adjusted by False Discovery Rate [FDR] to control for multiple testing (Benjamini et al., 2005, Genetics 171:783). Genes significantly regulated by N and/or bZIP1 were then selected with a FDR cutoff of 5% while genes significantly regulated by the interaction of N and bZIP1 [NXbZIP1] were selected with a p-val [ANOVA] cutoff of 0.01. Only unambiguous probes were included. Heatmaps were created using Multiple Experiment Viewer software [TIGR; http://www.tm4.org/mev/]. The significance of overlaps of gene sets were calculated using the genesect [R] script (Krouk et al., 2010, Genome Biology 11:R123) or the hypergeometric method [R].

[00327] Analysis of microarray data without CHX treatment: Analysis was identical to with CHX except a 2-way ANOVA with N and bZIP1 as factors was used to identify differentially expressed genes.

[00328] Micro Chromatin Immunoprecipitation. For each combination of protoplast treatments (see above), an unsorted suspension of protoplasts containing approximately 5,000-10,000 GR::bZIP1 transfected cells was incubated with gentle rotation in 1% formahaldeyde in W5 buffer for 7 minutes, then washed with W5 buffer and frozen in liquid N2. μChIP was performed according to Dahl et al, 2008 (Dahl et al., 2008, Nucleic Acids Research, 36:e15) with a few modifications. The GR::bZIP1-DNA complexes were captured using anti-GR antibody [GR [P-20] -Santa Cruz biotech] bound to Protein A beads [Life Biotechnologies]. A washing step with LiCl buffer [0.25M LiCl, 1% Na deoxycholate, 10mM Tris–HCl (pH8), 1% NP-40] was added in between the

wash with RIPA buffer and TE (Dahl et al., 2008, Nucleic Acids Research, 36:e15). After elution from the beads, the ChIP material and the INPUT DNA were cleaned and concentrated using QIAGEN MinElute Kit [QIAGEN]. The protoplast suspension used for micro ChIP was not FACS sorted to maintain a comparable incubation time between the samples that were used for microarray analyses and for micro ChIP. Additionally, FACS sorting of transformed cells was not required to identify DNA targets, as it is required for microarray studies.

[00329] ChIP-Seq library prep. The ChIP DNA and Input DNA were prepared for Illumina HiSeq sequencing platform following the Illumina ChIP-Seq protocol [Illumina, San Diego, CA] with modifications. Barcoded adaptors and enrichment primers [BiOO Scientific, TX, USA] were used according to the manufacturer's protocol. The concentration and the quality of the libraries was determined by the Qubit Fluorometric DNA Assay [InVitrogen, NY, USA], DNA 12000 Bioanalzyer chip [Agilent, CA, USA] and KAPA Quant Library Kit for Illumina [KAPA Biosystems, MA, USA]. A total of 8 libraries were then pooled equimolarly and sequenced on two lanes of an Illumina HiSeq platform for 100 cycles in paired-end configuration [Cold Spring Harbor Lab, NY].

[00330] ChIP-Seq Analysis. Reads obtained from the four treatments were filtered and aligned to the Arabidopsis thaliana genome [TAIR10] and clonal reads were removed. The ChIP alignment data was compared to its partner Input DNA and peaks were called using the QuEST package (Valouev et al., 2008, Nature Methods 5:829.) with a ChIP seeding enrichment ≥ 5, and extension and background enrichments ≥ 2. These regions were overlapped with the genome annotation to identify genes within 500bp downstream of the peak. The gene lists from multiple treatments were largely overlapping sets and hence were pooled to generate a single list of 850 genes that show significant binding of bZIP1. Due to technical issues, the experimental design used for ChIP-Seq precludes the observation of significant differences between the genes bound by bZIP1 under the different treatment conditions. This is because the samples fixed for ChIP included a variable number of transfected cells that were not sorted by FACS.

[00331] Cis-element Motif Analysis. 1 Kb regions upstream of the TSS (Transcription Start Site) for target genes were extracted based on TAIR10 annotation and submitted to the *Elefinder* program (Li et al., 2011, Plant physiology 156:2124.) or

MEME (53) to determine over-representation of known binding sites. (Different parameters used in specific cases were notified in the paper if applicable). The E-value of significance for each motif was used to cluster the occurrence of motifs in the various subsets using the HCL algorithm in MeV (Saeed et al., 2006, Methods in Enzymology 411:134). Motifs that show a higher specificity to a particular category or a sub-group were identified with the PTM algorithm in MeV. *De novo* motif identification was performed on 1Kb upstream sequence of the genes regulated by bZIP1 from microarray and ChIP-Seq data separately using the MEME suite (Bailey et al., 2009, Nucleic Acids Research 37:W202).

7.3. RESULTS

[00332] Perturbation of a TF *and* the signal it transduces uncovers context-dependent primary TF target genes. To discern mechanisms by which TFs controlling GRNs respond to a signal perceived *in vivo*, *both* a TF (bZIP1) *and* a metabolic signal that it transduces (nitrogen, N) were perturbed (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939; Obertello et al., 2010, BMC systems biology 4:111). The Arabidopsis TF bZIP1 was transiently overexpressed as a glucocorticoid receptor fusion (35S::GR-bZIP1) in a rapid cell-based system called *TARGET* (*T*ransient *A*ssay *R*eporting *G*enome-wide *E*ffects of *T*ranscription factors) (Bargmann et al., 2013, Molecular Plant 6(3):978) and genome-wide responses were monitored (Fig. 1). The GR-TF fusion enabled temporal induction of the nuclear localization of the TF using dexamethasone (DEX), as performed previously *in planta* (Eklund et al., 2010, Plant Cell 22:349) and in the cell-based *TARGET* system (Bargmann et al., 2013, Molecular Plant 6(3):978). In detail, Arabidopsis root protoplast cells overexpressing the 35S::GR-bZIP fusion protein were sequentially treated as follows: i) pre-treatment with an external metabolic signal (nitrogen, +/-N), followed by ii) CHX to block the synthesis of proteins, and iii) DEX to induce bZIP1 nuclear import of the GR-TF fusion (Fig. 1). Importantly, the addition of CHX blocks translation of mRNAs of bZIP1 primary targets, enabling identification of primary TF targets based solely on their TF-induced regulation (Bargmann et al., 2013, Molecular Plant 6(3):978; et al., 2010, Plant Cell 22:349). This sequence of treatments enabled identification of i) bZIP1 primary targets based on *either* TF-induced gene

regulation *or* TF-binding and ii) the "context-dependence" of TF-target gene regulation (i.e. response to both TF *and* signal perturbation).

Discovery of bZIP1 primary targets by *either* gene regulation *or* promoter binding. Transcriptome analysis using ATH1 Affymetrix Gene Chips was performed on cells transfected with 35S::GR-bZIP1 and subjected to the N, CHX and DEX treatments shown in Fig. 1C, in order to identify the primary targets regulated by bZIP1 in the context of the N-signal it transduces. ANOVA analysis identified 1,218 genes significantly regulated (FDR <0.05) in response to DEX-induced bZIP1 nuclear import (Fig. 10A; Fig. 10B; Table 4 and 5). 328 genes responded significantly to the N-signal in protoplasts, and show significant intersections with N-responses observed with a similar N-treatment (NH_4NO_3) and/or similar tissue (root) *in planta* (*pval* <0.001) (Fig. 13; Table 4) (Krouk et al., 2010, Genome biology 11:R123; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939; Palenchar et al., 2004, Genome Biology 5:R91; Gutierrez et al., 2007, Genome Biology 8:R7). With regard to signal perturbation, the N-responsive genes (328 genes) (Fig. 13) identified in the cell-based system, overlap significantly with the N-responsive genes identified from *in planta* studies (Krouk et al., 2010, Genome biology 11:R123; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939; Palenchar et al., 2004, Genome Biology 5:R91; Gutierrez et al., 2007, Genome Biology 8:R7) with a similar N-treatment (NH4NO3) and/or similar tissue (root) (pval <0.001 by Genesect) underscoring their *in planta* relevance. These N-responsive genes were also significantly enriched (pval=8.8E-13) with genes responsive to N across all root cell-types (Gifford et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:803), suggesting the root protoplasts used in this study has an even representation of different root cell types.

TABLE 4.

Genes identified by ANOVA and ChIP-Seq analysis.

Microarray Analysis		
Category of Genes		Number of Genes
Significantly regulated by ANOVA factor	Nitrogen (FDR<0.05)	328
	bZIP1* (FDR<0.05)	1218
	NitrogenXbZIP1 (pval<0.01)	108
	bZIP1* (FDR<0.05) AND NitrogenXbZIP1* (pval<0.01)	48
ChIP-SEQ Analysis		

bZIP1 bound genes*	850

* genes considered as TF primary targets in this study.

TABLE 5.

A. Significantly over-represented GO terms in the DEX up-regulated genes (+CHX)

	Term	p-value
GO:0042221	response to chemical stimulus	1.75E-07
GO:0050896	response to stimulus	1.75E-07
GO:0009628	response to abiotic stimulus	2.22E-05
GO:0009310	amine catabolic process	3.66E-05
GO:0010033	response to organic substance	5.33E-05
GO:0009063	cellular amino acid catabolic process	0.000127
GO:0016054	organic acid catabolic process	0.000239
GO:0046395	carboxylic acid catabolic process	0.000239
GO:0009719	response to endogenous stimulus	0.000436
GO:0006950	response to stress	0.000529
GO:0009651	response to salt stress	0.000747
GO:0044282	small molecule catabolic process	0.000899
GO:0080167	response to karrikin	0.000899
GO:0009725	response to hormone stimulus	0.00146
GO:0006970	response to osmotic stress	0.00171
GO:0009081	branched chain family amino acid metabolic process	0.00197
GO:0009737	response to abscisic acid stimulus	0.00553

B. Significantly over-represented GO terms in the DEX down-regulated genes (+CHX)

	Term	p-value
GO:0050896	response to stimulus	8.89E-16
GO:0006952	defense response	6.77E-12
GO:0042221	response to chemical stimulus	6.77E-12
GO:0006950	response to stress	1.19E-10
GO:0010033	response to organic substance	5.79E-10
GO:0051707	response to other organism	3.57E-09
GO:0009607	response to biotic stimulus	1.37E-08
GO:0051704	multi-organism process	1.37E-08
GO:0010200	response to chitin	2.84E-08
GO:0009620	response to fungus	1.24E-07
GO:0031347	regulation of defense response	3.60E-07
GO:0080134	regulation of response to stress	3.72E-07
GO:0002376	immune system process	3.79E-06
GO:0009743	response to carbohydrate stimulus	1.72E-05
GO:0048583	regulation of response to stimulus	1.96E-05
GO:0009719	response to endogenous stimulus	2.45E-05

GO:0050832	defense response to fungus	2.95E-05
GO:0009611	response to wounding	9.30E-05
GO:0031348	negative regulation of defense response	0.000105
GO:0045087	innate immune response	0.000151
GO:0006955	immune response	0.000172
GO:0009753	response to jasmonic acid stimulus	0.000241
GO:0002682	regulation of immune system process	0.000326
GO:0031408	oxylipin biosynthetic process	0.00076
GO:0045088	regulation of innate immune response	0.00125
GO:0050776	regulation of immune response	0.00125
GO:0016310	phosphorylation	0.00135
GO:0031407	oxylipin metabolic process	0.0014
GO:0006468	protein phosphorylation	0.00169
GO:0006793	phosphorus metabolic process	0.00194
GO:0006796	phosphate metabolic process	0.00194
GO:0009695	jasmonic acid biosynthetic process	0.0022
GO:0008219	cell death	0.00326
GO:0009694	jasmonic acid metabolic process	0.00326
GO:0009725	response to hormone stimulus	0.00326
GO:0009863	salicylic acid mediated signaling pathway	0.00326
GO:0016265	death	0.00326
GO:0050794	regulation of cellular process	0.00326
GO:0071446	cellular response to salicylic acid stimulus	0.00326
GO:0009737	response to abscisic acid stimulus	0.00331
GO:0006334	nucleosome assembly	0.00467
GO:0034728	nucleosome organization	0.00467
GO:0010941	regulation of cell death	0.00486
GO:0048584	positive regulation of response to stimulus	0.00497
GO:0065004	protein-DNA complex assembly	0.00529
GO:0071824	protein-DNA complex subunit organization	0.00529
GO:0042742	defense response to bacterium	0.0057
GO:0060548	negative regulation of cell death	0.0057
GO:0045727	positive regulation of translation	0.00575
GO:0009409	response to cold	0.00577
GO:0031349	positive regulation of defense response	0.00577
GO:0009751	response to salicylic acid stimulus	0.00661
GO:0050789	regulation of biological process	0.00785
GO:0010185	regulation of cellular defense response	0.00856
GO:0010193	response to ozone	0.00856
GO:0032270	positive regulation of cellular protein metabolic process	0.00856
GO:0051247	positive regulation of protein metabolic process	0.00856
GO:0012501	programmed cell death	0.00886

[00333] Forty-eight bZIP1 primary targets (FDR<0.05) were uncovered that show a significant TF x N-signal interaction (*pval* < 0.01) (Table 6). These genes responding to bZIP1 x N interactions form four distinct expression clusters (Fig. 14A) that can be

viewed as a context-dependent bZIP1 GRN (Fig. 14B). Intriguingly, cluster 4 genes, whose induction is completely dependent on the bZIP1 x N interaction, are enriched with N-regulated biological processes such as auxin stimulus, circadian, and response to organic substance (Fig. 14A). These 1,218 genes (including the 48 bZIP1 x N responsive genes) are deemed to be *primary targets* of bZIP1, as gene responses to DEX-induced TF nuclear import were assayed in the presence of CHX, which blocks regulation of secondary targets controlled by other TFs downstream of bZIP1 (Bargmann et al., 2013, Molecular Plant 6(3):978). Thus, bZIP1 primary targets are expected to be regulated in response to TF perturbation under both +CHX and –CHX conditions. A significant overlap (*pval*<0.001) was observed between the bZIP1-regulated genes identified in +CHX samples and –CHX samples.

TABLE 6.
Genes that are regualted by DEX (FDR<0.05) and also regulated by the interaction of N and DEX (pval<0.01) forming 4 clusters based on their expression patterns by Hierachical clustering in Mev

Locus	Symbol	Fullname
A. Cluster 1		
AT4G39190		
AT1G55610	BRL1	BRI1 like
AT3G49350		
AT3G23820	GAE6	UDP-D-glucuronate 4-epimerase 6
AT4G33960		
AT5G54470	BBX29	B-box domain protein 29
AT2G26390		
B. Cluster 2		
AT3G59900	ARGOS	AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE
AT5G39710	EMB2745	EMBRYO DEFECTIVE 2745
AT4G28940		
AT4G30560	ATCNGC9	cyclic nucleotide gated channel 9
AT3G15520		
AT1G56510	ADR2	ACTIVATED DISEASE RESISTANCE 2
AT2G39900	WLIM2a	WLIM2a
AT3G63390		
AT3G14360		
AT3G53280	CYP71B5	cytochrome p45 71b5
AT5G61210	ATSNAP33	
C. Cluster 3		
AT2G04500		
AT3G05210	ERCC1	
AT3G30396		
AT1G13280	AOC4	allene oxide cyclase 4
AT2G28630	KCS12	3-ketoacyl-CoA synthase 12

AT4G33420		
AT2G31380	BBX25	B-box domain protein 25
AT3G60290		
AT2G02700		
AT5G64100		
AT4G37240		
AT4G20350		
AT1G64160	AtDIR5	
AT1G15050	IAA34	indole-3-acetic acid inducible 34
AT1G10090		
AT1G13270	MAP1B	METHIONINE AMINOPEPTIDASE 1B
AT3G55150	ATEXO7H1	exocyst subunit exo7 family protein H1
AT3G48650		
AT2G39570	ACR9	ACT domain repeats 9
AT2G24130		
AT5G28050		
AT4G25620		
AT1G21410	SKP2A	
AT1G01490		
D. Cluster 4		
AT3G60690		
AT3G48360	ATBT2	
AT4G37540	LBD39	LOB domain-containing protein 39
AT5G59350		
AT5G04630	CYP77A9	cytochrome P45, family 77, subfamily A, polypeptide 9
AT4G38340		

[00334] To next identify primary bZIP1 targets whose promoter was *bound* by the GR-bZIP1 fusion protein either directly or indirectly through an interacting TF partner in a protein complex, a micro-ChIP protocol (Dahl et al., 2008, Nucleic Acids Research 36:e15) was adapted using anti-GR antibodies to pull down genomic regions bound to bZIP1 (Fig. 1C). Micro-ChIP and transcriptome data were derived from cells expressing 35S::GR-bZIP1 in parallel (Fig. 1C). Genic regions enriched in the ChIP DNA bound to GR-bZIP1 (peak seeding >=5 fold; extension >= 2 fold) compared to the background (input DNA), were identified using the QuEST peak-calling algorithm (Valouev et al., 2008, Nature Methods 5:829) (Fig. 10A). This analysis identified 850 target genes with significant bZIP1 binding (FDR <0.05) (Fig. 10D), which includes several validated bZIP1 target genes (e.g. ASN1 and ProDH) previously uncovered by ChIP-qPCR *in planta* (Dietrich et al., 2011, The Plant Cell 23:381-395).

[00335] It was confirmed that the 1,218 genes responding to bZIP1 perturbation and the 850 genes with significant binding to bZIP1 are enriched in bZIP1 primary targets by *cis*-regulatory motif analysis using MEME (Bailey et al., 2009, Nucleic Acids Research 37:W202) and *elefinder* (Li et al., 2011, Plant physiology 156:2124), which searches for known bZIP1 binding sites. Genes *induced* or *bound* by bZIP1 (644 genes) showed a highly significant overrepresentation of "G/C-box" (Fig. 10 C&E), a *cis*-element previously shown to bind bZIP1 *in vitro* (Kang et al., 2010, Molecular Plant 3:361). A distinct bZIP-binding motif called the "GCN4 binding motif" (Onodera et al., 2001, The Journal of Biological Chemistry 276:14139) was significantly over-represented in the 574 genes *repressed* in response to bZIP1 perturbation (Fig. 10C). The GCN4 motif has been reported to mediate nitrogen and amino acid starvation sensing in both yeast and plants (Hill et al., 1986, Science 234:451; Muller et al., 1993, The Plant Journal: for cell and molecular biology 4:343), suggesting a functional conservation between bZIP1 and nutrient sensing. Lastly, the $FORC^{A}$ motif, previously implicated in integrating light and defense signaling (Evrard et al., 2009. BMC Plant Biology 9:2), was shown to be over-represented in the 850 bZIP1 bound genes (Fig. 10E), consistent with the known role of bZIP1 *in planta* (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361; Hanson et al., 2007, The Plant Journal 53:935).

[00336] **Identification of temporal modes of bZIP1 primary target gene regulation.** Mechanisms underlying temporal, signal-mediated modes of TF action were identified by integrating results from transcriptome and ChIP-Seq, and then performing analysis of signal context, biological function, and *cis*-element enrichment in bZIP1 primary target genes (Fig. 10A). bZIP1-regulated primary TF targets (1,218 genes) were compared with the bZIP1-bound TF-targets (663 out of 850 genes, because 187 are not on the ATH1 microarray) (Fig. 11A). This analysis identified three classes of *primary* TF targets (Fig. 11A) that represent distinct modes-of-action for bZIP1: Class I: 473 genes with TF binding *only*; Class II: 190 genes that are TF bound *and* regulated; and Class III: 1,028 genes that are regulated by, but not bound to the TF (Fig. 11A). All three classes of bZIP1 primary targets are: i) enriched in known bZIP1 binding sites (Fig. 12B); ii) overlap significantly with genes previously shown to be regulated by bZIP1 from *in planta* studies (Kang et al., 2010, Molecular Plant 3:361; Gutierrez et al., 2008, Proc.

Natl. Acad. Sci. U.S.A. 105:4939) (Fig. 11B; Fig. 15); iii) shared significant GO terms associated with known bZIP1 functions (e.g. Stimulus/Stress) (Fig. 11A); and iv) overlap with genes induced by carbon-starvation and darkness (Krouk et al., 2009, PLoS Computer Biology 5:e1000326) (Fig. 16), which is consistent with the known role of bZIP1 *in planta* (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361; Hanson et al., 2007, The Plant Journal 53:935). In addition to these common features, the three classes of bZIP1 primary target genes show distinguishing features.

[00337] In planta cross-validation of the three classes of bZIP1 primary targets. The *in vivo* relevance of all three classes of bZIP1 primary targets was validated based on comparison to targets identified *in planta* in i) a constitutive bZIP1 overexpression line (Kang et al., 2010, Molecular Plant 3:361) (122/449 genes; p-val <0.001) (Fig. 11B) and ii) predicted from an organic-N regulatory network (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939) (14/27 genes; p-val <0.001) (Fig. 15). Additionally, the potential relevance was determined for each bZIP1-target class in the signaling pathways previously associated with bZIP1 regulation *in planta*, including sugar (Kang et al., 2010, Molecular Plant 3:361) and light (Baena-Gonzalez et al., 2007, Nature 448:938). Intersections with genes repressed by carbon (C) and light (L) (Krouk et al., 2009, PLoS Computer Biology 5:e1000326) in roots and shoots (Fig. 16) were highly significant (p-val <0.001) across all three classes of bZIP1 primary targets identified. This result is consistent with previous reports that bZIP1 is a master regulator in response to light and sugar starvation (Weltmeier et al., 2008, Plant Molecular Biology 69:107; Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361; Hanson et al., 2007, The Plant Journal 53:935).

[00338] Cis-element analysis of the three classes of bZIP1 targets. Cis-element analysis of each of the three subclasses of bZIP1 regulated gene targets show enrichment of known bZIP binding sites (Fig. 12B). Genes that either bind to bZIP1 or are activated by bZIP1 (Class I, IIA and IIIA), show significant over-representation of the known bZIP1 binding site "ACGT" box: including G-box, C-box or hybrid G/C-box (Kang et al., 2010, Molecular Plant 3:361) (Fig. 12B; Fig. 17). By contrast, genes that are repressed by bZIP1 do not have the canonical "ACGT" core, and instead posses the

GCN4 binding motif for the bZIP family - as well as a W-box (Fig. 12B; Fig. 17). Interestingly, the GCN4 motif was reported to mediate nitrogen and amino acid starvation sensing in both yeast and plants (Onodera et al., 2001, The Journal of Biological Chemistry 276:14139; Hill et al., 1986, Science 234:451; Muller et al., 1993, The Plant Journal: for cell and molecular biology 4:343), suggesting a link between bZIP1 and nutrient sensing. A non-exclusive alternative interpretation is that bZIP1 may work with a WRKY family partner to repress primary target genes.

[00339] Class I "poised" bZIP1 targets: TF Binding, No regulation. This class of bZIP1 primary targets were specifically and significantly overrepresented in genes involved in "regulation of transcription" and "calcium transport" (FDR<0.01) (Fig. 11A). These functions suggest that bZIP1 may serve as a master TF, that is bound to and *"poised"* to activate these downstream regulatory genes in response to a signal not provided in the experimental set-up, or that requires a TF partner not present in root cell protoplasts.

[00340] Class II "active" bZIP1 targets: TF Binding and Regulation. The 190 primary bZIP1 target genes in Class II, represents a 29% overlap (p-val<0.001) between the transcriptome and ChIP-Seq data, which compares favorably to such overlaps in other TF studies *in planta* (23 % ABI3 (Monke et al., 2012, Nucleic Acids Research 40:8240); 25% PIL5 (Oh et al., 2009, The Plant Cell Online 21:403)). Class II genes are the classical "gold standard" set that are the *only* primary targets identified in other TF studies that require TF-binding to define primary targets. For bZIP1, these primary targets in Class II have an overrepresentation in genes involved in "response to stress/stimulus" (FDR<0.01), which was a term common to all three classes of bZIP1 targets. No class-specific GO-terms were identified for these "classic" Class II bZIP1 primary target genes (Fig. 11A).

[00341] Class III "transient" bZIP1 targets: TF Regulation, but no detectable TF binding. Unexpectedly, the Class III bZIP1 primary target genes, that are regulated by, but not detectably bound to the TF, turned out to be the largest set of bZIP1 primary target genes (1,028) detected in this study. The Class III genes were identified as primary bZIP1 targets based on gene regulation in response to the nuclear import of bZIP1 performed in the presence of CHX (to block activation of secondary targets), but were

not detected in the parallel ChIP-Seq analysis to be bound by bZIP1 directly or indirectly in a protein complex containing bZIP1. In either scenario – direct binding of bZIP1 to its gene target or bZIP1 binding via interacting TF partners – the bZIP1 target gene should be detected by ChIP-Seq if the interaction is stable. This led to the hypothesis that the Class III primary bZIP1 target genes that are regulated in response to DEX-induced bZIP1 nuclear import may be the result of a transient TF-target association not detectable by ChIP-Seq at the time of sampling. A series of results supports this view, and also indicates that the Class III "transient" bZIP1 primary targets are most relevant to the function of bZIP1 in transducing the N-signal provided. First, the Class III "transient" bZIP1 primary target genes show a substantial (117/328) and the most significant overlap with N-responsive genes (Fig. 13) identified in the study (Class IIIA: *pval*=2e-41; Class IIIB: *pval*=2e-29) compared to Classes I and II (Fig. 11A). Second, out of the 48 primary targets regulated by bZIP1 x N interaction (Fig. 14), 47 of these belong to Class III: Class IIIA (29 genes regulated by bZIP1 X N interaction) (*pval*=5e-22) and Class IIIB (18 genes regulated by bZIP1 x N interaction) (*pval*=5e-12) (Fig. 11A). This suggests that the bZIP1 regulation of Class III genes is likely modified by the N-signal, which may involve a post-translational modification of bZIP1 and/or by translational/transcription effects on its interacting partners (Fig. 1B). Third, only Class III bZIP1 primary targets showed a significant enrichment in genes involved in processes related to the N-signal including "amino acid metabolism", "phosphorus metabolism" and "signal transduction" (FDR<0.01) (Fig. 11A). Lastly, but most importantly, only Class IIIA bZIP1 primary targets are specifically enriched with genes that respond to N in a *transient* and rapid manner *in planta* (Fig. 11B) (Krouk et al., 2010, Genome Biology 11:R123), as discussed in detail below.

[00342] Class III "transient" bZIP1 target genes show an early and transient N-response *in planta*. To assess the significance of the three classes of bZIP1 targets identified in this cell-based system, the classes were compared to studies that have implicated bZIP1 as a master hub in mediating responses to N nutrient signals *in planta* (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939; Obertello et al., 2010, BMC Systems Biology 4:111). Indeed, all three classes of bZIP1 primary targets identified in this cell-based system were significantly enriched (*pval*<0.001) in genes

regulated by an identical nitrogen treatment (NH_4NO_3) in an *in planta* study (Fig. 11B) (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939). The link between *temporal* N nutrient signaling and the bZIP1 "transient" mode of action was investigated by comparing all three Classes of bZIP1 primary targets to a fine-scale, time-series dataset that uncovered dynamic N-responsive genes in roots (Krouk et al., 2010, Genome Biology 11:R123). This analysis shows that only Class IIIA "transient" bZIP1 targets genes are rapidly and transiently regulated by nitrogen treatments *in planta*, as follows: i) Rapid N-induction: Only Class IIIA "transient" bZIP1 primary targets show a significant overlap (pval<0.001) with *early* nitrate-responsive genes induced within 6 minutes following N-treatment (Krouk et al., 2009, PLoS Computer Biology 5:e1000326) (Fig. 11B). ii) Transient N-induction: Only Class IIIA "transient" bZIP1 *activated* targets are distinguished by their significant overlap (*pval*<0.001) with genes that show a *transient* response to nitrate-induction in roots from the *in planta* time-course study (Krouk et al., 2010, Genome Biology 11:R123) (Fig. 11B). Specifically, 20 Class IIIA bZIP1 primary target genes (Table 1) are transiently N-induced *in planta*, and specific gene induction kinetics (3-20 min) are shown for three sample genes (AT2G43400, AT4G38490, and AT5G04310) (Fig. 11B). These data support the notion that a temporal relationship between bZIP1 and the Class IIIA "transient" primary target genes likely mediates an early and transient response to the N-signal.

[00343] ***Cis*-element context analysis uncovers elements associated with signal x TF interactions**. A distinguishing feature of the Class III "transient" bZIP1 primary targets is their significant enrichment in genes responding to a bZIP1 x N-signal interaction (Fig. 10A). This could be a result of i) the post-translational modification of bZIP1 and/or ii) the transcriptional or post-translational modification of its interactors in response to N-signaling (Fig. 1B; Fig. 12A). To uncover evidence for possible bZIP1 TF partners, the class-specific enrichment of cis-elements in the promoters of genes in each of the three bZIP1 primary target classes was examined (Fig. 12B). The Class III "transient" bZIP1 primary target genes contained the largest number and most highly significant enrichment of *cis*-motifs, compared to the other classes of bZIP1 targets (Fig. 12B; Fig. 17). Specifically, promoters of Class IIIA genes (primary targets *activated* by bZIP1, but no detectable bZIP1 binding) are significantly enriched with bZIP family TF

binding sites (e.g. the TGA1 binding site (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118), ABRE binding site (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118), and GBF1/2/3 binding site (de Vetten et al., 1995, Plant Journal 7:589)). Other significant co-inherited cis-elements were specifically found in Class IIIA bZIP1 targets and include: MYB family TF binding sites (I-box (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118) and CCA1 motif (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118)), GATA promoter motif (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118), and the light responsive motif SORLIP1 (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118). These findings suggest that Class IIIA "transient" TF-target genes may be co-activated by bZIP1 and other TFs, including other bZIP family members, for which there is *in vivo* evidence of association with bZIP1 (Kang et al., 2010, Molecular Plant 3:361; Ehlert et al., 2006, The Plant Journal 46:890). For the Class IIIB bZIP1 target genes (primary target genes *repressed* by bZIP1, but no detectable bZIP1 binding), a number of *cis*-elements implicated in light and temperature signaling were significantly over-represented in their promoters, including T-box, SORLREP1, LTRE, and HSE binding site (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118). Combined, the significant enrichment in Class III "transient" bZIP1 primary targets of genes i) early and ii) transiently regulated in response to a N-signal, iii) whose expression depends on a N x TF interaction, and iv) whose promoters are enriched in co-inherited cis-elements, support a model of temporal bZIP1-target association in response to the N-signal and/or a N-responsive interaction of bZIP1 with other TFs, as depicted in Fig. 12A.

7.4. DISCUSSION AND CONCLUDING REMARKS

[00344] A previously unrecognized "transient" mode of TF action was uncovered by a conceptual innovation in the experimental design to temporally perturb both a TF and signal, and in the integration and interpretation of TF-binding and TF-regulation data. This allowed for identification of primary TF targets based on *either* gene regulation *or* TF-binding, and the association of this regulation with a signal. This contrasts with previous studies of TFs in both plants and animals, where the identification of primary targets has been limited to TF-binding and/or the overlap between TF-regulation *and* TF-binding (Reeves et al., 2011, Plant Molecular Biology 75:347; Gorski et al., 2011,

Nucleic Acids Research 39:9536; Hull et al., 2013, BMC Genomics 14:92; Fujisawa et al., 2011, Planta 235:1107; Wagner et al., 2004, The Plant Journal: for cellular and molecular biology 39:273). The approach enabled discovery of a new class of "transient" TF targets that are regulated by the TF but not detectably bound by it, because of three complementary features of the system: i) the ability to temporally induce the nuclear import of the TF bZIP1 in the presence or absence of a signal; ii) the use of a protein synthesis inhibitor (CHX) to identify primary TF-targets based solely on gene regulation; and iii) the ability to perform transcriptome analysis and ChIP-Seq on the same samples which allowed direct data comparison. Combining these features enabled the distinction between three temporal modes of bZIP1 action in regulating primary TF-target genes: "poised", "active" and "transient". By examining the TF modes of action in the presence or absence of a signal it transduces (N), it was found that Class III "transient" gene targets (TF-regulated but not bound) were most relevant to the N-signal provided, as they show unique and significant: i) enrichment in N-responsive genes (Fig. 11A), ii) early and iii) transient induction by a N-signal (Fig. 11B), iv) regulation by TF x N-signal interactions (Fig. 11A), and v) GO-term enrichment in N-related processes (Fig. 11A). These features distinguish the Class III "transient" TF-target genes, compared to the other two classes of primary TF targets: "poised" and "active". It is noteworthy that the Class III "transient" TF-targets identified in the cell-based system also play an important role *in vivo* – based on significant overlap with *in planta* data (Fig. 11B). However, they would have been *dismissed* as *secondary TF-targets* in those *in planta* studies, and their role in mediating a dynamic GRN would have been missed.

[00345] This discovery suggests that the Class III "transient" TF-target genes are likely the result of a *temporal* association between bZIP1 with these targets, acting either directly on the primary target DNA and/or through TF partner interactions (Fig. 12A). In support of the role of TF partners in this temporal, N-signal mediated regulation, *cis*-element analysis revealed that the Class III "transient" bZIP1 target genes had the highest enrichment, both in number and in significance, of *cis*-elements that co-occurred with the bZIP1 binding site, compared to the inactive "poised" Class I genes and the constitutively "active" Class II genes (Fig. 12B). TFs associated with these co-occurring *cis*-elements include other bZIP family members and TFs belonging to the MYB family. Querying a

protein-protein interaction database (Katari et al., 2010, Plant physiology 152:500) revealed that bZIP1 interacts with 11 other members of the bZIP family (Table 7). Interestingly, 3 out of these 11 bZIP TFs shown to interact with bZIP1 *in vitro* (Katari et al., 2010, Plant physiology 152:500), were also determined to be primary targets of bZIP1 in this study (bZIP25, bZIP53, bZIP9), suggesting that bZIP1 regulates and activates some of its protein-interaction TF partners. The interactions between bZIP1 with bZIP25/53/9 have also been independently experimentally validated *in vivo* (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361; Ehlert et al., 2006, The Plant Journal 46:890). These data support the hypothesis that bZIP1 may be a master response gene that activates and interacts with specific bZIP family members, and/or potentially with members of the MYB family, to "temporally" co-regulate downstream genes in response to a N-signal.

TABLE 7.
bZIP1 protein-protein interaction partners.

At5g37780	ACAM-1, CAM1, TCH1, calmodulin 1
At1g66410	ACAM-4, CAM4, calmodulin 4
At5g21274	ACAM-6, CAM6, calmodulin 6
At2g41100	ATCAL4, TCH3, Calcium-binding EF hand family protein
At3g51920	ATCML9, CAM9, CML9, calmodulin 9
At2g41090	Calcium-binding EF-hand family protein
At3g43810	CAM7, calmodulin 7
At4g14640	CAM8, calmodulin 8
At5g41910	MED10A, Mediator complex, subunit Med10
At4g34590	ATB2, AtbZIP11, BZIP11, GBF6, G-box binding factor 6
At5g49450	AtbZIP1, bZIP1, basic leucine-zipper 1
At4g02640	ATBZIP10, BZO2H1, bZIP transcription factor family protein
At2g18160	ATBZIP2, bZIP2, GBF5, basic leucine-zipper 2
At3g54620	ATBZIP25, BZIP25, BZO2H4, basic leucine zipper 25
At1g59530	ATBZIP4, bZIP4, basic leucine-zipper 4
At3g30530	ATBZIP42, bZIP42, basic leucine-zipper 42
At1g75390	AtbZIP44, bZIP44, basic leucine-zipper 44
At3g62420	ATBZIP53, BZIP53, basic region/leucine zipper motif 53
At1g13600	AtbZIP58, bZIP58, basic leucine-zipper 58
At5g28770	AtbZIP63, BZO2H3, bZIP transcription factor family protein
At5g24800	ATBZIP9, BZIP9, BZO2H2, basic leucine zipper 9

[00346] To place these findings in perspective, the general field of GRN validation has focused on determining when and how TF binding does, or does not, result in gene

activation (Reeves et al., 2011, Plant Molecular Biology 75:347; Gorski et al, 2011, Nucleic Acids Research 39:9536). This focus has limited the field to studying the more stable and static "gold standard" interactions exemplified by the bZIP1 Class II genes (TF-bound and regulated). The discovery of the Class III "transient" TF-targets (TF-regulated, no binding) now opens the opposite question/perspective in the general field of transcriptional control: How and why can TF-induced changes in mRNA occur in the absence of stable TF binding? The simple explanation that the Class IIIA mRNA is stabilized by CHX or bZIP1 is not supported by the data, as +/-CHX results are comparable (Fig. 16), and there was no evidence for either bZIP1 regulated small RNAs or 3' UTR elements that could affect RNA stability in Class III genes. Therefore, these transient TF-target interactions may be conceptualized as the "hit-and-run" model of transcription, which posits that a TF can act as a trigger to organize a stable transcriptional complex, after which transcription by RNA polymerase II can continue without the TF being bound to the DNA (Schaffner, 1988, Nature 336:427-428).

[00347] In support of this "hit-and-run" model, the Class III "transient" genes are enriched in mRNAs with short half-lives (<2 hour) (Chiba et al., 2013, Plant & cell physiology 54:180) indicating that they are actively transcribed at the 5 hour time-point when the gene is induced by the TF but is not stably bound to it (Fig. 18). This "hit-and-run" model of TF action suggests a general mechanism for the deployment of an acute response to nutrient level change, in which a master regulatory TF transiently and rapidly activates a large set of genes in response to a signal. This "pioneer" TF responds to N-signals possibly by recruiting TF partners, as supported by the finding that Class III targets are most significantly enriched with cis-regulatory elements of known bZIP1 interactors.

[00348] The "transient", signal-induced association of a target with a TF can be analaogized to a "touch-and-go" (hit-and-run) landing or circuit maneuver used in aviation. This involves landing a plane on a runway and taking off again without coming to a full stop, allowing many landings in a short time. This maneuver also allows pilots to rapidly detect or avoid another plane or object on the runway, and could serve an analogous role for bZIP1 and its TF partners. The "touch-and-go" (hit-and-run) mode may enable bZIP1 to "direct", "detect" or "avoid" TFs on a gene target, or alternatively

to rapidly activate and leave the promoter "empty" for its TF partners to occupy. By contrast, the more traditional "stop-and-go" action requiring a full stop before taking off again, is a more stable maneuver which can be analogized to the classic Class II "gold standard" set, in which the TF lands (stably binds) and regulates a gene. While these more stable and static interactions have been the focus of most TF studies, the discovery of this new "touch-and-go" (hit-and-run) mode of TF action opens a new concept and field of inquiry in the study of dynamic GRNs in plants and animals.

8. EXAMPLE 3

8.1. PLANT GROWTH AND TREATMENT

[00349] Rice seeds (Oryza sativa ssp. japonica) were kindly provided by Dale Bumpers of the National Rice Research Center (AR, USA). Seeds were surface-sterilized and vernalized on 1x Murashige and Skoog (MS) basal salts (custom-made; GIBCO) with 0.5 mM ammonium succinate and 3 mM sucrose, 0.8% BactoAgar at pH 5.5 for 3 days in dark conditions at 27°C. Germinated seeds were transferred to a hydroponic system (Phytatray II, Sigma Aldrich) containing basal MS salts (custom-made; GIBCO) with 0.5 mM ammonium succinate and 3 mM sucrose at pH 5.5 to grow for 12 days under long-day (16 h light: 8 h dark) at 27°C, at light intensity of 180 $\mu E.s^{-1}.m^{-2}$. Media was replaced every 3 days and the plants were transferred to fresh media containing basal MS salts for 24 h prior treatment. On day 13, plants were transiently treated for 2 h at the start of their light cycle by adding Nitrogen (N) at a final concentration of 20 mM KNO_3 and 20 mM NH_4NO_3 (referred here as 1xN). Control plants were treated with KCl at a final concentration of 20 mM. After treatment, roots and shoots were harvested separately using a blade, and immediately submerged into liquid nitrogen and stored at -80°C prior to RNA extraction.

[00350] Arabidopsis seeds were placed for 2 days in the dark at 4°C to synchronize germination. Seeds were surface-sterilized and then transferred to a hydroponic system (Phytatray I, Sigma Aldrich) containing the same media previously described for rice (pH 5.7). Growth conditions were the same as in rice, except that plants were under 50 μE.s–

1.m–2 light intensity at 22°C. N-starvation and treatments were done as described above (Figure 19). RNA was isolated using TRIzol reagent following manufacturer's protocols.

8.2. MICROARRAY EXPERIMENTS AND ANALYSIS

[00351] cDNA synthesis, array hybridization and normalization of the signal intensities were performed according to the instructions provided by Affymetrix. Affymetrix Arabidopsis ATH1 Genome Array Chip and Rice Genome Array Chip were used for respective species. Data normalization was performed using the RMA (Robust Microarray Analysis) method in the Bioconductor package in R statistical environment. A two-way Analysis of Variance (ANOVA) was performed using custom-made function in R to identify probes that were differentially expressed following N treatment. The p-values for the model were corrected for multiple hypotheses testing using FDR correction at 5% (Benjamini and Hochberg, 1995, Journal of the Royal Statistical Society 57:289). The probes passing the cut-off ($p \leq 0.05$) for the model and, N treatment or interaction of N treatment and tissue, were deemed significant. A Tukey's HSD post-hoc analysis was performed on significant probes to determine the tissue specificity of N-regulation at p-value cut-off ≤ 0.05 and fold-change ≥ 1.5-fold (Figure 19). Affy probes mapping to more than one gene were disregarded resulting in a significant set of N-regulated 1417 Arabidopsis genes and 451 Rice genes (Figure 20).

[00352] Orthologous N-regulated genes between Rice and Arabidopsis were obtained using reverse Blast (Camacho et al., 2008, BMC Bioinformatics 10:421) with an e-value $\leq 1e^{-20}$, thereby allowing for multiple ortholog hits (Figure 20).

8.3. NETWORK ANALYSIS

[00353] A Rice Multinetwork was generated using the following interactions (Figure 21):

[00354] Metabolic interactions were obtained from RiceCyc (Dharmawardhana et al., 2013, Rice 6:15).

[00355] Protein-Protein interactions were obtained from the PRIN database (Gu et al., 2011, BMC Bioinformatics 12:161), and published work, which include experimentally determined and computationally predicted interactions (Ding et al., 2009, Plant

Physiology 149(3):1478; Rohila et al., 2006, The Plant Journal 46:1; Ho et al., 2012, The Rice Journal 5:15).

[00356] Predicted Regulatory interactions were created between a Transcription Factor (TF) and its putative target using TF family membership obtained from Grassius (Yilmaz et al., 2009, Plant Physiology 149:171) and identification of cis-regulatory motifs, obtained from AGRIS (Palaniswamy et al., 2006, Plant Physioloy 140:818), in 1000 bp upstream of promoter sequence of Target genes. Motifs were searched using the DNA pattern search tool from the RSA tools server with default parameters (van Helden, 2003, Nucleic Acids Research 31:3593).

[00357] The 451 N-regulated rice genes were queried against the Rice Multinetwork to create a N-regulated gene network in Rice. Additionally, conserved correlation edges between two N-regulated Rice genes were proposed if the respective Arabidopsis N-regulated orthologs were also correlated significantly in the same direction (both positively or negatively) with Pearson correlation coefficient ≥ 0.8. Predicted regulatory interactions were further restricted to those TF and Target pairs where the two were also significantly correlated (Pearson correlation coefficient ≥ 0.8 and p-value ≤ 0.01), which resulted in a network of 206 Rice genes, of which 21 are transcription factors, with 6,818 edges (Figure 21).

[00358] The network was further refined by removing conserved correlation edges that are not supported with predicted regulatory edges which resulted in a "N-regulated correlated network" containing 151 Rice genes, of which 16 were TFs (Table 8). All network visualizations were created using Cytoscape (v2.8.3) software (Shannon et al., 2003, Genome Research 13:2498).

TABLE 8.

Number of targets of transcription factors at each step in the network creation process.

		Rice Homology Network	Rice Core Network	Rice Core Correlated Network
Gene Locus ID	Gene Description	# of targets	# of targets	# of targets
LOC_Os01g64020	transcription factor HBP-1b, putative, expressed	246	124	44
LOC_Os01g64000	ABA response element binding factor, putative, expressed	136	78	34
LOC_Os06g41100	TGA10 transcription factor, putative, expressed	114	48	5
LOC_Os09g35030	sbCBF6, putative, expressed	108	64	1
LOC_Os01g08640	DNA binding protein, putative, expressed	108	58	28
LOC_Os05g37170	transcription factor TGA6, putative, expressed	86	53	9
LOC_Os04g42950	DNA binding protein, putative, expressed	84	36	6
LOC_Os02g06810	auxin response factor 6, putative, expressed	66		
LOC_Os04g55970	DNA binding protein, putative, expressed	63	30	4
LOC_Os03g04310	DNA binding protein, putative, expressed	52	20	4
LOC_Os08g07030	dehydration responsive element binding protein, putative, expressed	45		
LOC_Os09g26420	ethylene response factor, putative, expressed	30		
LOC_Os08g42550	AP2 domain containing protein, expressed	26	9	1
LOC_Os01g34060	DNA binding protein, putative, expressed	14	5	2
LOC_Os05g38140	bHLH transcription factor, putative, expressed	6		
LOC_Os03g47730	knotted1-interacting protein, putative, expressed	3		

[00359] A comparison of the number of TF targets at various network building steps as shown in Figure 21, demonstrates that TFs with the most targets are more likely to be conserved between Arabidopsis and Rice and therefore are candidates for further translational studies (Table 9). BioMaps (GO-term enrichment analysis) of the targets of all TFs present in the "N-regulated core network" revealed that targets of only two TFs, LOC_Os01g64000 and LOC_Os01g64020, are enriched for "nitrate assimilation" and "nitrate metabolic process" (Table 10). A closer look at the N-assimilation pathway in the N-regulated Core Network revealed a set of 7 Rice transcription factors, which are directly targeting the genes in the N-assimilation pathway (Table 11). Three of the 7 TFs were also present in the correlated core N-regulated network, which implies that these TF-target gene pairs have conserved N-response in both Arabidopsis and Rice (Table 11).

TABLE 9.

Rice and Arabidopsis orthologous transcription factors in the "N-regulated core network."

Rice Core Network				Arabidopsis Orthologs	
Gene Locus ID	Index	Rank	Gene Description	Ortholog Gene ID	Ortholog Gene Description
LOC_Os01G64020	114	2	transcription factor HBP-1b, putative, expressed	AT1G22070	TGA3, TGA1A-related gene 3
				AT1G77920	bZIP transcription factor family protein
				AT5G10030	OBF4, TGA4, TGACG motif-binding factor 4
				AT5G65210	TGA1, bZIP transcription factor family protein
LOC_Os01G64000	79	3	ABA response element binding factor, putative, expressed	AT3G56850	ABF3, DPBF3, ABA-responsive element binding protein 3
LOC_Os09G35030	64	3	sbc8f6, putative, expressed	AT1G63030	ddf2, integrase-type DNA-binding superfamily protein
LOC_Os01G06640	58	5	DNA binding protein, putative, expressed	AT3G23710	ATAIG1, BHLH32, TMO5, basic helix-loop-helix 32
LOC_Os05G37170	53	5	transcription factor TGA5, putative, expressed	AT1G22070	TGA3, TGA1A-related gene 3
				AT1G77920	bZIP transcription factor family protein
				AT5G10030	OBF4, TGA4, TGACG motif-binding factor 4
				AT5G65210	TGA1, bZIP transcription factor family protein
LOC_Os06g43100	46	6	TGA1B transcription factor, putative, expressed	AT1G22070	TGA3, TGA1A-related gene 3
				AT1G77920	bZIP transcription factor family protein
				AT5G10030	OBF4, TGA4, TGACG motif-binding factor 4
				AT5G65210	TGA1, bZIP transcription factor family protein
LOC_Os04G42950	46	7	DNA binding protein, putative, expressed	AT5G26660	ATMYB86, MYB86, myb domain protein 86
				AT5G60890	ATMYB34, ATR1, MYB34, myb domain protein 34
				AT5G61420	AtMYB28, HAG1, MYB28, PMG1, myb domain protein 28
LOC_Os04G52970	36	8	DNA binding protein, putative, expressed	AT1G75490	integrase-type DNA-binding superfamily protein/AINTEGUMENTA-like 6
				AT2G28550	RAP2.7, TOE3, related to AP2 7
				AT3G20840	PLT3, integrase-type DNA-binding superfamily protein
				AT3G54320	ANK1, ATWRI1, WRI, WRI1, integrase-type DNA-binding superfamily protein
				AT5G10510	AIL6, PLT3, AINTEGUMENTA-like 6
LOC_Os03G04310	29	9	DNA binding protein, putative, expressed	AT3G26744	ATICE1, ICE1, SCRM, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
LOC_Os08G42950	9	10	AP2 domain containing protein, expressed	AT1G23420	O-fucosyltransferase family protein
LOC_Os01G34060	5	11	DNA binding protein, putative, expressed	AT1G49010	Duplicated homeodomain-like superfamily protein
				AT3G18350	Homeodomain-like superfamily protein

TABLE 10.

BioMaps (Gene Ontology Enrichment Analysis) of N-regulated TF targets in the "N-regulated Core Network." Only LOC_OS01G64020 and LOC_OS01G64000 targets had over-represented GO-terms ("nitrate metabolic process" and "nitrate assimilation") (p-value cutoff ≤0.05).

Gene Locus ID	Gene Description	# of Targets in Rice Core Network (N-assimilation pathway)	Over-represented GO:Terms for targets
LOC_OS01G64020	transcription factor HBP-1b, putative, expressed	114 (5)	nitrate metabolic process (GO:0042126), nitrate assimilation (GO:0042128)
LOC_OS01G64000	ABA response element binding factor, putative, expressed	79 (4)	nitrate metabolic process (GO:0042126), nitrate assimilation (GO:0042128)

TABLE 11.

Rice and Arabidopsis orthologous transcription factors targeting the "N-assimilation pathway."

Rice TF Targets		Rice TFs		Arabidopsis Orthologs of Rice TF	
ID	Description	ID	Description	ID	Description
LOC_Os01g25494	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed	LOC_Os01g64020	transcription factor HBP-1b, putative, expressed	AT1G22070	TGA3, TGA1A-related gene 3
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed			AT1G77920	bZIP transcription factor family protein
LOC_Os02g53130	nitrate reductase, putative, expressed			AT5G10030	OBF4, TGA4, TGACG motif-binding factor 4
LOC_Os03g13250	peptide transporter PTR2, putative, expressed				
LOC_Os06g15370	peptide transporter PTR2, putative, expressed			AT5G65210	TGA1, bZIP transcription factor family protein
LOC_Os06g15370	peptide transporter PTR2, putative, expressed	LOC_Os01g64020	ABA response element binding factor, putative, expressed	AT3G56850	AREB3, DPBF3, ABA-responsive element binding protein 3
LOC_Os01g25494	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed				
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed				
LOC_Os02g53130	nitrate reductase, putative, expressed				
LOC_Os01g25494	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed	LOC_Os09g39030	abi3VP1, putative, expressed	AT1G63030	ddf2, integrase-type DNA-binding superfamily protein
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed				
LOC_Os03g13250	peptide transporter PTR2, putative, expressed				
LOC_Os06g15370	peptide transporter PTR2, putative, expressed	LOC_Os01g06640	DNA binding protein, putative, expressed	AT3G25710	ATAIG1, BHLH32, IND5, basic helix-loop-helix 32
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed				
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed	LOC_Os05g37370	transcription factor TGA6, putative, expressed	AT1G22070	TGA3, TGA1A-related gene 3
				AT1G77920	bZIP transcription factor family protein
				AT5G10030	OBF4, TGA4, TGACG motif-binding factor 4
LOC_Os03g13250	peptide transporter PTR2, putative, expressed			AT5G65210	TGA1, bZIP transcription factor family protein
LOC_Os02g10360	tyrosine aminotransferase, putative, expressed	LOC_Os03g04330	DNA binding protein, putative, expressed	AT3G26744	AtICE1, ICE1, SCRM, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
LOC_Os02g10360	tyrosine aminotransferase, putative, expressed	LOC_Os01g34060	DNA binding protein, putative, expressed	AT1G49010	Duplicated homeodomain-like superfamily protein
				AT3G16350	homeodomain-like superfamily protein

9. EXAMPLE 4

9.1. TRANSLATIONAL SYSTEMS BIOLOGY: TRANSLATING "NETWORK KNOWLEDGE" FROM ARABIDOPSIS TO MAIZE.

[00360] Recent advances in genome sequencing, functional genomics, and computational tools enable a systems-level understanding of key physiological and developmental processes in the model plant Arabidopsis, but translating this knowledge to enhancing agriculturally important phenotypes in crop species remains challenging. In this Example, network-connected modules were identified in a data poor crop (maize) by exploiting the extensive network knowledge in the model plant Arabidopsis. Translating the systems-knowledge from Arabidopsis to improve agriculturally important traits has been hindered by a gene-centric focus in crops, and a limited capacity to empirically derive gene regulatory networks at a population scale in germplasm relevant to future crop improvement. At the heart of this work below, is the combination of crop

transcriptome data with Arabidopsis "network-knowledge" to identify network modules associated with nitrogen use efficiency, NUE, an important trait in agriculture.

[00361] The surprising and unexpected result of this study is that the transfer of "network knowledge" from Arabidopsis to Maize, enabled the identification of a conserved N-regulatory network of 223 N-responsive genes including 15 TF hubs in Arabidopsis, and their 32 TF homologs in Maize (see Figure 22 and Table 36).

EXPERIMENTAL APPROACH

[00362] **Building maize networks exploiting Arabidopsis "network knowledge".** We used network analysis and systems biology tools housed in the VirtualPlant software platform (www.virtualplant.org) [Katari et al 2010], to translate knowledge from models-to-crops to aid in hypotheses translation to agriculture. We used a publicly available microarray N-treatment dataset of maize for this study [Yang et al. 2011]. The step-by-step analysis described below incorporates Arabidopsis "network knowledge" into the maize networks, and results in a conserved network of 223 genes that enable focused hypothesis generation on transcription factor (TF) hubs with translational value (see Figures 22 & 23, Table 36).

[00363] **The maize data**: Using functions in the software platform we developed to enable systems biology research, VirtualPlant maize (www.virtualplant.org) [Katari et al 2010], we identified 5,057 N-responsive genes from [Yang et al., 2011], which form a correlation network of 4,278 maize genes. This network is too large to enable focused hypothesis generation, and >50% of the maize genes are un-annotated. Below, we describe how to interpret/filter this maize transcriptome data in the context of Arabidopsis "network knowledge" to derive networks and focused hypothesis generation for testing. Specifically, we have identified a N-regulatory network conserved between Arabidopsis and Maize that contains 223 connected genes including the 15 Arabidopsis transcription factors that regulate this N-response network. The 4 most highly connected Arabidopsis TFs shown in Figures 22 and 23, and their 32 maize orthologs are listed in Table 36 (BLAST).

Translating Arabidopsis "network knowledge" to maize:

[00364] Step 1. Mapping maize genes to Arabidopsis:

The 5,057 N-responsive genes from maize were mapped to 3,756 Arabidopsis homologs using VirtualPlant maize, which uses the maize "best-hit" to Arabidopsis data provided by Phytozome (www.phytozome.net).

[00365] Step 2. Translating Arabidopsis "network knowledge" to maize:

To integrate "network knowledge" from Arabidopsis into the 3,756 maize N-regulated genes, we used the "gene network" function in VirtualPlant (i.e. protein:protein, metabolic, cis-binding, and text mining edges) and obtained a network of 2,262 connected maize genes. A GO (Gene Ontology) term over-representation test on this network identifies Nitrogen metabolic process ($p<1e-33$) and sulfur metabolic process ($p<0.005$) among the significant GO terms. To focus hypotheses for translational studies using conserved N-networks, we refined the maize translational network by selecting genes that are N-regulated in both maize and Arabidopsis in Step 3.

[00366] Step 3. Conserved N-response genes in maize and Arabidopsis:

A) An Arabidopsis nitrogen response gene set (1,254 genes) was created as a union of genes responsive in shoots [Gutierrez et. al., 2008] and roots [Wang et. al., 2004].

B) These 1,254 Arabidopsis genes and the 2,262 maize genes were intersected to produce a highly significant ($p <0.001$) overlapping gene list of 223 N-regulated genes. The regulatory edges in this conserved network were required to have a correlation of >0.7 or <-0.7 (within maize), as described in [Gutierrez et. al., 2008] and [Katari et. al., 2010]. BioMaps analysis in Virtual plant uncovers significant GO terms including photoperiodism (p-val <0.005) and nitrate transport (p-val <0.01) and 15 Arabidopsis TF hubs for focused hypothesis generation.

[00367] Step 4. Identifying network hubs and modules.

Using the VirtualPlant-meets-Cytoscape function, we generated a "hubbiness" table to identify the master regulatory nodes (TFs) in this core N-regulatory network conserved between maize and Arabidopsis. Remarkably, the 5 top TF hubs include TFs (CCA1, GLK1 and bZIP9) previously validated in Arabidopsis as major regulators of an organic-N response network to regulate genes involved in N-assimilation, including ASN1 [Gutierrez et. al., 2008, Wang et. al., 2004].

[00368] Step 5. Maize orthologs of network hubs.

Each of the 15 Arabidopsis TF hubs in the conserved cross-species network was mapped back to the Maize genome to determine the Maize ortholog for these key genes. The mapping was done using the one-to-many BLAST-based homology mapping function in VirtualPlant, which has an e-20 cut off. For each such mapping, we retained only those Maize orthologs that respond to the Nitrogen signal in the original N-treatment dataset from the field. Using these criteria, we obtained a list of 32 Maize TFs (Table 36) whose role in response to Nitrogen is conserved across Maize and Arabidopsis.

[00369] A conserved N-regulatory network module identifies TF hubs in a N-regulatory network: The TF hubs (Table 36) of this N-regulatory network conserved between maize and Arabidopsis (Figs. 22 & 23) provide a focus for network module identification, hypothesis testing and validation. For example, a conserved network module (Fig. 22) shows several TF hubs previously validated to regulate genes involved in N-assimilation in Arabidopsis [Gutierrez et al, 2008]. This network module also reinforces the discovery that nitrogen-regulation of CCA1 imparts nutrient regulation of N-assimilation and the circadian clock in Arabidopsis [Gutierrez et al., 2008] and now in maize. The individual gene members of such modules, and in particular the highly connected hubs, provide targets for investigation. These network modules can guide future breeding efforts to improve NUE by incorporating the higher performance alleles of connected genes into elite hybrid lines, for example. The biological role of these hubs and the genome-wide processes they affect can also be validated in a rapid screening method. We can use our rapid single-cell system called TARGET [Bargmann et al 2013; Para et al., 2014], to identify all of the functional targets of any given network TF hub using isolated maize protoplasts [Sheen 2001].

[00370] Identifying Arabidopsis bZIP1 orthologs in Maize (>40% homology). We showed that bZIP1 is a master TF involved in the N-response in Arabidopsis [Obertello et al 2010][Para et al., 2014]. The bZIP1 TF belongs to the S group of the bZIP family of transcription factors. The bZIP family was compared across Arabidopsis (75 genes), Maize (125 genes) and Rice (89 genes) using phylogenetic methods [Wei et. al., 2012] (Fig. 52). From this analysis we derived the orthologs of Arabidopsis bZIP1 gene in Rice and Maize, as below.

[00371] **The Maize orthologs of Arabidopsis bZIP1** are GRMZM2G093020 (ZmbZIP7) (SEQ ID NO. 69), AC203957.3_FG004 (ZmbZIP22), GRMZM2G361611 (ZmbZIP59*) (SEQ ID NO. 70),GRMZM2G444748 (ZmbZIP64*) (SEQ ID NO. 71), and GRMZM2G092137 (ZmbZIP87) (SEQ ID NO. 72). This set of maize orthologs was further filtered to choose the Maize gene with >40% homology to the Arabidopsis bZIP1 (AT5G49450) (SEQ ID NO. 73), as determined by the global protein alignment tool EMBOSS Needle [http://www.ebi.ac.uk/Tools/psa/emboss_needle/]. Based on this homology calculation, GRMZM2G092137 (ZmbZIP87) is the maize ortholog of Arabidopsis.

[00372] **The Rice orthologs of Arabidopsis bZIP1** are Os02g03960 (OsbZIP14, 41.4% Homology), Os08g26880 (OsbZIP65, 41.5% Homology) and Os09g13570 (OsbZIP71, 44.4% Homology) (See Fig. 52).

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10. EXAMPLE 5

10.1. INTRODUCTION

[00376] Signal propagation through gene regulatory networks (GRNs) enables organisms to rapidly respond to changes in environmental signals. For example, dynamic GRN studies in plants have uncovered genome-wide responses that occur within as little as three minutes following a nitrogen (N) nutrient signal perturbation (Kouk et al., 2010, Genome Biology 11:R123). Yet, many of the underlying rapid and temporal network connections between transcription factors (TFs) and their targets elude detection even in fine-scale time-course studies (Ni *et al.*, 2009, *Gene Dev* 23(11):1351-1363; Chang *et al.*, 2013, *Elife* 2:e00675), as current methods used (e.g. chromatin immunoprecipitation, ChIP) require stable TF-binding in at least one time-point to identify primary targets (Gorski et al, 2011, Nucleic Acids Research 39(22):9536-9548; Hughes et al., 2013, Genetics 195(1):9-36; Marchive et al., 2013, Nature Communications 4). However, recent models suggest that GRNs built solely on TF-binding data are insufficient to recapture transcriptional regulation (Biggin MD, 2011, Dev Cell 21(4):611-626; Walhout AJM, 2011, Genome Biol 12(4); Lickwar et al., 2012, Nature 484(7393):251-255). Compounding this dilemma, TFs have been found to stably bind to only a small percentage (5-32%) of the TF-regulated genes across eukaryotes (Gorski et al, 2011, Nucleic Acids Research 39(22):9536-9548; Hughes et al., 2013, Genetics 195(1):9-36; Marchive et al., 2013, Nature Communications 4; Monke et al., 2012, Nucleic Acids Research 40:8240l; Arenhart et al., 2014, Molecular plant 7(4):709-721; Bolduc et al., 2012, Gene Dev 26(15):1685-1690; Bianco et al., 2014, Cancer research 74(7):2015-2025). Since TF-binding is *required* to define the primary targets in current GRN studies, the large set of TF-regulated, but *not TF-bound* genes must be categorically dismissed as indirect or secondary targets (Gorski et al, 2011, Nucleic Acids Research 39(22):9536-9548; Hughes et al., 2013, Genetics 195(1):9-36; Arenhart et al., 2014, Molecular plant 7(4):709-721; Bolduc et al., 2012, Gene Dev 26(15):1685-1690; Bianco et al., 2014, Cancer research 74(7):2015-2025). Provided herein is an alternative - and more intriguing conclusion - that these typically dismissed targets comprise the "dark matter" of rapid and transient signal transduction that has previously eluded detection across eukaryotes.

[00377] To capture these rapid and dynamic network connections that elude detection by biochemical TF-binding assays, an approach was developed that can identify *primary*

targets based on a functional read out - TF-induced gene regulation – even in the absence of detectable TF-binding. This study focuses on the master TF bZIP1 (BASIC LEUCINE ZIPPER 1), a central integrator of metabolic signaling including sugar (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361-373; Dietrich et al., 2011, The Plant Cell 23:381-395) and N nutrient signals (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939; Obertello et al., 2010, BMC Systems Biology 4:111). To uncover the underlying dynamic GRNs, *both* bZIP1 *and* the N-signal it transduces were temporally perturbed in a cell-based system designed for temporal TF perturbation. This cell-based system named *TARGET* (*T*ransient *A*ssay *R*eporting *G*enome-wide *E*ffects of *T*ranscription factors), which involves inducible TF nuclear localization, is able to identify primary TF targets based solely on TF-induced gene regulation, as shown for a well-studied TF involved in plant hormone signaling - ABI3 (Bargmann et al., 2013, Molecular Plant 6(3):978). In this study, by adapting a micro-ChIP protocol (Dahl et al., 2008, Nucleic Acids Research, 36:e15) to the cell-based *TARGET* system, primary targets were monitored based on *either* TF-induced gene regulation *or* TF-binding quantified in the same cell samples, enabling a direct comparison. The use of isolated cells allowed the capture of rapid and transient regulatory events including the formation of TF-DNA complexes within 1-5 min from the onset of TF translocation to the nucleus. Such a short-lived interaction would likely be missed *in planta*, as effective protein-DNA cross-linking in intact plant tissues requires prolonged (for a minimum of 15 minutes) infiltration under vacuum. Unexpectedly, the primary TF targets that are regulated by, but not stably bound to bZIP1- termed "transient"- were the most biologically relevant to rapid transduction of the N-signal. These transient TF-targets include first-responder genes, induced as early as 3-6 minutes after N-signal perturbation *in planta* (Kouk et al., 2010, Genome Biology 11:R123). This discovery suggests that the current "gold-standard" of GRNs built solely on the intersection of TF-binding and TF-regulation data miss a large and important class of transient TF targets, which are at the heart of dynamic networks. Moreover, the shared features of these transient bZIP1 targets and their role in rapid N-signaling provides genome-wide support for a classic, but largely forgotten model of "hit-and-run" transcription (Schaffner, 1988, Nature 336:427-428). This transient mode-of-

action can enable a master TF to catalytically and rapidly activate a large set of genes in response to a signal.

10.2. MATERIALS AND METHODS

[00378] Plant Materials and DNA Constructs. Wild-type *Arabidopsis thaliana* seeds [Columbia ecotype (Col-0)] were vapor-phase sterilized, vernalized for 3 days, then 1 ml of seed were sown on agar plates containing 2.2 g/l custom made Murashige and Skoog salts without N or sucrose (Sigma-Aldrich), 1% [w/v] sucrose, 0.5 g/l MES hydrate (Sigma-Aldrich), 1 mM KNO3 and 2% [w/v] agar. Plants were grown vertically on plates in an Intellus environment controller (Percival Scientific, Perry, IA), whose light regime was set to 50 μmol $m^{-2}s^{-1}$ and 16h-light/8h-dark at constant temp of 22°C. The bZIP1 (At5g49450) cDNA in pENTR was obtained from the REGIA collection (Paz-Ares et al., 2002 *Comp Funct Genomics* 3(2):102-108) and was then cloned into the destination vector pBeaconRFP_GR used in the protoplast expression system (Bargmann et al., 2009, Plant physiology 149:1231) by LR recombination (Life Technologies). The pBeaconRFP_GR vector is available through the VIB website (http://gateway.psb.ugent.be/).

[00379] Protoplast Preparation, Transfection, Treatments and Cell Sorting. Root protoplasts were prepared, transfected and sorted as previously described (Bargmann et al., 2013, Molecular Plant 6(3):978; Yoo et al., 2007, Nature Protocols 2:1565; Bargmann et al., 2009, Plant physiology 149:1231). Briefly, roots of 10-day-old seedlings were harvested and treated with cell wall digesting enzymes (Cellulase and Macerozyme; Yakult, Japan) for 4 h. Cells were filtered and washed then transfected with 40 μg of pBeaconRFP_GR::bZIP1 plasmid DNA per 1 x 106 cells facilitated by polyethylene glycol treatment (PEG; Fluka 81242) for 25 minutes (Bargmann et al., 2009, Plant physiology 149:1231). Cells were washed drop-wise, concentrated by centrifugation, then resuspended in wash solution W5 (154 mM NaCl, 125mM $CaCl_2$, 5mM KCl, 5mM MES, 1mM Glucose) for overnight incubation at room temperature. Protoplast suspensions were treated sequentially with: 1) a N-signal treatment of either a 20 mM KNO3 and 20 mM NH4NO3 solution (N) or 20 mM KCl (control) for 2 h, 2) either CHX (35 μM in DMSO, Sigma-Aldrich) or solvent alone as mock for 20 min, and then 3) with either

DEX (10 μM in EtOH, Sigma-Aldrich) or solvent alone as mock for 5h at room temperature. Treated protoplast suspensions were FACS sorted as in (13): approximately 10,000 RFP-positive cells were FACS sorted directly into RLT buffer (QIAGEN) for RNA extraction.

[00380] RNA Extraction and Microarray. RNA from 6 replicates (3 treatment replicates and 2 biological replicates) was extracted from protoplasts using an RNeasy Micro Kit with RNase-free DNaseI Set (QIAGEN and quantified on a Bioanalyzer RNA Pico Chip (Agilent Technologies). RNA was then converted into cDNA, amplified and labeled with Ovation Pico WTA System V2 (NuGEN) and Encore Biotin Module (NuGEN), respectively. The labeled cDNA was hybridized, washed and stained on an ATH1-121501 Arabidopsis Genome Array (Affymetrix) using a Hybridization Control Kit (Affymetrix), a GeneChip Hybridization, Wash, and Stain Kit (Affymetrix), a GeneChip Fluidics Station 450 and a GeneChip Scanner (Affymetrix).

[00381] Analysis of microarray data with CHX treatment. Microarray intensities were normalized using the GCRMA (http://www.bioconductor.org/packages/2.11/bioc/html/gcrma.html) package. Differentially expressed genes were then determined by a 3-way ANOVA with N, DEX and biological replicates as factors. The raw p-value from ANOVA was adjusted by False Discovery Rate (FDR) to control for multiple testing (Benjamini et al., 2005, Genetics 171:783). Genes significantly regulated by the N-signal and/or DEX-induced bZIP1 nuclear localization were then selected with a FDR cutoff of 5%. Genes significantly regulated by the interaction of the N-signal and bZIP1 (N-signal x bZIP1) were selected with a p-val (ANOVA) cutoff of 0.01. Only unambiguous probes were included. Heat maps were created using Multiple Experiment Viewer software (TIGR; http://www.tm4.org/mev/). The significance of overlaps of gene sets were calculated using the GeneSect (R)script (Katari et al., 2010, Plant physiology 152:500) using the microarray as background. Hypergeometric distribution was used in one case (specified in the manuscript) to evaluate the enrichment of gene sets, when a specific background - N-responsive genes identified in different root cell types (Gifford et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:803-808)– was needed.

[00382] Filtering bZIP1 targets for the effects of protoplasting, and response to CHX or DEX. In this step, genes were filtered out whose expression states responded to protoplasting, or to treatments of DEX or CHX that were not related to the bZIP1 mediated regulation, in the following three steps: Filter 1: DEX-response filter: Genes responding to DEX independent of TF. Genes significantly induced/repressed by DEX-treatment in protoplasts transfected with the empty pBeanconRFP_GR plasmid (ANOVA analysis; FDR<0.05), were excluded from analysis (1.6% genes filtered). Filter 2: Protoplast-response filter: Genes induced by protoplasting. Genes that are induced by root protoplasting (Birnbaum K, *et al.*, 2003, *Science* 302(5652):1956-1960) were removed from the list of bZIP1 targets (12.3% genes filtered). Filter 3: DEX x CHX interaction filter. Genes whose DEX-regulation is modified by CHX. This filter removes genes from the analysis in cases where the effects of DEX-induced TF nuclear import on gene regulation are affected by CHX treatment. To do this, a 3-way ANOVA was performed (Factors Nitrogen, DEX, and CHX) and bZIP1 primary targets were identified whose gene expression regulation by the DEX-induced nuclear import of bZIP1 is different between +CHX and –CHX conditions (FDR cutoff of interaction term CHX*DEX<0.05). This eliminated genes that are regulated by bZIP1 in the presence of CHX, but not in the absence of CHX. This gene set may contain bZIP1 targets under a self-control negative feedback loop, and bZIP1 targets for which the half-lives of the transcripts affected by CHX. While the first case is potentially interesting, the second case represents the CHX artifact to be removed. Since it is difficult to differentiate between the two outcomes, these CHX-sensitive DEX-responsive genes dependent on bZIP1 were eliminated from the list of bZIP1 target genes (17.4% genes filtered), thus increasing precision over recall.

[00383] Micro-Chromatin Immunoprecipitation. For each combination of protoplast treatments (see above), an unsorted suspension of protoplasts containing approximately 5,000-10,000 GR::bZIP1 transfected cells was fixed for ChIP analysis, using an adapted version of the micro-ChIP protocol by Dahl et al (Dahl et al., 2008, Nucleic Acids Research 36:e15). The advantage in a ChIP analysis from protoplasts is that short-lived interactions would likely be missed in *planta* assays, as effective protein-DNA cross-linking in intact plant tissues requires prolonged (for a minimum of 15

minutes) infiltration under vacuum (Gendrel et al., 2005, Nat Methods 2(3):213- 218). Cells were incubated with gentle rotation in 1% formaldehyde in W5 buffer for 7 minutes, then washed with W5 buffer and frozen in liquid N2. μChIP was performed according to Dahl et al. (2008, Nucleic Acids Research 36:e15) with a few modifications below. The GR::bZIP1-DNA complexes were captured using anti-GR antibody [GR (P-20) (Santa Cruz biotech) bound to Protein-A beads (Life Biotechnologies)]. A washing step with LiCl buffer [0.25M LiCl, 1% Na deoxycholate, 10mM Tris–HCl (pH8), 1% NP-40] was added in between the wash with RIPA buffer and TE (Dahl et al., 2008, Nucleic Acids Research 36:e15). After elution from the beads, the ChIP material and the Input DNA were cleaned and concentrated using QIAGEN MiniElute Kit (QIAGEN). The protoplast suspension used for micro-ChIP was not FACS sorted in order to maintain a comparable incubation time between the samples that were used for microarray analyses and for micro ChIP. Importantly, while FACS sorting of transformed cells is required for microarray studies, it was not required to identify DNA targets using ChIP-seq.

[00384] ChIP-Seq library preparation. The ChIP DNA and Input DNA were prepared for Illumina HiSeq sequencing platform following the Illumina ChIP-Seq protocol (Illumina, San Diego, CA) with modifications. Barcoded adaptors and enrichment primers (BiOO Scientific, TX, USA) were used according to the manufacturer's protocol. The concentration and the quality of the libraries was determined by the Qubit Fluorometric DNA Assay (InVitrogen, NY, USA), DNA 12000 Bioanalzyer chip (Agilent, CA, USA) and KAPA Quant Library Kit for Illumina (KAPA Biosystems, MA, USA). A total of 8 libraries were then pooled in equimolar amounts and sequenced on two lanes of an Illumina HiSeq platform for 100 cycles in paired-end configuration (Cold Spring Harbor Lab, NY).

[00385] ChIP-Seq Analysis. Reads obtained from the four treatments (with DEX and N in the presence of CHX) were filtered and aligned to the *Arabidopsis thaliana* genome (TAIR10) and clonal reads were removed. The ChIP alignment data was compared to its partner Input DNA and peaks were called using the QuEST package (20) with a ChIP seeding enrichment ≥ 3, and extension and background enrichments ≥ 2. These regions were overlapped with the genome annotation to identify genes within 500bp downstream

of the peak. The gene lists from multiple treatments were largely overlapping sets, and hence were pooled to generate a single list of genes that show significant binding of bZIP1. Due to technical issues, the experimental design used for ChIP-Seq precludes the observation of significant differences between the genes bound by bZIP1 under the different treatment conditions. This is because the samples fixed for ChIP included a variable number of transfected cells that were not sorted by FACS.

[00386] The ChIP-seq studies were performed using a micro-ChIP protocol on ~ 10,000 cells, which result in a low DNA input, compared to standard ChIP studies. It has been shown that peak discovery from ChIP data becomes more challenging as the number of cells goes down (Fig. 3 in Gilfillan et al., 2012, Bmc Genomics, 13). Therefore, ChIP libraries made from these very low input-DNA samples have a higher level of background noise, necessitating lower peak calling thresholds. However, even with this caveat for micro-ChIP studies, we were able to recover 850 targets including several previously validated bZIP1 targets (ASN1 and ProDH) (Dietrich et al., 2011, The Plant Cell 23:381-395).

[00387] **Time-series ChIP-seq.** The ChIP time-series samples were pre-treated with a N-signal treatment of 20 mM KNO3 and 20 mM NH4NO3 solution (N) for 2 h, followed by CHX (35 μM in DMSO, Sigma-Aldrich) for 20 min. Protoplasts were then treated with DEX (10 μM in Ethanol, Sigma-Aldrich) and samples were harvested at 1, 5, 30 and 60 min after the start of the DEX-induced bZIP1 nuclear localization.

[00388] ***Cis*-element Motif Analysis.** 1 Kb regions upstream of the TSS (Transcription Start Site) for target genes were extracted based on TAIR10 annotation and submitted to the *Elefinder* program (all promoters from the genome as background) (Li et al., 2011, Plant physiology 156:2124-2140) or MEME (against a randomized dinucleotide background) (Bailey et al., 2009, Nucleic Acids Research 37:W202-208) to determine over-representation of known cis-element binding sites (different parameters used in specific cases were notified in the paper if applicable). The E-value of significance for each motif was used to cluster the occurrence of motifs in the various subsets using the HCL algorithm in MeV (Saeed et al., 2006, Methods in Enzymology 411:134-193). Motifs that show a higher specificity to a particular category or a sub-group were identified with the PTM algorithm in MeV. *De novo* motif identification was

performed on 1Kb upstream sequence of the genes regulated by bZIP1 from microarray and ChIP-Seq data separately using the MEME suite (Bailey et al., 2009, Nucleic Acids Research 37:W202-208).

[00389] **Accession numbers**. The raw data from all Microarray assays, were submitted to NCBI GEO and is available under the accession number GSE54049. The raw sequencing data from ChIP-Seq assays is available from NCBI SRA under the accession SRX425878.

10.3. RESULTS

[00390] **Temporal perturbation of *both* bZIP1 *and* the N-signal it transduces.** To identify how bZIP1 mediates the rapid propagation of a N-signal in a GRN, *both* bZIP1 *and* the N-signal it transduces were temporally perturbed in the cell-based *TARGET* system (Fig. 24 A&B) (Bargmann et al., 2013, Molecular Plant 6(3):978). bZIP1, which is ubiquitously expressed across all root cell-types (Birnbaum K, *et al.,* 2003, *Science* 302(5652):1956-1960), was transiently overexpressed in root protoplasts as a GR::bZIP1 fusion protein, enabling temporal induction of nuclear localization by dexamethasone (DEX) (Fig. 24A) (Bargmann et al., 2013, Molecular Plant 6(3):978). Transfected root cells expressing the GR::bZIP1 fusion protein were sequentially treated with: 1) inorganic nitrogen (+/-N), 2) cycloheximide (+/- CHX) and 3) dexamethasone (+/-DEX) (Fig. 24C). The N-treatment can induce post-translational modifications of bZIP1 (Baena-Gonzalez et al., 2007, Nature 448:938-942), or influence bZIP1 partners by transcriptional or post-transcriptional mechanisms (Fig. 24B). DEX-treatment induces TF nuclear import (Fig. 24A) (Bargmann et al., 2013, Molecular Plant 6(3):978). Further, genes regulated by DEX-induced TF import are deemed primary targets, as a CHX pre-treatment blocks translation of downstream regulators, as previously shown in the *TARGET* system (Bargmann et al., 2013, Molecular Plant 6(3):978) and *in planta* (Eklund et al., 2010, Plant Cell 22:349-363) (Fig. 24A). Importantly, to eliminate any side effects caused by CHX pre-treatment, only genes whose transcriptome response to DEX-induced TF nuclear import is the same in either the presence or absence of CHX were considered. Such bZIP1 primary targets identified based on gene regulation following DEX-induced TF import, were identified using Affymetrix ATH1 microarrays.

In parallel, primary targets identified by TF-binding were identified in a micro-ChIP-Seq assay (Dahl et al., 2008, Nucleic Acids Research 36:e15) using anti-GR antibodies. Both transcriptome and ChIP-seq data were obtained 5 hours after the DEX-induced nuclear import of bZIP1, from the same cell samples, enabling a direct comparison (Fig. 24 C&D). Regarding the N-signal, 328 N-responsive genes were identified in the cell-based experiments (Fig. 25; Table 12). These N-responsive genes significantly overlap with the N-responsive genes identified in whole seedlings exposed to a similar N-treatment (NH_4NO_3) (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939-4944), and from roots treated with nitrate (Wang et al., 2003, Plant Physiol. 132(2):556-567; Wang et al., 2004, Plant physiology 136(1):2512-2522), including a dynamic study (Krouk et al., 2010, Genome Biology 11:R123) (121/328, *p-val*<0.001) (Fig. 26; Table 13). The N-responsive genes in the cell-based experiments are enriched with genes that respond to N-treatment across all root cell-types *in planta* (*p-val* = 8.8E-13, hypergeometric distribution) (Gifford et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:803-808).

Table 12. N-responsive genes (FDR<0.05) in root protoplasts used in the TARGET system.

A. Genes that are up-regulated by N-treatment (FDR<0.05)		
Locus	**Symbol**	**FullName**
AT3G17790	ATACP5	
AT4G39260	ATGRP8	GLYCINE-RICH PROTEIN 8
AT3G20770	AtEIN3	
AT2G38530	cdf3	cell growth defect factor-3
AT3G47420	AtG3Pp1	Glycerol-3-phosphate permease 1
AT3G61860	At-RS31	arginine/serine-rich splicing factor 31
AT4G13250	NYC1	NON-YELLOW COLORING 1
AT4G24620	PGI	
AT5G19430		
AT4G11560		
AT5G24870		
AT1G20110		
AT2G01850	ATXTH27	
AT4G14930		
AT1G19730	ATH4	thioredoxin H-type 4
AT3G60750		
AT5G01340	AtmSFC1	
AT5G04540	AtMTM2	
AT3G56150	ATEIF3C-1	
AT5G48180	AtNSP5	
AT4G00940		
AT5G53460	GLT1	NADH-dependent glutamate synthase 1
AT1G25550		
AT4G36760	APP1	aminopeptidase P1

AT1G23820	SPDS1	spermidine synthase 1
AT3G10740	ARAF	ALPHA-L-ARABINOFURANOSIDASE
AT4G32070	Phox4	Phox4
AT2G21290		
AT5G07890		
AT3G62140		
AT3G19030		
AT5G11470		
AT4G17340	DELTA-TIP2	
AT1G04400	AT-PHH1	
AT3G49620	DIN11	DARK INDUCIBLE 11
AT2G26150	ATHSFA2	heat shock transcription factor A2
AT3G58610		
AT1G64190		
AT1G74310	ATHSP101	heat shock protein 11
AT2G26980	CIPK3	CBL-interacting protein kinase 3
AT4G12400	Hop3	Hop3
AT1G68720	ATTADA	ARABIDOPSIS THALIANA TRNA ADENOSINE DEAMINASE A
AT1G27300		
AT2G18550	ATHB21	homeobox protein 21
AT1G78050	PGM	phosphoglycerate/bisphosphoglycerate mutase
AT3G19290	ABF4	ABRE binding factor 4
AT4G27910	ATX4	
AT2G18050	HIS1-3	histone H1-3
AT5G12860	DiT1	dicarboxylate transporter 1
AT5G41670		
AT3G49630		
AT4G09620		
AT1G54050		
AT2G03270		
AT5G48570	ATFKBP65	
AT4G24000	ATCSLG2	ARABIDOPSIS THALIANA CELLULOSE SYNTHASE LIKE G2
AT1G65540	AtLETM2	
AT4G23440		
AT5G12030	AT-HSP17.6A	heat shock protein 17.6A
AT5G62900		
AT1G53540		
AT1G37130	ATNR2	ARABIDOPSIS NITRATE REDUCTASE 2
AT3G16050	A37	
AT1G58360	AAP1	amino acid permease 1
AT3G52340	ATSPP2	SUCROSE-PHOSPHATASE 2
AT2G16060	AHB1	hemoglobin 1
AT5G49470		
AT1G58080	ATATP-PRT1	ATP phosphoribosyl transferase 1
AT1G13300	HRS1	HYPERSENSITIVITY TO LOW PI-ELICITED PRIMARY ROOT SHORTENING 1
AT5G20790		
AT5G13180	ANAC083	NAC domain containing protein 83
AT5G49000		
AT5G63680		
AT1G06570	HPD	4-hydroxyphenylpyruvate dioxygenase
AT1G55510	BCDH BETA1	branched-chain alpha-keto acid decarboxylase E1 beta subunit
AT3G52490		
AT3G60690		

AT2G38400	AGT3	alanine:glyoxylate aminotransferase 3
AT4G23100	ATECS1	
AT1G09460		
AT4G38470	STY46	serine/threonine/tyrosine kinase 46
AT2G41190		
AT5G07010	ATST2A	ARABIDOPSIS THALIANA SULFOTRANSFERASE 2A
AT1G23190	PGM3	phosphoglucomutase 3
AT5G04630	CYP77A9	cytochrome P45, family 77, subfamily A, polypeptide 9
AT3G48360	ATBT2	
AT4G37540	LBD39	LOB domain-containing protein 39
AT1G49500		
AT1G80160	GLYI7	glyoxylase I 7
AT5G47560	ATSDAT	
AT1G53580	ETHE1	ETHE1-LIKE
AT4G34030	MCCB	3-methylcrotonyl-CoA carboxylase
AT3G49940	LBD38	LOB domain-containing protein 38
AT5G10210		
AT2G33150	KAT2	3-KETOACYL-COA THIOLASE 2
AT1G03790	SOM	SOMNUS
AT4G31240		
AT1G04410	c-NAD-MDH1	cytosolic-NAD-dependent malate dehydrogenase 1
AT3G13750	BGAL1	beta galactosidase 1
AT1G23870	ATTPS9	trehalose-phosphatase/synthase 9
AT1G62660		
AT5G54080	AtHGO	
AT4G09760		
AT4G38340		
AT5G52300	LTI65	LOW-TEMPERATURE-INDUCED 65
AT1G08190	ATVAM2	
AT1G14340		
AT2G45960	ATHH2	
AT1G23800	ALDH2B	aldehyde dehydrogenase 2B
AT3G01420	ALPHA-DOX1	alpha-dioxygenase 1
AT3G16240	AQP1	
AT5G04250		
AT4G33080		
AT2G42560		
AT5G13110	G6PD2	glucose-6-phosphate dehydrogenase 2
AT1G16170		
AT5G20885		
AT5G66400	ATDI8	ARABIDOPSIS THALIANA DROUGHT-INDUCED 8
AT3G45060	ATNRT2.6	ARABIDOPSIS THALIANA HIGH AFFINITY NITRATE TRANSPORTER 2.6
AT2G42750		
AT3G45300	ATIVD	
AT5G40450		
AT2G38800		
AT1G52320		
AT2G23030	SNRK2-9	SUCROSE NONFERMENTING 1-RELATED PROTEIN KINASE 2-9
AT4G35090	CAT2	catalase 2
AT3G42860		
AT3G53540	TRM19	TON1 Recruiting Motif 19
AT4G34000	ABF3	abscisic acid responsive elements-binding factor 3
AT3G27820	ATMDAR4	MONODEHYDROASCORBATE REDUCTASE 4

AT5G48250	BBX8	B-box domain protein 8
AT5G50850	MAB1	MACCI-BOU
AT1G30510	ATRFNR2	root FNR 2
AT1G63940	MDAR6	monodehydroascorbate reductase 6
AT3G26100		
AT5G65210	TGA1	TGACG sequence-specific binding protein 1
AT1G73920		
AT1G60710	ATB2	
AT5G15450	APG6	ALBINO AND PALE GREEN 6
AT3G48990	AAE3	ACYL-ACTIVATING ENZYME 3
AT2G15620	ATHNIR	ARABIDOPSIS THALIANA NITRITE REDUCTASE
AT5G39590		
AT1G68670		
AT5G65660		
AT3G61430	ATPIP1	ARABIDOPSIS THALIANA PLASMA MEMBRANE INTRINSIC PROTEIN 1
AT4G12340		
AT5G67420	ASL39	ASYMMETRIC LEAVES2-LIKE 39

B. genes that are down-regulated by N-treatment (FDR<0.05)

Locus	**Symbol**	**FullName**
AT1G56060		
AT1G53430		
AT3G21230	4CL5	4-coumarate:CoA ligase 5
AT4G02330	AtPME41	
AT4G01850	AtSAM2	
AT1G52200		
AT2G23270		
AT5G59480		
AT2G17220	Kin3	kinase 3
AT3G10640	VPS60.1	
AT5G58120		
AT5G61210	ATSNAP33	
AT1G10160		
AT3G15520		
AT4G19960	ATKUP9	
AT4G28940		
AT4G30560	ATCNGC9	cyclic nucleotide gated channel 9
AT2G38120	AtAUX1	
AT3G59900	ARGOS	AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE
AT4G28850	ATXTH26	
AT4G39720		
AT1G09920		
AT4G24580	REN1	ROP1 ENHANCER 1
AT4G39940	AKN2	APS-kinase 2
AT1G54690	G-H2AX	GAMMA H2AX
AT3G10940	LSF2	LIKE SEX4 2
AT5G01490	ATCAX4	
AT1G73530		
AT4G24350		
AT3G55630	ATDFD	DHFS-FPGS homolog D
AT5G43520		
AT1G74870		
AT2G35990	LOG2	LONELY GUY 2

AT1G32350	AOX1D	alternative oxidase 1D
AT3G56400	ATWRKY70	ARABIDOPSIS THALIANA WRKY DNA-BINDING PROTEIN 7
AT2G47140	AtSDR5	
AT4G26470		
AT1G73066		
AT2G43000	ANAC042	NAC domain containing protein 42
AT5G06720	ATPA2	peroxidase 2
AT1G09930	ATOPT2	oligopeptide transporter 2
AT1G09520		
AT4G25030		
AT1G18860	ATWRKY61	WRKY DNA-BINDING PROTEIN 61
AT2G39530		
AT3G02850	SKOR	STELAR K+ outward rectifier
AT5G24540	BGLU31	beta glucosidase 31
AT5G39680	EMB2744	EMBRYO DEFECTIVE 2744
AT1G16380	ATCHX1	
AT4G11170		
AT3G07390	AIR12	Auxin-Induced in Root cultures 12
AT5G44060		
AT1G35200		
AT1G72070		
AT2G25735		
AT2G32020		
AT3G10630		
AT1G53920	GLIP5	GDSL-motif lipase 5
AT1G18570	AtMYB51	myb domain protein 51
AT2G19570	AT-CDA1	
AT3G08750		
AT1G30370	DLAH	DAD1-like acylhydrolase
AT3G08730	ATPK1	ARABIDOPSIS THALIANA PROTEIN-SERINE KINASE 1
AT1G14540	PER4	peroxidase 4
AT5G15130	ATWRKY72	ARABIDOPSIS THALIANA WRKY DNA-BINDING PROTEIN 72
AT1G14550		
AT4G22720		
AT5G60250		
AT1G73510		
AT4G14368		
AT2G33710		
AT4G37900		
AT1G33590		
AT4G08770	Prx37	peroxidase 37
AT3G50790		
AT4G23570	SGT1A	
AT1G18390		
AT5G26920	CBP60G	Cam-binding protein 6-like G
AT1G05575		
AT3G01500	ATBCA1	BETA CARBONIC ANHYDRASE 1
AT1G68765	IDA	INFLORESCENCE DEFICIENT IN ABSCISSION
AT5G64650		
AT3G55090	ABCG16	ATP-binding cassette G16
AT4G17785	MYB39	myb domain protein 39
AT1G02900	ATRALF1	RAPID ALKALINIZATION FACTOR 1
AT3G57080	NRPE5	
AT5G05220		

AT3G22900	NRPD7	
AT1G03990		
AT4G04490	CRK36	cysteine-rich RLK (RECEPTOR-like protein kinase) 36
AT5G14740	BETA CA2	BETA CARBONIC ANHYDRASE 2
AT1G76550		
AT2G29330	TRI	tropinone reductase
AT5G45280		
AT5G64860	DPE1	disproportionating enzyme
AT1G54890		
AT4G18950		
AT1G02360		
AT1G10330		
AT1G76570		
AT2G44790	UCC2	uclacyanin 2
AT2G22870	EMB2001	embryo defective 21
AT2G42880	ATMPK20	MAP kinase 2
AT1G51680	4CL.1	4-COUMARATE:COA LIGASE 1
AT1G75960		
AT1G05670		
AT2G18190		
AT1G80240	DGR1	DUF642 L-GalL responsive gene 1
AT5G11910		
AT5G16770	AtMYB9	myb domain protein 9
AT1G17300		
AT5G40770	ATPHB3	prohibitin 3
AT1G22890		
AT5G65930	KCBP	KINESIN-LIKE CALMODULIN-BINDING PROTEIN
AT1G72280	AERO1	endoplasmic reticulum oxidoreductins 1
AT5G03620		
AT2G18180		
AT1G71400	AtRLP12	receptor like protein 12
AT3G29250	AtSDR4	
AT3G63220		
AT1G80850		
AT5G22270		
AT4G17486		
AT2G33820	ATMBAC1	
AT4G23690	AtDIR6	Arabidopsis thaliana dirigent protein 6
AT4G09650	ATPD	ATP synthase delta-subunit gene
AT1G03920		
AT2G43610		
AT3G22800		
AT1G13210	ACA.1	autoinhibited Ca2+/ATPase II
AT1G30750		
AT1G50590		
AT5G63040		
AT5G07110	PRA1.B6	prenylated RAB acceptor 1.B6
AT5G63780	SHA1	shoot apical meristem arrest 1
AT5G66390		
AT3G01280	ATVDAC1	ARABIDOPSIS THALIANA VOLTAGE DEPENDENT ANION CHANNEL 1
AT2G34610		
AT2G44380		
AT3G55150	ATEXO70H1	exocyst subunit exo7 family protein H1

AT3G49130		
AT5G41610	ATCHX18	ARABIDOPSIS THALIANA CATION/H+ EXCHANGER 18
AT1G10090		
AT1G64160	AtDIR5	
AT3G48650		
AT5G61440	ACHT5	atypical CYS HIS rich thioredoxin 5
AT4G37240		
AT5G64100		
AT3G46280		
AT5G24030	SLAH3	SLAC1 homologue 3
AT1G13280	AOC4	allene oxide cyclase 4
AT2G10640		
AT1G02450	NIMIN-1	
AT3G22920		
AT1G65840	ATPAO4	polyamine oxidase 4
AT3G30396		
AT3G05210	ERCC1	
AT5G58630	TRM31	TON1 Recruiting Motif 31
AT2G44370		
AT4G20870	ATFAH2	ARABIDOPSIS FATTY ACID HYDROXYLASE 2
AT5G02780	GSTL1	glutathione transferase lambda 1
AT1G16150	WAKL4	wall associated kinase-like 4
AT3G01175		
AT5G64120		
AT2G31380	BBX25	B-box domain protein 25
AT4G33420		
AT1G56150		
AT2G43620		
AT1G32930		
AT3G23230	AtERF98	
AT3G22890	APS1	ATP sulfurylase 1
AT1G68850		
AT3G23240	ATERF1	ETHYLENE RESPONSE FACTOR 1
AT1G71530		
AT4G26690	GDPDL3	Glycerophosphodiester phosphodiesterase (GDPD) like 3
AT5G17990	pat1	PHOSPHORIBOSYLANTHRANILATE TRANSFERASE 1
AT2G04500		
AT5G14470		
AT2G02180	TOM3	tobamovirus multiplication protein 3
AT5G48430		
AT5G67450	AZF1	zinc-finger protein 1

Table 13: Overlap of N-responsive genes in protoplasts vs. N-response studies performed in planta

At4g24620	PGI, PGI1, phosphoglucose isomerase 1
At3g49940	LBD38, LOB domain-containing protein 38
At1g52200	PLAC8 family protein
At3g61430	ATPIP1, PIP1, PIP1;1, PIP1A, plasma membrane intrinsic protein 1A
At3g58610	ketol-acid reductoisomerase
At3g21230	4CL5, 4-coumarate:CoA ligase 5

At1g73920	alpha/beta-Hydrolases superfamily protein
At5g15130	ATWRKY72, WRKY72, WRKY DNA-binding protein 72
At5g48180	NSP5, nitrile specifier protein 5
At4g35090	CAT2, catalase 2
At5g39590	TLD-domain containing nucleolar protein
At1g23870	ATTPS9, TPS9, TPS9, trehalose-phosphatase/synthase 9
At4g09620	Mitochondrial transcription termination factor family protein
At2g19570	AT-CDA1, CDA1, DESZ, cytidine deaminase 1
At5g43520	Cysteine/Histidine-rich C1 domain family protein
At1g05575	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: anaerobic respiration; LOCATED IN: endomembrane system; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G31945.1); Has 63 Blast hits to 63 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At1g37130	ATNR2, B29, CHL3, NIA2, NIA2-1, NR, NR2, nitrate reductase 2
At5g22270	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11600.1); Has 136 Blast hits to 136 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 136; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At5g04540	Myotubularin-like phosphatases II superfamily
At1g56150	SAUR-like auxin-responsive protein family
At5g67420	ASL39, LBD37, LOB domain-containing protein 37
At5g64100	Peroxidase superfamily protein
At3g19030	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pyridoxine biosynthetic process, homoserine biosynthetic process; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49500.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At5g20885	RING/U-box superfamily protein
At1g06570	HPD, PDS1, phytoene desaturation 1
At5g24870	RING/U-box superfamily protein
At5g04250	Cysteine proteinases superfamily protein
At2g01850	ATXTH27, EXGT-A3, XTH27, endoxyloglucan transferase A3
At3g07390	AIR12, auxin-responsive family protein
At1g02900	ATRALF1, RALF1, RALFL1, rapid alkalinization factor 1
At5g01340	Mitochondrial substrate carrier family protein
At1g60710	ATB2, NAD(P)-linked oxidoreductase superfamily protein
At4g00940	Dof-type zinc finger DNA-binding family protein
At2g02180	TOM3, tobamovirus multiplication protein 3
At1g68720	ATTADA, TADA, tRNA arginine adenosine deaminase
At4g39940	AKN2, APK2, APS-kinase 2
At3g48360	ATBT2, BT2, BTB and TAZ domain protein 2
At3g47420	ATPS3, PS3, phosphate starvation-induced gene 3
At5g12860	DiT1, dicarboxylate transporter 1
At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).
At4g19960	ATKUP9, HAK9, KT9, KUP9, K+ uptake permease 9

At1g13280	AOC4, allene oxide cyclase 4
At3g60750	Transketolase
At2g15620	ATHNIR, NIR, NIR1, nitrite reductase 1
At1g65840	ATPAO4, PAO4, polyamine oxidase 4
At5g24030	SLAH3, SLAC1 homologue 3
At2g16060	AHB1, ARATH GLB1, ATGLB1, GLB1, HB1, NSHB1, hemoglobin 1
At3g55150	ATEXO70H1, EXO70H1, exocyst subunit exo70 family protein H1
At2g23030	SNRK2-9, SNRK2.9, SNF1-related protein kinase 2.9
At1g58360	AAP1, NAT2, amino acid permease 1
At4g38340	Plant regulator RWP-RK family protein
At2g32020	Acyl-CoA N-acyltransferases (NAT) superfamily protein
At5g48570	ATFKBP65, FKBP65, ROF2, FKBP-type peptidyl-prolyl cis-trans isomerase family protein
At1g62660	Glycosyl hydrolases family 32 protein
At2g34610	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G30190.1); Has 342 Blast hits to 279 proteins in 74 species: Archae - 0; Bacteria - 7; Metazoa - 76; Fungi - 18; Plants - 51; Viruses - 0; Other Eukaryotes - 190 (source: NCBI BLink).
At1g49500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G19030.1); Has 24 Blast hits to 24 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At1g54690	G-H2AX, GAMMA-H2AX, H2AXB, HTA3, gamma histone variant H2AX
At2g33710	Integrase-type DNA-binding superfamily protein
At3g22890	APS1, ATP sulfurylase 1
At3g23240	ATERF1, ERF1, ethylene response factor 1
At1g54050	HSP20-like chaperones superfamily protein
At4g37540	LBD39, LOB domain-containing protein 39
At1g58080	ATATP-PRT1, ATP-PRT1, HISN1A, ATP phosphoribosyl transferase 1
At5g50850	MAB1, Transketolase family protein
At5g12030	AT-HSP17.6A, HSP17.6, HSP17.6A, heat shock protein 17.6A
At1g13300	HRS1, myb-like transcription factor family protein
At1g14340	RNA-binding (RRM/RBD/RNP motifs) family protein
At3g60690	SAUR-like auxin-responsive protein family
At2g43620	Chitinase family protein
At5g63780	SHA1, RING/FYVE/PHD zinc finger superfamily protein
At5g59480	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
At1g09460	Carbohydrate-binding X8 domain superfamily protein
At5g13180	ANAC083, NAC083, VNI2, NAC domain containing protein 83
At5g62900	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G50090.1); Has 157 Blast hits to 157 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 157; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At4g34000	ABF3, DPBF5, abscisic acid responsive elements-binding factor 3
At2g39530	Uncharacterised protein family (UPF0497)
At2g17220	Protein kinase superfamily protein
At1g64190	6-phosphogluconate dehydrogenase family protein
At1g14540	Peroxidase superfamily protein
At1g33590	Leucine-rich repeat (LRR) family protein

At1g78050	PGM, phosphoglycerate/bisphosphoglycerate mutase
At1g63940	MDAR6, monodehydroascorbate reductase 6
At3g59900	ARGOS, auxin-regulated gene involved in organ size
At4g37900	Protein of unknown function (duplicated DUF1399)
At2g26980	CIPK3, SnRK3.17, CBL-interacting protein kinase 3
At1g50590	RmlC-like cupins superfamily protein
At5g26920	CBP60G, Cam-binding protein 60-like G
At4g34030	MCCB, 3-methylcrotonyl-CoA carboxylase
At5g64120	Peroxidase superfamily protein
At5g65210	TGA1, bZIP transcription factor family protein
At1g18390	Protein kinase superfamily protein
At1g14550	Peroxidase superfamily protein
At5g13110	G6PD2, glucose-6-phosphate dehydrogenase 2
At2g42880	ATMPK20, MPK20, MAP kinase 20
At3g10740	ARAF, ARAF1, ASD1, ATASD1, alpha-L-arabinofuranosidase 1
At2g44380	Cysteine/Histidine-rich C1 domain family protein
At5g53460	GLT1, NADH-dependent glutamate synthase 1
At5g16770	AtMYB9, MYB9, myb domain protein 9
At1g23190	Phosphoglucomutase/phosphomannomutase family protein
At3g48990	AMP-dependent synthetase and ligase family protein
At5g47560	ATSDAT, ATTDT, TDT, tonoplast dicarboxylate transporter
At1g76550	Phosphofructokinase family protein
At5g07010	ATST2A, ST2A, sulfotransferase 2A
At1g30510	ATRFNR2, RFNR2, root FNR 2
At1g30370	alpha/beta-Hydrolases superfamily protein
At1g68670	myb-like transcription factor family protein
At5g45280	Pectinacetylesterase family protein
At4g38470	ACT-like protein tyrosine kinase family protein
At1g16170	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G79660.1); Has 55 Blast hits to 55 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At5g41670	6-phosphogluconate dehydrogenase family protein
At2g43000	anac042, NAC042, NAC domain containing protein 42
At4g39720	VQ motif-containing protein
At1g51680	4CL.1, 4CL1, AT4CL1, 4-coumarate:CoA ligase 1
At3g55090	ABC-2 type transporter family protein
At5g15450	APG6, CLPB-P, CLPB3, casein lytic proteinase B3
At1g53920	GLIP5, GDSL-motif lipase 5
At5g07890	myosin heavy chain-related
At3g29250	NAD(P)-binding Rossmann-fold superfamily protein
At1g25550	myb-like transcription factor family protein
At5g48430	Eukaryotic asparty1 protease family protein

At4g37240	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G23690.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).

[00391] ***Primary targets of*** **bZIP1 can be identified by** ***either*** **TF-regulation** ***or*** **TF-binding.** bZIP1 primary targets were first identified based *solely* on TF-induced gene regulation. A total of 901 genes were identified as primary bZIP1 targets based on significant regulation in response to DEX-induced TF nuclear import, compared to minus DEX controls (ANOVA analysis; FDR adjusted p-value < 0.05) (Fig. 27A; Fig. 24D; Tables 14-16). These DEX-responsive genes are deemed to be *primary* targets of bZIP1, as pre-treatment of the samples with CHX (prior to DEX-induced TF nuclear import) blocks translation of mRNAs of primary bZIP1 targets, thus preventing changes in the mRNA levels of secondary targets in the GRN. To control for the potential side effects of CHX, this list of bZIP1 primary targets excluded genes whose DEX-induced mRNA response was altered by CHX treatment. With regard to the N-signal, 28 out of the 901 bZIP1 primary targets were regulated in response to a significant N-treatment x TF interaction (*p-val* < 0.01) (Fig. 28; Table 17). This could reflect a post-translational modification of bZIP1 by the N-signal, or the N-induced modification of bZIP1 partners at the transcriptional and/or post-translational level (Fig. 24B).

[00392] bZIP1 primary targets were next identified based *solely* on TF-DNA binding. Genes bound by bZIP1 were identified as genic regions enriched in the ChIP DNA, compared to the background (input DNA), using the QuEST peak-calling algorithm (Fig. 27C) (Valouev et al., 2008, Nature Methods 5:829-834). This identified 850 genes with significant bZIP1 binding (FDR <0.05) (Fig. 24D; Table 18), which included validated bZIP1 targets identified by single gene studies (e.g. ASN1 and ProDH) (Dietrich et al., 2011, The Plant Cell 23:381-395). It is noted that ChIP-seq can potentially detect genes directly bound to bZIP1, as well as genes indirectly bound by bZIP1 through bridging interactors. Thus, to independently assess whether *primary* targets identified either by TF-binding or TF-regulation were due to *direct* binding of bZIP1, *cis*-element analysis was performed (Fig. 27 B&D). The bZIP1-bound genes and the bZIP1 regulated genes,

are each highly significantly enriched in known bZIP1 binding sites, based on analysis of *de novo cis*-motifs using MEME (Bailey et al., 2009, Nucleic Acids Research 37:W202-208) or known *cis*-motif enrichment using Elefinder (Li et al., 2011, Plant physiology 156:2124-2140) (Fig. 27 B&D).

Table 14. Genes identified to be ZIP1 targets based on ANOVA analysis of transcriptome and/or by ChIP-Seq analysis.

Microarray Analysis		
Category of Genes		Number of Genes
Significantly regulated by ANOVA factor	Nitrogen (FDR<0.05)	328
	bZIP1 (FDR<0.05)	*901*
	NitrogenXbZIP1 (pval<0.01)	82
	bZIP1 (FDR<0.05) AND NitrogenXbZIP1 (pval<0.01)	*28*
ChIP-SEQ Analysis		
bZIP1 bound genes		*850*

In italic: genes considered as TF primary targets in this study.

Table 15. bZIP1 primary targets identified as genes up-regulated or down-regulated by DEX-induced nuclear import of bZIP1 (FDR<0.05).

A. Genes that are up-regulated by DEX (FDR<0.05)	**mean expression level (-N/-Dex)**	**mean expression level (-N/+Dex)**	**mean expression level (+N/-Dex)**	**mean expression level (+N/+Dex)**
AT3G01290	10184.42	11470.63	9717.07	11446.96
AT5G07440	7205.35	10345.22	7677.83	10608.98
AT1G73260	8932.55	9699.11	9311.45	10476.40
AT5G52050	8413.93	9799.60	8527.51	10023.89
AT3G30775	5957.48	9395.19	5816.87	9054.40
AT5G01600	4784.75	7836.06	5315.54	7812.26
AT3G60140	4631.95	7436.68	5268.33	7486.52
AT5G40780	6351.57	7390.86	6651.01	7327.18
AT5G12340	6655.56	7648.56	6683.99	7311.89
AT1G69490	4711.22	7387.64	4805.96	7198.73
AT3G45970	4244.45	6891.99	4430.99	6987.22
AT5G03380	5921.87	6920.93	6001.52	6778.08
AT5G28050	2746.82	7454.05	2832.16	6293.82
AT2G34600	5129.64	6443.44	5192.91	6111.11
AT5G64120	5699.56	7021.79	5052.95	6031.23
AT4G15610	5307.80	6201.30	5323.19	5859.60

AT1G80380	3193.36	5593.63	3482.22	5681.45
AT2G39200	5179.32	5821.64	5037.85	5665.74
AT3G56360	3523.14	5696.51	3522.84	5602.26
AT1G15040	2677.05	5590.67	2974.84	5585.75
AT5G66400	3990.79	4256.05	4625.69	5544.75
AT4G01870	4589.86	5531.82	4415.21	5483.60
AT5G56870	3710.66	5064.44	3959.70	5090.22
AT3G19390	2282.54	5063.88	2733.05	5028.37
AT5G06300	4016.04	4502.49	4312.07	4779.59
AT1G68440	2879.57	4408.78	3220.60	4635.18
AT1G10070	1991.74	4673.62	2354.02	4455.75
AT5G20150	2916.04	3829.24	3543.14	4451.22
AT1G23870	2774.60	3629.67	3635.51	4415.35
AT3G47960	2989.02	3938.43	3321.11	4262.19
AT5G47740	3367.67	3947.58	3614.82	4217.10
AT2G23170	3558.08	4503.52	3485.93	4165.23
AT4G38470	1408.69	3152.12	2007.53	4099.55
AT2G19800	2246.77	4333.96	2200.99	3882.93
AT5G67300	3211.67	3812.88	3290.90	3832.21
AT3G61260	2826.59	4226.43	2752.02	3824.18
AT2G38400	1970.17	3129.70	2516.19	3716.21
AT1G54100	2555.41	3120.81	3004.69	3689.79
AT5G49440	2727.51	3759.00	2516.28	3613.92
AT1G67480	1002.02	3773.82	1059.32	3525.08
AT1G64660	1905.16	3536.41	2134.11	3434.33
AT1G25275	2905.62	3755.00	2568.03	3299.31
AT4G33150	1814.47	2840.47	2230.03	3288.96
AT3G04070	2724.93	3390.50	2797.02	3266.73
AT5G57655	2290.70	2911.98	2555.48	3247.33
AT5G43580	2427.72	3256.69	2635.41	3222.34
AT4G35770	948.38	3140.55	1314.57	3177.19
AT5G11090	2078.24	2784.47	2283.94	3085.78
AT1G08830	2441.65	2922.21	2469.18	2780.36
AT3G56240	2353.08	2907.75	2327.40	2728.18
AT1G79340	2204.62	2609.32	2337.77	2721.73
AT5G54500	2372.67	3095.73	2004.25	2690.71
AT3G05200	1793.81	2231.06	1938.52	2553.69
AT4G36040	1903.75	2772.28	1948.94	2551.54
AT1G68620	1757.50	2432.63	1713.98	2503.30
AT1G11260	1818.65	2621.83	1712.04	2398.40
AT4G32950	481.13	2304.42	619.27	2368.04
AT4G20860	1743.34	2314.59	1847.07	2193.24
AT1G14330	1769.07	2184.54	1787.45	2156.24
AT3G14990	1486.66	2353.45	1600.26	2108.65
AT4G15550	1482.06	1895.48	1505.45	2052.15
AT5G50200	1702.01	2185.46	1724.26	2040.88
AT4G37790	1516.07	2019.80	1563.38	2034.09
AT1G03090	1196.37	1905.17	1458.24	2014.86
AT2G33150	1467.96	1678.65	1719.03	2011.98

AT1G43160	1640.78	2089.38	1677.85	2004.44
AT5G05340	1990.71	2455.06	1675.36	1997.69
AT1G22360	1435.43	1834.51	1651.79	1940.94
AT5G64260	1833.49	2167.71	1692.73	1935.14
AT1G32460	1457.27	2439.73	1366.24	1929.38
AT1G29400	1732.04	2012.76	1657.37	1917.29
AT5G11520	1366.90	1831.79	1466.17	1910.76
AT4G39780	1312.50	1899.95	1496.49	1897.93
AT5G67310	1827.99	2284.68	1585.68	1860.24
AT5G08350	73.19	1944.64	79.08	1798.98
AT3G15450	1476.21	1901.72	1501.24	1773.58
AT5G28610	1341.26	1888.26	1387.43	1761.45
AT4G03510	953.82	1726.31	968.89	1759.19
AT2G38750	1213.34	1600.58	1313.42	1695.27
AT5G67320	1596.01	2100.45	1420.94	1678.29
AT3G14770	643.54	1627.16	767.40	1620.43
AT1G27100	1301.70	1680.26	1281.77	1598.90
AT1G69890	1143.76	1882.02	1024.97	1556.08
AT5G61600	1383.51	1762.18	1271.92	1552.54
AT1G80460	1202.78	1535.00	1168.86	1548.39
AT5G48430	1757.39	2322.30	1372.87	1508.49
AT3G11410	1189.35	1363.58	1210.84	1479.68
AT4G27260	1018.07	1484.79	1009.82	1464.57
AT3G51730	907.42	1308.15	1001.97	1457.17
AT1G04410	946.12	1162.96	1212.68	1441.19
AT2G02800	1173.58	1632.63	1183.50	1407.36
AT2G32660	1135.17	1410.73	1132.61	1400.63
AT3G43430	905.85	1670.63	819.65	1400.22
AT3G55450	1238.32	1609.73	1068.06	1354.31
AT1G08930	1194.49	1381.44	1091.15	1306.69
AT5G44380	1054.14	1584.83	983.22	1289.14
AT3G52060	867.54	1171.26	825.77	1284.28
AT3G15630	970.70	1691.80	902.42	1237.34
AT1G08920	843.98	1132.36	964.58	1195.78
AT1G30820	610.39	1245.12	725.50	1164.67
AT4G34350	630.77	988.61	876.35	1164.52
AT5G16110	798.11	1210.43	756.99	1139.91
AT4G38060	885.30	1080.25	916.81	1109.34
AT3G19930	669.32	1349.89	603.66	1089.31
AT3G06850	705.39	1259.52	746.19	1072.72
AT1G68410	917.29	1179.01	921.44	1054.98
AT3G12320	768.10	957.25	887.47	1030.97
AT1G18270	554.66	1117.09	589.44	1007.85
AT4G15630	660.42	1000.90	631.83	1003.19
AT1G15380	677.06	949.20	711.13	1002.44
AT4G30490	790.90	982.97	819.52	992.49
AT5G20250	295.01	1063.61	377.67	976.27
AT3G45300	527.47	768.10	788.61	968.78
AT3G15950	637.26	1011.75	601.23	948.72

AT5G65110	645.46	1043.94	629.59	925.59
AT3G46690	512.82	889.96	495.74	921.56
AT2G39210	530.68	850.67	614.41	890.85
AT5G41610	493.04	1077.30	399.49	882.34
AT4G24220	595.64	978.37	543.62	877.62
AT5G04040	492.68	886.80	594.52	877.26
AT1G28130	569.60	844.63	506.85	876.67
AT5G67420	206.65	326.20	733.39	876.59
AT1G76990	511.46	794.92	531.69	869.96
AT5G24530	533.88	826.44	559.74	845.58
AT4G18340	257.55	1111.63	246.45	834.12
AT5G10450	700.33	846.43	688.08	822.06
AT3G17110	530.43	585.81	570.25	819.94
AT2G32510	497.35	774.09	529.25	811.11
AT1G29760	610.06	780.86	724.85	788.34
AT1G22830	535.37	873.50	565.71	787.30
AT2G30600	358.04	829.99	331.61	780.48
AT1G22190	620.74	786.03	592.52	768.94
AT1G58180	440.02	836.01	428.79	761.66
AT2G31390	481.43	580.20	596.80	761.61
AT3G29240	326.16	792.83	352.29	756.15
AT3G49790	474.90	852.12	449.07	731.71
AT2G38820	295.83	728.53	332.08	715.79
AT1G08720	633.75	805.71	610.86	709.33
AT4G01026	499.36	799.47	501.33	689.90
AT1G26270	437.10	749.41	455.57	684.98
AT4G21440	518.10	847.63	390.31	677.20
AT5G54080	466.34	563.21	571.81	670.32
AT1G62570	480.50	653.30	563.75	668.93
AT1G76410	477.22	685.02	530.84	665.41
AT4G32870	600.84	739.01	436.98	652.54
AT5G45630	293.64	851.38	248.54	650.24
AT3G51840	456.42	561.01	539.55	649.19
AT1G55510	359.48	505.19	438.72	632.62
AT1G76240	416.87	627.84	476.67	628.97
AT3G16150	73.84	851.91	77.41	622.58
AT5G40450	425.44	515.17	539.91	610.18
AT2G23450	477.27	663.73	456.64	608.98
AT5G49360	100.52	564.27	138.45	583.56
AT4G10840	411.43	503.25	459.63	553.75
AT5G15190	245.58	502.01	320.39	540.57
AT2G44670	312.67	631.34	285.27	535.16
AT3G61060	163.22	600.33	208.76	531.13
AT2G12400	323.07	500.47	366.46	529.50
AT3G13460	433.42	520.52	408.87	525.71
AT1G06570	263.25	395.08	327.78	518.78
AT2G26280	431.35	509.69	443.22	516.43
AT5G04740	413.67	480.88	418.89	506.93
AT2G14170	302.99	514.20	317.60	505.01

AT1G02860	290.17	632.44	310.74	504.02
AT4G13430	356.83	440.33	378.32	502.99
AT1G72770	250.42	475.96	359.01	501.13
AT1G55020	222.81	510.73	247.00	500.39
AT3G54620	384.47	486.84	414.77	496.60
AT1G65840	487.99	619.99	440.66	490.79
AT3G54140	301.69	421.20	364.28	486.97
AT4G39730	304.20	457.54	298.99	467.18
AT4G17950	378.17	463.37	417.61	466.59
AT4G01120	171.46	448.16	195.47	455.26
AT1G01490	296.79	504.22	354.46	455.22
AT1G16150	389.48	664.54	258.23	451.86
AT3G57890	359.52	398.76	365.14	448.61
AT3G23230	477.73	720.03	284.96	446.59
AT3G51860	359.25	406.42	347.34	439.13
AT1G61660	376.46	482.03	340.63	433.51
AT2G39570	147.42	576.87	162.97	427.86
AT1G67810	258.42	466.67	261.45	418.71
AT1G63180	293.52	504.12	298.99	418.36
AT5G16970	274.42	361.16	293.68	417.10
AT5G63620	321.59	383.09	361.31	415.60
AT4G29950	248.77	424.65	265.88	410.83
AT3G46440	296.17	388.65	320.64	407.40
AT3G01175	360.83	535.86	283.40	405.06
AT3G17420	277.61	422.27	317.09	397.44
AT1G66470	226.02	346.31	299.54	391.92
AT3G46280	386.23	572.31	286.47	390.51
AT3G57540	246.02	338.91	315.59	386.72
AT3G53150	309.42	429.81	287.16	383.79
AT1G03790	223.72	293.00	296.24	383.24
AT1G61740	204.52	373.13	248.24	382.22
AT5G61590	169.36	322.75	217.79	369.15
AT4G23880	246.89	339.77	230.07	368.41
AT4G15620	220.23	431.88	163.64	360.52
AT5G64460	232.76	344.86	270.38	357.94
AT1G75450	201.99	431.13	186.76	355.21
AT2G15695	223.60	335.08	210.60	354.64
AT3G17440	235.08	325.79	244.52	350.48
AT3G20410	260.99	397.46	248.52	347.30
AT3G19920	181.43	297.01	181.99	347.01
AT2G27490	265.83	366.46	281.46	346.25
AT1G75230	298.68	362.99	303.28	344.29
AT5G37260	183.58	323.24	191.07	338.89
AT3G48690	136.33	376.40	124.31	333.70
AT5G06980	229.34	369.71	276.34	328.19
AT4G28040	126.83	311.27	164.96	326.75
AT1G35580	249.68	388.17	229.39	326.38
AT5G24470	237.51	330.86	230.82	321.05
AT4G14420	278.60	365.61	218.88	314.73

AT2G25900	230.39	321.40	271.91	312.60
AT5G18630	212.25	282.12	248.33	301.33
AT5G13740	148.46	287.89	167.62	297.04
AT1G03100	184.63	398.39	169.38	294.96
AT1G49670	246.84	272.38	248.68	292.52
AT1G54740	50.65	279.25	63.67	287.90
AT3G03170	188.22	240.68	195.94	280.19
AT1G67470	233.81	347.51	219.61	279.31
AT1G06520	246.49	338.83	194.75	277.92
AT1G56700	173.77	270.96	225.74	276.90
AT3G13450	115.41	292.52	112.43	273.07
AT1G03610	176.69	299.85	197.11	271.81
AT3G14050	184.59	249.89	184.11	269.92
AT5G46590	54.42	277.55	61.46	267.30
AT1G11380	112.85	259.85	131.99	263.86
AT5G66030	210.45	277.21	211.28	262.39
AT2G43060	121.21	237.36	133.52	261.39
AT4G30550	176.17	235.71	202.63	257.78
AT1G56145	153.41	292.27	152.77	256.92
AT1G19700	210.69	250.61	214.73	256.72
AT2G17500	213.62	274.99	194.47	253.08
AT4G03080	218.91	264.94	211.69	252.74
AT4G24330	166.59	259.57	205.16	252.10
AT5G18610	137.12	200.94	163.91	244.41
AT5G43190	173.58	276.27	162.71	243.92
AT3G11340	103.93	253.84	95.09	242.44
AT1G69570	53.47	280.68	66.82	240.47
AT5G16120	166.52	193.99	185.28	239.74
AT1G03080	141.88	212.23	177.46	237.30
AT5G47390	214.99	261.98	197.83	237.13
AT5G02780	208.46	325.07	147.70	230.92
AT1G08630	86.59	305.91	81.73	227.16
AT2G22080	167.39	214.32	161.86	226.72
AT3G61070	159.27	230.78	167.05	222.96
AT5G49690	134.05	194.00	132.84	222.19
AT4G15280	162.18	216.41	177.44	221.97
AT1G48840	138.48	191.27	166.86	220.61
AT1G23550	115.16	205.81	126.48	219.78
AT3G52710	185.70	224.55	173.68	219.41
AT4G26290	100.09	204.28	99.72	217.88
AT1G66070	187.56	241.42	186.15	214.37
AT1G71980	87.74	200.94	104.80	211.66
AT5G27350	169.81	217.50	181.09	209.46
AT4G30170	81.34	235.80	82.59	204.62
AT1G76160	149.85	241.80	165.87	203.41
AT3G16800	136.82	188.05	163.34	203.20
AT4G15545	156.88	210.11	145.84	202.89
AT2G29380	133.78	205.70	133.94	195.73
AT3G05390	162.24	261.87	157.21	195.25

AT4G32320	139.86	219.65	135.38	194.46
AT1G23880	108.11	207.96	154.52	193.41
AT5G43430	167.02	202.42	152.23	192.88
AT5G02810	115.69	171.62	147.36	191.61
AT4G33910	133.44	231.40	133.01	188.06
AT3G16910	132.96	200.97	129.81	187.98
AT4G37540	23.62	63.65	56.50	187.59
AT5G07080	174.68	247.22	134.82	185.93
AT5G24030	177.37	240.76	142.93	183.54
AT3G57020	115.75	152.78	139.84	183.40
AT1G17190	92.87	188.86	111.21	180.24
AT3G14780	137.88	158.41	144.07	179.84
AT4G14500	124.89	193.26	132.77	179.33
AT1G08090	90.27	189.04	104.52	177.75
AT3G60690	63.78	115.19	80.58	175.69
AT3G55150	68.56	258.96	42.22	174.54
AT5G16960	123.23	167.73	131.78	171.56
AT2G46270	77.59	150.29	99.41	171.54
AT5G17640	107.49	190.13	121.67	171.17
AT3G20860	102.93	177.80	86.02	170.02
AT3G45060	88.06	139.17	146.70	169.39
AT1G67880	141.83	194.88	147.45	169.14
AT5G26740	88.42	165.00	91.06	165.11
AT5G43830	124.16	213.01	108.34	164.50
AT1G32200	94.05	141.29	96.44	163.07
AT5G04770	106.01	197.32	98.70	162.60
AT5G18850	87.29	173.24	106.32	161.22
AT4G17140	125.32	158.91	129.87	160.87
AT3G15610	127.30	184.88	138.02	159.29
AT1G18260	121.01	130.77	129.39	157.84
AT4G39070	81.16	197.76	78.43	157.28
AT1G13080	56.39	132.02	56.78	155.59
AT4G27657	89.63	155.91	96.74	153.67
AT1G68850	191.27	332.59	80.41	153.54
AT3G22930	120.29	248.25	108.40	152.64
AT4G37590	107.97	167.29	121.12	152.57
AT5G59220	121.92	147.72	123.64	151.98
AT4G35780	101.85	146.06	104.35	151.98
AT1G31480	103.91	150.30	117.73	151.70
AT5G57630	99.77	156.71	119.20	151.17
AT1G21310	110.32	184.92	105.96	143.26
AT4G32300	84.23	150.08	79.46	142.38
AT1G66170	143.51	216.29	88.76	141.44
AT5G27920	51.23	141.94	55.44	140.96
AT2G40170	66.43	140.44	63.41	139.40
AT5G13750	79.95	151.37	81.87	139.08
AT5G65630	109.66	146.68	116.75	138.71
AT4G32960	108.46	144.34	116.28	138.12
AT3G47500	103.77	139.68	110.41	137.67

AT5G03720	74.31	137.22	89.23	137.53
AT4G36670	93.16	179.25	91.44	133.77
AT4G20870	109.56	213.99	77.04	133.70
AT5G56100	95.00	127.73	90.07	133.47
AT5G18170	58.10	106.68	83.00	132.91
AT2G44360	111.72	152.31	114.74	131.90
AT5G61510	97.58	121.52	105.48	131.82
AT3G14067	84.56	132.94	109.50	131.21
AT5G23050	79.96	112.81	85.27	128.37
AT1G09460	51.78	96.15	68.09	128.23
AT5G60200	57.29	113.64	51.11	127.35
AT3G62650	83.14	114.05	100.20	127.07
AT5G56180	93.37	125.51	108.00	126.69
AT1G61810	55.96	171.39	50.57	126.49
AT4G36790	93.30	121.16	92.98	124.48
AT2G28200	80.09	107.22	66.42	122.50
AT5G18650	80.20	119.46	94.34	121.87
AT1G66550	16.87	178.52	8.85	121.01
AT2G43400	80.72	117.84	102.26	120.82
AT4G24060	74.58	116.88	79.81	120.75
AT1G60940	89.47	114.81	94.79	120.19
AT5G13110	50.81	55.50	85.60	117.80
AT1G73240	84.91	120.96	82.12	115.06
AT3G47640	88.22	124.31	95.33	113.52
AT1G79700	99.25	144.06	84.18	110.96
AT5G67450	137.07	197.99	91.95	108.74
AT4G01030	80.36	134.69	62.12	108.14
AT5G07070	79.82	107.17	83.36	107.96
AT3G54630	35.72	138.03	32.62	106.41
AT5G57660	57.73	90.98	77.73	105.82
AT5G10210	21.30	48.72	64.20	102.49
AT3G29160	78.64	120.24	79.77	98.18
AT1G63700	78.58	105.41	68.50	95.18
AT4G37220	49.77	108.81	49.51	94.74
AT5G05440	83.03	131.52	73.58	93.44
AT3G56000	72.31	96.23	66.14	92.92
AT2G19350	68.37	78.86	72.52	92.41
AT4G31240	52.21	69.75	70.95	92.27
AT4G38500	32.40	67.18	48.08	88.95
AT1G75220	77.58	101.05	73.89	87.30
AT2G19810	66.83	96.10	60.49	87.19
AT3G49060	71.49	102.76	76.53	86.88
AT4G36730	70.75	99.16	72.19	86.62
AT1G57680	80.22	119.55	70.72	85.92
AT1G52240	24.19	113.85	24.24	84.31
AT2G39130	60.17	77.61	62.96	83.54
AT1G15050	26.09	148.94	25.21	82.55
AT1G07250	65.31	70.10	59.97	80.93
AT1G28260	38.14	59.37	53.22	80.56

AT3G06780	69.06	95.10	65.59	80.51
AT1G79350	77.83	99.11	70.96	80.08
AT1G14340	44.89	51.11	62.44	78.79
AT5G49650	58.97	83.31	69.58	76.81
AT1G20300	42.65	75.93	44.46	76.36
AT2G39980	43.88	88.55	40.86	74.51
AT5G58620	64.50	88.80	63.60	72.85
AT2G22870	88.47	110.12	61.46	70.40
AT3G15260	52.85	64.15	55.86	70.34
AT1G75800	35.21	55.46	43.50	69.04
AT3G02550	42.17	91.77	38.20	67.55
AT1G18460	37.13	60.92	42.38	66.81
AT5G13760	47.74	66.43	54.92	66.73
AT1G26730	49.92	91.39	52.09	66.01
AT2G35230	55.94	73.72	45.53	65.92
AT3G14760	30.68	107.79	22.41	65.15
AT3G50780	50.65	62.62	44.75	64.77
AT1G69910	54.48	71.77	51.52	64.24
AT5G39040	48.05	70.13	45.72	64.19
AT3G51540	38.50	68.02	37.25	63.50
AT2G41190	6.86	45.71	15.34	62.77
AT5G20050	51.77	72.19	47.39	62.08
AT1G32930	63.44	86.24	44.68	61.75
AT2G01570	46.85	71.90	51.08	61.62
AT3G14740	26.43	87.61	24.95	58.46
AT3G24520	35.14	63.23	34.03	58.25
AT2G40420	40.27	53.19	45.52	58.14
AT1G18330	26.34	54.45	37.77	57.86
AT3G49940	23.55	32.95	38.48	52.17
AT3G57420	29.77	51.55	31.01	50.89
AT3G16170	38.77	48.49	44.68	50.20
AT5G47560	17.64	31.89	28.49	49.55
AT3G27690	14.62	72.47	13.43	49.52
AT4G33420	47.88	90.04	43.70	48.00
AT2G19320	24.44	42.04	20.39	47.63
AT1G66890	11.36	50.55	10.69	46.58
AT3G14750	32.16	55.23	29.39	45.87
AT4G38490	23.46	40.16	28.81	45.63
AT2G26600	34.19	45.31	33.79	44.77
AT3G54960	24.86	44.56	25.62	43.05
AT1G08980	34.96	47.23	25.50	42.02
AT3G13965	35.28	45.80	27.62	41.19
AT2G02040	31.00	37.83	30.63	40.12
AT1G67070	21.84	44.07	19.20	38.23
AT5G47240	8.75	37.13	10.66	37.97
AT1G67510	31.53	52.76	20.67	37.92
AT5G06690	32.61	57.90	29.49	36.67
AT1G06560	27.24	35.93	28.73	34.64
AT5G19090	19.12	32.24	22.01	34.38

AT1G64670	13.42	38.93	13.04	33.64
AT4G01330	23.71	37.06	27.66	33.62
AT5G59590	26.63	34.86	25.22	33.14
AT3G22920	27.78	61.59	17.92	32.41
AT4G38340	14.34	15.20	19.22	30.49
AT4G38480	10.86	22.11	13.01	30.31
AT1G15060	21.88	31.42	23.75	29.48
AT2G03220	18.19	29.62	19.33	27.68
AT1G10060	6.06	19.90	6.33	26.91
AT1G22400	19.68	27.72	19.28	25.25
AT3G15440	17.92	24.49	18.42	24.07
AT4G23870	10.43	19.24	9.65	23.39
AT3G15620	15.25	34.17	11.40	22.99
AT2G02700	18.77	35.42	22.59	22.72
AT5G52250	13.84	20.92	14.12	22.51
AT1G64010	13.47	26.14	14.03	22.13
AT5G67440	12.57	24.98	12.56	22.07
AT5G03550	15.43	19.74	13.92	21.98
AT2G37440	10.35	21.93	11.17	21.62
AT1G42480	17.86	25.22	17.67	21.38
AT4G27480	11.87	20.41	11.65	21.02
AT1G03870	6.85	36.12	6.04	21.00
AT3G15650	11.63	25.13	9.63	20.65
AT3G02150	16.33	22.41	16.55	20.49
AT1G10560	13.15	18.66	15.05	20.25
AT5G20885	8.36	11.31	13.58	20.01
AT1G30900	14.17	22.25	14.04	18.91
AT5G51850	10.59	15.80	13.04	17.91
AT1G76185	9.06	12.95	9.57	17.54
AT1G51820	14.48	29.13	11.64	17.32
AT3G19400	11.02	21.42	10.14	17.18
AT5G63800	13.42	20.95	14.00	16.50
AT3G52490	9.07	12.77	10.98	15.69
AT2G03740	7.17	24.53	5.19	15.60
AT2G28120	7.11	14.95	6.95	15.21
AT3G03470	10.74	11.23	11.17	13.91
AT3G60510	9.09	17.53	10.61	13.77
AT1G68400	11.34	20.12	10.76	13.07
AT5G01590	8.10	15.68	7.19	11.21
AT1G12080	5.10	19.09	5.14	10.96
AT2G31380	10.73	17.66	9.54	10.27
AT1G11780	7.50	8.31	7.75	10.21
AT1G63710	6.48	11.95	6.23	9.70
AT4G16690	6.14	8.67	6.33	9.51
AT3G01270	7.93	13.97	6.75	9.12
AT2G01860	6.16	8.89	6.91	9.11
AT5G03350	6.09	8.50	5.72	8.74
AT2G10640	7.04	14.98	5.78	8.73
AT4G01110	7.63	8.89	7.20	8.58

AT3G30396	7.82	14.39	6.03	8.50
AT3G18980	7.17	8.50	7.11	8.38
AT5G04310	5.80	7.82	5.66	8.19
AT1G20340	4.92	16.33	4.92	8.19
AT4G19810	6.62	7.83	6.37	7.42
AT1G03600	5.81	7.32	5.90	6.94
AT2G28630	6.31	12.16	5.64	6.79
AT4G38200	5.45	5.78	5.70	6.77
AT3G28510	5.31	6.30	5.30	6.55
AT1G02670	4.97	7.19	5.44	6.53
AT5G04630	5.19	5.07	5.16	6.43
AT3G24310	5.10	5.34	5.26	6.31
AT2G41200	5.07	5.59	4.99	5.81
B. Genes that are down-regulated by DEX (FDR<0.05)	**mean expression level (-N/-Dex)**	**mean expression level (-N/+Dex)**	**mean expression level (+N/-Dex)**	**mean expression level (+N/+Dex)**
AT2G38470	10594.94	9805.00	10690.91	9439.25
AT3G57450	10275.67	9151.09	9958.55	8270.15
AT3G45640	8895.22	8082.87	8991.34	7649.50
AT2G41730	7745.15	7011.42	7278.40	6457.43
AT4G30280	7638.56	7227.50	7735.48	6672.97
AT2G38870	7550.52	5944.54	6578.59	5449.26
AT5G64310	7247.82	6331.15	7483.09	6501.53
AT5G02230	7230.54	6000.23	7098.06	5757.55
AT1G30370	7198.83	6096.88	6392.67	4996.87
AT2G35980	6887.25	5915.12	6900.24	6080.70
AT2G17660	6519.25	6035.21	7218.16	6322.89
AT1G14540	6503.27	5600.91	5905.89	4876.12
AT5G13190	6327.96	5777.02	6277.25	5641.66
AT4G12720	5417.69	4831.47	5626.66	4720.71
AT3G06490	5298.66	4516.36	5209.36	4230.12
AT5G19240	5206.39	4093.63	4888.19	3710.43
AT1G14550	5125.17	3201.22	3718.19	2242.62
AT1G78100	4689.46	3678.75	4742.38	3865.18
AT4G34150	4607.37	4291.35	4572.67	3996.05
AT2G27390	4566.43	3837.18	4464.66	3801.81
AT4G08850	4428.08	4007.17	4267.77	3829.57
AT1G56060	4412.46	3059.50	3859.42	2460.41
AT3G52400	4286.43	3807.93	4148.80	3653.63
AT4G40040	4135.05	3616.24	3965.38	3614.05
AT4G32020	3994.28	3119.61	3736.47	3114.00
AT3G53730	3945.81	3259.21	4221.20	3631.17
AT5G08240	3875.35	3274.32	3788.89	3294.04
AT3G62720	3800.72	3410.65	3918.77	3158.22
AT1G73010	3512.54	2948.47	4400.95	3492.79
AT1G70130	3413.86	2346.61	3432.51	2378.90
AT5G47910	3328.40	3079.49	3463.66	2840.76
AT4G02380	3292.06	2079.41	3198.37	2088.63

AT2G23270	3149.67	1677.37	2305.40	1208.21
AT5G41810	3111.61	2679.01	3039.98	2659.79
AT4G17230	3054.74	2738.50	3105.45	2656.17
AT2G30130	2997.40	2304.29	3366.78	2457.53
AT2G22500	2981.76	2536.55	3104.64	2641.18
AT3G02800	2956.62	2435.58	2501.23	2086.28
AT2G31880	2880.46	2387.48	2754.07	2290.80
AT4G11360	2822.28	2152.72	2401.20	1756.26
AT3G21070	2814.10	2300.53	2588.43	2215.90
AT1G06760	2776.71	2378.31	2853.96	2519.50
AT1G51920	2773.17	1979.42	2214.57	1517.34
AT3G24550	2722.50	2655.04	2851.78	2564.13
AT3G02880	2715.25	2563.73	2713.98	2352.20
AT5G51190	2664.80	2220.62	2418.21	1944.26
AT1G11210	2645.36	2160.38	3164.87	2356.86
AT2G06050	2616.60	2165.16	2711.72	2128.88
AT2G01450	2579.51	2177.06	2716.31	2140.39
AT5G44610	2554.63	2138.70	2434.61	1936.00
AT5G62350	2356.45	1655.92	2504.33	1559.98
AT4G22470	2292.25	1969.35	2081.97	1738.58
AT2G22470	2273.65	1776.05	2061.53	1672.60
AT1G52200	2223.03	1509.49	1794.15	1240.12
AT4G39260	2222.20	1848.46	2425.54	2171.34
AT5G66070	2187.98	1822.99	2143.00	1836.79
AT4G01850	2159.94	1177.09	1656.44	936.20
AT4G37910	2039.79	1589.72	1708.63	1426.12
AT4G24160	1998.33	1756.43	1899.18	1586.29
AT4G32060	1969.28	1557.50	1840.41	1513.36
AT2G19570	1967.42	1602.44	1658.96	1249.48
AT5G61210	1920.02	1836.03	1854.71	1498.34
AT5G07310	1917.88	1485.37	2045.93	1539.41
AT1G13340	1867.19	1491.57	1944.69	1536.05
AT2G17220	1821.13	1578.15	1680.18	1256.00
AT1G80820	1802.73	1554.35	1839.63	1563.73
AT3G13650	1722.32	901.05	1328.90	762.96
AT5G48540	1708.97	1409.01	1678.11	1375.50
AT1G04440	1701.41	1560.40	1762.71	1487.92
AT3G55960	1694.09	1446.07	1693.87	1399.27
AT4G30290	1653.42	1210.90	2032.78	1267.09
AT4G28350	1653.13	1171.60	1439.88	1176.22
AT3G11820	1600.50	1325.60	1566.12	1278.85
AT1G59910	1591.72	1364.44	1646.71	1393.59
AT5G07620	1569.64	1126.48	1339.31	1038.34
AT5G44070	1567.49	1174.12	1195.05	1001.80
AT3G17020	1555.88	1411.42	1574.25	1369.51
AT3G59080	1536.13	1236.25	1350.16	1102.62
AT3G61390	1524.35	1139.96	1463.77	830.00
AT5G60680	1522.99	1052.96	1329.86	1009.48
AT4G22820	1520.78	1316.01	1544.71	1311.00

AT4G40030	1509.28	1144.40	1388.30	1028.36
AT2G28570	1453.74	1102.83	1338.15	1081.58
AT1G16670	1432.88	1244.29	1390.31	1188.06
AT1G55920	1416.03	1028.24	1171.04	960.14
AT5G39670	1332.60	1026.04	1354.50	999.29
AT2G25735	1322.34	1095.95	1075.97	794.10
AT1G28190	1320.00	1083.64	1321.61	1112.49
AT1G72060	1292.51	1074.21	1075.49	836.87
AT5G62390	1283.87	1092.32	1285.84	1090.86
AT3G18250	1276.11	843.37	941.65	678.63
AT4G18880	1273.25	1066.78	1254.86	948.83
AT3G49720	1223.58	1045.45	1140.05	960.26
AT2G25250	1156.23	798.81	1091.29	789.02
AT1G02400	1125.76	824.28	1042.52	815.59
AT3G50900	1123.55	910.84	1304.73	953.10
AT1G17370	1117.83	820.42	998.40	784.41
AT5G65020	1116.90	955.98	1226.70	1082.21
AT4G25030	1106.98	910.25	898.93	760.64
AT5G49620	1094.51	923.27	1155.71	887.29
AT5G66880	1075.21	846.26	1061.06	939.67
AT4G34180	1054.26	916.35	957.82	882.79
AT3G22160	1027.28	773.11	897.50	660.04
AT3G10640	1011.64	891.22	960.27	772.48
AT5G58110	1009.27	882.17	1068.85	822.53
AT1G72070	991.01	759.65	756.53	543.38
AT2G26380	986.98	727.38	841.17	548.62
AT5G06720	979.96	470.49	598.64	278.98
AT3G52360	912.90	699.55	1017.10	882.60
AT4G30470	894.34	752.07	1057.46	688.34
AT4G37180	889.54	672.72	918.95	755.82
AT5G57340	881.06	713.57	951.94	693.08
AT3G44720	874.87	704.84	803.58	638.68
AT1G18210	865.92	721.87	841.77	668.69
AT4G37900	847.54	719.50	577.15	462.63
AT4G38420	832.76	469.66	572.49	293.99
AT3G09020	817.18	715.83	739.90	575.96
AT5G26030	800.07	590.54	678.60	552.31
AT3G08760	796.60	564.43	743.38	551.95
AT3G21230	790.87	554.21	669.69	431.90
AT1G32350	774.03	454.60	499.64	344.20
AT2G32030	770.33	558.70	609.13	426.36
AT5G60350	757.40	531.49	814.90	509.35
AT1G51915	752.57	369.57	551.41	272.93
AT1G09920	750.89	629.51	570.88	531.45
AT2G39660	749.80	565.80	707.07	492.75
AT1G78340	729.18	554.44	642.19	535.97
AT3G54150	727.23	552.33	660.76	486.37
AT5G37770	718.69	580.26	685.02	541.13
AT1G20510	706.29	597.83	783.87	542.51

AT2G19190	685.28	400.28	553.52	376.68
AT1G18890	678.67	590.44	785.53	608.15
AT5G14930	677.86	497.36	720.33	477.00
AT3G54200	669.01	578.02	677.09	506.17
AT1G73510	666.96	518.32	417.74	307.73
AT4G31780	661.82	508.60	656.34	477.88
AT3G05490	657.57	387.27	502.10	374.36
AT1G63830	650.19	546.39	642.66	480.94
AT3G28580	647.41	558.14	727.50	526.40
AT5G39680	642.29	368.12	352.34	206.80
AT4G24390	636.82	379.19	424.50	269.58
AT5G42830	630.34	319.86	363.41	229.22
AT4G28085	624.10	500.53	545.49	449.97
AT1G09940	619.64	520.36	623.27	495.64
AT2G24180	614.05	486.07	674.28	520.77
AT2G26290	611.67	428.70	605.78	441.57
AT3G04120	598.45	487.62	571.67	505.88
AT4G37730	590.41	387.61	477.88	298.68
AT1G51620	589.71	397.80	544.85	392.83
AT4G30530	586.26	446.12	544.76	414.90
AT2G20960	582.08	455.39	507.30	397.68
AT4G33300	577.05	444.58	530.56	412.41
AT3G10630	572.60	447.96	428.14	305.24
AT1G19220	567.55	359.63	469.34	391.68
AT1G74590	566.35	322.51	478.94	298.72
AT2G42350	552.15	400.88	505.70	405.11
AT2G26190	540.73	404.79	481.87	356.94
AT2G39110	538.72	429.26	558.14	369.80
AT1G11310	537.13	491.58	514.83	415.15
AT2G41630	535.84	443.16	541.46	421.65
AT3G47550	527.25	450.86	543.54	436.06
AT4G00330	517.44	441.24	499.60	354.96
AT2G38830	513.49	403.57	440.46	328.92
AT4G37940	506.95	427.75	507.13	447.15
AT3G08710	506.90	409.13	464.95	366.87
AT5G62630	505.16	417.40	449.98	328.76
AT5G51390	500.46	316.95	473.91	283.61
AT2G21120	490.38	428.08	506.41	417.25
AT3G55630	480.92	339.84	277.84	198.71
AT5G41100	479.59	388.13	397.73	320.80
AT2G43000	476.73	217.41	281.93	127.29
AT4G11350	473.60	370.33	422.41	394.08
AT4G16780	469.56	300.33	378.03	236.91
AT5G04720	448.61	368.00	406.96	337.63
AT2G46140	439.56	347.42	407.54	279.81
AT4G36900	437.23	362.76	496.33	369.50
AT2G42430	436.12	313.08	401.95	295.15
AT5G59510	427.55	250.69	417.49	218.37
AT2G47130	418.63	310.91	388.64	238.18

AT3G48090	417.97	371.87	453.22	357.78
AT4G18890	417.22	378.73	425.34	345.77
AT3G61850	416.47	307.85	502.52	311.56
AT2G39700	415.94	312.42	314.64	262.48
AT4G39890	413.32	343.49	419.01	295.70
AT5G59480	408.82	251.29	324.14	202.63
AT5G45750	402.86	343.76	360.93	285.44
AT5G60250	401.41	302.26	322.78	233.26
AT3G09270	395.41	298.12	336.49	238.53
AT1G71450	394.30	191.87	215.77	136.56
AT1G10160	384.80	242.75	234.68	206.77
AT1G65690	384.45	291.73	338.94	280.36
AT1G24140	376.60	282.18	369.70	244.70
AT4G02200	375.43	306.60	344.27	252.99
AT4G29670	374.13	285.58	360.31	292.47
AT4G14368	372.74	299.65	250.04	185.77
AT1G34750	371.50	331.40	383.80	302.44
AT5G54170	368.19	277.24	379.24	282.00
AT4G31000	366.31	244.84	283.94	217.10
AT5G12880	364.45	296.84	344.63	228.53
AT1G79160	359.73	250.73	377.09	258.36
AT1G18860	355.43	239.05	237.25	162.56
AT2G17120	354.39	243.88	280.12	224.50
AT5G66640	352.37	224.36	297.84	170.23
AT3G54040	352.28	235.31	288.67	169.22
AT5G24620	349.85	279.62	286.06	257.58
AT4G23010	346.37	284.66	326.72	216.42
AT1G70530	330.15	264.52	340.91	262.10
AT4G01720	329.46	195.87	290.78	169.55
AT2G26560	328.67	217.69	238.05	148.38
AT2G19710	321.11	275.00	305.59	252.88
AT3G28740	320.29	195.94	326.46	209.90
AT4G21390	318.39	254.61	322.11	249.73
AT3G55950	314.00	208.52	276.03	198.12
AT5G65870	313.09	207.66	295.96	209.03
AT1G53430	311.41	218.88	263.74	162.28
AT1G57630	301.78	179.80	292.68	189.47
AT5G01540	296.89	218.77	286.07	206.48
AT5G53130	290.17	253.21	273.00	217.14
AT1G75540	289.25	229.29	284.86	267.65
AT2G16430	288.37	242.09	340.20	274.37
AT2G24240	285.10	179.59	310.84	197.68
AT2G47140	274.18	144.79	162.65	85.14
AT4G30210	271.35	213.19	253.06	190.97
AT4G39940	263.87	201.21	161.80	131.95
AT3G21080	263.37	158.47	191.66	96.73
AT3G25070	260.11	185.94	248.21	168.51
AT1G17310	259.77	180.69	208.28	171.07
AT3G52430	259.01	182.07	316.62	174.16

AT3G05510	254.46	156.80	167.87	152.16
AT1G07130	252.68	188.29	259.23	185.23
AT4G12070	251.34	182.24	238.72	212.56
AT3G29670	245.29	195.88	260.11	214.41
AT5G24430	242.79	172.19	249.47	172.19
AT5G44350	237.68	182.15	249.92	175.38
AT3G02790	237.46	154.39	218.06	166.72
AT3G03020	235.62	167.21	208.94	173.60
AT4G40020	233.07	172.14	187.39	145.78
AT3G43250	230.33	168.91	216.98	138.94
AT5G22530	227.62	149.07	210.52	102.89
AT2G01150	226.39	183.45	300.00	200.26
AT3G59900	224.19	143.94	119.47	108.04
AT2G27690	223.63	173.37	229.40	140.60
AT5G40010	223.44	149.11	179.26	112.00
AT3G20510	220.97	185.82	197.76	157.64
AT1G18570	215.25	167.37	173.04	121.02
AT1G07000	212.12	189.78	224.52	166.21
AT1G61560	206.08	111.67	134.07	78.72
AT5G46710	204.13	115.24	178.68	98.07
AT1G08510	202.66	158.09	182.44	166.13
AT3G11840	200.71	146.58	164.44	123.71
AT4G00080	200.58	139.69	241.23	160.09
AT1G61370	198.89	161.66	184.72	130.95
AT5G43520	196.01	137.87	113.86	85.56
AT3G07390	194.86	130.69	122.34	91.62
AT3G23090	187.47	130.73	152.74	118.35
AT2G44090	187.45	138.06	158.65	115.52
AT3G47380	184.44	82.64	149.15	70.09
AT4G11850	175.57	124.51	143.86	117.19
AT3G19630	175.34	126.04	183.13	146.21
AT2G41890	172.57	103.33	202.75	115.01
AT3G16030	172.35	117.74	137.15	97.15
AT5G22690	170.36	144.46	158.94	116.55
AT1G74870	166.63	95.53	99.13	70.00
AT1G73066	165.80	111.21	123.41	95.52
AT1G05060	165.30	80.42	131.75	65.50
AT1G44830	163.47	72.94	126.20	56.04
AT3G14360	159.92	70.48	109.23	66.97
AT1G07520	159.28	135.21	149.96	112.75
AT4G01700	158.84	88.10	131.39	73.00
AT5G10400	158.79	103.88	124.58	86.10
AT3G63390	157.00	98.40	107.62	104.12
AT2G11520	148.26	116.99	126.40	105.06
AT3G53130	146.81	130.51	175.82	112.17
AT2G34930	144.25	81.36	130.87	61.45
AT1G29250	140.47	89.92	101.42	95.01
AT1G30040	140.10	84.66	120.28	64.56
AT2G39530	137.58	83.44	84.55	50.39

AT1G32690	137.33	97.19	110.85	84.09
AT2G42360	137.30	82.50	142.29	78.23
AT2G22680	134.47	104.98	141.50	109.21
AT3G02770	133.37	110.31	139.56	90.55
AT5G57500	132.87	62.88	78.12	45.79
AT2G37940	132.34	112.90	132.46	114.85
AT4G21780	128.86	99.03	110.50	78.21
AT1G80530	127.35	88.43	128.13	70.73
AT5G62680	127.34	88.09	107.42	78.22
AT1G66090	124.24	84.29	110.97	71.78
AT1G48320	123.74	65.39	90.36	48.64
AT3G27110	120.14	98.59	116.86	95.35
AT3G23820	119.79	114.87	144.10	108.77
AT1G74710	119.70	78.43	128.49	75.38
AT2G37840	119.50	93.26	118.62	92.18
AT5G48175	115.84	87.46	96.02	69.89
AT3G09405	115.62	72.35	102.70	47.74
AT1G07750	113.10	83.54	125.44	86.83
AT5G09980	110.04	75.78	106.56	64.75
AT3G53280	109.25	49.15	81.72	45.51
AT3G01820	108.90	78.79	97.13	73.82
AT2G44450	107.93	81.49	100.31	62.24
AT3G44735	105.44	70.03	84.11	62.64
AT1G53980	103.44	57.11	81.68	40.82
AT3G17700	102.91	70.63	83.73	57.39
AT2G16500	102.35	70.20	91.71	74.38
AT5G10750	101.55	65.81	97.39	74.41
AT5G60800	101.43	63.70	94.64	66.92
AT1G10650	100.69	70.18	116.03	74.97
AT1G53440	99.13	61.54	86.87	42.22
AT1G16380	98.90	59.21	53.67	40.07
AT3G04630	98.30	65.67	67.35	58.42
AT2G40180	97.56	49.67	70.53	32.23
AT5G25190	96.39	53.81	96.36	55.40
AT2G45080	93.74	49.21	97.93	49.04
AT3G08750	93.07	65.98	71.04	38.94
AT5G63770	92.87	79.12	115.58	71.90
AT3G49350	92.15	88.09	128.98	90.92
AT4G09570	90.60	69.84	86.66	60.25
AT2G20150	89.57	49.56	48.52	33.97
AT4G37400	88.98	75.23	94.82	56.32
AT2G04160	88.96	69.59	92.04	59.41
AT5G52240	88.72	69.14	68.60	63.23
AT1G24150	82.18	49.97	88.44	50.10
AT3G03660	78.51	35.64	51.51	26.41
AT1G05710	78.04	50.95	65.42	45.80
AT1G28390	77.59	49.23	62.11	56.64
AT4G02330	76.52	32.55	59.17	21.47
AT5G41680	76.34	44.71	85.15	58.78

AT3G48850	76.26	26.22	41.82	26.39
AT1G05800	76.23	22.18	76.25	18.98
AT1G53920	75.05	52.32	55.22	33.42
AT2G32220	74.40	47.77	60.82	33.68
AT4G39840	73.11	51.49	70.31	38.51
AT2G37810	73.02	34.00	50.68	24.68
AT2G22750	72.42	54.77	62.63	40.93
AT2G01880	70.53	60.05	73.81	53.64
AT4G19960	69.95	45.98	45.27	38.32
AT4G11370	69.74	49.88	67.25	47.44
AT1G05055	68.76	48.32	57.59	42.69
AT4G15120	68.53	43.90	50.95	39.99
AT1G52560	67.76	28.42	83.14	34.54
AT4G30080	66.84	52.74	80.29	50.25
AT1G29860	66.78	36.25	46.75	30.49
AT4G14630	64.86	37.68	52.74	35.81
AT5G38210	63.74	41.46	55.84	32.01
AT5G66620	63.09	49.06	59.64	47.29
AT4G38000	62.11	49.69	79.63	58.88
AT5G65600	61.42	30.17	38.14	21.61
AT5G07870	60.63	40.51	56.74	26.82
AT2G24600	60.55	47.27	55.85	38.17
AT2G26480	59.95	39.35	67.91	40.83
AT2G38010	59.18	41.36	65.07	46.06
AT5G58120	58.25	51.88	50.62	35.19
AT1G21830	58.10	45.98	63.22	37.68
AT1G77030	56.83	36.04	38.03	31.58
AT1G63480	56.33	32.70	53.25	34.52
AT4G28940	55.88	30.46	27.12	24.99
AT2G46150	55.77	30.19	42.67	25.63
AT5G41550	54.53	39.88	47.68	34.78
AT3G49220	54.38	30.24	50.59	30.68
AT4G17260	51.13	29.62	34.86	24.60
AT3G09000	50.81	34.37	39.21	31.70
AT3G27160	49.43	37.26	45.09	38.05
AT4G11170	44.31	26.55	25.21	17.90
AT1G44100	43.23	30.10	50.34	31.34
AT5G56760	43.19	33.63	44.35	37.50
AT4G34320	43.13	35.74	39.56	29.61
AT1G17750	42.72	26.80	48.52	22.57
AT1G70940	42.16	31.28	50.67	34.90
AT2G35910	41.06	32.08	31.72	23.72
AT1G59850	40.89	23.62	35.25	22.56
AT5G62070	39.79	34.81	40.01	33.58
AT3G50480	38.95	27.53	26.65	14.65
AT1G53050	35.29	27.77	35.59	25.51
AT5G13870	34.95	26.45	38.18	25.58
AT1G63040	33.11	22.87	38.04	23.62
AT5G67570	32.93	20.46	25.77	21.88

AT1G58080	32.56	21.90	53.15	40.06
AT1G73750	31.67	24.34	27.29	20.16
AT4G02360	31.22	26.07	30.44	22.52
AT3G10190	30.27	20.52	25.16	19.98
AT4G26120	30.12	17.27	28.82	15.97
AT5G58787	30.05	21.31	38.13	26.25
AT4G36680	28.74	20.86	24.64	20.30
AT5G22550	28.35	22.42	27.37	20.72
AT1G67050	25.58	18.34	23.54	13.63
AT3G60910	24.33	16.11	20.90	16.63
AT3G05360	24.26	18.61	23.71	17.17
AT1G57560	24.10	16.49	19.77	12.56
AT2G34920	23.56	13.89	23.48	12.28
AT3G20900	23.47	14.59	21.99	15.22
AT4G39030	23.17	13.34	21.70	12.18
AT1G68150	23.14	17.01	26.38	17.18
AT1G51940	22.71	12.54	18.28	9.88
AT4G40080	22.23	15.63	20.82	15.38
AT1G18580	21.46	13.98	18.34	16.83
AT5G07860	21.44	16.18	23.14	14.60
AT1G32310	21.29	16.66	22.55	14.12
AT5G24540	21.22	11.80	11.17	6.14
AT1G74430	20.83	12.64	14.95	10.57
AT5G52670	19.63	13.72	21.70	12.29
AT1G44130	19.52	12.57	17.14	10.14
AT1G24625	18.35	15.12	16.45	13.12
AT1G19190	17.18	12.74	15.52	11.54
AT5G44990	16.17	9.98	12.07	8.38
AT3G63410	15.85	10.19	11.73	9.37
AT1G60030	14.88	9.35	12.78	8.11
AT3G54980	14.83	13.99	14.70	13.30
AT1G35560	14.73	11.88	17.54	12.13
AT2G41380	14.68	10.15	11.08	9.95
AT5G38310	13.79	7.34	7.83	6.66
AT1G15890	13.73	10.78	11.14	9.25
AT1G09520	12.31	10.95	10.78	9.84
AT1G56510	11.50	6.85	7.35	6.40
AT1G36640	11.24	7.31	7.70	5.61
AT1G35200	11.01	8.27	8.33	5.35
AT5G40540	10.60	8.85	11.62	8.49
AT4G27720	10.47	8.94	12.78	8.64
AT4G33960	10.43	10.34	12.36	9.41
AT2G46590	10.15	7.44	9.91	6.51
AT2G21560	10.04	8.09	14.38	9.82
AT1G14480	9.06	5.96	7.07	5.94
AT3G50760	8.95	7.09	8.54	7.09
AT2G17040	8.67	5.06	8.13	4.96
AT2G19130	8.62	6.93	7.97	7.00
AT1G11000	8.36	6.90	8.58	5.95

AT2G16870	7.87	6.66	6.93	5.96
AT3G61900	6.57	6.11	7.57	6.19
AT4G23440	5.43	5.36	6.00	5.54
AT4G30560	5.33	4.99	4.92	4.92
AT5G39710	5.21	4.99	4.98	4.98
AT2G39900	5.15	4.95	4.98	4.95
AT1G55610	5.00	4.96	5.43	4.98

Table 16. Significantly over-represented GO terms (FDR <0.01) identified for genes up-regulated or down-regulated by DEX-induced nuclear import of bZIP1 (FDR<0.05).

A. Significantly over-represented GO terms in the DEX up-regulated genes			
	Term	**p-value**	**Genes**
GO:0009310	amine catabolic process	0.000255	AT4G33150|AT3G30775|AT2G43400|AT1G08630|AT5G43430|AT1G64660|AT1G03090|AT1G65840|AT5G54080
GO:0042221	response to chemical stimulus	0.000255	AT1G08720|AT1G08920|AT5G66400|AT2G40170|AT2G22080|AT4G13430|AT4G37790|AT2G34600|AT1G54100|AT5G37260|AT3G51860|AT5G61590|AT5G47390|AT5G16970|AT2G38750|AT4G37220|AT5G16960|AT1G04410|AT1G49670|AT3G11410|AT4G32320|AT5G67450|AT5G07440|AT1G08090|AT5G54500|AT5G50200|AT2G23170|AT1G08830|AT3G56240|AT1G55020|AT4G33420|AT1G20340|AT4G27260|AT5G59220|AT1G28130|AT2G19810|AT3G05200|AT2G46270|AT5G03720|AT3G23230|AT5G01600|AT1G73260|AT1G08930|AT5G39040|AT5G44380|AT1G18330|AT5G13740|AT4G30170|AT4G35770|AT1G16150|AT1G15050|AT2G14170|AT1G80460|AT5G10450|AT1G43160|AT4G39070|AT5G67300|AT3G14050|AT3G14990|AT4G21440|AT1G02860|AT3G30775|AT5G18170|AT1G68850|AT4G34350|AT2G01570|AT3G60690|AT5G05340|AT1G17190
GO:0050896	response to stimulus	0.000255	AT1G08920|AT2G43400|AT2G33150|AT5G02810|AT2G40170|AT2G22080|AT4G13430|AT4G37790|AT1G54100|AT1G02670|AT5G61590|AT5G47390|AT3G54960|AT2G38750|AT4G37220|AT5G16960|AT1G04410|AT1G49670|AT3G11410|AT4G32320|AT5G07440|AT1G08090|AT5G54500|AT1G08830|AT1G25275|AT3G15950|AT4G33420|AT4G27260|AT5G59220|AT1G28130|AT5G24470|AT2G46270|AT5G03720|AT3G23230|AT1G06520|AT5G67320|AT1G73260|AT5G39040|AT5G40780|AT4G30170|AT4G35770|AT1G16150|AT1G31480|AT1G80460|AT5G24530|AT1G75800|AT1G43160|AT2G39980|AT4G39070|AT3G14050|AT3G14990|AT1G60940|AT3G15620|AT5G06980|AT1G02860|AT3G47640|AT3G30775|AT1G68850|AT2G26280|AT5G13750|AT3G45060|AT1G17190|AT5G67440|AT5G27350|AT1G08720|AT5G20150|AT5G66400|AT5G47740|AT5G52250|AT4G24220|AT2G34600|AT5G37260|AT3G51860|AT5G16970|AT3G61060|AT3G27690|AT5G67450|AT5G47240|AT5G50200|AT2G23170|AT4G01120|AT5G61510|AT3G56240|AT1G55020|AT1G20340|AT5G43580|AT5G04770|AT2G39200|AT2G19810|AT3G05200|AT5G01600|AT1G08930|AT4G37590|AT5G44380|AT1G18330|AT5G13740|AT4G36040|AT1G15050|AT2G14170|AT1G13080|AT5G64120|AT5G10450|AT5G20250|AT5G67300|AT2G32660|AT4G21440|AT1G75230|AT5G18170|AT4G34350|AT2G01570|AT3G60690|AT5G05340|AT5G61600
GO:0016054	organic acid catabolic process	0.000434	AT3G30775|AT2G43400|AT2G33150|AT5G43430|AT1G64660|AT4G33150|AT3G51840|AT1G08630|AT5G65110|AT1G03090|AT5G54080

GO:0046395	carboxylic acid catabolic process	0.000434	AT3G30775|AT2G43400|AT2G33150|AT5G43430|AT1G64660|AT4G33150|AT3G51840|AT1G08630|AT5G65110|AT1G03090|AT5G54080
GO:0009063	cellular amino acid catabolic process	0.000585	AT4G33150|AT3G30775|AT2G43400|AT1G08630|AT5G43430|AT1G64660|AT1G03090|AT5G54080
GO:0009628	response to abiotic stimulus	0.00178	AT1G08720|AT1G08920|AT2G43400|AT5G02810|AT5G66400|AT5G52250|AT1G54100|AT5G37260|AT5G61590|AT5G47390|AT2G38750|AT1G04410|AT3G11410|AT3G27690|AT5G67450|AT5G07440|AT4G01120|AT5G61510|AT1G08830|AT1G25275|AT3G56240|AT3G15950|AT1G20340|AT5G59220|AT5G24470|AT5G03720|AT1G06520|AT5G67320|AT5G01600|AT1G73260|AT1G08930|AT5G40780|AT4G37590|AT1G18330|AT1G31480|AT1G80460|AT1G13080|AT5G20250|AT1G43160|AT2G39980|AT4G39070|AT5G67300|AT1G60940|AT3G15620|AT5G06980|AT4G21440|AT5G18170|AT2G01570|AT5G13750|AT3G45060|AT1G17190|AT5G67440
GO:0006950	response to stress	0.00375	AT1G08920|AT2G33150|AT2G22080|AT1G54100|AT1G02670|AT5G61590|AT5G47390|AT3G54960|AT2G38750|AT4G37220|AT5G16960|AT1G04410|AT1G49670|AT3G11410|AT4G32320|AT5G07440|AT1G08830|AT3G15950|AT4G33420|AT5G59220|AT5G03720|AT5G67320|AT1G73260|AT4G30170|AT4G35770|AT1G43160|AT3G14050|AT1G60940|AT1G02860|AT3G47640|AT3G30775|AT1G68850|AT2G26280|AT1G17190|AT1G08720|AT5G20150|AT5G66400|AT5G47740|AT4G24220|AT5G37260|AT5G16970|AT3G61060|AT5G67450|AT5G47240|AT5G50200|AT3G56240|AT1G55020|AT5G43580|AT2G39200|AT2G19810|AT5G01600|AT1G08930|AT5G44380|AT1G18330|AT4G36040|AT2G14170|AT1G13080|AT5G64120|AT5G10450|AT5G20250|AT5G67300|AT2G32660|AT4G21440|AT1G75230|AT5G18170|AT2G01570|AT5G05340|AT5G61600
GO:0006979	response to oxidative stress	0.00375	AT2G19810|AT2G22080|AT5G01600|AT1G73260|AT1G08830|AT3G56240|AT5G16970|AT3G30775|AT1G68850|AT4G33420|AT5G44380|AT4G30170|AT5G16960|AT4G35770|AT5G05340|AT2G14170|AT1G49670|AT4G32320
GO:0009081	branched chain family amino acid metabolic process	0.0044	AT1G18270|AT1G10070|AT5G43430|AT1G10060|AT1G03090|AT2G43400
GO:0044282	small molecule catabolic process	0.00497	AT3G30775|AT2G43400|AT2G33150|AT5G43430|AT3G51840|AT4G33150|AT5G65110|AT1G03090|AT1G18270|AT1G64660|AT1G80460|AT1G08630|AT5G54080
GO:0048878	chemical homeostasis	0.00601	AT3G47640|AT1G20340|AT5G24030|AT5G13740|AT2G23170|AT4G27260|AT5G47560|AT3G51860|AT1G28130|AT5G01600|AT3G56240
B. Significantly over-represented GO terms in the DEX down-regulated genes			
	Term	**p-value**	**Genes**

GO:0050896	response to stimulus	4.68E-09	AT4G23440|AT3G52360|AT4G17230|AT4G16780|AT5G24620|AT2G35980|AT1G80820|AT4G17260|AT2G46140|AT4G34180|AT3G11840|AT5G62390|AT3G02880|AT3G24550|AT1G61560|AT1G18890|AT4G02200|AT4G30080|AT5G44070|AT3G61850|AT5G01540|AT1G11210|AT4G12720|AT1G09940|AT2G01150|AT5G51190|AT1G13340|AT3G44720|AT2G17040|AT4G39260|AT1G55920|AT1G20510|AT3G61900|AT4G33300|AT3G45640|AT2G38870|AT3G25070|AT1G57630|AT1G07520|AT3G06490|AT2G34930|AT3G17020|AT3G50480|AT5G62680|AT1G80530|AT5G61210|AT5G44610|AT5G66070|AT2G26560|AT3G07390|AT1G73010|AT2G40180|AT4G11360|AT1G56510|AT5G63770|AT4G11170|AT2G41380|AT5G25190|AT5G65020|AT3G13650|AT2G06050|AT3G52430|AT4G37910|AT1G11000|AT5G06720|AT5G66880|AT3G59900|AT5G48540|AT1G18570|AT2G04160|AT3G05360|AT2G39660|AT1G72060|AT5G37770|AT1G11310|AT1G15890|AT3G48090|AT5G04720|AT4G26120|AT4G34150|AT4G39030|AT1G52560|AT1G05710|AT5G24540|AT5G22690|AT3G52400|AT2G17660|AT1G05055|AT3G28740|AT4G02380|AT2G19190|AT1G52200|AT1G17750|AT1G74430|AT1G05800|AT1G66090|AT3G17700|AT1G30040|AT4G14630|AT1G14550|AT5G26030|AT4G11850|AT5G09980|AT5G41550|AT5G58120|AT3G28580|AT2G38470|AT1G19220|AT4G18880|AT3G11820|AT2G26380|AT1G74710|AT2G16870|AT2G16500|AT1G57560|AT1G70940|AT5G47910|AT1G02400|AT5G54170|AT2G46590|AT1G14540|AT3G09270|AT5G49620
GO:0006952	defense response	3.03E-08	AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT4G23440|AT1G11000|AT1G57630|AT2G35980|AT1G18570|AT5G41550|AT5G58120|AT2G38470|AT2G34930|AT3G05360|AT2G39660|AT5G37770|AT3G11840|AT1G11310|AT3G11820|AT2G26380|AT1G74710|AT1G61560|AT2G26560|AT1G15890|AT3G48090|AT5G04720|AT2G16870|AT4G39030|AT5G44070|AT5G47910|AT1G56510|AT4G12720|AT5G22690|AT4G11170|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT4G39260|AT1G05800|AT3G13650|AT1G66090|AT4G33300
GO:0006950	response to stress	9.90E-08	AT4G23440|AT2G35980|AT1G80820|AT4G17260|AT2G46140|AT4G34180|AT3G11840|AT5G62390|AT3G24550|AT1G61560|AT4G02200|AT5G44070|AT1G11210|AT4G12720|AT1G09940|AT1G13340|AT4G39260|AT1G55920|AT1G20510|AT4G33300|AT3G45640|AT2G38870|AT3G25070|AT1G57630|AT3G06490|AT2G34930|AT3G17020|AT5G44610|AT2G26560|AT1G73010|AT1G56510|AT5G63770|AT4G11170|AT5G65020|AT3G13650|AT2G06050|AT3G52430|AT4G37910|AT1G11000|AT5G66880|AT5G06720|AT1G18570|AT3G05360|AT2G39660|AT1G72060|AT5G37770|AT1G11310|AT1G15890|AT3G48090|AT5G04720|AT4G34150|AT4G39030|AT1G52560|AT5G22690|AT3G52400|AT1G05055|AT3G28740|AT4G02380|AT2G19190|AT1G52200|AT1G17750|AT1G05800|AT1G66090|AT4G14630|AT1G14550|AT5G26030|AT4G11850|AT5G41550|AT5G58120|AT2G38470|AT3G11820|AT2G26380|AT1G74710|AT2G16870|AT2G16500|AT5G47910|AT5G54170|AT2G46590|AT1G14540|AT5G49620
GO:0051707	response to other organism	1.21E-06	AT3G45640|AT2G06050|AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT5G24620|AT2G35980|AT1G18570|AT2G38470|AT3G06490|AT2G34930|AT3G50480|AT2G39660|AT5G61210|AT1G11310|AT3G11820|AT1G74710|AT3G24550|AT1G61560|AT2G26560|AT3G48090|AT4G39030|AT5G44070|AT5G47910|AT1G56510|AT4G12720|AT5G24540|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G17700

GO:0009607	response to biotic stimulus	2.35E-06	AT3G45640|AT2G06050|AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT5G24620|AT2G35980|AT1G18570|AT2G38470|AT3G06490|AT2G34930|AT3G50480|AT2G39660|AT5G61210|AT5G62390|AT1G11310|AT3G11820|AT1G74710|AT3G24550|AT1G61560|AT2G26560|AT3G48090|AT4G39030|AT5G44070|AT5G47910|AT1G56510|AT4G12720|AT5G24540|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G17700
GO:0051704	multi-organism process	2.77E-06	AT3G45640|AT2G06050|AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT5G24620|AT2G35980|AT1G18570|AT2G38470|AT3G06490|AT2G34930|AT3G50480|AT2G39660|AT5G61210|AT1G11310|AT3G11820|AT1G74710|AT3G24550|AT1G61560|AT2G26560|AT3G48090|AT4G39030|AT5G44070|AT5G47910|AT1G56510|AT4G12720|AT5G24540|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G17700
GO:0002376	immune system process	1.12E-05	AT3G48090|AT3G52430|AT2G16870|AT3G25070|AT4G11850|AT4G23440|AT1G57630|AT1G56510|AT2G35980|AT4G12720|AT5G41550|AT5G58120|AT5G22690|AT3G05360|AT5G37770|AT3G11840|AT4G39260|AT1G11310|AT1G74710|AT1G66090|AT1G61560|AT2G26560
GO:0042221	response to chemical stimulus	1.18E-05	AT2G06050|AT3G52430|AT4G37910|AT4G17230|AT5G06720|AT5G66880|AT3G59900|AT4G16780|AT1G18570|AT2G04160|AT4G17260|AT2G46140|AT1G72060|AT5G37770|AT3G11840|AT5G62390|AT3G02880|AT3G48090|AT4G26120|AT1G18890|AT4G02200|AT4G30080|AT5G44070|AT5G01540|AT1G52560|AT1G11210|AT1G05710|AT4G12720|AT1G09940|AT5G51190|AT3G52400|AT1G13340|AT2G17660|AT4G02380|AT1G52200|AT2G17040|AT1G17750|AT4G39260|AT1G74430|AT3G61900|AT3G45640|AT1G14550|AT3G25070|AT5G26030|AT1G07520|AT5G09980|AT3G28580|AT2G38470|AT3G06490|AT1G19220|AT4G18880|AT5G61210|AT5G44610|AT3G11820|AT5G66070|AT2G26560|AT3G07390|AT2G16500|AT1G57560|AT2G40180|AT4G11360|AT4G11170|AT2G41380|AT5G25190|AT1G14540|AT5G65020|AT3G09270|AT5G49620
GO:0031348	negative regulation of defense response	3.00E-05	AT3G25070|AT1G11310|AT3G52400|AT3G11820|AT4G39030|AT1G74710|AT3G52430
GO:0045087	innate immune response	6.55E-05	AT3G48090|AT3G52430|AT2G16870|AT3G25070|AT4G11850|AT4G23440|AT1G57630|AT1G56510|AT4G12720|AT5G41550|AT5G58120|AT5G22690|AT5G37770|AT4G39260|AT1G11310|AT1G74710|AT1G66090|AT1G61560|AT2G26560
GO:0006955	immune response	7.49E-05	AT3G48090|AT3G52430|AT2G16870|AT3G25070|AT4G11850|AT4G23440|AT1G57630|AT1G56510|AT4G12720|AT5G41550|AT5G58120|AT5G22690|AT5G37770|AT4G39260|AT1G11310|AT1G74710|AT1G66090|AT1G61560|AT2G26560
GO:0009620	response to fungus	0.000103	AT2G06050|AT2G38470|AT3G06490|AT2G34930|AT2G38870|AT3G52400|AT2G39660|AT5G47910|AT1G56510|AT1G11310|AT3G11820|AT1G05800|AT1G74710|AT3G24550|AT1G61560
GO:0080134	regulation of response to stress	0.000169	AT3G45640|AT1G11310|AT3G11820|AT2G31880|AT3G52430|AT4G12720|AT3G25070|AT3G52400|AT4G39030|AT1G74710|AT3G05360

GO:0016310	phosphorylation	0.00018	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT1G16670|AT2G41890|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT2G39660|AT1G70530|AT3G02880|AT1G53430|AT1G61370|AT3G24550|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT2G39110|AT1G17750|AT4G08850|AT1G53050|AT4G39940
GO:0031347	regulation of defense response	0.000214	AT1G11310|AT3G11820|AT2G31880|AT3G52430|AT4G12720|AT3G25070|AT3G52400|AT4G39030|AT1G74710|AT3G05360
GO:0010033	response to organic substance	0.000224	AT3G52430|AT4G17230|AT5G66880|AT3G59900|AT4G16780|AT1G18570|AT2G04160|AT4G17260|AT5G37770|AT3G11840|AT5G62390|AT3G02880|AT3G48090|AT4G26120|AT1G18890|AT4G30080|AT5G01540|AT1G05710|AT5G51190|AT3G52400|AT2G17040|AT1G17750|AT4G39260|AT1G74430|AT3G61900|AT3G45640|AT3G25070|AT1G07520|AT5G09980|AT3G28580|AT2G38470|AT3G06490|AT1G19220|AT4G18880|AT5G61210|AT5G44610|AT3G11820|AT5G66070|AT3G07390|AT1G57560|AT2G40180|AT4G11360|AT5G25190|AT5G49620
GO:0006468	protein phosphorylation	0.000235	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT1G16670|AT2G41890|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT2G39660|AT1G70530|AT3G02880|AT1G53430|AT1G61370|AT3G24550|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT2G39110|AT1G17750|AT4G08850|AT1G53050
GO:0006793	phosphorus metabolic process	0.000373	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT1G16670|AT2G41890|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT2G39660|AT1G70530|AT3G02880|AT1G53430|AT1G61370|AT3G24550|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT3G02800|AT2G39110|AT1G17750|AT4G08850|AT1G53050|AT4G39940
GO:0006796	phosphate metabolic process	0.000373	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT1G16670|AT2G41890|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT2G39660|AT1G70530|AT3G02880|AT1G53430|AT1G61370|AT3G24550|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT3G02800|AT2G39110|AT1G17750|AT4G08850|AT1G53050|AT4G39940
GO:0050832	defense response to fungus	0.00054	AT2G38470|AT2G34930|AT2G38870|AT3G52400|AT2G39660|AT5G47910|AT1G56510|AT1G11310|AT3G11820|AT1G05800|AT1G74710|AT1G61560
GO:0008219	cell death	0.000593	AT5G22690|AT3G48090|AT5G04720|AT2G16870|AT3G25070|AT4G23440|AT1G11000|AT1G11310|AT4G12720|AT1G66090|AT5G41550|AT1G61560|AT5G58120|AT4G33300|AT2G26560|AT1G15890
GO:0016265	death	0.000593	AT5G22690|AT3G48090|AT5G04720|AT2G16870|AT3G25070|AT4G23440|AT1G11000|AT1G11310|AT4G12720|AT1G66090|AT5G41550|AT1G61560|AT5G58120|AT4G33300|AT2G26560|AT1G15890

GO:0010200	response to chitin	0.00127	AT3G45640|AT2G17040|AT3G11840|AT1G07520|AT2G38470|AT4G18880|AT5G51190|AT4G26120|AT5G66070|AT4G17230|AT4G11360
GO:0048583	regulation of response to stimulus	0.00199	AT3G45640|AT3G52430|AT3G25070|AT3G52400|AT4G39030|AT3G05360|AT5G66880|AT4G09570|AT1G11310|AT3G11820|AT2G31880|AT4G12720|AT1G74710
GO:0012501	programmed cell death	0.00424	AT5G22690|AT3G48090|AT5G04720|AT2G16870|AT3G25070|AT4G23440|AT4G12720|AT1G66090|AT5G41550|AT5G58120|AT4G33300|AT2G26560|AT1G15890
GO:0006979	response to oxidative stress	0.0049	AT3G45640|AT3G48090|AT1G14550|AT5G26030|AT2G16500|AT5G06720|AT1G52560|AT1G11210|AT4G12720|AT1G09940|AT1G13340|AT4G02380|AT1G14540|AT1G52200|AT1G72060|AT5G37770
GO:0006464	protein modification process	0.0081	AT5G40540|AT1G55610|AT2G41890|AT2G17220|AT2G19130|AT5G38210|AT2G39660|AT3G11840|AT3G02880|AT1G53430|AT3G24550|AT2G11520|AT1G18890|AT5G57500|AT4G12720|AT5G65600|AT1G04440|AT1G17750|AT4G08850|AT3G45640|AT3G25070|AT5G41680|AT1G16670|AT3G61390|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT1G70530|AT1G61370|AT3G08760|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT2G38830|AT2G39110|AT1G53050

Table 17. Genes regulated by DEX-induced nuclear import of bZIP1 (FDR<0.05) and by the interaction of N-signal and DEX-induced nuclear import of bZIP1 (p-val<0.01).

Cluster1	
At4g37540	LBD39, LOB domain-containing protein 39
At5g04630	CYP77A9, cytochrome P450, family 77, subfamily A, polypeptide 9
At3g60690	SAUR-like auxin-responsive protein family
At4g38340	NLP3;Plant regulator RWP-RK family protein
Cluster2	
At4g33420	Peroxidase superfamily protein
At2g31380	STH, salt tolerance homologue
At3g30396	transposable element gene
At1g15050	IAA34, indole-3-acetic acid inducible 34
At5g28050	Cytidine/deoxycytidylate deaminase family protein
At1g01490	Heavy metal transport/detoxification superfamily protein
At2g39570	ACT domain-containing protein
At3g55150	ATEXO70H1, EXO70H1, exocyst subunit exo70 family protein H1
At2g28630	KCS12, 3-ketoacyl-CoA synthase 12
At2g02700	Cysteine/Histidine-rich C1 domain family protein
Cluster3	
At1g55610	BRL1, BRI1 like
At4g33960	unknown protein;
At3g23820	GAE6, UDP-D-glucuronate 4-epimerase 6
At3g49350	Ypt/Rab-GAP domain of gyp1p superfamily protein
Cluster4	

At1g56510	ADR2, WRR4, Disease resistance protein (TIR-NBS-LRR class)
At3g14360	alpha/beta-Hydrolases superfamily protein
At3g59900	ARGOS, auxin-regulated gene involved in organ size
At4g30560	ATCNGC9, CNGC9, cyclic nucleotide gated channel 9
At5g61210	ATSNAP33, ATSNAP33B, SNAP33, SNP33, soluble N-ethylmaleimide-sensitive factor adaptor protein 33
At5g39710	EMB2745, Tetratricopeptide repeat (TPR)-like superfamily protein
At3g63390	unknown protein;
At4g28940	Phosphorylase superfamily protein
At2g39900	GATA type zinc finger transcription factor family protein
At3g53280	CYP71B5, cytochrome p450 71b5

Table 18. Genes bound by GR::bZIP1 as detected by ChIP-seq with anti-GR antibody.

bZIP1 bound genes	**present in ATH1 microarray by unambiguous probes**		
AT1G01060	YES	LHY	LATE ELONGATED HYPOCOTYL
AT1G01460	YES	ATPIPK11	
AT1G01470	YES	LEA14	LATE EMBRYOGENESIS ABUNDANT 14
AT1G01550	YES	BPS1	BYPASS 1
AT1G01560	YES	ATMPK11	MAP kinase 11
AT1G01720	YES	ANAC2	Arabidopsis NAC domain containing protein 2
AT1G01725	YES		
AT1G03850	YES	ATGRXS13	glutaredoxin 13
AT1G04530	YES	TPR4	tetratricopeptide repeat 4
AT1G05330	YES		
AT1G05340	YES		
AT1G05680	YES	UGT74E2	Uridine diphosphate glycosyltransferase 74E2
AT1G06760	YES		
AT1G08510	YES	FATB	fatty acyl-ACP thioesterases B
AT1G08940	YES		
AT1G09070	YES	(AT)SRC2	SOYBEAN GENE REGULATED BY COLD-2
AT1G09080	YES	BIP3	binding protein 3
AT1G09930	YES	ATOPT2	oligopeptide transporter 2
AT1G10170	YES	ATNFXL1	NF-X-like 1
AT1G11560	YES		
AT1G11670	YES		
AT1G12960	YES		
AT1G13210	YES	ACA.1	autoinhibited Ca2+/ATPase II
AT1G13260	YES	EDF4	ETHYLENE RESPONSE DNA BINDING FACTOR 4
AT1G13270	YES	MAP1B	METHIONINE AMINOPEPTIDASE 1B
AT1G14040	YES		
AT1G14530	YES	THH1	TOM THREE HOMOLOG 1
AT1G14540	YES	PER4	peroxidase 4
AT1G14550	YES		

AT1G14560	YES		
AT1G15010	YES		
AT1G15040	YES	GAT	glutamine amidotransferase
AT1G15080	YES	ATLPP2	LIPID PHOSPHATE PHOSPHATASE 2
AT1G16640	YES		
AT1G16670	YES		
AT1G17180	YES	ATGSTU25	glutathione S-transferase TAU 25
AT1G17420	YES	ATLOX3	Arabidopsis thaliana lipoxygenase 3
AT1G17850	YES		
AT1G17860	YES		
AT1G17870	YES	ATEGY3	ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN-LIKE 3
AT1G18210	YES		
AT1G18310	YES		
AT1G18740	YES		
AT1G19020	YES		
AT1G19025	YES		
AT1G19180	YES	JAZ1	jasmonate-zim-domain protein 1
AT1G19190	YES		
AT1G19210	YES		
AT1G19770	YES	ATPUP14	purine permease 14
AT1G20440	YES	AtCOR47	
AT1G20450	YES	ERD1	EARLY RESPONSIVE TO DEHYDRATION 1
AT1G21850	YES	sks8	SKU5 similar 8
AT1G22070	YES	TGA3	TGA1A-related gene 3
AT1G22080	YES		
AT1G22190	YES	RAP2.4	related to AP2 4
AT1G22200	YES		
AT1G22570	YES		
AT1G22830	YES		
AT1G22840	YES	ATCYTC-A	CYTOCHROME C-A
AT1G23480	YES	ATCSLA3	cellulose synthase-like A3
AT1G23710	YES		
AT1G25400	YES		
AT1G25550	YES		
AT1G25560	YES	EDF1	ETHYLENE RESPONSE DNA BINDING FACTOR 1
AT1G27100	YES		
AT1G27720	YES	TAF4	TBP-associated factor 4
AT1G27730	YES	STZ	salt tolerance zinc finger
AT1G27760	YES	ATSAT32	SALT-TOLERANCE 32
AT1G27770	YES	ACA1	autoinhibited Ca2+-ATPase 1
AT1G28280	YES		
AT1G28480	YES	GRX48	
AT1G29395	YES	COR413-TM1	COLD REGULATED 314 THYLAKOID MEMBRANE 1
AT1G29400	YES	AML5	MEI2-like protein 5
AT1G29680	YES		
AT1G29690	YES	CAD1	constitutively activated cell death 1
AT1G30135	YES	JAZ8	jasmonate-zim-domain protein 8
AT1G30370	YES	DLAH	DAD1-like acylhydrolase

AT1G30700	YES		
AT1G30740	YES		
AT1G31820	YES	PUT1	POLYAMINE UPTAKE TRANSPORTER 1
AT1G32070	YES	ATNSI	nuclear shuttle interacting
AT1G32640	YES	ATMYC2	
AT1G32920	YES		
AT1G32930	YES		
AT1G33590	YES		
AT1G35140	YES	EXL1	EXORDIUM like 1
AT1G35910	YES	TPPD	trehalose-6-phosphate phosphatase D
AT1G42560	YES	ATMLO9	ARABIDOPSIS THALIANA MILDEW RESISTANCE LOCUS O 9
AT1G42990	YES	ATBZIP6	basic region/leucine zipper motif 6
AT1G43160	YES	RAP2.6	related to AP2 6
AT1G43900	YES		
AT1G43910	YES		
AT1G45145	YES	ATH5	THIOREDOXIN H-TYPE 5
AT1G49520	YES		
AT1G50750	YES		
AT1G52890	YES	ANAC19	NAC domain containing protein 19
AT1G53720	YES	ATCYP59	CYCLOPHILIN 59
AT1G53830	YES	ATPME2	pectin methylesterase 2
AT1G53840	YES	ATPME1	pectin methylesterase 1
AT1G55450	YES		
AT1G56050	YES		
AT1G56060	YES		
AT1G56590	YES	ZIP4	ZIG SUPPRESSOR 4
AT1G56660	YES		
AT1G56670	YES		
AT1G58210	YES	EMB1674	EMBRYO DEFECTIVE 1674
AT1G58420	YES		
AT1G59590	YES	ZCF37	
AT1G59600	YES	ZCW7	
AT1G59870	YES	ABCG36	ATP-binding cassette G36
AT1G60190	YES	AtPUB19	
AT1G61340	YES	AtFBS1	
AT1G61360	YES		
AT1G61820	YES	BGLU46	beta glucosidase 46
AT1G61870	YES	PPR336	pentatricopeptide repeat 336
AT1G61890	YES		
AT1G62300	YES	ATWRKY6	
AT1G62570	YES	FMO GS-OX4	flavin-monooxygenase glucosinolate S-oxygenase 4
AT1G62790	YES		
AT1G64390	YES	AtGH9C2	glycosyl hydrolase 9C2
AT1G64660	YES	ATMGL	methionine gamma-lyase
AT1G64670	YES	BDG1	BODYGUARD1
AT1G65510	YES		
AT1G65520	YES	ATECI1	ARABIDOPSIS THALIANA DELTA(3), DELTA(2)-ENOYL COA ISOMERASE 1

AT1G66160	YES	ATCMPG1	
AT1G66170	YES	MMD1	MALE MEIOCYTE DEATH 1
AT1G68440	YES		
AT1G68670	YES		
AT1G68760	YES	ATNUDT1	ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 1
AT1G68765	YES	IDA	INFLORESCENCE DEFICIENT IN ABSCISSION
AT1G68840	YES	AtRAV2	
AT1G69220	YES	SIK1	
AT1G69490	YES	ANAC29	Arabidopsis NAC domain containing protein 29
AT1G69760	YES		
AT1G69880	YES	ATH8	thioredoxin H-type 8
AT1G69890	YES		
AT1G69930	YES	ATGSTU11	glutathione S-transferase TAU 11
AT1G70420	YES		
AT1G71530	YES		
AT1G71697	YES	ATCK1	choline kinase 1
AT1G72520	YES	ATLOX4	Arabidopsis thaliana lipoxygenase 4
AT1G73010	YES	AtPPsPase1	pyrophosphate-specific phosphatase1
AT1G73080	YES	ATPEPR1	PEP1 RECEPTOR 1
AT1G73500	YES	ATMKK9	
AT1G73510	YES		
AT1G73530	YES		
AT1G73540	YES	atnudt21	nudix hydrolase homolog 21
AT1G74310	YES	ATHSP11	heat shock protein 11
AT1G74450	YES		
AT1G74930	YES	ORA47	
AT1G76170	YES		
AT1G76180	YES	ERD14	EARLY RESPONSE TO DEHYDRATION 14
AT1G76600	YES		
AT1G76640	YES		
AT1G76650	YES	CML38	calmodulin-like 38
AT1G78080	YES	RAP2.4	related to AP2 4
AT1G78290	YES	SNRK2-8	SNF1-RELATED PROTEIN KINASE 2-8
AT1G78340	YES	ATGSTU22	glutathione S-transferase TAU 22
AT1G79400	YES	ATCHX2	cation/H+ exchanger 2
AT1G79990	YES		
AT1G80010	YES	FRS8	FAR1-related sequence 8
AT1G80380	YES		
AT1G80820	YES	ATCCR2	
AT1G80840	YES	ATWRKY4	
AT1G80850	YES		
AT1G80930	YES		
AT2G01300	YES		
AT2G01670	YES	atnudt17	nudix hydrolase homolog 17
AT2G03750	YES		
AT2G03760	YES	AtSOT1	
AT2G04040	YES	ATDTX1	
AT2G04050	YES		

AT2G04880	YES	ATWRKY1	
AT2G04890	YES	SCL21	SCARECROW-like 21
AT2G05710	YES	ACO3	aconitase 3
AT2G05720	YES		
AT2G05940	YES	RIPK	RPM1-induced protein kinase
AT2G07050	YES	CAS1	cycloartenol synthase 1
AT2G17080	YES		
AT2G17660	YES		
AT2G17670	YES		
AT2G17840	YES	ERD7	EARLY-RESPONSIVE TO DEHYDRATION 7
AT2G18190	YES		
AT2G18210	YES		
AT2G18240	YES		
AT2G18690	YES		
AT2G20560	YES		
AT2G20570	YES	ATGLK1	ARABIDOPSIS GOLDEN2-LIKE 1
AT2G22470	YES	AGP2	arabinogalactan protein 2
AT2G22500	YES	ATPUMP5	PLANT UNCOUPLING MITOCHONDRIAL PROTEIN 5
AT2G22760	YES		
AT2G22860	YES	ATPSK2	phytosulfokine 2 precursor
AT2G22870	YES	EMB21	embryo defective 21
AT2G22880	YES		
AT2G23120	YES		
AT2G23170	YES	GH3.3	
AT2G23320	YES	AtWRKY15	
AT2G23810	YES	TET8	tetraspanin8
AT2G24570	YES	ATWRKY17	
AT2G24850	YES	TAT	TYROSINE AMINOTRANSFERASE
AT2G25460	YES		
AT2G25490	YES	EBF1	EIN3-binding F box protein 1
AT2G25735	YES		
AT2G26530	YES	AR781	
AT2G26690	YES		
AT2G27080	YES		
AT2G27090	YES		
AT2G28400	YES		
AT2G29080	YES	ftsh3	FTSH protease 3
AT2G29470	YES	ATGSTU3	glutathione S-transferase tau 3
AT2G29480	YES	ATGSTU2	glutathione S-transferase tau 2
AT2G29490	YES	ATGSTU1	glutathione S-transferase TAU 1
AT2G30040	YES	MAPKKK14	mitogen-activated protein kinase kinase kinase 14
AT2G30240	YES	ATCHX13	
AT2G30250	YES	ATWRKY25	
AT2G31690	YES		
AT2G32020	YES		
AT2G32120	YES	HSP7T-2	heat-shock protein 7T-2
AT2G32150	YES		
AT2G32220	YES		
AT2G33710	YES		

AT2G34910	YES		
AT2G35410	YES		
AT2G35930	YES	AtPUB23	
AT2G35980	YES	ATNHL1	ARABIDOPSIS NDR1/HIN1-LIKE 1
AT2G36220	YES		
AT2G36230	YES	APG1	ALBINO AND PALE GREEN 1
AT2G36950	YES		
AT2G37430	YES	ZAT11	zinc finger of Arabidopsis thaliana 11
AT2G37975	YES		
AT2G38240	YES		
AT2G38470	YES	ATWRKY33	WRKY DNA-BINDING PROTEIN 33
AT2G38480	YES		
AT2G38830	YES		
AT2G39190	YES	ATATH8	
AT2G39200	YES	ATMLO12	MILDEW RESISTANCE LOCUS O 12
AT2G39660	YES	BIK1	botrytis-induced kinase1
AT2G39670	YES		
AT2G39990	YES	AteIF3f	Arabidopsis thaliana eukaryotic translation initiation factor 3 subunit F
AT2G40000	YES	ATHSPRO2	ARABIDOPSIS ORTHOLOG OF SUGAR BEET HS1 PRO-1 2
AT2G40140	YES	ATSZF2	
AT2G41000	YES		
AT2G41010	YES	ATCAMBP25	calmodulin (CAM)-binding protein of 25 kDa
AT2G41100	YES	ATCAL4	ARABIDOPSIS THALIANA CALMODULIN LIKE 4
AT2G41110	YES	ATCAL5	
AT2G41410	YES		
AT2G41430	YES	CID1	CTC-Interacting Domain 1
AT2G41620	YES		
AT2G41630	YES	TFIIB	transcription factor IIB
AT2G41640	YES		
AT2G41730	YES		
AT2G41740	YES	ATVLN2	
AT2G41790	YES		
AT2G41800	YES		
AT2G41890	YES		
AT2G43130	YES	ARA-4	
AT2G43290	YES	MSS3	multicopy suppressors of snf4 deficiency in yeast 3
AT2G44790	YES	UCC2	uclacyanin 2
AT2G44840	YES	ATERF13	ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13
AT2G45400	YES	BEN1	
AT2G45810	YES		
AT2G45820	YES		
AT2G46140	YES		
AT2G46260	YES	LRB1	light-response BTB 1
AT2G46390	YES	SDH8	succinate dehydrogenase 8
AT2G46400	YES	ATWRKY46	WRKY DNA-BINDING PROTEIN 46
AT2G46420	YES		

AT2G46830	YES	AtCCA1	
AT2G47000	YES	ABCB4	ATP-binding cassette B4
AT2G47550	YES		
AT2G47950	YES		
AT3G01280	YES	ATVDAC1	ARABIDOPSIS THALIANA VOLTAGE DEPENDENT ANION CHANNEL 1
AT3G01290	YES	AtHIR2	
AT3G01560	YES		
AT3G01830	YES		
AT3G01840	YES	LYK2	LysM-containing receptor-like kinase 2
AT3G02040	YES	AtGDPD1	
AT3G02480	YES		
AT3G02840	YES		
AT3G02850	YES	SKOR	STELAR K+ outward rectifier
AT3G02880	YES		
AT3G03810	YES	EDA3	embryo sac development arrest 3
AT3G03890	YES		
AT3G04070	YES	anac47	NAC domain containing protein 47
AT3G04120	YES	GAPC	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT
AT3G04130	YES		
AT3G04730	YES	IAA16	indoleacetic acid-induced protein 16
AT3G05310	YES	MIRO3	MIRO-related GTP-ase 3
AT3G06490	YES	AtMYB18	myb domain protein 18
AT3G06500	YES	A/N-InvC	alkaline/neutral invertase C
AT3G06510	YES	ATSFR2	SENSITIVE TO FREEZING 2
AT3G08580	YES	AAC1	ADP/ATP carrier 1
AT3G08590	YES	iPGAM2	2,3-biphosphoglycerate-independent phosphoglycerate mutase 2
AT3G08610	YES		
AT3G09440	YES		
AT3G09940	YES	ATMDAR3	ARABIDOPSIS THALIANA MONODEHYDROASCORBATE REDUCTASE 3
AT3G10300	YES		
AT3G10920	YES	ATMSD1	ARABIDOPSIS MANGANESE SUPEROXIDE DISMUTASE 1
AT3G10930	YES		
AT3G10985	YES	ATWI-12	ARABIDOPSIS THALIANA WOUND-INDUCED PROTEIN 12
AT3G12120	YES	FAD2	fatty acid desaturase 2
AT3G12320	YES		
AT3G13310	YES		
AT3G13320	YES	atcax2	
AT3G13790	YES	ATBFRUCT1	
AT3G13920	YES	EIF4A1	eukaryotic translation initiation factor 4A1
AT3G14940	YES	ATPPC3	phosphoenolpyruvate carboxylase 3
AT3G14990	YES	AtDJ1A	DJ-1 homolog A
AT3G15210	YES	ATERF-4	ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4
AT3G15450	YES		

AT3G15460	YES		
AT3G15500	YES	ANAC55	NAC domain containing protein 55
AT3G15620	YES	UVR3	UV REPAIR DEFECTIVE 3
AT3G15630	YES		
AT3G16857	YES	ARR1	response regulator 1
AT3G16860	YES	COBL8	COBRA-like protein 8 precursor
AT3G17390	YES	MAT4	METHIONINE ADENOSYLTRANSFERASE 4
AT3G19020	YES		
AT3G19030	YES		
AT3G19240	YES		
AT3G19570	YES	QWRF1	QWRF domain containing 1
AT3G19580	YES	AZF2	zinc-finger protein 2
AT3G19930	YES	ATSTP4	SUGAR TRANSPORTER 4
AT3G21070	YES	ATNADK-1	NAD KINASE 1
AT3G21500	YES	DXL1	DXS-like 1
AT3G22370	YES	AOX1A	alternative oxidase 1A
AT3G22380	YES	TIC	TIME FOR COFFEE
AT3G22900	YES	NRPD7	
AT3G22910	YES		
AT3G23170	YES		
AT3G23250	YES	ATMYB15	MYB DOMAIN PROTEIN 15
AT3G23460	YES		
AT3G24050	YES	GATA1	GATA transcription factor 1
AT3G24170	YES	ATGR1	glutathione-disulfide reductase
AT3G24550	YES	ATPERK1	proline-rich extensin-like receptor kinase 1
AT3G24560	YES	RSY3	RASPBERRY 3
AT3G25250	YES	AGC2	
AT3G25600	YES		
AT3G25610	YES		
AT3G25650	YES	ASK15	SKP1-like 15
AT3G25655	YES	IDL1	inflorescence deficient in abscission (IDA)-like 1
AT3G25780	YES	AOC3	allene oxide cyclase 3
AT3G27510	YES		
AT3G28690	YES		
AT3G29010	YES		
AT3G29290	YES	emb276	embryo defective 276
AT3G30775	YES	AT-POX	
AT3G44260	YES	AtCAF1a	CCR4- associated factor 1a
AT3G45730	YES		
AT3G45740	YES		
AT3G45970	YES	ATEXLA1	expansin-like A1
AT3G45980	YES	H2B	HISTONE H2B
AT3G46620	YES	AtRDUF1	Arabidopsis thaliana RING and Domain of Unknown Function 1117 1
AT3G47340	YES	ASN1	glutamine-dependent asparagine synthase 1
AT3G48520	YES	CYP94B3	cytochrome P45, family 94, subfamily B, polypeptide 3
AT3G49000	YES		
AT3G49530	YES	ANAC62	NAC domain containing protein 62
AT3G49780	YES	ATPSK3 (FORMER SYMBOL)	

AT3G49790	YES		
AT3G50900	YES		
AT3G50910	YES		
AT3G50930	YES	BCS1	cytochrome BC1 synthesis
AT3G50960	YES	PLP3a	phosducin-like protein 3 homolog
AT3G50970	YES	LTI3	LOW TEMPERATURE-INDUCED 3
AT3G50980	YES	XERO1	dehydrin xero 1
AT3G51920	YES	ATCML9	
AT3G52450	YES	AtPUB22	
AT3G52700	YES		
AT3G52710	YES		
AT3G52800	YES		
AT3G52810	YES	ATPAP21	PURPLE ACID PHOSPHATASE 21
AT3G52930	YES	AtFBA8	
AT3G53480	YES	ABCG37	ATP-binding cassette G37
AT3G53510	YES	ABCG2	ATP-binding cassette G2
AT3G53600	YES		
AT3G53610	YES	ATRAB8	RAB GTPase homolog 8
AT3G53760	YES	ATGCP4	
AT3G54150	YES		
AT3G55440	YES	ATCTIMC	CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE
AT3G55620	YES	eIF6A	eukaryotic initiation facor 6A
AT3G55630	YES	ATDFD	DHFS-FPGS homolog D
AT3G55640	YES		
AT3G55970	YES	ATJRG21	
AT3G55980	YES	ATSZF1	
AT3G56800	YES	ACAM-3	CALMODULIN 3
AT3G56880	YES		
AT3G57450	YES		
AT3G57460	YES		
AT3G59350	YES		
AT3G59360	YES	ATUTR6	UDP-GALACTOSE TRANSPORTER 6
AT3G60130	YES	BGLU16	beta glucosidase 16
AT3G60140	YES	BGLU3	BETA GLUCOSIDASE 3
AT3G61190	YES	BAP1	BON association protein 1
AT3G61640	YES	AGP2	arabinogalactan protein 2
AT3G61890	YES	ATHB-12	homeobox 12
AT3G62260	YES		
AT3G62410	YES	CP12	CP12 DOMAIN-CONTAINING PROTEIN 1
AT3G63380	YES		
AT4G00170	YES		
AT4G00690	YES	ULP1B	UB-like protease 1B
AT4G01370	YES	ATMPK4	MAP kinase 4
AT4G02380	YES	AtLEA5	Arabidopsis thaliana late embryogenensis abundant like 5
AT4G02880	YES		
AT4G04500	YES	CRK37	cysteine-rich RLK (RECEPTOR-like protein kinase) 37
AT4G05050	YES	UBQ11	ubiquitin 11
AT4G05100	YES	AtMYB74	myb domain protein 74
AT4G05320	YES	UBI1	ubiquitin 1

AT4G08850	YES		
AT4G08950	YES	EXO	EXORDIUM
AT4G09630	YES		
AT4G11280	YES	ACS6	1-aminocyclopropane-1-carboxylic acid (acc) synthase 6
AT4G11350	YES		
AT4G11360	YES	RHA1B	RING-H2 finger A1B
AT4G11560	YES		
AT4G11570	YES		
AT4G11670	YES		
AT4G12720	YES	AtNUDT7	Arabidopsis thaliana Nudix hydrolase homolog 7
AT4G12730	YES	FLA2	FASCICLIN-like arabinogalactan 2
AT4G13390	YES	EXT12	extensin 12
AT4G15610	YES		
AT4G16670	YES		
AT4G16680	YES		
AT4G16820	YES	PLA-I{beta]2	phospholipase A I beta 2
AT4G16830	YES		
AT4G17490	YES	ATERF6	ethylene responsive element binding factor 6
AT4G17500	YES	ATERF-1	ethylene responsive element binding factor 1
AT4G17520	YES		
AT4G17615	YES	ATCBL1	ARABIDOPSIS THALIANA CALCINEURIN B-LIKE PROTEIN
AT4G18170	YES	ATWRKY28	
AT4G18880	YES	AT-HSFA4A	ARABIDOPSIS THALIANA HEAT SHOCK TRANSCRIPTION FACTOR A4A
AT4G19200	YES		
AT4G19210	YES	ABCE2	ATP-binding cassette E2
AT4G20000	YES		
AT4G20830	YES		
AT4G20840	YES		
AT4G20860	YES		
AT4G20870	YES	ATFAH2	ARABIDOPSIS FATTY ACID HYDROXYLASE 2
AT4G21120	YES	AAT1	amino acid transporter 1
AT4G21490	YES	NDB3	NAD(P)H dehydrogenase B3
AT4G21820	YES		
AT4G21850	YES	ATMSRB9	methionine sulfoxide reductase B9
AT4G22720	YES		
AT4G23190	YES	AT-RLK3	RECEPTOR LIKE PROTEIN KINASE 3
AT4G24390	YES	AFB4	auxin signaling F-box 4
AT4G24570	YES	DIC2	dicarboxylate carrier 2
AT4G24580	YES	REN1	ROP1 ENHANCER 1
AT4G25570	YES	ACYB-2	
AT4G25580	YES		
AT4G25810	YES	XTH23	xyloglucan endotransglucosylase/hydrolase 23
AT4G25820	YES	ATXTH14	
AT4G26040	YES		
AT4G26180	YES		
AT4G27270	YES		
AT4G27280	YES		

AT4G27580	YES		
AT4G27652	YES		
AT4G27654	YES		
AT4G27657	YES		
AT4G28460	YES		
AT4G29780	YES		
AT4G29790	YES		
AT4G30210	YES	AR2	
AT4G30280	YES	ATXTH18	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 18
AT4G30290	YES	ATXTH19	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 19
AT4G30430	YES	TET9	tetraspanin9
AT4G30440	YES	GAE1	UDP-D-glucuronate 4-epimerase 1
AT4G30530	YES	GGP1	gamma-glutamyl peptidase 1
AT4G30600	YES		
AT4G31550	YES	ATWRKY11	
AT4G31800	YES	ATWRKY18	ARABIDOPSIS THALIANA WRKY DNA-BINDING PROTEIN 18
AT4G31805	YES		
AT4G32020	YES		
AT4G32920	YES		
AT4G33666	YES		
AT4G33670	YES		
AT4G33780	YES		
AT4G33920	YES		
AT4G33925	YES	SSN2	suppressor of sni1 2
AT4G33950	YES	ATOST1	OPEN STOMATA 1
AT4G34150	YES		
AT4G34160	YES	CYCD3	
AT4G34410	YES	RRTF1	redox responsive transcription factor 1
AT4G35580	YES	CBNAC	calmodulin-binding NAC protein
AT4G36010	YES		
AT4G36040	YES	J11	DnaJ11
AT4G36500	YES		
AT4G36640	YES		
AT4G37010	YES	CEN2	centrin 2
AT4G37260	YES	ATMYB73	
AT4G37270	YES	ATHMA1	ARABIDOPSIS THALIANA HEAVY METAL ATPASE 1
AT4G37370	YES	CYP81D8	cytochrome P45, family 81, subfamily D, polypeptide 8
AT4G37590	YES	MEL1	MAB4/ENP/NPY1-LIKE 1
AT4G37610	YES	BT5	BTB and TAZ domain protein 5
AT4G37770	YES	ACS8	1-amino-cyclopropane-1-carboxylate synthase 8
AT4G37900	YES		
AT4G37910	YES	mtHsc7-1	mitochondrial heat shock protein 7-1
AT4G38420	YES	sks9	SKU5 similar 9
AT4G39080	YES	VHA-A3	vacuolar proton ATPase A3
AT4G39090	YES	RD19	RESPONSIVE TO DEHYDRATION 19
AT4G39260	YES	ATGRP8	GLYCINE-RICH PROTEIN 8

AT4G39640	YES	GGT1	gamma-glutamyl transpeptidase 1
AT4G40030	YES		
AT4G40040	YES		
AT5G01380	YES		
AT5G01500	YES	TAAC	thylakoid ATP/ADP carrier
AT5G01510	YES	RUS5	ROOT UV-B SENSITIVE 5
AT5G01540	YES	LecRK-VI.2	L-type lectin receptor kinase-VI.2
AT5G01600	YES	ATFER1	ARABIDOPSIS THALIANA FERRETIN 1
AT5G01750	YES		
AT5G01820	YES	ATCIPK14	
AT5G01950	YES		
AT5G01960	YES		
AT5G02020	YES	SIS	Salt Induced Serine rich
AT5G02230	YES		
AT5G02240	YES		
AT5G02810	YES	APRR7	
AT5G02820	YES	BIN5	BRASSINOSTEROID INSENSITIVE 5
AT5G03210	YES	AtDIP2	
AT5G03380	YES		
AT5G03610	YES		
AT5G04330	YES	CYP84A4	CYTOCHROME P45 84A4
AT5G04750	YES		
AT5G05410	YES	DREB2	DEHYDRATION-RESPONSIVE ELEMENT BINDING PROTEIN 2
AT5G05420	YES		
AT5G05600	YES		
AT5G05790	YES		
AT5G06290	YES	2-Cys Prx B	2-cysteine peroxiredoxin B
AT5G06300	YES	LOG7	LONELY GUY 7
AT5G06320	YES	NHL3	NDR1/HIN1-like 3
AT5G07440	YES	GDH2	glutamate dehydrogenase 2
AT5G07450	YES	CYCP4;3	cyclin p4;3
AT5G07730	YES		
AT5G07740	YES		
AT5G08230	YES		
AT5G08240	YES		
AT5G09990	YES	PROPEP5	elicitor peptide 5 precursor
AT5G10180	YES	AST68	ARABIDOPSIS SULFATE TRANSPORTER 68
AT5G10630	YES		
AT5G10690	YES		
AT5G10695	YES		
AT5G10700	YES		
AT5G10710	YES		
AT5G11090	YES		
AT5G11650	YES		
AT5G11670	YES	ATNADP-ME2	Arabidopsis thaliana NADP-malic enzyme 2
AT5G11740	YES	AGP15	arabinogalactan protein 15
AT5G12340	YES		
AT5G13200	YES		

AT5G13220	YES	JAS1	JASMONATE-ASSOCIATED 1
AT5G13470	YES		
AT5G14730	YES		
AT5G14740	YES	BETA CA2	BETA CARBONIC ANHYDRASE 2
AT5G15090	YES	ATVDAC3	ARABIDOPSIS THALIANA VOLTAGE DEPENDENT ANION CHANNEL 3
AT5G15130	YES	ATWRKY72	ARABIDOPSIS THALIANA WRKY DNA-BINDING PROTEIN 72
AT5G15980	YES		
AT5G17330	YES	GAD	glutamate decarboxylase
AT5G17350	YES		
AT5G17360	YES		
AT5G17460	YES		
AT5G17650	YES		
AT5G18270	YES	ANAC87	Arabidopsis NAC domain containing protein 87
AT5G18310	YES		
AT5G18475	YES		
AT5G19110	YES		
AT5G19240	YES		
AT5G20150	YES	ATSPX1	ARABIDOPSIS THALIANA SPX DOMAIN GENE 1
AT5G20230	YES	ATBCB	blue-copper-binding protein
AT5G20240	YES	PI	PISTILLATA
AT5G24590	YES	ANAC91	Arabidopsis NAC domain containing protein 91
AT5G24650	YES		
AT5G24800	YES	ATBZIP9	ARABIDOPSIS THALIANA BASIC LEUCINE ZIPPER 9
AT5G24930	YES	ATCOL4	
AT5G25280	YES		
AT5G25930	YES		
AT5G26030	YES	ATFC-I	
AT5G26340	YES	ATSTP13	SUGAR TRANSPORT PROTEIN 13
AT5G26360	YES		
AT5G26760	YES		
AT5G27420	YES	ATL31	Arabidopsis toxicos en levadura 31
AT5G35735	YES		
AT5G36260	YES		
AT5G37500	YES	GORK	gated outwardly-rectifying K+ channel
AT5G37770	YES	CML24	CALMODULIN-LIKE 24
AT5G39580	YES		
AT5G39670	YES		
AT5G39680	YES	EMB2744	EMBRYO DEFECTIVE 2744
AT5G40690	YES		
AT5G40780	YES	LHT1	lysine histidine transporter 1
AT5G41080	YES	AtGDPD2	
AT5G41810	YES		
AT5G42050	YES		
AT5G42370	YES		
AT5G42380	YES	CML37	calmodulin like 37
AT5G42830	YES		
AT5G43440	YES		

AT5G43450	YES		
AT5G43580	YES	UPI	UNUSUAL SERINE PROTEASE INHIBITOR
AT5G44320	YES		
AT5G44330	YES		
AT5G45110	YES	ATNPR3	
AT5G45140	YES	NRPC2	nuclear RNA polymerase C2
AT5G45350	YES		
AT5G45630	YES		
AT5G46780	YES		
AT5G47200	YES	ATRAB1A	RAB GTPase homolog 1A
AT5G47210	YES		
AT5G47220	YES	ATERF-2	ETHYLENE RESPONSE FACTOR- 2
AT5G47230	YES	ATERF-5	ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR-5
AT5G47910	YES	ATRBOHD	
AT5G47960	YES	ATRABA4C	RAB GTPase homolog A4C
AT5G47970	YES		
AT5G49030	YES	OVA2	ovule abortion 2
AT5G49220	YES		
AT5G49480	YES	ATCP1	Ca2+-binding protein 1
AT5G49520	YES	ATWRKY48	ARABIDOPSIS THALIANA WRKY DNA-BINDING PROTEIN 48
AT5G50900	YES		
AT5G52050	YES		
AT5G52400	YES	CYP715A1	cytochrome P45, family 715, subfamily A, polypeptide 1
AT5G52410	YES		
AT5G52750	YES		
AT5G53110	YES		
AT5G54490	YES	PBP1	pinoid-binding protein 1
AT5G55140	YES		
AT5G55780	YES		
AT5G56340	YES	ATCRT1	
AT5G56980	YES		
AT5G57190	YES	PSD2	phosphatidylserine decarboxylase 2
AT5G57500	YES		
AT5G57510	YES		
AT5G57550	YES	XTH25	xyloglucan endotransglucosylase/hydrolase 25
AT5G57560	YES	TCH4	Touch 4
AT5G57720	YES		
AT5G58060	YES	ATGP1	
AT5G58070	YES	ATTIL	TEMPERATURE-INDUCED LIPOCALIN
AT5G59450	YES		
AT5G59490	YES		
AT5G59820	YES	AtZAT12	
AT5G59830	YES		
AT5G61520	YES		
AT5G61890	YES		
AT5G61910	YES		
AT5G62520	YES	SRO5	similar to RCD one 5

AT5G62530	YES	ALDH12A1	aldehyde dehydrogenase 12A1
AT5G63130	YES		
AT5G63780	YES	SHA1	shoot apical meristem arrest 1
AT5G63790	YES	ANAC12	NAC domain containing protein 12
AT5G64120	YES		
AT5G64240	YES	AtMC3	metacaspase 3
AT5G64310	YES	AGP1	arabinogalactan protein 1
AT5G64650	YES		
AT5G64660	YES	ATCMPG2	
AT5G64905	YES	PROPEP3	elicitor peptide 3 precursor
AT5G65205	YES		
AT5G65300	YES		
AT5G65660	YES		
AT5G66055	YES	AKRP	ankyrin repeat protein
AT5G66060	YES		
AT5G66460	YES	AtMAN7	
AT5G67080	YES	MAPKKK19	mitogen-activated protein kinase kinase kinase 19
AT5G67300	YES	ATMYB44	ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 44
AT5G67310	YES	CYP81G1	cytochrome P45, family 81, subfamily G, polypeptide 1
AT5G67420	YES	ASL39	ASYMMETRIC LEAVES2-LIKE 39
AT5G67560	YES	ARLA1D	ADP-ribosylation factor-like A1D
AT1G01471	NO		
AT1G02520	NO	ABCB11	ATP-binding cassette B11
AT1G02530	NO	ABCB12	ATP-binding cassette B12
AT1G02590	NO		
AT1G02600	NO		
AT1G02920	NO	ATGST11	ARABIDOPSIS GLUTATHIONE S-TRANSFERASE 11
AT1G02930	NO	ATGST1	ARABIDOPSIS GLUTATHIONE S-TRANSFERASE 1
AT1G03220	NO		
AT1G05320	NO		
AT1G05675	NO		
AT1G07135	NO		
AT1G08950	NO		
AT1G09690	NO		
AT1G09932	NO		
AT1G10155	NO	ATPP2-A1	phloem protein 2-A1
AT1G11550	NO		
AT1G13350	NO		
AT1G13360	NO		
AT1G14549	NO		
AT1G14870	NO	AtPCR2	
AT1G15015	NO		
AT1G15030	NO		
AT1G15045	NO		
AT1G15090	NO		
AT1G16635	NO		
AT1G17147	NO		
AT1G18200	NO	AtRABA6b	RAB GTPase homolog A6B
AT1G18300	NO	atnudt4	nudix hydrolase homolog 4

AT1G18745	NO		
AT1G21395	NO		
AT1G24160	NO		
AT1G27695	NO		
AT1G29640	NO		
AT1G30720	NO		
AT1G30730	NO		
AT1G32928	NO		
AT1G42980	NO		
AT1G49610	NO		
AT1G53625	NO		
AT1G55340	NO		
AT1G56240	NO	AtPP2-B13	phloem protein 2-B13
AT1G56242	NO		
AT1G57690	NO		
AT1G57980	NO		
AT1G57990	NO	ATPUP18	purine permease 18
AT1G61880	NO		
AT1G62870	NO		
AT1G68770	NO		
AT1G68845	NO		
AT1G69130	NO		
AT1G69290	NO		
AT1G69300	NO		
AT1G70390	NO		
AT1G70780	NO		
AT1G70782	NO	CPuORF28	conserved peptide upstream open reading frame 28
AT1G71520	NO		
AT1G71528	NO		
AT1G74929	NO		
AT1G76680	NO	ATOPR1	ARABIDOPSIS 12-OXOPHYTODIENOATE REDUCTASE 1
AT1G76690	NO	ATOPR2	ARABIDOPSIS 12-OXOPHYTODIENOATE REDUCTASE 2
AT1G78830	NO		
AT1G78850	NO		
AT1G79240	NO		
AT1G79980	NO		
AT2G07772	NO		
AT2G17190	NO		
AT2G17830	NO		
AT2G18193	NO		
AT2G19260	NO		
AT2G20562	NO		
AT2G23118	NO		
AT2G23321	NO		
AT2G25130	NO		
AT2G30020	NO		
AT2G31030	NO	ORP1B	OSBP(oxysterol binding protein)-related protein 1B
AT2G31345	NO		
AT2G32190	NO		

AT2G32210	NO		
AT2G36770	NO		
AT2G36800	NO	DOGT1	don-glucosyltransferase 1
AT2G38230	NO	ATPDX1.1	ARABIDOPSIS THALIANA PYRIDOXINE BIOSYNTHESIS 1.1
AT2G38823	NO		
AT2G41415	NO		
AT2G41440	NO		
AT2G43120	NO		
AT2G45390	NO		
AT2G45950	NO	ASK2	SKP1-like 2
AT2G46995	NO		
AT3G02030	NO		
AT3G02468	NO	CPuORF9	conserved peptide upstream open reading frame 9
AT3G02470	NO	SAMDC	S-adenosylmethionine decarboxylase
AT3G10815	NO		
AT3G10986	NO		
AT3G11950	NO		
AT3G13080	NO	ABCC3	ATP-binding cassette C3
AT3G13300	NO	VCS	VARICOSE
AT3G13432	NO		
AT3G13600	NO		
AT3G14362	NO	DVL19	DEVIL 19
AT3G18950	NO		
AT3G18952	NO		
AT3G23470	NO		
AT3G25597	NO		
AT3G29000	NO		
AT3G30770	NO		
AT3G46080	NO		
AT3G46090	NO	ZAT7	
AT3G47790	NO	ABCA8	ATP-binding cassette A8
AT3G48515	NO		
AT3G49570	NO	LSU3	RESPONSE TO LOW SULFUR 3
AT3G49796	NO		
AT3G56790	NO		
AT3G62420	NO	ATBZIP53	basic region/leucine zipper motif 53
AT3G62422	NO	CPuORF3	conserved peptide upstream open reading frame 3
AT4G01360	NO	BPS3	BYPASS 3
AT4G03635	NO		
AT4G05048	NO	U49.1	
AT4G08555	NO		
AT4G09040	NO		
AT4G12731	NO		
AT4G12735	NO		
AT4G13395	NO	DVL1	DEVIL 1
AT4G15760	NO	MO1	monooxygenase 1
AT4G17616	NO		
AT4G20920	NO		

AT4G21830	NO	ATMSRB7	methionine sulfoxide reductase B7
AT4G21910	NO		
AT4G21920	NO		
AT4G22590	NO	TPPG	trehalose-6-phosphate phosphatase G
AT4G22592	NO	CPuORF27	conserved peptide upstream open reading frame 27
AT4G22710	NO	CYP76A2	cytochrome P45, family 76, subfamily A, polypeptide 2
AT4G23550	NO	ATWRKY29	
AT4G23560	NO	AtGH9B15	glycosyl hydrolase 9B15
AT4G24565	NO		
AT4G27585	NO		
AT4G28470	NO	ATRPN1B	
AT4G32480	NO		
AT4G34131	NO	UGT73B3	UDP-glucosyl transferase 73B3
AT4G34412	NO		
AT4G36648	NO		
AT4G37390	NO	AUR3	AUXIN UPREGULATED 3
AT4G37608	NO		
AT5G01542	NO		
AT5G01595	NO		
AT5G02815	NO		
AT5G03204	NO		
AT5G06310	NO	AtPOT1b	protection of telomeres 1b
AT5G06990	NO		
AT5G08770	NO		
AT5G08780	NO		
AT5G08790	NO	anac81	Arabidopsis NAC domain containing protein 81
AT5G13210	NO		
AT5G15960	NO	KIN1	
AT5G15970	NO	AtCor6.6	
AT5G18480	NO	PGSIP6	plant glycogenin-like starch initiation protein 6
AT5G19230	NO		
AT5G20010	NO	ATRAN1	ARABIDOPSIS THALIANA RAS-RELATED NUCLEAR PROTEIN
AT5G20225	NO		
AT5G21930	NO	ATHMA8	ARABIDOPSIS HEAVY METAL ATPASE 8
AT5G21940	NO		
AT5G24630	NO	BIN4	brassinosteroid-insensitive4
AT5G24640	NO		
AT5G36920	NO		
AT5G39581	NO		
AT5G40700	NO		
AT5G40880	NO		
AT5G42053	NO		
AT5G43570	NO		
AT5G43620	NO		
AT5G43650	NO	BHLH92	
AT5G47229	NO		
AT5G51730	NO		
AT5G53300	NO	UBC1	ubiquitin-conjugating enzyme 1

AT5G53588	NO	CPuORF5	conserved peptide upstream open reading frame 5
AT5G53590	NO		
AT5G53592	NO		
AT5G54100	NO		
AT5G55870	NO		
AT5G56975	NO		
AT5G57010	NO		
AT5G57015	NO	ckl12	casein kinase I-like 12
AT5G61900	NO	BON	
AT5G64320	NO		
AT5G64401	NO		
AT5G65207	NO		
AT5G65687	NO		
AT5G65690	NO	PCK2	phosphoenolpyruvate carboxykinase 2

[00393] Integration of TF-regulation and TF-binding data identifies three modes-of-action for bZIP1 and its primary targets: *poised, stable,* and *transient.* To understand the underlying mechanisms by which bZIP1 propagates N-signals through a GRN, *primary* targets identified *either* by TF-induced gene regulation *or* TF-binding were integrated. To enable a direct comparison of transcriptome and TF-binding data, of the 850 genes bound to bZIP1, 187 genes not represented on the ATH1 microarray were omitted. 136 genes that did not pass the stringent filters for effects of protoplasting, DEX, or CHX treatment were also omitted. This resulted in a filtered total of 527 bZIP1 bound genes (Fig. 29A). The resulting list of 1,308 high-confidence primary targets of bZIP1 identified *either* by TF-mediated gene regulation (901 genes) *or* TF-binding (527 genes) were integrated and analyzed for biological relevance to the N-signal (Fig. 29). The intersection of the TF-regulation and TF-binding data identified three classes of primary targets, representing distinct modes-of-action for bZIP1 in N-signal propagation (Fig. 29A; Table 19). Class I targets (407 genes) were deemed "*Poised*", as they are bound to bZIP1 but show no significant TF-induced gene regulation. Class II targets (120 genes), are deemed "*Stable*", as they are both bound *and* regulated by bZIP1. Unexpectedly, Class III targets (781 genes) - the largest class of bZIP1 primary target genes - were deemed "*Transient*" as they are regulated by bZIP1 perturbation, but not detectably bound to it. We note that these are not indirect TF targets, as ChIP-seq is able to detect direct or indirect binding by bZIP1, *i.e.*, as part of a protein complex. They also cannot be dismissed as secondary targets of bZIP1, as they are regulated in response to DEX-

induced bZIP1 perturbation performed in the presence of CHX, which blocks the regulation of secondary targets.

Table 19. Classes of bZIP1 primary targets: Class I, Poised; Class II Stable (IIA induced; IIB repressed); and Class III transient (IIIA induced, IIIB repressed) listed as 5 subclasses. Gene annotations are from TAIR10.

Class I. BN: Bind but no regulation		
At1g14560	Mitochondrial substrate carrier family protein	Class I
At2g23120	Late embryogenesis abundant protein, group 6	Class I
At5g57720	AP2/B3-like transcriptional factor family protein	Class I
At5g02820	BIN5, RHL2, Spo11/DNA topoisomerase VI, subunit A protein	Class I
At4g09630	Protein of unknown function (DUF616)	Class I
At3g52700	unknown protein; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At1g16640	AP2/B3-like transcriptional factor family protein	Class I
At3g10920	ATMSD1, MEE33, MSD1, manganese superoxide dismutase 1	Class I
At1g61820	BGLU46, beta glucosidase 46	Class I
At4g39080	VHA-A3, vacuolar proton ATPase A3	Class I
At1g53720	ATCYP59, CYP59, cyclophilin 59	Class I
At3g29290	emb2076, Pentatricopeptide repeat (PPR) superfamily protein	Class I
At1g64390	AtGH9C2, GH9C2, glycosyl hydrolase 9C2	Class I
At5g01500	TAAC, thylakoid ATP/ADP carrier	Class I
At3g45980	H2B, HTB9, Histone superfamily protein	Class I
At1g32920	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to wounding; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G32928.1); Has 42 Blast hits to 42 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At4g23190	AT-RLK3, CRK11, cysteine-rich RLK (RECEPTOR-like protein kinase) 11	Class I
At2g36230	APG10, HISN3, Aldolase-type TIM barrel family protein	Class I
At2g26690	Major facilitator superfamily protein	Class I
At1g73080	ATPEPR1, PEPR1, PEP1 receptor 1	Class I
At4g35580	NTL9, NAC transcription factor-like 9	Class I
At4g33950	ATOST1, OST1, P44, SNRK2-6, SNRK2.6, SRK2E, Protein kinase superfamily protein	Class I
At5g67560	ARLA1D, ATARLA1D, ADP-ribosylation factor-like A1D	Class I
At5g10180	AST68, SULTR2;1, slufate transporter 2;1	Class I
At5g42370	Calcineurin-like metallo-phosphoesterase superfamily protein	Class I
At5g26760	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At4g17615	ATCBL1, CBL1, SCABP5, calcineurin B-like protein 1	Class I
At1g29690	CAD1, MAC/Perforin domain-containing protein	Class I
At3g16857	ARR1, RR1, response regulator 1	Class I
At3g15500	ANAC055, ATNAC3, NAC055, NAC3, NAC domain containing protein 3	Class I
At5g64650	Ribosomal protein L17 family protein	Class I
At3g13790	ATBFRUCT1, ATCWINV1, Glycosyl hydrolases family 32 protein	Class I

At5g05600	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Class I
At4g01370	ATMPK4, MPK4, MAP kinase 4	Class I
At2g41430	CID1, ERD15, LSR1, dehydration-induced protein (ERD15)	Class I
At3g22900	NRPD7, RNA polymerase Rpb7-like, N-terminal domain	Class I
At1g14040	EXS (ERD1/XPR1/SYG1) family protein	Class I
At3g52930	Aldolase superfamily protein	Class I
At2g29080	ftsh3, FTSH protease 3	Class I
At4g16680	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class I
At4g39640	GGT1, gamma-glutamyl transpeptidase 1	Class I
At2g32120	HSP70T-2, heat-shock protein 70T-2	Class I
At1g23480	ATCSLA03, ATCSLA3, CSLA03, CSLA03, CSLA3, cellulose synthase-like A3	Class I
At1g15080	ATLPP2, ATPAP2, LPP2, lipid phosphate phosphatase 2	Class I
At3g13320	atcax2, CAX2, cation exchanger 2	Class I
At1g43900	Protein phosphatase 2C family protein	Class I
At2g04040	ATDTX1, TX1, MATE efflux family protein	Class I
At3g56800	acam-3, CAM3, calmodulin 3	Class I
At2g30240	ATCHX13, CHX13, Cation/hydrogen exchanger family protein	Class I
At4g12730	FLA2, FASCICLIN-like arabinogalactan 2	Class I
At5g53110	RING/U-box superfamily protein	Class I
At5g05790	Duplicated homeodomain-like superfamily protein	Class I
At3g19020	Leucine-rich repeat (LRR) family protein	Class I
At5g17360	BEST Arabidopsis thaliana protein match is: DNA LIGASE 6 (TAIR:AT1G66730.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	Class I
At3g25610	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	Class I
At1g61890	MATE efflux family protein	Class I
At5g56980	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G26130.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At5g07730	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61360.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At3g59360	ATUTR6, UTR6, UDP-galactose transporter 6	Class I
At5g44320	Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)	Class I
At4g33666	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 11 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At5g42050	DCD (Development and Cell Death) domain protein	Class I
At4g19210	ATRLI2, RLI2, RNAse l inhibitor protein 2	Class I
At5g43450	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Class I
At2g07050	CAS1, cycloartenol synthase 1	Class I
At1g60190	ARM repeat superfamily protein	Class I
At1g68840	EDF2, RAP2.8, RAV2, TEM2, related to ABI3/VP1 2	Class I

At4g36640	Sec14p-like phosphatidylinositol transfer family protein	Class I
At3g53480	ABCG37, ATPDR9, PDR9, PIS1, pleiotropic drug resistance 9	Class I
At2g31690	alpha/beta-Hydrolases superfamily protein	Class I
At5g61910	DCD (Development and Cell Death) domain protein	Class I
At1g35140	EXL7, PHI-1, Phosphate-responsive 1 family protein	Class I
At3g04730	IAA16, indoleacetic acid-induced protein 16	Class I
At2g45400	BEN1, NAD(P)-binding Rossmann-fold superfamily protein	Class I
At1g30700	FAD-binding Berberine family protein	Class I
At4g00170	Plant VAMP (vesicle-associated membrane protein) family protein	Class I
At4g39090	RD19, RD19A, Papain family cysteine protease	Class I
At1g05330	unknown protein; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At5g01750	Protein of unknown function (DUF567)	Class I
At3g10985	ATWI-12, SAG20, WI12, senescence associated gene 20	Class I
At5g10690	pentatricopeptide (PPR) repeat-containing protein / CBS domain-containing protein	Class I
At3g17390	MAT4, MTO3, SAMS3, S-adenosylmethionine synthetase family protein	Class I
At2g18690	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF975 (InterPro:IPR010380); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18680.1); Has 213 Blast hits to 211 proteins in 20 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 205; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At3g52800	A20/AN1-like zinc finger family protein	Class I
At2g38480	Uncharacterised protein family (UPF0497)	Class I
At5g52750	Heavy metal transport/detoxification superfamily protein	Class I
At2g18190	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class I
At5g52400	CYP715A1, cytochrome P450, family 715, subfamily A, polypeptide 1	Class I
At1g11670	MATE efflux family protein	Class I
At4g25570	ACYB-2, Cytochrome b561/ferric reductase transmembrane protein family	Class I
At4g34160	CYCD3, CYCD3;1, CYCLIN D3;1	Class I
At3g22370	AOX1A, ATAOX1A, alternative oxidase 1A	Class I
At1g01550	BPS1, Protein of unknown function (DUF793)	Class I
At3g23250	ATMYB15, ATY19, MYB15, myb domain protein 15	Class I
At3g53610	ATRAB8, AtRab8B, AtRABE1a, RAB8, RAB GTPase homolog 8	Class I
At5g45110	ATNPR3, NPR3, NPR1-like protein 3	Class I
At5g45140	NRPC2, nuclear RNA polymerase C2	Class I
At3g50980	XERO1, dehydrin xero 1	Class I
At5g58060	ATGP1, ATYKT61, YKT61, SNARE-like superfamily protein	Class I
At1g79990	structural molecules	Class I
At5g03210	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 7 growth stages; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At5g57550	XTH25, XTR3, xyloglucan endotransglucosylase/hydrolase 25	Class I
At1g61360	S-locus lectin protein kinase family protein	Class I
At3g19240	Vacuolar import/degradation, Vid27-related protein	Class I
At5g66060	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Class I
At4g04500	CRK37, cysteine-rich RLK (RECEPTOR-like protein kinase) 37	Class I

At1g32070	ATNSI, NSI, nuclear shuttle interacting	Class I
At5g49220	Protein of unknown function (DUF789)	Class I
At2g04050	MATE efflux family protein	Class I
At1g09070	(AT)SRC2, SRC2, soybean gene regulated by cold-2	Class I
At5g55780	Cysteine/Histidine-rich C1 domain family protein	Class I
At5g06290	2-Cys Prx B, 2CPB, 2-cysteine peroxiredoxin B	Class I
At1g12960	Ribosomal protein L18e/L15 superfamily protein	Class I
At3g46620	zinc finger (C3HC4-type RING finger) family protein	Class I
At3g55640	Mitochondrial substrate carrier family protein	Class I
At5g01960	RING/U-box superfamily protein	Class I
At1g35910	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	Class I
At1g29680	Protein of unknown function (DUF1264)	Class I
At1g14530	THH1, Protein of unknown function (DUF1084)	Class I
At5g06320	NHL3, NDR1/HIN1-like 3	Class I
At1g05680	UGT74E2, Uridine diphosphate glycosyltransferase 74E2	Class I
At4g27270	Quinone reductase family protein	Class I
At3g50970	LTI30, XERO2, dehydrin family protein	Class I
At5g64240	AtMC3, MC3, metacaspase 3	Class I
At3g02040	SRG3, senescence-related gene 3	Class I
At4g05320	UBQ10, polyubiquitin 10	Class I
At3g16860	COBL8, COBRA-like protein 8 precursor	Class I
At5g04750	F1F0-ATPase inhibitor protein, putative	Class I
At4g36500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G18210.1); Has 50 Blast hits to 50 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At5g17460	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to salt stress; LOCATED IN: mitochondrion; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At3g49530	ANAC062, NAC062, NTL6, NAC domain containing protein 62	Class I
At1g22080	Cysteine proteinases superfamily protein	Class I
At4g37260	ATMYB73, MYB73, myb domain protein 73	Class I
At5g02240	NAD(P)-binding Rossmann-fold superfamily protein	Class I
At1g01720	ANAC002, ATAF1, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Class I
At5g13470	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	Class I
At1g59870	ABCG36, ATABCG36, ATPDR8, PDR8, PEN3, ABC-2 and Plant PDR ABC-type transporter family protein	Class I
At3g52450	PUB22, plant U-box 22	Class I
At1g49520	SWIB complex BAF60b domain-containing protein	Class I
At1g78290	SNRK2-8, SNRK2.8, SRK2C, Protein kinase superfamily protein	Class I
At3g63380	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	Class I
At5g25930	Protein kinase family protein with leucine-rich repeat domain	Class I
At4g24580	REN1, Rho GTPase activation protein (RhoGAP) with PH domain	Class I
At1g80850	DNA glycosylase superfamily protein	Class I

At5g37500	GORK, gated outwardly-rectifying K+ channel	Class I
At4g21850	ATMSRB9, MSRB9, methionine sulfoxide reductase B9	Class I
At3g09440	Heat shock protein 70 (Hsp 70) family protein	Class I
At3g14940	ATPPC3, PPC3, phosphoenolpyruvate carboxylase 3	Class I
At2g27090	Protein of unknown function (DUF630 and DUF632)	Class I
At3g45730	unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At5g63780	SHA1, RING/FYVE/PHD zinc finger superfamily protein	Class I
At3g08590	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	Class I
At2g40000	ATHSPRO2, HSPRO2, ortholog of sugar beet HS1 PRO-1 2	Class I
At5g66055	AKRP, EMB16, EMB2036, ankyrin repeat protein	Class I
At1g17870	ATEGY3, EGY3, ethylene-dependent gravitropism-deficient and yellow-green-like 3	Class I
At1g69220	SIK1, Protein kinase superfamily protein	Class I
At5g20240	PI, K-box region and MADS-box transcription factor family protein	Class I
At1g68760	ATNUDT1, ATNUDX1, NUDX1, NUDX1, nudix hydrolase 1	Class I
At1g20440	AtCOR47, COR47, RD17, cold-regulated 47	Class I
At1g19180	JAZ1, TIFY10A, jasmonate-zim-domain protein 1	Class I
At5g52410	CONTAINS InterPro DOMAIN/s: S-layer homology domain (InterPro:IPR001119); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23890.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At5g39580	Peroxidase superfamily protein	Class I
At5g15980	Pentatricopeptide repeat (PPR) superfamily protein	Class I
At3g24050	GATA1, GATA transcription factor 1	Class I
At1g61870	PPR336, pentatricopeptide repeat 336	Class I
At5g10710	INVOLVED IN: chromosome segregation, cell division; LOCATED IN: chromosome, centromeric region, nucleus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Centromere protein Cenp-O (InterPro:IPR018464); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At1g50750	Plant mobile domain protein family	Class I
At5g05420	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	Class I
At1g09080	BIP3, Heat shock protein 70 (Hsp 70) family protein	Class I
At1g58210	EMB1674, kinase interacting family protein	Class I
At5g02020	Encodes a protein involved in salt tolerance, names SIS (Salt Induced Serine rich).	Class I
At2g39190	ATATH8, Protein kinase superfamily protein	Class I
At1g62790	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	Class I
At4g26040	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At3g23460	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Class I
At2g36950	Heavy metal transport/detoxification superfamily protein	Class I
At5g04330	Cytochrome P450 superfamily protein	Class I
At2g23320	WRKY15, WRKY DNA-binding protein 15	Class I
At2g23810	TET8, tetraspanin8	Class I
At3g03890	FMN binding	Class I
At1g17180	ATGSTU25, GSTU25, glutathione S-transferase TAU 25	Class I
At1g56660	unknown protein; Has 665200 Blast hits to 205811 proteins in 4684 species: Archae - 3320; Bacteria - 107592; Metazoa - 249086; Fungi - 76753; Plants - 38542; Viruses - 3008; Other Eukaryotes - 186899 (source: NCBI BLink).	Class I

At4g33670	NAD(P)-linked oxidoreductase superfamily protein	Class I
At1g05340	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32210.1); Has 189 Blast hits to 189 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 21; Plants - 168; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At3g55440	ATCTIMC, CYTOTPI, TPI, triosephosphate isomerase	Class I
At3g49000	RNA polymerase III subunit RPC82 family protein	Class I
At4g25820	ATXTH14, XTH14, XTR9, xyloglucan endotransglucosylase/hydrolase 14	Class I
At1g27770	ACA1, PEA1, autoinhibited Ca2+-ATPase 1	Class I
At5g09990	PROPEP5, elicitor peptide 5 precursor	Class I
At5g10630	Translation elongation factor EF1A/initiation factor IF2gamma family protein	Class I
At4g16830	Hyaluronan / mRNA binding family	Class I
At3g13920	EIF4A1, RH4, TIF4A1, eukaryotic translation initiation factor 4A1	Class I
At1g25550	myb-like transcription factor family protein	Class I
At5g24650	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	Class I
At3g59350	Protein kinase superfamily protein	Class I
At2g29470	ATGSTU3, GST21, GSTU3, glutathione S-transferase tau 3	Class I
At4g33925	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At4g25580	CAP160 protein	Class I
At2g03750	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class I
At1g42990	ATBZIP60, BZIP60, BZIP60, basic region/leucine zipper motif 60	Class I
At5g36260	Eukaryotic aspartyl protease family protein	Class I
At1g78080	RAP2.4, related to AP2 4	Class I
At2g37975	Yos1-like protein	Class I
At5g55140	ribosomal protein L30 family protein	Class I
At3g08610	unknown protein; Has 40 Blast hits to 40 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At5g57190	PSD2, phosphatidylserine decarboxylase 2	Class I
At1g27720	TAF4, TAF4B, TBP-associated factor 4B	Class I
At1g30740	FAD-binding Berberine family protein	Class I
At2g24570	ATWRKY17, WRKY17, WRKY DNA-binding protein 17	Class I
At2g44790	UCC2, uclacyanin 2	Class I
At3g49780	ATPSK3 (FORMER SYMBOL), ATPSK4, PSK4, phytosulfokine 4 precursor	Class I
At3g51920	ATCML9, CAM9, CML9, calmodulin 9	Class I
At5g65660	hydroxyproline-rich glycoprotein family protein	Class I
At3g19030	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pyridoxine biosynthetic process, homoserine biosynthetic process; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49500.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At4g11570	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	Class I
At4g11560	bromo-adjacent homology (BAH) domain-containing protein	Class I
At3g19580	AZF2, ZF2, zinc-finger protein 2	Class I
At5g44330	Tetratricopeptide repeat (TPR)-like superfamily protein	Class I
At4g21820	binding;calmodulin binding	Class I

At3g08580	AAC1, ADP/ATP carrier 1	Class I
At5g66460	Glycosyl hydrolase superfamily protein	Class I
At1g74450	Protein of unknown function (DUF793)	Class I
At2g41110	ATCAL5, CAM2, calmodulin 2	Class I
At4g37270	ATHMA1, HMA1, heavy metal atpase 1	Class I
At1g29395	COR413-TM1, COR413IM1, COR414-TM1, COLD REGULATED 314 INNER MEMBRANE 1	Class I
At1g20450	ERD10, LTI29, LTI45, Dehydrin family protein	Class I
At1g32640	ATMYC2, JAI1, JIN1, MYC2, RD22BP1, ZBF1, Basic helix-loop-helix (bHLH) DNA-binding family protein	Class I
At5g47960	ATRABA4C, RABA4C, SMG1, RAB GTPase homolog A4C	Class I
At3g03810	EDA30, O-fucosyltransferase family protein	Class I
At1g62300	ATWRKY6, WRKY6, WRKY family transcription factor	Class I
At4g13390	Proline-rich extensin-like family protein	Class I
At2g39990	AteIF3f, EIF2, eIF3F, eukaryotic translation initiation factor 2	Class I
At5g59450	GRAS family transcription factor	Class I
At5g01380	Homeodomain-like superfamily protein	Class I
At4g37370	CYP81D8, cytochrome P450, family 81, subfamily D, polypeptide 8	Class I
At1g13210	ACA.l, autoinhibited Ca2+/ATPase II	Class I
At2g41620	Nucleoporin interacting component (Nup93/Nic96-like) family protein	Class I
At2g41740	ATVLN2, VLN2, villin 2	Class I
At5g18475	Pentatricopeptide repeat (PPR) superfamily protein	Class I
At2g17840	ERD7, Senescence/dehydration-associated protein-related	Class I
At2g25490	EBF1, FBL6, EIN3-binding F box protein 1	Class I
At4g20840	FAD-binding Berberine family protein	Class I
At1g53830	ATPME2, PME2, pectin methylesterase 2	Class I
At5g59830	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13660.2); Has 174 Blast hits to 139 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 172; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Class I
At1g01060	LHY, LHY1, Homeodomain-like superfamily protein	Class I
At1g31820	Amino acid permease family protein	Class I
At1g80010	FRS8, FAR1-related sequence 8	Class I
At2g45810	DEA(D/H)-box RNA helicase family protein	Class I
At1g55450	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Class I
At1g21850	sks8, SKU5 similar 8	Class I
At5g50900	ARM repeat superfamily protein	Class I
At3g56880	VQ motif-containing protein	Class I
At1g76180	ERD14, Dehydrin family protein	Class I
At4g25810	XTH23, XTR6, xyloglucan endotransglycosylase 6	Class I
At3g24170	ATGR1, GR1, glutathione-disulfide reductase	Class I
At5g47210	Hyaluronan / mRNA binding family	Class I
At5g07450	CYCP4;3, cyclin p4;3	Class I
At2g39670	Radical SAM superfamily protein	Class I
At1g56670	GDSL-like Lipase/Acylhydrolase superfamily protein	Class I
At5g08230	Tudor/PWWP/MBT domain-containing protein	Class I
At3g24560	RSY3, Adenine nucleotide alpha hydrolases-like superfamily protein	Class I
At1g17860	Kunitz family trypsin and protease inhibitor protein	Class I
At3g57460	catalytics;metal ion binding	Class I

At2g20570	ATGLK1, GLK1, GPRI1, GBF's pro-rich region-interacting factor 1	Class I
At3g21500	DXPS1, 1-deoxy-D-xylulose 5-phosphate synthase 1	Class I
At3g25650	ASK15, SK15, SKP1-like 15	Class I
At5g46780	VQ motif-containing protein	Class I
At5g43440	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Class I
At3g50910	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66480.1); Has 76 Blast hits to 75 proteins in 28 species: Archae - 0; Bacteria - 10; Metazoa - 7; Fungi - 2; Plants - 49; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).	Class I
At4g26180	Mitochondrial substrate carrier family protein	Class I
At3g25250	AGC2, AGC2-1, AtOXI1, OXI1, AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	Class I
At1g59600	ZCW7, ZCW7	Class I
At2g05720	Transducin/WD40 repeat-like superfamily protein	Class I
At2g43290	MSS3, Calcium-binding EF-hand family protein	Class I
At3g53760	ATGCP4, GCP4, GAMMA-TUBULIN COMPLEX PROTEIN 4	Class I
At5g11670	ATNADP-ME2, NADP-ME2, NADP-malic enzyme 2	Class I
At5g07740	actin binding	Class I
At5g27420	ATL31, CNI1, carbon/nitrogen insensitive 1	Class I
At3g15460	Ribosomal RNA processing Brix domain protein	Class I
At5g47230	ATERF-5, ATERF5, ERF5, ethylene responsive element binding factor 5	Class I
At3g62410	CP12, CP12-2, CP12 domain-containing protein 2	Class I
At5g03610	GDSL-like Lipase/Acylhydrolase superfamily protein	Class I
At4g05050	UBQ11, ubiquitin 11	Class I
At1g22200	Endoplasmic reticulum vesicle transporter protein	Class I
At4g32920	glycine-rich protein	Class I
At5g59820	RHL41, ZAT12, C2H2-type zinc finger family protein	Class I
At5g49030	OVA2, tRNA synthetase class I (I, L, M and V) family protein	Class I
At1g68670	myb-like transcription factor family protein	Class I
At5g26360	TCP-1/cpn60 chaperonin family protein	Class I
At5g24800	ATBZIP9, BZIP9, BZO2H2, basic leucine zipper 9	Class I
At4g00690	ULP1B, UB-like protease 1B	Class I
At3g06500	Plant neutral invertase family protein	Class I
At1g80930	MIF4G domain-containing protein / MA3 domain-containing protein	Class I
At1g69880	ATH8, TH8, thioredoxin H-type 8	Class I
At5g24930	ATCOL4, COL4, CONSTANS-like 4	Class I
At2g46260	BTB/POZ/Kelch-associated protein	Class I
At1g19020	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48180.1); Has 88 Blast hits to 88 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 88; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At1g68765	IDA, Putative membrane lipoprotein	Class I
At1g56590	ZIP4, Clathrin adaptor complexes medium subunit family protein	Class I
At5g01820	ATCIPK14, ATSR1, CIPK14, SnRK3.15, SR1, serine/threonine protein kinase 1	Class I
At4g05100	AtMYB74, MYB74, myb domain protein 74	Class I
At5g58070	ATTIL, TIL, temperature-induced lipocalin	Class I
At5g15090	ATVDAC3, VDAC3, voltage dependent anion channel 3	Class I
At3g06510	ATSFR2, SFR2, Glycosyl hydrolase superfamily protein	Class I
At2g40140	ATSZF2, CZF1, SZF2, ZFAR1, zinc finger (CCCH-type) family protein	Class I
At3g50960	PLP3a, phosducin-like protein 3 homolog	Class I

At1g17850	Rhodanese/Cell cycle control phosphatase superfamily protein	Class I
At1g28280	VQ motif-containing protein	Class I
At4g36010	Pathogenesis-related thaumatin superfamily protein	Class I
At3g44260	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	Class I
At5g35735	Auxin-responsive family protein	Class I
At1g01725	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G00530.1); Has 20 Blast hits to 20 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At3g45740	hydrolase family protein / HAD-superfamily protein	Class I
At3g55620	emb1624, Translation initiation factor IF6	Class I
At5g63790	ANAC102, NAC102, NAC domain containing protein 102	Class I
At2g34910	BEST Arabidopsis thaliana protein match is: root hair specific 4 (TAIR:AT1G30850.1); Has 43 Blast hits to 43 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At5g01510	RUS5, Protein of unknown function, DUF647	Class I
At2g43130	ARA-4, ARA4, ATRAB11F, ATRABA5C, RABA5C, P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class I
At3g22380	TIC, time for coffee	Class I
At1g45145	ATH5, ATTRX5, LIV1, TRX5, thioredoxin H-type 5	Class I
At1g22070	TGA3, TGA1A-related gene 3	Class I
At5g14740	BETA CA2, CA18, CA2, carbonic anhydrase 2	Class I
At2g18240	Rer1 family protein	Class I
At2g46420	Plant protein 1589 of unknown function	Class I
At5g56340	ATCRT1, RING/U-box superfamily protein	Class I
At5g18310	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48500.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At3g28690	Protein kinase superfamily protein	Class I
At3g15210	ATERF-4, ATERF4, ERF4, RAP2.5, ethylene responsive element binding factor 4	Class I
At1g69760	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26920.1); Has 51 Blast hits to 51 proteins in 15 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 7; Plants - 29; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Class I
At2g46390	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At2g17080	Arabidopsis protein of unknown function (DUF241)	Class I
At1g76170	2-thiocytidine tRNA biosynthesis protein, TtcA	Class I
At5g61890	Integrase-type DNA-binding superfamily protein	Class I
At2g20560	DNAJ heat shock family protein	Class I
At4g30600	signal recognition particle receptor alpha subunit family protein	Class I
At3g19570	Family of unknown function (DUF566)	Class I

At5g11740	AGP15, ATAGP15, arabinogalactan protein 15	Class I
At1g04530	Tetratricopeptide repeat (TPR)-like superfamily protein	Class I
At2g29490	ATGSTU1, GST19, GSTU1, glutathione S-transferase TAU 1	Class I
At5g61520	Major facilitator superfamily protein	Class I
At4g02880	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G03290.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At1g43910	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class I
At2g30250	ATWRKY25, WRKY25, WRKY DNA-binding protein 25	Class I
At4g08950	EXO, Phosphate-responsive 1 family protein	Class I
At4g20830	FAD-binding Berberine family protein	Class I
At1g18740	Protein of unknown function (DUF793)	Class I
At3g01560	Protein of unknown function (DUF1421)	Class I
At5g10700	Peptidyl-tRNA hydrolase II (PTH2) family protein	Class I
At2g41410	Calcium-binding EF-hand family protein	Class I
At4g33780	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: short hypocotyl in white light1 (TAIR:AT1G69935.1); Has 40 Blast hits to 40 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At3g60130	BGLU16, beta glucosidase 16	Class I
At1g42560	ATMLO9, MLO9, Seven transmembrane MLO family protein	Class I
At2g35930	PUB23, plant U-box 23	Class I
At3g04130	Tetratricopeptide repeat (TPR)-like superfamily protein	Class I
At5g49480	ATCP1, CP1, Ca2+-binding protein 1	Class I
At4g37010	CEN2, centrin 2	Class I
At3g52810	ATPAP21, PAP21, purple acid phosphatase 21	Class I
At1g10170	ATNFXL1, NFXL1, NF-X-like 1	Class I
At2g41000	Chaperone DnaJ-domain superfamily protein	Class I
At1g33590	Leucine-rich repeat (LRR) family protein	Class I
At5g64905	PROPEP3, elicitor peptide 3 precursor	Class I
At5g62530	ALDH12A1, ATP5CDH, P5CDH, aldehyde dehydrogenase 12A1	Class I
At1g79400	ATCHX2, CHX2, cation/H+ exchanger 2	Class I
At4g16670	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region	Class I
At4g27652	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27657.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At5g25280	serine-rich protein-related	Class I
At2g03760	AtSOT1, AtSOT12, ATST1, RAR047, SOT12, ST, ST1, sulphotransferase 12	Class I
At1g01460	ATPIPK11, PIPK11, Phosphatidylinositol-4-phosphate 5-kinase, core	Class I
At4g11670	Protein of unknown function (DUF810)	Class I
At4g27580	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, cell wall; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class I
At3g05310	MIRO3, MIRO-related GTP-ase 3	Class I

At3g12120	FAD2, fatty acid desaturase 2	Class I
At4g28460	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; Has 8 Blast hits to 8 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At2g17670	Tetratricopeptide repeat (TPR)-like superfamily protein	Class I
At3g61640	AGP20, AtAGP20, arabinogalactan protein 20	Class I
At4g18170	ATWRKY28, WRKY28, WRKY DNA-binding protein 28	Class I
At4g31805	WRKY family transcription factor	Class I
At1g76600	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: nucleolus, nucleus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21010.1); Has 220 Blast hits to 220 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 220; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At1g65510	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: LP.06 six leaves visible, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage, LP.08 eight leaves visible; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G65486.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class I
At2g46830	CCA1, circadian clock associated 1	Class I
At4g30440	GAE1, UDP-D-glucuronate 4-epimerase 1	Class I
At5g65205	NAD(P)-binding Rossmann-fold superfamily protein	Class I
At5g40690	CONTAINS InterPro DOMAIN/s: EF-Hand 1, calcium-binding site (InterPro:IPR018247); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41730.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	Class I
At1g74310	ATHSP101, HOT1, HSP101, heat shock protein 101	Class I
At5g01950	Leucine-rich repeat protein kinase family protein	Class I
At1g56050	GTP-binding protein-related	Class I
At1g22840	ATCYTC-A, CYTC-1, CYTOCHROME C-1	Class I
At4g19200	proline-rich family protein	Class I
At1g19025	DNA repair metallo-beta-lactamase family protein	Class I
At2g05710	ACO3, aconitase 3	Class I
At1g08940	Phosphoglycerate mutase family protein	Class I
At2g47000	ABCB4, ATPGP4, MDR4, PGP4, ATP binding cassette subfamily B4	Class I
At3g27510	Cysteine/Histidine-rich C1 domain family protein	Class I
At4g27280	Calcium-binding EF-hand family protein	Class I
At1g71697	ATCK1, CK, CK1, choline kinase 1	Class I
At4g21490	NDB3, NAD(P)H dehydrogenase B3	Class I
At5g47970	Aldolase-type TIM barrel family protein	Class I
At1g18310	glycosyl hydrolase family 81 protein	Class I
At1g71530	Protein kinase superfamily protein	Class I
At2g32150	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	Class I
At1g59590	ZCF37, ZCF37	Class I
At1g19770	ATPUP14, PUP14, purine permease 14	Class I

At4g29790	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G19390.1); Has 538 Blast hits to 357 proteins in 124 species: Archae - 0; Bacteria - 74; Metazoa - 109; Fungi - 58; Plants - 105; Viruses - 2; Other Eukaryotes - 190 (source: NCBI BLink).	Class I
At1g27760	ATSAT32, SAT32, interferon-related developmental regulator family protein / IFRD protein family	Class I
At1g11560	Oligosaccharyltransferase complex/magnesium transporter family protein	Class I
At2g04880	ATWRKY1, WRKY1, ZAP1, zinc-dependent activator protein-1	Class I
At1g53840	ATPME1, PME1, pectin methylesterase 1	Class I
ClassIIA. BA: bind and activate		
At1g69490	ANAC029, ATNAP, NAP, NAC-like, activated by AP3/PI	Class IIA
At5g03380	Heavy metal transport/detoxification superfamily protein	Class IIA
At2g23170	GH3.3, Auxin-responsive GH3 family protein	Class IIA
At1g66170	MMD1, RING/FYVE/PHD zinc finger superfamily protein	Class IIA
At4g20860	FAD-binding Berberine family protein	Class IIA
At3g12320	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G06980.4); Has 102 Blast hits to 102 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 98; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Class IIA
At5g06300	Putative lysine decarboxylase family protein	Class IIA
At3g15630	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52720.1); Has 61 Blast hits to 61 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 61; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIA
At3g19930	ATSTP4, STP4, sugar transporter 4	Class IIA
At1g43160	RAP2.6, related to AP2 6	Class IIA
At3g01290	SPFH/Band 7/PHB domain-containing membrane-associated protein family	Class IIA
At2g39200	ATMLO12, MLO12, Seven transmembrane MLO family protein	Class IIA
At3g14990	Class I glutamine amidotransferase-like superfamily protein	Class IIA
At1g69890	Protein of unknown function (DUF569)	Class IIA
At4g15610	Uncharacterised protein family (UPF0497)	Class IIA
At3g15450	Aluminium induced protein with YGL and LRDR motifs	Class IIA
At1g62570	FMO GS-OX4, flavin-monooxygenase glucosinolate S-oxygenase 4	Class IIA
At1g29400	AML5, ML5, MEI2-like protein 5	Class IIA
At1g32930	Galactosyltransferase family protein	Class IIA
At5g67420	ASL39, LBD37, LOB domain-containing protein 37	Class IIA
At5g64120	Peroxidase superfamily protein	Class IIA
At3g30775	AT-POX, ATPDH, ATPOX, ERD5, PRO1, PRODH, Methylenetetrahydrofolate reductase family protein	Class IIA
At1g22830	Tetratricopeptide repeat (TPR)-like superfamily protein	Class IIA
At1g22190	Integrase-type DNA-binding superfamily protein	Class IIA
At2g22870	EMB2001, P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class IIA
At5g11090	serine-rich protein-related	Class IIA
At5g07440	GDH2, glutamate dehydrogenase 2	Class IIA
At5g67310	CYP81G1, cytochrome P450, family 81, subfamily G, polypeptide 1	Class IIA
At1g68440	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G25400.2); Has 86 Blast hits to 86 proteins in 29 species: Archae - 0; Bacteria - 6; Metazoa - 27; Fungi - 11; Plants - 24; Viruses - 0; Other Eukaryotes - 18 (source: NCBI	Class IIA

	BLink).	
At1g15040	Class I glutamine amidotransferase-like superfamily protein	Class IIA
At5g43580	Serine protease inhibitor, potato inhibitor I-type family protein	Class IIA
At3g49790	Carbohydrate-binding protein	Class IIA
At5g52050	MATE efflux family protein	Class IIA
At5g12340	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G28190.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class IIA
At4g27657	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	Class IIA
At5g02810	APRR7, PRR7, pseudo-response regulator 7	Class IIA
At3g45970	ATEXLA1, ATEXPL1, ATHEXP BETA 2.1, EXLA1, EXPL1, expansin-like A1	Class IIA
At4g20870	ATFAH2, FAH2, fatty acid hydroxylase 2	Class IIA
At1g64670	BDG1, alpha/beta-Hydrolases superfamily protein	Class IIA
At3g60140	BGLU30, DIN2, SRG2, Glycosyl hydrolase superfamily protein	Class IIA
At1g64660	ATMGL, MGL, methionine gamma-lyase	Class IIA
At5g67300	ATMYB44, ATMYBR1, MYB44, MYBR1, myb domain protein r1	Class IIA
At5g20150	ATSPX1, SPX1, SPX domain gene 1	Class IIA
At4g36040	Chaperone DnaJ-domain superfamily protein	Class IIA
At5g40780	LHT1, lysine histidine transporter 1	Class IIA
At1g80380	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Class IIA
At1g27100	Actin cross-linking protein	Class IIA
At3g15620	UVR3, DNA photolyase family protein	Class IIA
At5g01600	ATFER1, FER1, ferretin 1	Class IIA
At3g52710	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36220.1); Has 64 Blast hits to 64 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIA
At3g04070	anac047, NAC047, NAC domain containing protein 47	Class IIA
At4g37590	NPY5, Phototropic-responsive NPH3 family protein	Class IIA
At5g45630	Protein of unknown function, DUF584	Class IIA
ClassIIB. BR: bind and repress		
At3g50900	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66490.1); Has 45 Blast hits to 45 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At5g57500	Galactosyltransferase family protein	Class IIB
At1g19190	alpha/beta-Hydrolases superfamily protein	Class IIB
At2g25735	unknown protein; Has 31 Blast hits to 31 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB

At1g56060	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32210.1); Has 180 Blast hits to 180 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 10; Plants - 170; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At4g08850	Leucine-rich repeat receptor-like protein kinase family protein	Class IIB
At5g08240	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23160.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 1; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At3g21070	ATNADK-1, NADK1, NAD kinase 1	Class IIB
At4g37910	mtHsc70-1, mitochondrial heat shock protein 70-1	Class IIB
At4g12720	AtNUDT7, ATNUDX7, GFG1, NUDT7, MutT/nudix family protein	Class IIB
At3g02880	Leucine-rich repeat protein kinase family protein	Class IIB
At3g06490	AtMYB108, BOS1, MYB108, myb domain protein 108	Class IIB
At1g18210	Calcium-binding EF-hand family protein	Class IIB
At5g26030	ATFC-I, FC-I, FC1, ferrochelatase 1	Class IIB
At3g55630	ATDFD, DFD, DHFS-FPGS homolog D	Class IIB
At4g24390	RNI-like superfamily protein	Class IIB
At2g41730	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At5g41810	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64340.1); Has 876 Blast hits to 690 proteins in 132 species: Archae - 0; Bacteria - 38; Metazoa - 180; Fungi - 112; Plants - 59; Viruses - 2; Other Eukaryotes - 485 (source: NCBI BLink).	Class IIB
At5g02230	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	Class IIB
At1g16670	Protein kinase superfamily protein	Class IIB
At3g04120	GAPC, GAPC-1, GAPC1, glyceraldehyde-3-phosphate dehydrogenase C subunit 1	Class IIB
At2g32220	Ribosomal L27e protein family	Class IIB
At5g37770	CML24, TCH2, EF hand calcium-binding protein family	Class IIB
At2g38470	ATWRKY33, WRKY33, WRKY DNA-binding protein 33	Class IIB
At4g30290	ATXTH19, XTH19, xyloglucan endotransglucosylase/hydrolase 19	Class IIB
At5g39670	Calcium-binding EF-hand family protein	Class IIB
At1g08510	FATB, fatty acyl-ACP thioesterases B	Class IIB
At3g57450	unknown protein; Has 65 Blast hits to 65 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At2g35980	ATNHL10, NHL10, YLS9, Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	Class IIB
At3g24550	ATPERK1, PERK1, proline extensin-like receptor kinase 1	Class IIB
At1g80820	ATCCR2, CCR2, cinnamoyl coa reductase	Class IIB
At4g34150	Calcium-dependent lipid-binding (CaLB domain) family protein	Class IIB
At5g01540	LECRKA4.1, lectin receptor kinase a4.1	Class IIB
At1g14540	Peroxidase superfamily protein	Class IIB
At2g41630	TFIIB, transcription factor IIB	Class IIB
At2g38830	Ubiquitin-conjugating enzyme/RWD-like protein	Class IIB
At3g54150	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Class IIB
At4g11350	Protein of unknown function (DUF604)	Class IIB
At4g37900	Protein of unknown function (duplicated DUF1399)	Class IIB
At4g30210	AR2, ATR2, P450 reductase 2	Class IIB
At4g02380	AtLEA5, SAG21, senescence-associated gene 21	Class IIB

At1g73510	unknown protein; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At2g41890	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein	Class IIB
At1g14550	Peroxidase superfamily protein	Class IIB
At4g30280	ATXTH18, XTH18, xyloglucan endotransglucosylase/hydrolase 18	Class IIB
At5g39680	EMB2744, Pentatricopeptide repeat (PPR) superfamily protein	Class IIB
At4g39260	ATGRP8, CCR1, GR-RBP8, GRP8, cold, circadian rhythm, and RNA binding 1	Class IIB
At4g38420	sks9, SKU5 similar 9	Class IIB
At2g46140	Late embryogenesis abundant protein	Class IIB
At1g78340	ATGSTU22, GSTU22, glutathione S-transferase TAU 22	Class IIB
At2g39660	BIK1, botrytis-induced kinase1	Class IIB
At4g18880	AT-HSFA4A, HSF A4A, heat shock transcription factor A4A	Class IIB
At4g40040	Histone superfamily protein	Class IIB
At4g11360	RHA1B, RING-H2 finger A1B	Class IIB
At4g30530	Class I glutamine amidotransferase-like superfamily protein	Class IIB
At1g30370	alpha/beta-Hydrolases superfamily protein	Class IIB
At4g40030	Histone superfamily protein	Class IIB
At5g47910	ATRBOHD, RBOHD, respiratory burst oxidase homologue D	Class IIB
At5g64310	AGP1, ATAGP1, arabinogalactan protein 1	Class IIB
At5g42830	HXXXD-type acyl-transferase family protein	Class IIB
At1g73010	ATPS2, PS2, phosphate starvation-induced gene 2	Class IIB
At5g19240	Glycoprotein membrane precursor GPI-anchored	Class IIB
At1g06760	winged-helix DNA-binding transcription factor family protein	Class IIB
At2g22500	ATPUMP5, DIC1, UCP5, uncoupling protein 5	Class IIB
At4g32020	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25250.1); Has 65 Blast hits to 65 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 8; Plants - 54; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Class IIB
At2g17660	RPM1-interacting protein 4 (RIN4) family protein	Class IIB
At2g22470	AGP2, ATAGP2, arabinogalactan protein 2	Class IIB
ClassIIIA. NA: No binding but activation		
At3g15440	BEST Arabidopsis thaliana protein match is: RING/U-box superfamily protein (TAIR:AT3G15740.1); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At4g15280	UGT71B5, UDP-glucosyl transferase 71B5	ClassIIIA
At3g27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3	ClassIIIA
At5g67450	AZF1, ZF1, zinc-finger protein 1	ClassIIIA
At1g18460	alpha/beta-Hydrolases superfamily protein	ClassIIIA
At1g03600	PSB27, photosystem II family protein	ClassIIIA
At5g44380	FAD-binding Berberine family protein	ClassIIIA
At3g24310	ATMYB71, MYB305, myb domain protein 305	ClassIIIA
At3g14780	CONTAINS InterPro DOMAIN/s: Transposase, Ptta/En/Spm, plant (InterPro:IPR004252); BEST Arabidopsis thaliana protein match is: glucan synthase-like 4 (TAIR:AT3G14570.2); Has 315 Blast hits to 313 proteins in 50 species: Archae - 2; Bacteria - 16; Metazoa - 11; Fungi - 7; Plants - 181; Viruses - 2; Other Eukaryotes - 96 (source: NCBI BLink).	ClassIIIA
At5g65110	ACX2, ATACX2, acyl-CoA oxidase 2	ClassIIIA
At1g23870	ATTPS9, TPS9, TPS9, trehalose-phosphatase/synthase 9	ClassIIIA

At1g08720	ATEDR1, EDR1, Protein kinase superfamily protein	ClassIIIA
At3g03170	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24890.1); Has 184 Blast hits to 184 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 184; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At1g02860	BAH1, NLA, SPX (SYG1/Pho81/XPR1) domain-containing protein	ClassIIIA
At1g08830	CSD1, copper/zinc superoxide dismutase 1	ClassIIIA
At5g63800	BGAL6, MUM2, Glycosyl hydrolase family 35 protein	ClassIIIA
At4g37790	HAT22, Homeobox-leucine zipper protein family	ClassIIIA
At3g02150	PTF1, TCP13, TFPD, plastid transcription factor 1	ClassIIIA
At5g64460	Phosphoglycerate mutase family protein	ClassIIIA
At2g33150	KAT2, PED1, PKT3, peroxisomal 3-ketoacyl-CoA thiolase 3	ClassIIIA
At1g06570	HPD, PDS1, phytoene desaturation 1	ClassIIIA
At3g14750	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67170.1); Has 4036 Blast hits to 3091 proteins in 519 species: Archae - 61; Bacteria - 669; Metazoa - 1503; Fungi - 255; Plants - 421; Viruses - 4; Other Eukaryotes - 1123 (source: NCBI BLink).	ClassIIIA
At1g18330	EPR1, RVE7, Homeodomain-like superfamily protein	ClassIIIA
At3g49060	U-box domain-containing protein kinase family protein	ClassIIIA
At3g16800	Protein phosphatase 2C family protein	ClassIIIA
At1g72770	HAB1, homology to ABI1	ClassIIIA
At5g20050	Protein kinase superfamily protein	ClassIIIA
At1g18260	HCP-like superfamily protein	ClassIIIA
At2g26280	CID7, CTC-interacting domain 7	ClassIIIA
At5g13760	Plasma-membrane choline transporter family protein	ClassIIIA
At1g55020	ATLOX1, LOX1, lipoxygenase 1	ClassIIIA
At5g03720	AT-HSFA3, HSFA3, heat shock transcription factor A3	ClassIIIA
At1g76240	Arabidopsis protein of unknown function (DUF241)	ClassIIIA
At3g11340	UDP-Glycosyltransferase superfamily protein	ClassIIIA
At3g16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	ClassIIIA
At2g34600	JAZ7, TIFY5B, jasmonate-zim-domain protein 7	ClassIIIA
At3g43430	RING/U-box superfamily protein	ClassIIIA
At2g41200	unknown protein; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At1g75230	DNA glycosylase superfamily protein	ClassIIIA
At1g52240	ATROPGEF11, PIRF1, ROPGEF11, RHO guanyl-nucleotide exchange factor 11	ClassIIIA
At1g13080	CYP71B2, cytochrome P450, family 71, subfamily B, polypeptide 2	ClassIIIA
At1g68400	leucine-rich repeat transmembrane protein kinase family protein	ClassIIIA
At1g56145	Leucine-rich repeat transmembrane protein kinase	ClassIIIA
At5g61510	GroES-like zinc-binding alcohol dehydrogenase family protein	ClassIIIA
At2g26600	Glycosyl hydrolase superfamily protein	ClassIIIA
At1g02670	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ClassIIIA
At1g14340	RNA-binding (RRM/RBD/RNP motifs) family protein	ClassIIIA
At2g41190	Transmembrane amino acid transporter family protein	ClassIIIA
At1g06520	ATGPAT1, GPAT1, glycerol-3-phosphate acyltransferase 1	ClassIIIA
At1g23880	NHL domain-containing protein	ClassIIIA
At3g52060	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	ClassIIIA
At1g08980	AMI1, ATAMI1, ATTOC64-I, TOC64-I, amidase 1	ClassIIIA
At5g37260	CIR1, RVE2, Homeodomain-like superfamily protein	ClassIIIA

At4g23880	unknown protein; Has 73 Blast hits to 69 proteins in 22 species: Archae - 0; Bacteria - 4; Metazoa - 9; Fungi - 2; Plants - 18; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink).	ClassIIIA
At4g38200	SEC7-like guanine nucleotide exchange family protein	ClassIIIA
At5g59590	UGT76E2, UDP-glucosyl transferase 76E2	ClassIIIA
At1g25275	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 18 Blast hits to 18 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At2g29380	HAI3, highly ABA-induced PP2C gene 3	ClassIIIA
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1	ClassIIIA
At5g57655	xylose isomerase family protein	ClassIIIA
At4g01110	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G01453.1); Has 273 Blast hits to 272 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 273; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At3g54960	ATPDI1, ATPDIL1-3, PDI1, PDIL1-3, PDI-like 1-3	ClassIIIA
At3g54620	ATBZIP25, BZIP25, BZO2H4, basic leucine zipper 25	ClassIIIA
At1g03870	FLA9, FASCICLIN-like arabinoogalactan 9	ClassIIIA
At3g19400	Cysteine proteinases superfamily protein	ClassIIIA
At3g13965	pseudogene, hypothetical protein	ClassIIIA
At4g32960	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32970.1); Has 106 Blast hits to 106 proteins in 39 species: Archae - 0; Bacteria - 0; Metazoa - 62; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	ClassIIIA
At5g51850	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62170.1); Has 384 Blast hits to 375 proteins in 79 species: Archae - 0; Bacteria - 14; Metazoa - 135; Fungi - 31; Plants - 92; Viruses - 0; Other Eukaryotes - 112 (source: NCBI BLink).	ClassIIIA
At3g29240	Protein of unknown function (DUF179)	ClassIIIA
At3g29160	AKIN11, ATKIN11, KIN11, SNRK1.2, SNF1 kinase homolog 11	ClassIIIA
At5g56100	glycine-rich protein / oleosin	ClassIIIA
At5g47740	Adenine nucleotide alpha hydrolases-like superfamily protein	ClassIIIA
At1g03100	Pentatricopeptide repeat (PPR) superfamily protein	ClassIIIA
At1g67480	Galactose oxidase/kelch repeat superfamily protein	ClassIIIA
At5g08350	GRAM domain-containing protein / ABA-responsive protein-related	ClassIIIA
At3g23230	Integrase-type DNA-binding superfamily protein	ClassIIIA
At4g28040	nodulin MtN21 /EamA-like transporter family protein	ClassIIIA
At5g47560	ATSDAT, ATTDT, TDT, tonoplast dicarboxylate transporter	ClassIIIA
At5g04040	SDP1, Patatin-like phospholipase family protein	ClassIIIA
At4g27480	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	ClassIIIA
At1g08930	ERD6, Major facilitator superfamily protein	ClassIIIA
At3g15650	alpha/beta-Hydrolases superfamily protein	ClassIIIA
At1g79700	Integrase-type DNA-binding superfamily protein	ClassIIIA
At3g24520	AT-HSFC1, HSFC1, heat shock transcription factor C1	ClassIIIA
At4g36730	GBF1, G-box binding factor 1	ClassIIIA
At4g01030	pentatricopeptide (PPR) repeat-containing protein	ClassIIIA
At1g79340	AtMC4, MC4, metacaspase 4	ClassIIIA
At1g10560	ATPUB18, PUB18, plant U-box 18	ClassIIIA

At2g43400	ETFQO, electron-transfer flavoprotein:ubiquinone oxidoreductase	ClassIIIA
At5g56180	ARP8, ARP8, ATARP8, actin-related protein 8	ClassIIIA
At5g18170	GDH1, glutamate dehydrogenase 1	ClassIIIA
At4g16690	ATMES16, MES16, methyl esterase 16	ClassIIIA
At2g32510	MAPKKK17, mitogen-activated protein kinase kinase kinase 17	ClassIIIA
At1g76185	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G20460.1); Has 37 Blast hits to 37 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At2g44360	unknown protein; Has 23 Blast hits to 23 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At3g45300	ATIVD, IVD, IVDH, isovaleryl-CoA-dehydrogenase	ClassIIIA
At3g22920	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	ClassIIIA
At4g39730	Lipase/lipooxygenase, PLAT/LH2 family protein	ClassIIIA
At4g14500	Polyketide cyclase/dehydrase and lipid transport superfamily protein	ClassIIIA
At3g14740	RING/FYVE/PHD zinc finger superfamily protein	ClassIIIA
At3g13450	DIN4, Transketolase family protein	ClassIIIA
At3g05200	ATL6, RING/U-box superfamily protein	ClassIIIA
At2g28120	Major facilitator superfamily protein	ClassIIIA
At2g02700	Cysteine/Histidine-rich C1 domain family protein	ClassIIIA
At4g26290	unknown protein; Has 9 Blast hits to 9 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	ClassIIIA
At4g30170	Peroxidase family protein	ClassIIIA
At3g11410	AHG3, ATPP2CA, PP2CA, protein phosphatase 2CA	ClassIIIA
At1g10060	ATBCAT-1, BCAT-1, branched-chain amino acid transaminase 1	ClassIIIA
At1g63710	CYP86A7, cytochrome P450, family 86, subfamily A, polypeptide 7	ClassIIIA
At3g49940	LBD38, LOB domain-containing protein 38	ClassIIIA
At3g22930	CML11, calmodulin-like 11	ClassIIIA
At2g19320	unknown protein; Has 9 Blast hits to 9 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At4g34350	CLB6, HDR, ISPH, 4-hydroxy-3-methylbut-2-enyl diphosphate reductase	ClassIIIA
At5g61590	Integrase-type DNA-binding superfamily protein	ClassIIIA
At2g28630	KCS12, 3-ketoacyl-CoA synthase 12	ClassIIIA
At2g19800	MIOX2, myo-inositol oxygenase 2	ClassIIIA
At3g56240	CCH, copper chaperone	ClassIIIA
At1g56700	Peptidase C15, pyroglutamyl peptidase I-like	ClassIIIA
At5g67440	NPY3, Phototropic-responsive NPH3 family protein	ClassIIIA
At5g43190	Galactose oxidase/kelch repeat superfamily protein	ClassIIIA
At2g15695	Protein of unknown function DUF829, transmembrane 53	ClassIIIA
At5g16110	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02555.1); Has 133 Blast hits to 133 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At1g66890	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: 50S ribosomal protein-related (TAIR:AT5G16200.1); Has 36 Blast hits to 36 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA

At3g57540	Remorin family protein	ClassIIIA
At1g61740	Sulfite exporter TauE/SafE family protein	ClassIIIA
At1g67470	Protein kinase superfamily protein	ClassIIIA
At5g49440	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIA
At4g01870	tolB protein-related	ClassIIIA
At4g21440	ATM4, ATMYB102, MYB102, MYB102, MYB-like 102	ClassIIIA
At4g29950	Ypt/Rab-GAP domain of gyp1p superfamily protein	ClassIIIA
At3g51860	ATCAX3, ATHCX1, CAX1-LIKE, CAX3, cation exchanger 3	ClassIIIA
At1g16150	WAKL4, wall associated kinase-like 4	ClassIIIA
At1g67880	beta-1,4-N-acetylglucosaminyltransferase family protein	ClassIIIA
At1g08630	THA1, threonine aldolase 1	ClassIIIA
At1g28130	GH3.17, Auxin-responsive GH3 family protein	ClassIIIA
At3g55150	ATEXO70H1, EXO70H1, exocyst subunit exo70 family protein H1	ClassIIIA
At1g76160	sks5, SKU5 similar 5	ClassIIIA
At4g37220	Cold acclimation protein WCOR413 family	ClassIIIA
At2g31380	STH, salt tolerance homologue	ClassIIIA
At3g14050	AT-RSH2, ATRSH2, RSH2, RELA/SPOT homolog 2	ClassIIIA
At3g14770	Nodulin MtN3 family protein	ClassIIIA
At5g57630	CIPK21, SnRK3.4, CBL-interacting protein kinase 21	ClassIIIA
At5g24530	DMR6, 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	ClassIIIA
At3g56000	ATCSLA14, CSLA14, cellulose synthase like A14	ClassIIIA
At1g15060	Uncharacterised conserved protein UCP031088, alpha/beta hydrolase	ClassIIIA
At2g28200	C2H2-type zinc finger family protein	ClassIIIA
At4g33420	Peroxidase superfamily protein	ClassIIIA
At5g18650	CHY-type/CTCHY-type/RING-type Zinc finger protein	ClassIIIA
At1g66070	Translation initiation factor eIF3 subunit	ClassIIIA
At2g10640	transposable element gene	ClassIIIA
At5g18610	Protein kinase superfamily protein	ClassIIIA
At4g15620	Uncharacterised protein family (UPF0497)	ClassIIIA
At5g50200	ATNRT3.1, NRT3.1, WR3, nitrate transmembrane transporters	ClassIIIA
At4g01330	Protein kinase superfamily protein	ClassIIIA
At5g46590	anac096, NAC096, NAC domain containing protein 96	ClassIIIA
At2g39570	ACT domain-containing protein	ClassIIIA
At5g04740	ACT domain-containing protein	ClassIIIA
At1g08920	ESL1, ERD (early response to dehydration) six-like 1	ClassIIIA
At1g09460	Carbohydrate-binding X8 domain superfamily protein	ClassIIIA
At4g38060	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65480.1); Has 63 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At3g57420	Protein of unknown function (DUF288)	ClassIIIA
At5g54080	HGO, homogentisate 1,2-dioxygenase	ClassIIIA
At3g06780	glycine-rich protein	ClassIIIA
At2g22080	unknown protein; Has 96314 Blast hits to 34847 proteins in 1702 species: Archae - 612; Bacteria - 27969; Metazoa - 24311; Fungi - 12153; Plants - 4409; Viruses - 1572; Other Eukaryotes - 25288 (source: NCBI BLink).	ClassIIIA
At1g49670	NQR, ARP protein (REF)	ClassIIIA

At2g03740	late embryogenesis abundant domain-containing protein / LEA domain-containing protein	ClassIIIA
At5g56870	BGAL4, beta-galactosidase 4	ClassIIIA
At4g33150	LKR, LKR/SDH, SDH, lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme	ClassIIIA
At1g23550	SRO2, similar to RCD one 2	ClassIIIA
At2g12400	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25270.1); Has 177 Blast hits to 172 proteins in 23 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 0; Plants - 164; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).	ClassIIIA
At1g12080	Vacuolar calcium-binding protein-related	ClassIIIA
At5g01590	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 59 proteins in 31 species: Archae - 0; Bacteria - 20; Metazoa - 1; Fungi - 2; Plants - 33; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	ClassIIIA
At4g19810	Glycosyl hydrolase family protein with chitinase insertion domain	ClassIIIA
At3g17440	ATNPSN13, NPSN13, novel plant snare 13	ClassIIIA
At5g03350	Legume lectin family protein	ClassIIIA
At2g44670	Protein of unknown function (DUF581)	ClassIIIA
At5g28050	Cytidine/deoxycytidylate deaminase family protein	ClassIIIA
At5g10450	14-3-3lambda, AFT1, GRF6, G-box regulating factor 6	ClassIIIA
At4g23870	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11020.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At1g69910	Protein kinase superfamily protein	ClassIIIA
At5g13110	G6PD2, glucose-6-phosphate dehydrogenase 2	ClassIIIA
At1g14330	Galactose oxidase/kelch repeat superfamily protein	ClassIIIA
At1g06560	NOL1/NOP2/sun family protein	ClassIIIA
At3g16170	AMP-dependent synthetase and ligase family protein	ClassIIIA
At5g20250	DIN10, Raffinose synthase family protein	ClassIIIA
At5g49690	UDP-Glycosyltransferase superfamily protein	ClassIIIA
At1g07250	UGT71C4, UDP-glucosyl transferase 71C4	ClassIIIA
At3g51540	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G08670.1); Has 22744 Blast hits to 9965 proteins in 783 species: Archae - 64; Bacteria - 2760; Metazoa - 8515; Fungi - 3864; Plants - 499; Viruses - 702; Other Eukaryotes - 6340 (source: NCBI BLink).	ClassIIIA
At3g30396	transposable element gene	ClassIIIA
At1g67510	Leucine-rich repeat protein kinase family protein	ClassIIIA
At2g39130	Transmembrane amino acid transporter family protein	ClassIIIA
At5g23050	AAE17, acyl-activating enzyme 17	ClassIIIA
At1g22360	AtUGT85A2, UGT85A2, UDP-glucosyl transferase 85A2	ClassIIIA
At2g32660	AtRLP22, RLP22, receptor like protein 22	ClassIIIA
At1g54740	Protein of unknown function (DUF3049)	ClassIIIA
At1g03080	kinase interacting (KIP1-like) family protein	ClassIIIA
At4g38490	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIA

At4g36790	Major facilitator superfamily protein	ClassIIIA
At4g38480	Transducin/WD40 repeat-like superfamily protein	ClassIIIA
At3g61070	PEX11E, peroxin 11E	ClassIIIA
At3g45060	ATNRT2.6, NRT2.6, high affinity nitrate transporter 2.6	ClassIIIA
At4g33910	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	ClassIIIA
At1g58180	ATBCA6, BCA6, beta carbonic anhydrase 6	ClassIIIA
At1g71980	Protease-associated (PA) RING/U-box zinc finger family protein	ClassIIIA
At1g57680	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031277 (InterPro:IPR016971); Has 70 Blast hits to 70 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 66; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	ClassIIIA
At3g46280	protein kinase-related	ClassIIIA
At1g30820	CTP synthase family protein	ClassIIIA
At3g13460	ECT2, evolutionarily conserved C-terminal region 2	ClassIIIA
At4g17140	pleckstrin homology (PH) domain-containing protein	ClassIIIA
At5g16120	alpha/beta-Hydrolases superfamily protein	ClassIIIA
At1g04410	Lactate/malate dehydrogenase family protein	ClassIIIA
At4g27260	GH3.5, WES1, Auxin-responsive GH3 family protein	ClassIIIA
At1g66470	RHD6, ROOT HAIR DEFECTIVE6	ClassIIIA
At2g02040	ATPTR2, ATPTR2-B, NTR1, PTR2, PTR2-B, peptide transporter 2	ClassIIIA
At3g05390	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF248, methyltransferase putative (InterPro:IPR004159); BEST Arabidopsis thaliana protein match is: S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (TAIR:AT4G01240.1); Has 507 Blast hits to 498 proteins in 33 species: Archae - 4; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 493; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	ClassIIIA
At4g03510	ATRMA1, RMA1, RING membrane-anchor 1	ClassIIIA
At3g20860	ATNEK5, NEK5, NIMA-related kinase 5	ClassIIIA
At3g62650	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G47485.1); Has 57 Blast hits to 57 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At1g54100	ALDH7B4, aldehyde dehydrogenase 7B4	ClassIIIA
At3g47500	CDF3, cycling DOF factor 3	ClassIIIA
At5g13750	ZIFL1, zinc induced facilitator-like 1	ClassIIIA
At3g51730	saposin B domain-containing protein	ClassIIIA
At1g67810	SUFE2, sulfur E2	ClassIIIA
At3g52490	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	ClassIIIA
At3g48690	ATCXE12, CXE12, alpha/beta-Hydrolases superfamily protein	ClassIIIA
At3g55450	PBL1, PBS1-like 1	ClassIIIA
At1g68620	alpha/beta-Hydrolases superfamily protein	ClassIIIA
At3g54140	ATPTR1, PTR1, peptide transporter 1	ClassIIIA
At4g24330	Protein of unknown function (DUF1682)	ClassIIIA
At1g64010	Serine protease inhibitor (SERPIN) family protein	ClassIIIA
At2g46270	GBF3, G-box binding factor 3	ClassIIIA

At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	ClassIIIA
At1g73260	ATKTI1, KTI1, kunitz trypsin inhibitor 1	ClassIIIA
At1g75800	Pathogenesis-related thaumatin superfamily protein	ClassIIIA
At5g07080	HXXXD-type acyl-transferase family protein	ClassIIIA
At1g21310	ATEXT3, EXT3, RSH, extensin 3	ClassIIIA
At1g61810	BGLU45, beta-glucosidase 45	ClassIIIA
At4g32300	SD2-5, S-domain-2 5	ClassIIIA
At1g65840	ATPAO4, PAO4, polyamine oxidase 4	ClassIIIA
At5g47390	myb-like transcription factor family protein	ClassIIIA
At5g61600	ERF104, ethylene response factor 104	ClassIIIA
At5g24030	SLAH3, SLAC1 homologue 3	ClassIIIA
At5g15190	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; Has 7 Blast hits to 7 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At4g38340	NLP3;Plant regulator RWP-RK family protein	ClassIIIA
At1g10070	ATBCAT-2, BCAT-2, branched-chain amino acid transaminase 2	ClassIIIA
At2g19350	Eukaryotic protein of unknown function (DUF872)	ClassIIIA
At4g31240	protein kinase C-like zinc finger protein	ClassIIIA
At5g40450	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIA
At1g69570	Dof-type zinc finger DNA-binding family protein	ClassIIIA
At1g11260	ATSTP1, STP1, sugar transporter 1	ClassIIIA
At4g37540	LBD39, LOB domain-containing protein 39	ClassIIIA
At3g20410	CPK9, calmodulin-domain protein kinase 9	ClassIIIA
At5g27920	F-box family protein	ClassIIIA
At4g01026	PYL7, RCAR2, PYR1-like 7	ClassIIIA
At4g35780	ACT-like protein tyrosine kinase family protein	ClassIIIA
At3g06850	BCE2, DIN3, LTA1, 2-oxoacid dehydrogenases acyltransferase family protein	ClassIIIA
At1g76410	ATL8, RING/U-box superfamily protein	ClassIIIA
At1g20340	DRT112, PETE2, Cupredoxin superfamily protein	ClassIIIA
At1g55510	BCDH BETA1, branched-chain alpha-keto acid decarboxylase E1 beta subunit	ClassIIIA
At4g35770	ATSEN1, DIN1, SEN1, SEN1, Rhodanese/Cell cycle control phosphatase superfamily protein	ClassIIIA
At5g47240	atnudt8, NUDT8, nudix hydrolase homolog 8	ClassIIIA
At3g14760	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: LP.04 four leaves visible, LP.02 two leaves visible; Has 63 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At3g60690	SAUR-like auxin-responsive protein family	ClassIIIA

At1g32460	unknown protein; Has 19 Blast hits to 19 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At2g35230	IKU1, IKU1, VQ motif-containing protein	ClassIIIA
At5g54500	FQR1, flavodoxin-like quinone reductase 1	ClassIIIA
At5g43830	Aluminium induced protein with YGL and LRDR motifs	ClassIIIA
At1g51820	Leucine-rich repeat protein kinase family protein	ClassIIIA
At1g63180	UGE3, UDP-D-glucose/UDP-D-galactose 4-epimerase 3	ClassIIIA
At3g61260	Remorin family protein	ClassIIIA
At2g38750	ANNAT4, annexin 4	ClassIIIA
At4g32870	Polyketide cyclase/dehydrase and lipid transport superfamily protein	ClassIIIA
At3g47960	Major facilitator superfamily protein	ClassIIIA
At5g05340	Peroxidase superfamily protein	ClassIIIA
At2g38400	AGT3, alanine:glyoxylate aminotransferase 3	ClassIIIA
At5g66030	ATGRIP, GRIP, Golgi-localized GRIP domain-containing protein	ClassIIIA
At3g56360	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05250.1); Has 45 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At5g18850	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	ClassIIIA
At2g31390	pfkB-like carbohydrate kinase family protein	ClassIIIA
At5g03550	BEST Arabidopsis thaliana protein match is: TRAF-like family protein (TAIR:AT2G42460.1); Has 137 Blast hits to 125 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 137; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At1g42480	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3456 (InterPro:IPR021852); Has 177 Blast hits to 177 proteins in 59 species: Archae - 0; Bacteria - 0; Metazoa - 140; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	ClassIIIA
At4g30490	AFG1-like ATPase family protein	ClassIIIA
At2g25900	ATCTH, ATTZF1, Zinc finger C-x8-C-x5-C-x3-H type family protein	ClassIIIA
At3g54630	CONTAINS InterPro DOMAIN/s: Kinetochore protein Ndc80 (InterPro:IPR005550); Has 24780 Blast hits to 15608 proteins in 1321 species: Archae - 545; Bacteria - 2969; Metazoa - 12597; Fungi - 2181; Plants - 1581; Viruses - 39; Other Eukaryotes - 4868 (source: NCBI BLink).	ClassIIIA
At1g66550	ATWRKY67, WRKY67, WRKY DNA-binding protein 67	ClassIIIA
At4g39780	Integrase-type DNA-binding superfamily protein	ClassIIIA
At1g75450	ATCKX5, ATCKX6, CKX5, cytokinin oxidase 5	ClassIIIA
At2g01570	RGA, RGA1, GRAS family transcription factor family protein	ClassIIIA
At4g38470	ACT-like protein tyrosine kinase family protein	ClassIIIA
At1g35580	CINV1, cytosolic invertase 1	ClassIIIA
At1g11380	PLAC8 family protein	ClassIIIA
At1g48840	Plant protein of unknown function (DUF639)	ClassIIIA
At1g60940	SNRK2-10, SNRK2.10, SRK2B, SNF1-related protein kinase 2.10	ClassIIIA

At1g31480	SGR2, shoot gravitropism 2 (SGR2)	ClassIIIA
At3g19390	Granulin repeat cysteine protease family protein	ClassIIIA
At4g15545	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16520.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIA
At1g32200	ACT1, ATS1, phospholipid/glycerol acyltransferase family protein	ClassIIIA
At1g61660	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	ClassIIIA
At1g18270	ketose-bisphosphate aldolase class-II family protein	ClassIIIA
At5g59220	HAI1, highly ABA-induced PP2C gene 1	ClassIIIA
At5g48430	Eukaryotic aspartyl protease family protein	ClassIIIA
At5g06690	WCRKC1, WCRKC thioredoxin 1	ClassIIIA
At2g40170	ATEM6, EM6, GEA6, Stress induced protein	ClassIIIA
At5g06980	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12320.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIA
At3g03470	CYP89A9, cytochrome P450, family 87, subfamily A, polypeptide 9	ClassIIIA
At1g67070	DIN9, PMI2, Mannose-6-phosphate isomerase, type I	ClassIIIA
At5g05440	PYL5, RCAR8, Polyketide cyclase/dehydrase and lipid transport superfamily protein	ClassIIIA
At1g80460	GLI1, NHO1, Actin-like ATPase superfamily protein	ClassIIIA
At2g39210	Major facilitator superfamily protein	ClassIIIA
At5g63620	GroES-like zinc-binding alcohol dehydrogenase family protein	ClassIIIA
At1g73240	CONTAINS InterPro DOMAIN/s: Nucleoporin protein Ndc1-Nup (InterPro:IPR019049); Has 36 Blast hits to 36 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At2g30600	BTB/POZ domain-containing protein	ClassIIIA
At5g04310	Pectin lyase-like superfamily protein	ClassIIIA
At4g18340	Glycosyl hydrolase superfamily protein	ClassIIIA
At5g16960	Zinc-binding dehydrogenase family protein	ClassIIIA
At4g15630	Uncharacterised protein family (UPF0497)	ClassIIIA
At2g03220	ATFT1, ATFUT1, FT1, MUR2, fucosyltransferase 1	ClassIIIA
At3g50780	BEST Arabidopsis thaliana protein match is: BTB/POZ domain-containing protein (TAIR:AT1G63850.1); Has 298 Blast hits to 298 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 0; Plants - 287; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	ClassIIIA
At5g65630	GTE7, global transcription factor group E7	ClassIIIA
At1g28260	Telomerase activating protein Est1	ClassIIIA
At3g02550	LBD41, LOB domain-containing protein 41	ClassIIIA
At3g14067	Subtilase family protein	ClassIIIA
At5g26740	Protein of unknown function (DUF300)	ClassIIIA
At4g36670	Major facilitator superfamily protein	ClassIIIA
At1g19700	BEL10, BLH10, BEL1-like homeodomain 10	ClassIIIA
At5g64260	EXL2, EXORDIUM like 2	ClassIIIA
At1g75220	Major facilitator superfamily protein	ClassIIIA
At2g40420	Transmembrane amino acid transporter family protein	ClassIIIA
At1g30900	BP80-3;3, VSR3;3, VSR6, VACUOLAR SORTING RECEPTOR 6	ClassIIIA
At5g20885	RING/U-box superfamily protein	ClassIIIA
At5g52250	Transducin/WD40 repeat-like superfamily protein	ClassIIIA
At3g46440	UXS5, UDP-XYL synthase 5	ClassIIIA

At5g13740	ZIF1, zinc induced facilitator 1	ClassIIIA
At1g11780	oxidoreductase, 2OG-Fe(II) oxygenase family protein	ClassIIIA
At5g43430	ETFBETA, electron transfer flavoprotein beta	ClassIIIA
At5g60200	TMO6, TARGET OF MONOPTEROS 6	ClassIIIA
At5g16970	AER, AT-AER, alkenal reductase	ClassIIIA
At3g57020	Calcium-dependent phosphotriesterase superfamily protein	ClassIIIA
At5g02780	GSTL1, glutathione transferase lambda 1	ClassIIIA
At5g39040	ALS1, ATTAP2, TAP2, transporter associated with antigen processing protein 2	ClassIIIA
At5g19090	Heavy metal transport/detoxification superfamily protein	ClassIIIA
At4g24220	AWI31, VEP1, NAD(P)-binding Rossmann-fold superfamily protein	ClassIIIA
At1g03790	SOM, Zinc finger C-x8-C-x5-C-x3-H type family protein	ClassIIIA
At2g38820	Protein of unknown function (DUF506)	ClassIIIA
At1g20300	Pentatricopeptide repeat (PPR) superfamily protein	ClassIIIA
At3g46690	UDP-Glycosyltransferase superfamily protein	ClassIIIA
At3g15610	Transducin/WD40 repeat-like superfamily protein	ClassIIIA
At3g01175	Protein of unknown function (DUF1666)	ClassIIIA
At1g76990	ACR3, ACT domain repeat 3	ClassIIIA
At1g68410	Protein phosphatase 2C family protein	ClassIIIA
At5g27350	SFP1, Major facilitator superfamily protein	ClassIIIA
At4g32320	APX6, ascorbate peroxidase 6	ClassIIIA
At5g11520	ASP3, YLS4, aspartate aminotransferase 3	ClassIIIA
At2g14170	ALDH6B2, aldehyde dehydrogenase 6B2	ClassIIIA
At1g63700	EMB71, MAPKKK4, YDA, Protein kinase superfamily protein	ClassIIIA
At1g68850	Peroxidase superfamily protein	ClassIIIA
At3g15260	Protein phosphatase 2C family protein	ClassIIIA
At5g04630	CYP77A9, cytochrome P450, family 77, subfamily A, polypeptide 9	ClassIIIA
At3g01270	Pectate lyase family protein	ClassIIIA
At1g26730	EXS (ERD1/XPR1/SYG1) family protein	ClassIIIA
At2g37440	DNAse I-like superfamily protein	ClassIIIA
At5g49650	XK-2, XK2, xylulose kinase-2	ClassIIIA
At1g26270	Phosphatidylinositol 3- and 4-kinase family protein	ClassIIIA
At5g28610	BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT5G28630.1); Has 1536 Blast hits to 1202 proteins in 136 species: Archae - 0; Bacteria - 8; Metazoa - 888; Fungi - 120; Plants - 71; Viruses - 39; Other Eukaryotes - 410 (source: NCBI BLink).	ClassIIIA
At5g04770	ATCAT6, CAT6, cationic amino acid transporter 6	ClassIIIA
At4g10840	Tetratricopeptide repeat (TPR)-like superfamily protein	ClassIIIA
At2g43060	IBH1, ILI1 binding bHLH 1	ClassIIIA
At4g03080	BSL1, BRI1 suppressor 1 (BSU1)-like 1	ClassIIIA
At5g57660	ATCOL5, COL5, CONSTANS-like 5	ClassIIIA
At5g07070	CIPK2, SnRK3.2, CBL-interacting protein kinase 2	ClassIIIA
At4g15550	IAGLU, indole-3-acetate beta-D-glucosyltransferase	ClassIIIA
At2g01860	EMB975, Tetratricopeptide repeat (TPR)-like superfamily protein	ClassIIIA
At5g58620	zinc finger (CCCH-type) family protein	ClassIIIA
At1g15050	IAA34, indole-3-acetic acid inducible 34	ClassIIIA
At5g66400	ATDI8, RAB18, Dehydrin family protein	ClassIIIA
At2g19810	CCCH-type zinc finger family protein	ClassIIIA
At3g17420	GPK1, glyoxysomal protein kinase 1	ClassIIIA
At3g47640	PYE, basic helix-loop-helix (bHLH) DNA-binding superfamily protein	ClassIIIA
At3g53150	UGT73D1, UDP-glucosyl transferase 73D1	ClassIIIA

At5g67320	HOS15, WD-40 repeat family protein	ClassIIIA
At3g17110	pseudogene, glycine-rich protein	ClassIIIA
At3g61060	AtPP2-A13, PP2-A13, phloem protein 2-A13	ClassIIIA
At1g01490	Heavy metal transport/detoxification superfamily protein	ClassIIIA
At5g41610	ATCHX18, CHX18, cation/H+ exchanger 18	ClassIIIA
At3g57890	Tubulin binding cofactor C domain-containing protein	ClassIIIA
At4g17950	AT hook motif DNA-binding family protein	ClassIIIA
At4g01120	ATBZIP54, GBF2, G-box binding factor 2	ClassIIIA
At3g51840	ACX4, ATG6, ATSCX, acyl-CoA oxidase 4	ClassIIIA
At4g32950	Protein phosphatase 2C family protein	ClassIIIA
At4g24060	Dof-type zinc finger DNA-binding family protein	ClassIIIA
At1g79350	EMB1135, RING/FYVE/PHD zinc finger superfamily protein	ClassIIIA
At2g39980	HXXXD-type acyl-transferase family protein	ClassIIIA
At3g15950	NAI2, DNA topoisomerase-related	ClassIIIA
At2g27490	ATCOAE, dephospho-CoA kinase family	ClassIIIA
At3g60510	ATP-dependent caseinolytic (Clp) protease/crotonase family protein	ClassIIIA
At3g28510	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ClassIIIA
At4g39070	B-box zinc finger family protein	ClassIIIA
At1g22400	ATUGT85A1, UGT85A1, UDP-Glycosyltransferase superfamily protein	ClassIIIA
At2g02800	APK2B, protein kinase 2B	ClassIIIA
At4g14420	HR-like lesion-inducing protein-related	ClassIIIA
At4g30550	Class I glutamine amidotransferase-like superfamily protein	ClassIIIA
At1g03610	Protein of unknown function (DUF789)	ClassIIIA
At2g23450	Protein kinase superfamily protein	ClassIIIA
At4g13430	ATLEUC1, IIL1, isopropyl malate isomerase large subunit 1	ClassIIIA
At3g19920	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64230.1); Has 217 Blast hits to 217 proteins in 16 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIA
At5g49360	ATBXL1, BXL1, beta-xylosidase 1	ClassIIIA
At1g29760	Putative adipose-regulatory protein (Seipin)	ClassIIIA
At4g38500	Protein of unknown function (DUF616)	ClassIIIA
At1g15380	Lactoylglutathione lyase / glyoxalase I family protein	ClassIIIA
At2g17500	Auxin efflux carrier family protein	ClassIIIA
At5g24470	APRR5, PRR5, pseudo-response regulator 5	ClassIIIA
At1g03090	MCCA, methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA)	ClassIIIA
At3g18980	ETP1, EIN2 targeting protein1	ClassIIIA
At3g16910	AAE7, ACN1, acyl-activating enzyme 7	ClassIIIA
At1g17190	ATGSTU26, GSTU26, glutathione S-transferase tau 26	ClassIIIA
At5g18630	alpha/beta-Hydrolases superfamily protein	ClassIIIA
At5g17640	Protein of unknown function (DUF1005)	ClassIIIA
ClassIIIB. NR: no binding but repression		
At1g56510	ADR2, WRR4, Disease resistance protein (TIR-NBS-LRR class)	ClassIIIB
At1g74710	ATICS1, EDS16, ICS1, SID2, ADC synthase superfamily protein	ClassIIIB
At2g17040	anac036, NAC036, NAC domain containing protein 36	ClassIIIB
At1g57630	Toll-Interleukin-Resistance (TIR) domain family protein	ClassIIIB

At3g63390	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At1g67050	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G38320.1); Has 617 Blast hits to 318 proteins in 80 species: Archae - 0; Bacteria - 16; Metazoa - 141; Fungi - 62; Plants - 128; Viruses - 2; Other Eukaryotes - 268 (source: NCBI BLink).	ClassIIIB
At1g73750	Uncharacterised conserved protein UCP031088, alpha/beta hydrolase	ClassIIIB
At3g05490	RALFL22, ralf-like 22	ClassIIIB
At1g15890	Disease resistance protein (CC-NBS-LRR class) family	ClassIIIB
At2g46590	DAG2, Dof-type zinc finger DNA-binding family protein	ClassIIIB
At2g44450	BGLU15, beta glucosidase 15	ClassIIIB
At1g05800	DGL, alpha/beta-Hydrolases superfamily protein	ClassIIIB
At1g32690	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35200.1); Has 45 Blast hits to 45 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At5g44350	ethylene-responsive nuclear protein -related	ClassIIIB
At4g30560	ATCNGC9, CNGC9, cyclic nucleotide gated channel 9	ClassIIIB
At4g26120	Ankyrin repeat family protein / BTB/POZ domain-containing protein	ClassIIIB
At3g10630	UDP-Glycosyltransferase superfamily protein	ClassIIIB
At4g39890	AtRABH1c, RABH1c, RAB GTPase homolog H1C	ClassIIIB
At3g61390	RING/U-box superfamily protein	ClassIIIB
At3g07390	AIR12, auxin-responsive family protein	ClassIIIB
At2g23270	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stem, sperm cell, root, stamen; EXPRESSED DURING: 4 anthesis; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37290.1); Has 36 Blast hits to 35 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At4g22820	A20/AN1-like zinc finger family protein	ClassIIIB
At1g51620	Protein kinase superfamily protein	ClassIIIB
At4g39940	AKN2, APK2, APS-kinase 2	ClassIIIB
At1g10160	transposable element gene	ClassIIIB
At3g19630	Radical SAM superfamily protein	ClassIIIB
At2g44090	Ankyrin repeat family protein	ClassIIIB
At1g58080	ATATP-PRT1, ATP-PRT1, HISN1A, ATP phosphoribosyl transferase 1	ClassIIIB
At3g55960	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	ClassIIIB
At3g48850	PHT3;2, phosphate transporter 3;2	ClassIIIB
At1g53980	Ubiquitin-like superfamily protein	ClassIIIB
At1g74430	ATMYB95, ATMYBCP66, MYB95, myb domain protein 95	ClassIIIB
At5g40540	Protein kinase superfamily protein	ClassIIIB
At4g14368	Regulator of chromosome condensation (RCC1) family protein	ClassIIIB
At2g16500	ADC1, ARGDC, ARGDC1, SPE1, arginine decarboxylase 1	ClassIIIB
At3g05360	AtRLP30, RLP30, receptor like protein 30	ClassIIIB
At1g20510	OPCL1, OPC-8:0 CoA ligase1	ClassIIIB
At3g17020	Adenine nucleotide alpha hydrolases-like superfamily protein	ClassIIIB
At2g42360	RING/U-box superfamily protein	ClassIIIB

At1g24625	ZFP7, zinc finger protein 7	ClassIIIB
At5g41550	Disease resistance protein (TIR-NBS-LRR class) family	ClassIIIB
At2g41380	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ClassIIIB
At5g65870	ATPSK5, PSK5, PSK5, phytosulfokine 5 precursor	ClassIIIB
At4g11850	MEE54, PLDGAMMA1, phospholipase D gamma 1	ClassIIIB
At3g13650	Disease resistance-responsive (dirigent-like protein) family protein	ClassIIIB
At5g56760	ATSERAT1;1, SAT-52, SAT5, SERAT1;1, serine acetyltransferase 1;1	ClassIIIB
At1g75540	STH2, salt tolerance homolog2	ClassIIIB
At1g53430	Leucine-rich repeat transmembrane protein kinase	ClassIIIB
At1g74590	ATGSTU10, GSTU10, glutathione S-transferase TAU 10	ClassIIIB
At5g52670	Copper transport protein family	ClassIIIB
At3g44735	ATPSK3, PSK1, PSK3, PHYTOSULFOKINE 3 PRECURSOR	ClassIIIB
At3g18250	Putative membrane lipoprotein	ClassIIIB
At1g28190	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12340.1); Has 166 Blast hits to 162 proteins in 36 species: Archae - 0; Bacteria - 2; Metazoa - 15; Fungi - 5; Plants - 124; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink).	ClassIIIB
At3g02770	Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	ClassIIIB
At5g25190	Integrase-type DNA-binding superfamily protein	ClassIIIB
At4g00330	CRCK2, calmodulin-binding receptor-like cytoplasmic kinase 2	ClassIIIB
At1g53050	Protein kinase superfamily protein	ClassIIIB
At1g05060	unknown protein; Has 34 Blast hits to 34 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At3g09020	alpha 1,4-glycosyltransferase family protein	ClassIIIB
At1g30040	ATGA2OX2, GA2OX2, GA2OX2, gibberellin 2-oxidase	ClassIIIB
At5g24430	Calcium-dependent protein kinase (CDPK) family protein	ClassIIIB
At4g21390	B120, S-locus lectin protein kinase family protein	ClassIIIB
At1g70130	Concanavalin A-like lectin protein kinase family protein	ClassIIIB
At2g04160	AIR3, Subtilisin-like serine endopeptidase family protein	ClassIIIB
At3g20510	Transmembrane proteins 14C	ClassIIIB
At3g10640	VPS60.1, SNF7 family protein	ClassIIIB
At5g58787	RING/U-box superfamily protein	ClassIIIB
At2g34920	EDA18, RING/U-box superfamily protein	ClassIIIB
At1g44130	Eukaryotic aspartyl protease family protein	ClassIIIB
At4g37940	AGL21, AGAMOUS-like 21	ClassIIIB
At4g27720	Major facilitator superfamily protein	ClassIIIB
At5g22530	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G22520.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At1g17310	MADS-box transcription factor family protein	ClassIIIB
At1g35560	TCP family transcription factor	ClassIIIB
At4g40020	Myosin heavy chain-related protein	ClassIIIB
At1g24140	Matrixin family protein	ClassIIIB
At1g11210	Protein of unknown function (DUF761)	ClassIIIB
At1g48320	Thioesterase superfamily protein	ClassIIIB
At5g12880	proline-rich family protein	ClassIIIB
At1g10650	SBP (S-ribonuclease binding protein) family protein	ClassIIIB
At3g09270	ATGSTU8, GSTU8, glutathione S-transferase TAU 8	ClassIIIB

At1g29250	Alba DNA/RNA-binding protein	ClassIIIB
At3g61850	DAG1, Dof-type zinc finger DNA-binding family protein	ClassIIIB
At1g78100	F-box family protein	ClassIIIB
At4g00080	UNE11, Plant invertase/pectin methylesterase inhibitor superfamily protein	ClassIIIB
At1g32350	AOX1D, alternative oxidase 1D	ClassIIIB
At3g49350	Ypt/Rab-GAP domain of gyp1p superfamily protein	ClassIIIB
At1g80530	Major facilitator superfamily protein	ClassIIIB
At1g55610	BRL1, BRI1 like	ClassIIIB
At5g13870	EXGT-A4, XTH5, xyloglucan endotransglucosylase/hydrolase 5	ClassIIIB
At4g28085	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At1g07750	RmlC-like cupins superfamily protein	ClassIIIB
At3g50480	HR4, homolog of RPW8 4	ClassIIIB
At3g21230	4CL5, 4-coumarate:CoA ligase 5	ClassIIIB
At5g60350	unknown protein; Has 110 Blast hits to 97 proteins in 36 species: Archae - 0; Bacteria - 10; Metazoa - 39; Fungi - 2; Plants - 5; Viruses - 0; Other Eukaryotes - 54 (source: NCBI BLink).	ClassIIIB
At3g09000	proline-rich family protein	ClassIIIB
At3g25070	RIN4, RPM1 interacting protein 4	ClassIIIB
At3g11840	PUB24, plant U-box 24	ClassIIIB
At2g11520	CRCK3, calmodulin-binding receptor-like cytoplasmic kinase 3	ClassIIIB
At5g24540	BGLU31, beta glucosidase 31	ClassIIIB
At2g19130	S-locus lectin protein kinase family protein	ClassIIIB
At5g48540	receptor-like protein kinase-related family protein	ClassIIIB
At4g24160	alpha/beta-Hydrolases superfamily protein	ClassIIIB
At1g09940	HEMA2, Glutamyl-tRNA reductase family protein	ClassIIIB
At3g59080	Eukaryotic aspartyl protease family protein	ClassIIIB
At3g27110	Peptidase family M48 family protein	ClassIIIB
At4g16780	ATHB-2, ATHB2, HAT4, HB-2, homeobox protein 2	ClassIIIB
At5g44070	ARA8, ATPCS1, CAD1, PCS1, phytochelatin synthase 1 (PCS1)	ClassIIIB
At5g66880	SNRK2-3, SNRK2.3, SRK2I, sucrose nonfermenting 1(SNF1)-related protein kinase 2.3	ClassIIIB
At5g49620	AtMYB78, MYB78, myb domain protein 78	ClassIIIB
At5g22550	Plant protein of unknown function (DUF247)	ClassIIIB
At3g21080	ABC transporter-related	ClassIIIB
At3g03020	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 5 Blast hits to 5 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At5g59510	DVL18, RTFL5, ROTUNDIFOLIA like 5	ClassIIIB
At3g53730	Histone superfamily protein	ClassIIIB
At1g19220	ARF11, ARF19, IAA22, auxin response factor 19	ClassIIIB
At1g18890	ATCDPK1, CDPK1, CPK10, calcium-dependent protein kinase 1	ClassIIIB
At3g44720	ADT4, arogenate dehydratase 4	ClassIIIB
At4g11170	Disease resistance protein (TIR-NBS-LRR class) family	ClassIIIB
At5g07620	Protein kinase superfamily protein	ClassIIIB
At3g54980	Pentatricopeptide repeat (PPR) superfamily protein	ClassIIIB
At5g06720	ATPA2, PA2, peroxidase 2	ClassIIIB

At5g41100	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT3G26910.2); Has 1503 Blast hits to 1197 proteins in 220 species: Archae - 4; Bacteria - 108; Metazoa - 481; Fungi - 318; Plants - 186; Viruses - 39; Other Eukaryotes - 367 (source: NCBI BLink).	ClassIIIB
At4g02360	Protein of unknown function, DUF538	ClassIIIB
At4g09570	ATCPK4, CPK4, calcium-dependent protein kinase 4	ClassIIIB
At1g51940	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	ClassIIIB
At5g65020	ANNAT2, annexin 2	ClassIIIB
At3g48090	ATEDS1, EDS1, alpha/beta-Hydrolases superfamily protein	ClassIIIB
At1g70530	CRK3, cysteine-rich RLK (RECEPTOR-like protein kinase) 3	ClassIIIB
At4g12070	unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At1g63040	a pseudogene member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The translated product contains one AP2 domain. There are 17 members in this subfamily including TINY.	ClassIIIB
At2g01150	RHA2B, RING-H2 finger protein 2B	ClassIIIB
At4g25030	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45410.3); Has 125 Blast hits to 125 proteins in 36 species: Archae - 2; Bacteria - 31; Metazoa - 0; Fungi - 4; Plants - 88; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At2g32030	Acyl-CoA N-acyltransferases (NAT) superfamily protein	ClassIIIB
At3g60910	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ClassIIIB
At1g68150	ATWRKY9, WRKY9, WRKY DNA-binding protein 9	ClassIIIB
At2g06050	DDE1, OPR3, oxophytodienoate-reductase 3	ClassIIIB
At5g62680	Major facilitator superfamily protein	ClassIIIB
At5g45750	AtRABA1c, RABA1c, RAB GTPase homolog A1C	ClassIIIB
At4g18890	BEH3, BES1/BZR1 homolog 3	ClassIIIB
At2g27390	proline-rich family protein	ClassIIIB
At4g23440	Disease resistance protein (TIR-NBS class)	ClassIIIB
At2g22680	Zinc finger (C3HC4-type RING finger) family protein	ClassIIIB
At3g54040	PAR1 protein	ClassIIIB
At4g37730	AtbZIP7, bZIP7, basic leucine-zipper 7	ClassIIIB
At4g30080	ARF16, auxin response factor 16	ClassIIIB
At3g43250	Family of unknown function (DUF572)	ClassIIIB
At2g46150	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	ClassIIIB
At5g61210	ATSNAP33, ATSNAP33B, SNAP33, SNP33, soluble N-ethylmaleimide-sensitive factor adaptor protein 33	ClassIIIB
At5g57340	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At5g07870	HXXXD-type acyl-transferase family protein	ClassIIIB
At5g54170	Polyketide cyclase/dehydrase and lipid transport superfamily protein	ClassIIIB
At1g13340	Regulator of Vps4 activity in the MVB pathway protein	ClassIIIB

At5g48175	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: hypocotyl, male gametophyte, root; BEST Arabidopsis thaliana protein match is: Glycosyl hydrolase superfamily protein (TAIR:AT3G09260.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At1g07130	ATSTN1, STN1, Nucleic acid-binding, OB-fold-like protein	ClassIIIB
At2g30130	ASL5, LBD12, PCK1, Lateral organ boundaries (LOB) domain family protein	ClassIIIB
At4g17230	SCL13, SCARECROW-like 13	ClassIIIB
At3g05510	Phospholipid/glycerol acyltransferase family protein	ClassIIIB
At1g18570	AtMYB51, BW51A, BW51B, HIG1, MYB51, myb domain protein 51	ClassIIIB
At3g27160	GHS1, Ribosomal protein S21 family protein	ClassIIIB
At2g39700	ATEXP4, ATEXPA4, ATHEXP ALPHA 1.6, EXPA4, expansin A4	ClassIIIB
At4g40080	ENTH/ANTH/VHS superfamily protein	ClassIIIB
At1g57560	AtMYB50, MYB50, myb domain protein 50	ClassIIIB
At2g25250	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32020.1); Has 30 Blast hits to 30 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At2g28570	unknown protein; Has 13 Blast hits to 13 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At1g66090	Disease resistance protein (TIR-NBS class)	ClassIIIB
At1g44100	AAP5, amino acid permease 5	ClassIIIB
At3g11820	AT-SYR1, ATSYP121, ATSYR1, PEN1, SYP121, SYR1, syntaxin of plants 121	ClassIIIB
At4g01850	AtSAM2, MAT2, SAM-2, SAM2, S-adenosylmethionine synthetase 2	ClassIIIB
At2g24240	BTB/POZ domain with WD40/YVTN repeat-like protein	ClassIIIB
At1g32310	unknown protein; Has 28 Blast hits to 28 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At5g67570	DG1, EMB1408, EMB246, Tetratricopeptide repeat (TPR)-like superfamily protein	ClassIIIB
At4g11370	RHA1A, RING-H2 finger A1A	ClassIIIB
At1g60030	ATNAT7, NAT7, nucleobase-ascorbate transporter 7	ClassIIIB
At1g18860	ATWRKY61, WRKY61, WRKY DNA-binding protein 61	ClassIIIB
At1g18580	GAUT11, galacturonosyltransferase 11	ClassIIIB
At1g79160	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16500.1); Has 104 Blast hits to 102 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At2g19710	Regulator of Vps4 activity in the MVB pathway protein	ClassIIIB
At4g01720	AtWRKY47, WRKY47, WRKY family transcription factor	ClassIIIB
At2g37840	Protein kinase superfamily protein	ClassIIIB
At4g39840	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 20719 Blast hits to 6096 proteins in 607 species: Archae - 22; Bacteria - 3243; Metazoa - 4364; Fungi - 2270; Plants - 237; Viruses - 128; Other Eukaryotes - 10455 (source: NCBI BLink).	ClassIIIB
At4g32060	calcium-binding EF hand family protein	ClassIIIB
At1g70940	ATPIN3, PIN3, Auxin efflux carrier family protein	ClassIIIB
At2g26290	ARSK1, root-specific kinase 1	ClassIIIB

At1g44830	Integrase-type DNA-binding superfamily protein	ClassIIIB
At5g43520	Cysteine/Histidine-rich C1 domain family protein	ClassIIIB
At4g28350	Concanavalin A-like lectin protein kinase family protein	ClassIIIB
At2g20960	pEARLI4, Arabidopsis phospholipase-like protein (PEARLI 4) family	ClassIIIB
At3g49220	Plant invertase/pectin methylesterase inhibitor superfamily	ClassIIIB
At5g52240	AtMAPR5, ATMP1, MSBP1, membrane steroid binding protein 1	ClassIIIB
At1g09520	LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Zinc finger, PHD-type, conserved site (InterPro:IPR019786); BEST Arabidopsis thaliana protein match is: PHD finger family protein (TAIR:AT3G17460.1); Has 56 Blast hits to 56 proteins in 17 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 4; Plants - 46; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	ClassIIIB
At1g04440	CKL13, casein kinase like 13	ClassIIIB
At3g08750	F-box and associated interaction domains-containing protein	ClassIIIB
At4g17260	Lactate/malate dehydrogenase family protein	ClassIIIB
At3g63410	APG1, E37, IEP37, VTE3, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	ClassIIIB
At3g23820	GAE6, UDP-D-glucuronate 4-epimerase 6	ClassIIIB
At1g51920	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stem, stamen; EXPRESSED DURING: 4 anthesis; Has 22 Blast hits to 22 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At4g34180	Cyclase family protein	ClassIIIB
At1g52560	HSP20-like chaperones superfamily protein	ClassIIIB
At3g49720	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, Golgi apparatus, plasma membrane, membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65810.1); Has 64 Blast hits to 64 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At3g28740	CYP81D1, Cytochrome P450 superfamily protein	ClassIIIB
At3g52360	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35850.1); Has 34 Blast hits to 34 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At3g17700	ATCNGC20, CNBT1, CNGC20, cyclic nucleotide-binding transporter 1	ClassIIIB
At4g33300	ADR1-L1, ADR1-like 1	ClassIIIB
At3g52400	ATSYP122, SYP122, syntaxin of plants 122	ClassIIIB
At3g20900	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At5g14930	SAG101, senescence-associated gene 101	ClassIIIB
At1g35200	60S ribosomal protein L4/L1 (RPL4B), pseudogene, similar to 60S ribosomal protein L4 (fragment) GB:P49691 from (Arabidopsis thaliana); blastp match of 50% identity and 6.3e-17 P-value to SP|Q9XF97|RL4_PRUAR 60S ribosomal protein L4 (L1). (Apricot) {Prunus armeniaca}	ClassIIIB
At5g38310	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	ClassIIIB

At3g23090	TPX2 (targeting protein for Xklp2) protein family	ClassIIIB
At5g63770	ATDGK2, DGK2, diacylglycerol kinase 2	ClassIIIB
At5g13190	CONTAINS InterPro DOMAIN/s: LPS-induced tumor necrosis factor alpha factor (InterPro:IPR006629); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At4g30470	NAD(P)-binding Rossmann-fold superfamily protein	ClassIIIB
At1g29860	ATWRKY71, WRKY71, WRKY DNA-binding protein 71	ClassIIIB
At4g28940	Phosphorylase superfamily protein	ClassIIIB
At1g72070	Chaperone DnaJ-domain superfamily protein	ClassIIIB
At2g45080	cycp3;1, cyclin p3;1	ClassIIIB
At2g01880	ATPAP7, PAP7, purple acid phosphatase 7	ClassIIIB
At1g34750	Protein phosphatase 2C family protein	ClassIIIB
At1g09920	TRAF-type zinc finger-related	ClassIIIB
At2g38010	Neutral/alkaline non-lysosomal ceramidase	ClassIIIB
At1g21830	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF740 (InterPro:IPR008004); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G44608.1); Has 49 Blast hits to 49 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At1g74870	RING/U-box superfamily protein	ClassIIIB
At3g10190	Calcium-binding EF-hand family protein	ClassIIIB
At4g37400	CYP81F3, cytochrome P450, family 81, subfamily F, polypeptide 3	ClassIIIB
At1g07000	ATEXO70B2, EXO70B2, exocyst subunit exo70 family protein B2	ClassIIIB
At1g73066	Leucine-rich repeat family protein	ClassIIIB
At2g39530	Uncharacterised protein family (UPF0497)	ClassIIIB
At5g62070	IQD23, IQ-domain 23	ClassIIIB
At3g45640	ATMAPK3, ATMPK3, MPK3, mitogen-activated protein kinase 3	ClassIIIB
At1g11000	ATMLO4, MLO4, Seven transmembrane MLO family protein	ClassIIIB
At2g26480	UGT76D1, UDP-glucosyl transferase 76D1	ClassIIIB
At4g02200	Drought-responsive family protein	ClassIIIB
At5g07310	Integrase-type DNA-binding superfamily protein	ClassIIIB
At2g16430	ATPAP10, PAP10, purple acid phosphatase 10	ClassIIIB
At5g44610	MAP18, PCAP2, microtubule-associated protein 18	ClassIIIB
At4g36680	Tetratricopeptide repeat (TPR)-like superfamily protein	ClassIIIB
At4g21780	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At4g22470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	ClassIIIB
At5g60800	Heavy metal transport/detoxification superfamily protein	ClassIIIB
At4g34320	Protein of unknown function (DUF677)	ClassIIIB
At2g47130	NAD(P)-binding Rossmann-fold superfamily protein	ClassIIIB
At5g65600	Concanavalin A-like lectin protein kinase family protein	ClassIIIB
At1g17370	UBP1B, oligouridylate binding protein 1B	ClassIIIB
At1g28390	Protein kinase superfamily protein	ClassIIIB
At4g36900	DEAR4, RAP2.10, related to AP2 10	ClassIIIB
At2g35910	RING/U-box superfamily protein	ClassIIIB
At5g44990	Glutathione S-transferase family protein	ClassIIIB
At4g31780	MGD1, MGDA, monogalactosyl diacylglycerol synthase 1	ClassIIIB
At5g51190	Integrase-type DNA-binding superfamily protein	ClassIIIB

At4g23010	ATUTR2, UTR2, UDP-galactose transporter 2	ClassIIIB
At5g10400	Histone superfamily protein	ClassIIIB
At4g02330	ATPMEPCRB, Plant invertase/pectin methylesterase inhibitor superfamily	ClassIIIB
At2g34930	disease resistance family protein / LRR family protein	ClassIIIB
At2g43000	anac042, NAC042, NAC domain containing protein 42	ClassIIIB
At5g58110	chaperone binding;ATPase activators	ClassIIIB
At1g14480	Ankyrin repeat family protein	ClassIIIB
At1g17750	AtPEPR2, PEPR2, PEP1 receptor 2	ClassIIIB
At5g62630	HIPL2, hipl2 protein precursor	ClassIIIB
At5g51390	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	ClassIIIB
At5g07860	HXXXD-type acyl-transferase family protein	ClassIIIB
At4g38000	DOF4.7, DNA binding with one finger 4.7	ClassIIIB
At2g39900	GATA type zinc finger transcription factor family protein	ClassIIIB
At3g29670	HXXXD-type acyl-transferase family protein	ClassIIIB
At2g17120	LYM2, lysm domain GPI-anchored protein 2 precursor	ClassIIIB
At1g52200	PLAC8 family protein	ClassIIIB
At2g39110	Protein kinase superfamily protein	ClassIIIB
At1g55920	ATSERAT2;1, SAT1, SAT5, SERAT2;1, serine acetyltransferase 2;1	ClassIIIB
At4g01700	Chitinase family protein	ClassIIIB
At2g31880	EVR, SOBIR1, Leucine-rich repeat protein kinase family protein	ClassIIIB
At3g62720	ATXT1, XT1, XXT1, xylosyltransferase 1	ClassIIIB
At2g26380	Leucine-rich repeat (LRR) family protein	ClassIIIB
At2g47140	NAD(P)-binding Rossmann-fold superfamily protein	ClassIIIB
At2g19570	AT-CDA1, CDA1, DESZ, cytidine deaminase 1	ClassIIIB
At3g14360	alpha/beta-Hydrolases superfamily protein	ClassIIIB
At2g37940	AtIPCS2, Arabidopsis Inositol phosphorylceramide synthase 2	ClassIIIB
At5g60680	Protein of unknown function, DUF584	ClassIIIB
At5g41680	Protein kinase superfamily protein	ClassIIIB
At3g47380	Plant invertase/pectin methylesterase inhibitor superfamily protein	ClassIIIB
At5g62390	ATBAG7, BAG7, BCL-2-associated athanogene 7	ClassIIIB
At1g07520	GRAS family transcription factor	ClassIIIB
At4g39030	EDS5, SID1, MATE efflux family protein	ClassIIIB
At3g53130	CYP97C1, LUT1, Cytochrome P450 superfamily protein	ClassIIIB
At1g77030	hydrolases, acting on acid anhydrides, in phosphorus-containing anhydrides;ATP-dependent helicases;nucleic acid binding;ATP binding;RNA binding;helicases	ClassIIIB
At3g22160	VQ motif-containing protein	ClassIIIB
At2g42430	ASL18, LBD16, lateral organ boundaries-domain 16	ClassIIIB
At3g61900	SAUR-like auxin-responsive protein family	ClassIIIB
At5g66070	RING/U-box superfamily protein	ClassIIIB
At2g22750	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	ClassIIIB
At1g02400	ATGA2OX4, ATGA2OX6, DTA1, GA2OX6, gibberellin 2-oxidase 6	ClassIIIB
At1g51915	cryptdin protein-related	ClassIIIB
At4g19960	ATKUP9, HAK9, KT9, KUP9, K+ uptake permease 9	ClassIIIB
At4g31000	Calmodulin-binding protein	ClassIIIB
At2g26560	PLA IIA, PLA2A, PLP2, PLP2, phospholipase A 2A	ClassIIIB
At5g10750	Protein of unknown function (DUF1336)	ClassIIIB
At3g55950	ATCRR3, CCR3, CRINKLY4 related 3	ClassIIIB

At3g50760	GATL2, galacturonosyltransferase-like 2	ClassIIIB
At4g29670	ACHT2, atypical CYS HIS rich thioredoxin 2	ClassIIIB
At2g37810	Cysteine/Histidine-rich C1 domain family protein	ClassIIIB
At3g52430	ATPAD4, PAD4, alpha/beta-Hydrolases superfamily protein	ClassIIIB
At1g36640	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: sperm cell, root; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G36622.1); Has 14 Blast hits to 14 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At2g20150	unknown protein; Has 5 Blast hits to 5 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At3g08710	ATH9, TH9, TRX H9, thioredoxin H-type 9	ClassIIIB
At3g02800	Tyrosine phosphatase family protein	ClassIIIB
At2g24180	CYP71B6, cytochrome p450 71b6	ClassIIIB
At2g27690	CYP94C1, cytochrome P450, family 94, subfamily C, polypeptide 1	ClassIIIB
At5g46710	PLATZ transcription factor family protein	ClassIIIB
At3g02790	zinc finger (C2H2 type) family protein	ClassIIIB
At3g53280	CYP71B5, cytochrome p450 71b5	ClassIIIB
At5g62350	Plant invertase/pectin methylesterase inhibitor superfamily protein	ClassIIIB
At5g40010	AATP1, AAA-ATPase 1	ClassIIIB
At5g38210	Protein kinase family protein	ClassIIIB
At2g21560	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G39190.1); Has 3685 Blast hits to 2305 proteins in 270 species: Archae - 0; Bacteria - 156; Metazoa - 1145; Fungi - 322; Plants - 177; Viruses - 6; Other Eukaryotes - 1879 (source: NCBI BLink).	ClassIIIB
At1g59910	Actin-binding FH2 (formin homology 2) family protein	ClassIIIB
At5g58120	Disease resistance protein (TIR-NBS-LRR class) family	ClassIIIB
At5g59480	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	ClassIIIB
At3g01820	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ClassIIIB
At1g63480	AT hook motif DNA-binding family protein	ClassIIIB
At3g04630	WDL1, WVD2-like 1	ClassIIIB
At2g17220	Protein kinase superfamily protein	ClassIIIB
At1g16380	ATCHX1, CHX1, Cation/hydrogen exchanger family protein	ClassIIIB
At1g61370	S-locus lectin protein kinase family protein	ClassIIIB
At3g09405	Pectinacetylesterase family protein	ClassIIIB
At3g47550	RING/FYVE/PHD zinc finger superfamily protein	ClassIIIB
At3g59900	ARGOS, auxin-regulated gene involved in organ size	ClassIIIB
At1g24150	ATFH4, FH4, formin homologue 4	ClassIIIB
At2g16870	Disease resistance protein (TIR-NBS-LRR class) family	ClassIIIB
At2g42350	RING/U-box superfamily protein	ClassIIIB
At5g66620	DAR6, DA1-related protein 6	ClassIIIB
At4g33960	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G15830.1); Has 32 Blast hits to 32 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	ClassIIIB
At3g16030	CES101, lectin protein kinase family protein	ClassIIIB
At5g22690	Disease resistance protein (TIR-NBS-LRR class) family	ClassIIIB

At1g11310	ATMLO2, MLO2, PMR2, Seven transmembrane MLO family protein	ClassIIIB
At1g59850	ARM repeat superfamily protein	ClassIIIB
At2g21120	Protein of unknown function (DUF803)	ClassIIIB
At1g05710	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	ClassIIIB
At1g71450	Integrase-type DNA-binding superfamily protein	ClassIIIB
At4g37180	Homeodomain-like superfamily protein	ClassIIIB
At1g61560	ATMLO6, MLO6, Seven transmembrane MLO family protein	ClassIIIB
At5g39710	EMB2745, Tetratricopeptide repeat (TPR)-like superfamily protein	ClassIIIB
At1g05055	ATGTF2H2, GTF2H2, general transcription factor II H2	ClassIIIB
At3g03660	WOX11, WUSCHEL related homeobox 11	ClassIIIB
At5g09980	PROPEP4, elicitor peptide 4 precursor	ClassIIIB
At2g26190	calmodulin-binding family protein	ClassIIIB
At3g54200	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	ClassIIIB
At1g53440	Leucine-rich repeat transmembrane protein kinase	ClassIIIB
At5g60250	zinc finger (C3HC4-type RING finger) family protein	ClassIIIB
At1g63830	PLAC8 family protein	ClassIIIB
At3g08760	ATSIK, Protein kinase superfamily protein	ClassIIIB
At5g66640	DAR3, DA1-related protein 3	ClassIIIB
At5g53130	ATCNGC1, CNGC1, cyclic nucleotide gated channel 1	ClassIIIB
At3g28580	P-loop containing nucleoside triphosphate hydrolases superfamily protein	ClassIIIB
At4g15120	VQ motif-containing protein	ClassIIIB
At2g24600	Ankyrin repeat family protein	ClassIIIB
At2g01450	ATMPK17, MPK17, MAP kinase 17	ClassIIIB
At1g65690	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	ClassIIIB
At1g53920	GLIP5, GDSL-motif lipase 5	ClassIIIB
At2g38870	Serine protease inhibitor, potato inhibitor I-type family protein	ClassIIIB
At2g40180	ATHPP2C5, PP2C5, phosphatase 2C5	ClassIIIB
At5g04720	ADR1-L2, ADR1-like 2	ClassIIIB
At1g72060	serine-type endopeptidase inhibitors	ClassIIIB
At5g24620	Pathogenesis-related thaumatin superfamily protein	ClassIIIB
At2g19190	FRK1, FLG22-induced receptor-like kinase 1	ClassIIIB
At4g14630	GLP9, germin-like protein 9	ClassIIIB

[00394] To next explore the biological relevance of the three distinct classes of primary bZIP1 targets, the following features were examined: (1) enrichment of *cis*-regulatory elements (Fig. 30); (2) comparison to bZIP1 regulated genes *in planta* (Fig. 29B), and (3) biological relevance to N-signal transduction in isolated cells (Fig. 29A & 29C) and *in planta* (Fig. 29C). This comparative analysis uncovered features common to all three classes of bZIP1 targets, as well as specific features of Class III transient targets that are uniquely relevant to rapid N-signal propagation. The features *shared* by all three classes of bZIP1 *primary* targets are: i) bZIP1-binding sites: all three classes of genes deemed to be bZIP1 primary targets share enrichment of known bZIP1 binding sites in their promoters ($E<0.01$, Fig. 30). ii) *In planta* relevance to bZIP1: all three classes of

bZIP1 primary targets identified in the cell-based *TARGET* system were validated by their significant overlap with bZIP1-regulated genes identified in transgenic plants, either by comparison to a 35S::bZIP1 overexpression line (100/449 genes; 22% overlap; *p-val* <0.001) or a T-DNA insertion mutant in bZIP1 (89/488 genes; 18.2% overlap; *p-val*<0.001) (Kang et al., 2010, Molecular Plant 3:361-373) (Fig. 29B). iii) N-regulation *in planta*: bZIP1 was predicted to be a master regulator in N-response (Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939-4944; Obertello et al., 2010, BMC systems biology 4:111), and in support of this, all three classes of bZIP1 primary targets in protoplasts are significantly enriched with N-responsive genes *in planta* (Krouk et al., 2010, Genome Biology 11:R123; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939-4944; Wang et al., 2003, Plant Physiol. 132(2):556-567; Wang et al., 2004, Plant physiology 136(1):2512-2522) (438/1,308 genes, p-val<0.001) (Fig. 29C). iv) known bZIP1 functions: all three classes of targets show enrichment of GO-terms associated with other known bZIP1 functions (e.g. Stimulus/Stress) (Fig. 31). Specifically, bZIP1 is reported as a master regulator in response to darkness and sugar starvation (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361-373). Consistent with this, all three classes of bZIP1 primary targets share a significant overlap (*p-val* <0.001) with genes induced by sugar starvation and extended darkness (Krouk et al., 2009, PLoS Comput Biol 5(3):e1000326).

[00395] In addition to these common features consistent with the role of bZIP1 *in planta* (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361-373; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939-4944), distinctive features for the Class III transient bZIP1 primary targets specifically relevant to rapid N-signaling were uncovered. These class-specific features are outlined below.

[00396] ***Class I "Poised" targets (TF Binding only).*** Class I bZIP1 primary targets (407 genes) that are bound, but not regulated by bZIP1, are significantly enriched in genes involved in response to biotic/abiotic stimuli, and transport of divalent ions (FDR<0.01) (Fig. 29A; Fig. 31). They are also significantly enriched in the known bZIP1 binding site "hybrid ACGT box" (E=3.5e-4), supporting that they are valid primary targets of bZIP1 (Fig. 30). This suggests that bZIP1 is bound to and poised to activate

these target genes, possibly in response to a signal or a TF partner not present in the experimental conditions.

[00397] ***Class II "Stable" targets (TF Binding and Regulation).*** Class II targets (120 genes) are regulated and bound by bZIP1. This 23% overlap (*p-val*<0.001) between transcriptome and ChIP-Seq data (Fig. 29A), is comparable to the relatively low overlap observed for other TF perturbation studies performed *in planta* [23 % ABI3 (Monke et al., 2012, Nucleic Acids Research 40:8240l); 5% ASR5 (Arenhart et al., 2014, Molecular plant 7(4):709-721); KNOTTED1 20%-30% (Bolduc et al., 2012, Gene Dev 26(15):1685-1690)] and in other eukaryotes [8% BRCA1 (Gorski et al, 2011, Nucleic Acids Research 39(22):9536-9548); LRH-1 32% (Bianco et al., 2014, Cancer research 74(7):2015-2025)]. Thus, the Class II "stable" bZIP1 targets correspond to the "gold standard" set typically identified in TF studies across eukaryotes (Gorski et al, 2011, Nucleic Acids Research 39(22):9536-9548; Hughes et al., 2013, Genetics 195(1):9-36; Monke et al., 2012, Nucleic Acids Research 40:8240l; Arenhart et al., 2014, Molecular plant 7(4):709-721; Bolduc et al., 2012, Gene Dev 26(15):1685-1690; Bianco et al., 2014, Cancer research 74(7):2015-2025). Further, the *cis*-element analysis suggests the novel finding that bZIP1 functions to activate or repress target gene expression via two distinct binding sites (Fig. 30). The targets activated by bZIP1 (Class IIA), are significantly enriched with the hybrid ACGT box bZIP1 binding site (E=2.5e-8) (Fig. 30). By contrast, genes repressed by bZIP1 (Class IIB) are enriched with the bZIP binding site GCN4 (E=1.3e-3) (Fig. 30). Interestingly, the GCN4 motif was reported to mediate N and amino acid starvation sensing in yeast (Hill et al., 1986, Science 234:451-457), suggesting a conserved link between bZIPs and nutrient sensing across eukaryotes. Finally, Class II targets share the "Stimulus/Stress" GO terms with other classes, but surprisingly, no significant biological terms unique to Class II targets were identified (Fig. 29A and Fig. 31).

[00398] ***Class III "Transient" targets (TF Regulation, but no detectable TF binding).*** Unexpectedly, the largest group of bZIP1 primary targets (781 genes), is represented by the Class III "transient" targets i.e., primary targets regulated by bZIP1 perturbation but not detectably bound by it (Fig. 29A). Paradoxically, Class IIIA "transient" targets that are activated by bZIP1 are the most significantly enriched in the

known bZIP1 binding site (E=1.3e-52) (Fig. 30), despite their lack of detectable bZIP1 binding. Class IIIB targets repressed by bZIP1 are significantly enriched in a distinct bZIP binding site "GCN4" (E=3.8e-3) (Fig. 30). Intriguingly, both of these known bZIP1-binding sites in the Class III transient genes are also observed in the Class II stable target genes (TF-bound and regulated) (Fig. 30). The lack of detectable TF-binding for Class III targets likely represents a transient or weak interaction of bZIP1 and these primary targets, rather than an indirect interaction, as the ChIP-Seq protocol can also detect indirect binding (e.g. via interacting TF partners). The trivial explanation that the mRNAs for Class IIIA genes are stabilized by CHX or bZIP1 is not supported by the data, as the CHX effect was accounted for by filtering out genes whose response to DEX-induced nuclear localization of bZIP1 is altered by CHX-treatment. Instead, the Class III primary targets likely represent a transient interaction between bZIP1 and its targets. Indeed, 41 genes from Class III transient targets have detectable bZIP1 binding at one or more of the earlier time-points (1, 5, 30, 60 min) measured by ChIP-Seq, following DEX-induced TF nuclear import (Fig. 29D; Table 20). These Class III transient genes are uniquely relevant to rapid N-signaling, as described below.

Table 20: Class III bZIP1-regulated genes that show evidence of bZIP1 binding at early (1, 5, 30 or 60 min), but not at a 5hr time point.

At4g14368	Regulator of chromosome condensation (RCC1) family protein
At1g10060	ATBCAT-1, BCAT-1, branched-chain amino acid transaminase 1
At1g18460	alpha/beta-Hydrolases superfamily protein
At3g60690	SAUR-like auxin-responsive protein family
At2g37840	Protein kinase superfamily protein
At3g14780	CONTAINS InterPro DOMAIN/s: Transposase, Ptta/En/Spm, plant (InterPro:IPR004252); BEST Arabidopsis thaliana protein match is: glucan synthase-like 4 (TAIR:AT3G14570.2); Has 315 Blast hits to 313 proteins in 50 species: Archae - 2; Bacteria - 16; Metazoa - 11; Fungi - 7; Plants - 181; Viruses - 2; Other Eukaryotes - 96 (source: NCBI BLink).
At3g01820	P-loop containing nucleoside triphosphate hydrolases superfamily protein
At1g30820	CTP synthase family protein
At1g73240	CONTAINS InterPro DOMAIN/s: Nucleoporin protein Ndc1-Nup (InterPro:IPR019049); Has 36 Blast hits to 36 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At4g17140	pleckstrin homology (PH) domain-containing protein

At1g04410	Lactate/malate dehydrogenase family protein
At5g59590	UGT76E2, UDP-glucosyl transferase 76E2
At1g53430	Leucine-rich repeat transmembrane protein kinase
At1g11000	ATMLO4, MLO4, Seven transmembrane MLO family protein
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1
At1g08830	CSD1, copper/zinc superoxide dismutase 1
At3g02150	PTF1, TCP13, TFPD, plastid transcription factor 1
At5g24430	Calcium-dependent protein kinase (CDPK) family protein
At3g51840	ACX4, ATG6, ATSCX, acyl-CoA oxidase 4
At1g06570	HPD, PDS1, phytoene desaturation 1
At4g19810	Glycosyl hydrolase family protein with chitinase insertion domain
At5g01590	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 59 proteins in 31 species: Archae - 0; Bacteria - 20; Metazoa - 1; Fungi - 2; Plants - 33; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).
At1g77030	hydrolases, acting on acid anhydrides, in phosphorus-containing anhydrides;ATP-dependent helicases;nucleic acid binding;ATP binding;RNA binding;helicases
At3g15950	NAI2, DNA topoisomerase-related
At5g43430	ETFBETA, electron transfer flavoprotein beta
At4g34180	Cyclase family protein
At1g19220	ARF11, ARF19, IAA22, auxin response factor 19
At1g08630	THA1, threonine aldolase 1
At1g67510	Leucine-rich repeat protein kinase family protein
At4g38340	Plant regulator RWP-RK family protein (NLP3)
At1g57560	AtMYB50, MYB50, myb domain protein 50
At4g38500	Protein of unknown function (DUF616)
At5g53130	ATCNGC1, CNGC1, cyclic nucleotide gated channel 1
At1g03090	MCCA, methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA)
At1g44100	AAP5, amino acid permease 5
At3g61850	DAG1, Dof-type zinc finger DNA-binding family protein
At1g18270	ketose-bisphosphate aldolase class-II family protein
At1g26730	EXS (ERD1/XPR1/SYG1) family protein
At5g46710	PLATZ transcription factor family protein
At3g48850	PHT3;2, phosphate transporter 3;2
At2g02700	Cysteine/Histidine-rich C1 domain family protein

[00399] The Class III *transient* bZIP1 primary targets comprise "first responders" in rapid N-signaling. In line with its role as a master regulator in a N-response gene network, all three classes of bZIP1 primary targets uncovered in this cell-based study are significantly enriched with N-responsive genes observed in whole plants (Krouk et al., 2010, Genome Biology 11(12):R123; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939-4944; Wang et al., 2003, Plant Physiol. 132(2):556-567; Wang et al., 2004, Plant physiology 136(1):2512-2522) (Fig. 29C; overlap with the "union" of N-responsive genes *in planta*). Unexpectedly, the "transient" Class III bZIP1 targets - regulated by, but not stably bound to bZIP1 - are uniquely relevant to rapid and dynamic N-signaling *in planta* (Fig. 29C). This conclusion is based on the following evidence: *First*, the Class IIIA transient bZIP1 targets have the largest and most significant overlap ($p\text{-}val<0.001$; Fig. 29C) with the 147 genes *induced* by N-signals in this cell-based *TARGET* study (Table 12). *Second*, only Class III transient bZIP1 targets have a significant enrichment in genes involved in N-related biological processes (enrichment of GO terms $p\text{-}val<0.01$) including amino acid metabolism (Fig. 29A; Fig. 32; Table 21), a role also supported by *in planta* studies of bZIP1 (Dietrich et al., 2011, The Plant Cell 23:381-395). *Third*, the Class III transient genes comprise the bulk of the bZIP1 targets in the N-assimilation pathway (Fig. 33 & Table 22), including the "early N-responders", such as the high-affinity nitrate transporter, NRT2.1, induced rapidly (< 12 minutes) and transiently following N-signal perturbation *in planta* (Krouk et al., 2010, Genome Biology 11(12):R123). *Fourth*, the Class III transient targets exclusively comprise *all* of the genes regulated by a N-treatment x bZIP1 interaction (28 genes) (Fig. 29C; Fig. 28). These include well-known early mediators of N-signaling induced at 6-12 min after N-provision (Krouk et al., 2010, Genome Biology 11(12):R123), including the NIN-like transcription factor 3 (NLP3; At4g38340) (Konishi et al., 2013, Nature Communications 4: 1617), and the LBD39 transcription factor (At4g37540) (Rubin et al., 2009, The Plant Cell 21(11):3567-3584). NLP3 belongs to the NIN-like transcription factor family which plays an essential role in nitrate signaling (Konishi et al., 2013, Nature Communications 4: 1617). In this study, NLP3 is a transient bZIP1 target whose up-regulation by bZIP1 is dependent on the N-signal (Fig. 28; Table 17). LBD39, which has been reported to fine-tune the magnitude of the N-response *in planta* (Rubin et al.,

2009, The Plant Cell 21(11):3567-3584), is a transient bZIP1 target that is *only* induced by bZIP1 in the presence of the N-signal in this cell-based study (Fig. 28; Table 17). This N-signal x bZIP1 interaction could be a post-translational modification of bZIP1, reminiscent of its post-translational modification in response to other abiotic signals (e.g. sugar and stress signals) (Dietrich et al., 2011, The Plant Cell 23:381-395). The N-signal x bZIP1 interaction could also involve translational/transcriptional effects of the N-signal on its interacting TF partners, as depicted in Fig. 24B.

Table 21. Significantly over-represented GO terms (FDR adjusted p-val<0.01) identified for genes in each of the five subclasses of bZIP1 targets. (Nitrogen related biological processes are in **bold)**

	GO ID	Term	Observed Frequency	Expected Frequency	p-value	Genes
ClassI	GO:0006950	response to stress	86 out of 275 genes, 31.3%	2104 out of 15002 genes, 14%	1.69E-10	AT5G49480|AT1G17870|AT1G80850|AT4G23190|AT5G06320|AT3G09440|AT4G17615|AT2G40000|AT5G47230|AT3G17390|AT1G55450|AT3G50980|AT1G27760|AT5G15090|AT1G42560|AT3G52930|AT3G23250|AT1G09080|AT2G26690|AT3G06510|AT5G02020|AT1G74310|AT2G30250|AT1G19020|AT4G05100|AT2G05710|AT1G68760|AT3G44260|AT1G32920|AT3G52450|AT2G41430|AT3G22370|AT1G01060|AT5G14740|AT1G78080|AT3G13790|AT3G10920|AT3G15500|AT2G24570|AT5G59820|AT1G19180|AT3G19580|AT1G22070|AT2G43130|AT1G05680|AT1G45145|AT2G40140|AT2G32120|AT2G03760|AT1G42990|AT5G63790|AT4G39090|AT5G45110|AT5G64905|AT3G49530|AT1G01720|AT1G76180|AT5G39580|AT1G59870|AT3G51920|AT5G06290|AT5G61890|AT1G62300|AT3G55440|AT4G01370|AT2G46830|AT2G17840|AT1G73080|AT5G58070|AT4G39640|AT3G10985|AT1G20440|AT1G10170|AT4G37010|AT4G33950|AT5G62530|AT2G35930|AT1G29395|AT1G33590|AT3G50970|AT5G37500|AT1G20450|AT4G20830|AT1G32640|AT4G39080|AT1G71697
	GO:0009628	response to abiotic stimulus	66 out of 275 genes, 24%	1360 out of 15002 genes, 9.1%	1.69E-10	AT5G49480|AT1G17870|AT2G43130|AT1G05680|AT3G09440|AT2G40140|AT4G27280|AT4G17615|AT2G32120|AT2G03760|AT5G47230|AT3G17390|AT1G56590|AT1G55450|AT3G50980|AT1G27760|AT4G39090|AT3G49530|AT1G76180|AT3G51920|AT5G05600|AT5G06290|AT3G55440|AT4G01370|AT2G46830|AT3G52930|AT1G61890|AT4G37370|AT2G17840|AT5G58070|AT3G23250|AT1G09080|AT3G06510|AT5G02020|AT1G74310|AT1G20440|AT2G30250|AT2G47000|AT4G05100|AT1G10170|AT4G33950|AT1G78290|AT5G62530|AT2G05710|AT2G35930|AT1G29395|AT1G33590|AT3G50970|AT4G37270|AT3G52450|AT5G37500|AT3G62410|AT2G41430|AT1G20450|AT3G22370|AT1G80010|AT1G01060|AT1G32640|AT1G78080|AT3G13790|AT4G39080|AT3G10920|AT3G15500|AT5G59820|AT5G01500|AT3G19580

	GO:00 42221	response to chemical stimulus	79 out of 275 genes, 28.7%	1892 out of 15002 genes, 12.6%	5.36E-10	AT1G22070|AT1G17870|AT4G23190|AT1G68765|AT1G05680|AT3G15 210|AT1G45145|AT3G16857|AT3G09440|AT2G40140|AT1G43910|AT4 G17615|AT3G53480|AT2G32120|AT2G40000|AT2G03760|AT1G15080| AT5G47230|AT3G08590|AT1G42990|AT3G50980|AT5G63790|AT4G39 090|AT3G49530|AT4G34160|AT1G76180|AT1G59870|AT3G51920|AT3 G04730|AT1G62300|AT4G08950|AT3G55440|AT4G01370|AT2G46830| AT5G11670|AT3G52930|AT2G17840|AT5G27420|AT1G73080|AT4G39 640|AT3G23250|AT2G26690|AT1G74310|AT1G20440|AT5G02240|AT2 G25490|AT1G19020|AT2G47000|AT4G05100|AT1G10170|AT5G59450| AT3G46620|AT4G33950|AT3G13920|AT4G37260|AT2G05710|AT2G35 930|AT1G29395|AT3G50970|AT4G37270|AT3G52450|AT5G37500|AT3 G62410|AT2G41430|AT1G20450|AT4G20830|AT1G01060|AT1G32640| AT1G78080|AT3G10920|AT3G15500|AT3G52800|AT2G24570|AT4G05 320|AT2G04880|AT5G59820|AT1G19180|AT3G19580|AT2G23320
	GO:00 50896	response to stimulus	121 out of 275 genes, 44%	3689 out of 15002 genes, 24.6%	6.14E-10	AT5G49480|AT1G17870|AT1G80850|AT4G23190|AT3G15210|AT5G06 320|AT3G09440|AT4G27280|AT4G17615|AT2G40000|AT1G15080|AT5 G47230|AT3G17390|AT1G55450|AT3G50980|AT1G27760|AT5G15090| AT3G04730|AT4G08950|AT1G42560|AT3G52930|AT5G27420|AT3G23 250|AT1G09080|AT2G26690|AT3G06510|AT5G02020|AT1G74310|AT2 G30250|AT1G19020|AT2G47000|AT4G05100|AT5G59450|AT3G46620| AT1G78290|AT2G05710|AT1G68760|AT3G44260|AT1G32920|AT3G52 450|AT2G41430|AT3G22370|AT1G01060|AT5G14740|AT1G78080|AT3 G13790|AT3G10920|AT3G15500|AT4G36010|AT2G24570|AT2G04880| AT5G59820|AT5G01500|AT1G19180|AT3G19580|AT2G23320|AT1G22 070|AT2G43130|AT1G05680|AT1G68765|AT1G45145|AT3G16857|AT2 G40140|AT1G43910|AT3G53480|AT2G32120|AT2G03760|AT1G56590| AT3G08590|AT1G42990|AT5G63790|AT4G39090|AT5G45110|AT5G64 905|AT3G49530|AT1G01720|AT4G34160|AT1G76180|AT5G39580|AT1 G59870|AT3G51920|AT5G05600|AT5G06290|AT5G61890|AT1G62300| AT3G55440|AT4G01370|AT2G46830|AT5G11670|AT1G61890|AT4G37 370|AT2G17840|AT1G73080|AT5G58070|AT4G39640|AT3G10985|AT1 G20440|AT5G02240|AT2G25490|AT1G10170|AT4G37010|AT4G33950| AT3G13920|AT5G62530|AT4G37260|AT2G35930|AT1G29395|AT1G33 590|AT3G50970|AT4G37270|AT5G37500|AT3G62410|AT1G20450|AT4 G20830|AT1G80010|AT1G32640|AT4G39080|AT1G71697|AT3G52800| AT4G05320|AT1G29690
	GO:00 10033	response to organic substance	57 out of 275 genes, 20.7%	1148 out of 15002 genes, 7.7%	1.64E-09	AT1G22070|AT1G68765|AT1G05680|AT3G15210|AT3G16857|AT2G40 140|AT1G43910|AT4G17615|AT3G53480|AT2G40000|AT2G03760|AT1 G15080|AT5G47230|AT1G42990|AT3G49530|AT4G34160|AT1G76180| AT1G59870|AT3G51920|AT3G04730|AT1G62300|AT4G08950|AT4G01 370|AT2G46830|AT5G27420|AT1G73080|AT3G23250|AT2G26690|AT1 G20440|AT5G02240|AT2G25490|AT2G47000|AT4G05100|AT5G59450| AT3G46620|AT4G33950|AT4G37260|AT2G05710|AT2G35930|AT1G29 395|AT3G50970|AT3G52450|AT5G37500|AT3G62410|AT1G20450|AT1 G01060|AT1G32640|AT1G78080|AT3G15500|AT3G52800|AT2G24570| AT4G05320|AT2G04880|AT5G59820|AT1G19180|AT3G19580|AT2G23 320

	GO:00 10200	response to chitin	19 out of 275 genes, 6.9%	127 out of 15002 genes, 0.8%	2.22E-09	AT5G27420|AT1G32640|AT3G49530|AT2G40140|AT4G37260|AT1G42 990|AT3G19580|AT5G59450|AT3G15210|AT3G46620|AT5G59820|AT5 G47230|AT3G23250|AT2G35930|AT3G52800|AT2G23320|AT1G62300| AT2G24570|AT3G52450
	GO:00 09743	response to carbohydrat e stimulus	21 out of 275 genes, 7.6%	203 out of 15002 genes, 1.4%	8.31E-08	AT5G27420|AT3G49530|AT4G34160|AT5G59450|AT3G15210|AT3G46 620|AT5G59820|AT5G47230|AT3G23250|AT1G62300|AT3G52450|AT1 G32640|AT2G40140|AT4G37260|AT1G42990|AT3G19580|AT2G35930| AT3G52800|AT3G62410|AT2G23320|AT2G24570
	GO:00 06970	response to osmotic stress	29 out of 275 genes, 10.5%	425 out of 15002 genes, 2.8%	3.21E-07	AT5G49480|AT4G05100|AT1G10170|AT1G05680|AT3G51920|AT1G01 060|AT4G33950|AT5G62530|AT1G78080|AT4G39080|AT3G55440|AT3 G10920|AT4G01370|AT2G46830|AT2G05710|AT4G17615|AT3G52930| AT2G17840|AT5G58070|AT2G03760|AT5G59820|AT3G23250|AT1G55 450|AT5G02020|AT1G20440|AT3G19580|AT1G27760|AT2G30250|AT4 G39090
	GO:00 09651	response to salt stress	28 out of 275 genes, 10.2%	397 out of 15002 genes, 2.6%	3.21E-07	AT5G49480|AT4G05100|AT1G10170|AT1G05680|AT3G51920|AT1G01 060|AT4G33950|AT5G62530|AT1G78080|AT4G39080|AT3G55440|AT3 G10920|AT4G01370|AT2G46830|AT2G05710|AT4G17615|AT3G52930| AT2G17840|AT5G58070|AT2G03760|AT5G59820|AT3G23250|AT1G55 450|AT5G02020|AT3G19580|AT1G27760|AT2G30250|AT4G39090
	GO:00 09415	response to water	20 out of 275 genes, 7.3%	211 out of 15002 genes, 1.4%	5.96E-07	AT1G76180|AT1G05680|AT3G51920|AT3G50970|AT4G33950|AT3G52 450|AT1G32640|AT1G78080|AT5G37500|AT1G20440|AT3G19580|AT3 G15500|AT3G50980|AT2G35930|AT1G29395|AT4G39090|AT4G17615| AT2G41430|AT1G20450|AT2G17840
	GO:00 09414	response to water deprivation	19 out of 275 genes, 6.9%	202 out of 15002 genes, 1.3%	1.46E-06	AT1G76180|AT1G05680|AT3G51920|AT3G50970|AT4G33950|AT3G52 450|AT1G32640|AT1G78080|AT5G37500|AT1G20440|AT3G19580|AT3 G15500|AT2G35930|AT1G29395|AT4G39090|AT4G17615|AT2G41430| AT1G20450|AT2G17840
	GO:00 09737	response to abscisic acid stimulus	24 out of 275 genes, 8.7%	340 out of 15002 genes, 2.3%	3.21E-06	AT4G05100|AT1G76180|AT1G05680|AT3G15210|AT1G59870|AT3G51 920|AT1G01060|AT4G33950|AT1G32640|AT4G37260|AT4G01370|AT2 G46830|AT1G43910|AT2G05710|AT1G29395|AT4G17615|AT5G27420| AT1G15080|AT3G50970|AT5G37500|AT1G20440|AT3G19580|AT1G20 450|AT5G02240
	GO:00 09266	response to temperature stimulus	25 out of 275 genes, 9.1%	399 out of 15002 genes, 2.7%	1.33E-05	AT3G49530|AT3G22370|AT1G17870|AT2G43130|AT1G76180|AT5G06 290|AT3G09440|AT2G40140|AT4G01370|AT1G29395|AT4G17615|AT2 G17840|AT2G32120|AT5G58070|AT5G59820|AT5G47230|AT3G50970| AT1G09080|AT3G17390|AT3G06510|AT5G37500|AT1G74310|AT1G20 440|AT2G30250|AT1G20450
	GO:00 09409	response to cold	19 out of 275 genes, 6.9%	269 out of 15002 genes, 1.8%	7.22E-05	AT3G49530|AT3G22370|AT1G76180|AT5G06290|AT2G40140|AT4G01 370|AT1G29395|AT4G17615|AT2G17840|AT5G58070|AT5G47230|AT5 G59820|AT3G50970|AT3G17390|AT3G06510|AT5G37500|AT1G20440| AT2G30250|AT1G20450
	GO:00 09719	response to endogenous stimulus	39 out of 275 genes, 14.2%	920 out of 15002 genes, 6.1%	8.19E-05	AT2G47000|AT4G05100|AT1G68765|AT1G05680|AT3G15210|AT4G33 950|AT3G16857|AT4G37260|AT1G43910|AT2G05710|AT1G29395|AT4 G17615|AT3G53480|AT1G15080|AT5G47230|AT3G50970|AT5G37500| AT1G20450|AT4G34160|AT1G76180|AT1G59870|AT3G51920|AT3G04 730|AT1G01060|AT4G08950|AT1G32640|AT1G78080|AT3G15500|AT4

						G01370|AT2G46830|AT5G27420|AT1G73080|AT3G23250|AT2G26690|AT1G19180|AT1G20440|AT3G19580|AT5G02240|AT2G25490
	GO:0042742	defense response to bacterium	15 out of 275 genes, 5.5%	201 out of 15002 genes, 1.3%	0.000464	AT1G22070|AT2G40000|AT5G15090|AT1G10170|AT4G23190|AT5G06320|AT1G59870|AT5G06290|AT4G33950|AT5G14740|AT1G19180|AT3G10920|AT4G39090|AT2G24570|AT5G45110
	GO:0009725	response to hormone stimulus	35 out of 275 genes, 12.7%	849 out of 15002 genes, 5.7%	0.000474	AT2G47000|AT4G05100|AT1G68765|AT1G05680|AT3G15210|AT4G33950|AT3G16857|AT4G37260|AT1G43910|AT2G05710|AT1G29395|AT4G17615|AT3G53480|AT1G15080|AT5G47230|AT3G50970|AT5G37500|AT1G20450|AT4G34160|AT1G76180|AT1G59870|AT3G51920|AT3G04730|AT1G01060|AT4G08950|AT1G32640|AT1G78080|AT4G01370|AT2G46830|AT5G27420|AT3G23250|AT1G20440|AT3G19580|AT5G02240|AT2G25490
	GO:0009607	response to biotic stimulus	28 out of 275 genes, 10.2%	610 out of 15002 genes, 4.1%	0.000597	AT1G22070|AT1G10170|AT4G23190|AT5G06320|AT4G33950|AT1G45145|AT2G40140|AT3G44260|AT2G40000|AT3G50970|AT1G42990|AT4G39090|AT2G41430|AT5G45110|AT3G49530|AT5G15090|AT5G39580|AT1G59870|AT5G06290|AT5G61890|AT5G14740|AT3G10920|AT4G36010|AT4G01370|AT2G24570|AT3G10985|AT1G19180|AT1G20440
	GO:0009753	response to jasmonic acid stimulus	13 out of 275 genes, 4.7%	158 out of 15002 genes, 1.1%	0.000597	AT1G73080|AT4G05100|AT3G15210|AT1G01060|AT3G23250|AT2G26690|AT1G32640|AT1G19180|AT5G37500|AT4G37260|AT3G15500|AT4G01370|AT2G46830
	GO:0051707	response to other organism	26 out of 275 genes, 9.5%	558 out of 15002 genes, 3.7%	0.000872	AT1G22070|AT1G10170|AT4G23190|AT5G06320|AT4G33950|AT1G45145|AT2G40140|AT2G40000|AT3G50970|AT4G39090|AT2G41430|AT5G45110|AT3G49530|AT5G15090|AT5G39580|AT1G59870|AT5G06290|AT5G61890|AT5G14740|AT3G10920|AT4G36010|AT4G01370|AT2G24570|AT3G10985|AT1G19180|AT1G20440
	GO:0070887	cellular response to chemical stimulus	20 out of 275 genes, 7.3%	374 out of 15002 genes, 2.5%	0.00127	AT1G22070|AT1G05680|AT3G15210|AT1G59870|AT4G33950|AT1G62300|AT1G32640|AT3G16857|AT1G78080|AT3G10920|AT3G15500|AT4G01370|AT1G29395|AT4G17615|AT3G53480|AT2G04880|AT1G15080|AT5G47230|AT1G19180|AT1G42990
	GO:0009617	response to bacterium	16 out of 275 genes, 5.8%	256 out of 15002 genes, 1.7%	0.00134	AT1G22070|AT2G40000|AT5G15090|AT1G10170|AT4G23190|AT5G06320|AT1G59870|AT5G06290|AT4G33950|AT5G14740|AT1G19180|AT3G10920|AT4G39090|AT2G24570|AT2G41430|AT5G45110
	GO:0051704	multi-organism process	26 out of 275 genes, 9.5%	589 out of 15002 genes, 3.9%	0.00182	AT1G22070|AT1G10170|AT4G23190|AT5G06320|AT4G33950|AT1G45145|AT2G40140|AT2G40000|AT3G50970|AT4G39090|AT2G41430|AT5G45110|AT3G49530|AT5G15090|AT5G39580|AT1G59870|AT5G06290|AT5G61890|AT5G14740|AT3G10920|AT4G36010|AT4G01370|AT2G24570|AT3G10985|AT1G19180|AT1G20440
	GO:0006952	defense response	30 out of 275 genes, 10.9%	747 out of 15002 genes, 5%	0.00242	AT1G22070|AT1G10170|AT4G23190|AT5G06320|AT4G33950|AT1G45145|AT2G40140|AT2G35930|AT1G33590|AT2G40000|AT2G03760|AT3G50970|AT3G52450|AT4G39090|AT5G45110|AT5G64905|AT3G49530|AT5G15090|AT5G39580|AT1G59870|AT5G06290|AT5G61890|AT5G14740|AT3G10920|AT4G01370|AT1G42560|AT2G24570|AT1G73080|AT1G19180|AT1G20440

	GO:0009631	cold acclimation	5 out of 275 genes, 1.8%	21 out of 15002 genes, 0.1%	0.00297	AT5G59820|AT1G20440|AT1G20450|AT1G29395|AT3G50970
	GO:0009642	response to light intensity	8 out of 275 genes, 2.9%	78 out of 15002 genes, 0.5%	0.0051	AT2G32120|AT1G17870|AT1G74310|AT1G10170|AT5G59820|AT4G37270|AT2G41430|AT2G17840
	GO:0072511	divalent inorganic cation transport	6 out of 275 genes, 2.2%	40 out of 15002 genes, 0.3%	0.00516	AT3G13320|AT4G37270|AT3G63380|AT1G59870|AT2G04040|AT1G27770
	GO:0080167	response to karrikin	10 out of 275 genes, 3.6%	127 out of 15002 genes, 0.8%	0.00564	AT3G13790|AT3G09440|AT1G05680|AT5G05600|AT4G27280|AT1G33590|AT3G52930|AT1G61890|AT4G37370|AT1G78290
	GO:0071310	cellular response to organic substance	17 out of 275 genes, 6.2%	337 out of 15002 genes, 2.2%	0.00701	AT1G22070|AT1G05680|AT3G15210|AT1G59870|AT4G33950|AT1G32640|AT3G16857|AT1G78080|AT3G15500|AT4G01370|AT4G17615|AT3G53480|AT2G04880|AT1G15080|AT5G47230|AT1G19180|AT1G42990
	GO:0009723	response to ethylene stimulus	10 out of 275 genes, 3.6%	134 out of 15002 genes, 0.9%	0.00789	AT4G05100|AT1G68765|AT3G15210|AT5G47230|AT1G01060|AT3G23250|AT1G78080|AT4G37260|AT2G46830|AT2G25490
ClassIIA	None					
ClassIIB	GO:0006950	response to stress	18 out of 49 genes, 36.7%	1943 out of 12802 genes, 15.2%	0.03	AT2G35980|AT1G80820|AT2G46140|AT3G24550|AT4G12720|AT4G39260|AT3G06490|AT1G73010|AT4G37910|AT2G39660|AT5G37770|AT4G34150|AT4G02380|AT1G14550|AT5G26030|AT2G38470|AT5G47910|AT1G14540
	GO:0006979	response to oxidative stress	6 out of 49 genes, 12.2%	271 out of 12802 genes, 2.1%	0.03	AT1G14550|AT5G26030|AT4G12720|AT4G02380|AT1G14540|AT5G37770
	GO:0009266	response to temperature stimulus	8 out of 49 genes, 16.3%	388 out of 12802 genes, 3%	0.03	AT4G34150|AT4G37910|AT5G47910|AT2G38470|AT1G80820|AT4G02380|AT5G37770|AT4G39260
	GO:0009409	response to cold	6 out of 49 genes, 12.2%	264 out of 12802 genes, 2.1%	0.03	AT4G34150|AT2G38470|AT1G80820|AT4G02380|AT5G37770|AT4G39260
	GO:0009620	response to fungus	5 out of 49 genes,	159 out of 12802	0.03	AT2G38470|AT3G06490|AT2G39660|AT5G47910|AT3G24550

			10.2%	genes, 1.2%		
	GO:0010411	xyloglucan metabolic process	2 out of 49 genes, 4.1%	6 out of 12802 genes, 0%	0.03	AT4G30280|AT4G30290
	GO:0042221	response to chemical stimulus	16 out of 49 genes, 32.7%	1763 out of 12802 genes, 13.8%	0.03	AT4G37910|AT2G46140|AT5G37770|AT3G02880|AT5G01540|AT4G12720|AT2G17660|AT4G02380|AT4G39260|AT1G14550|AT5G26030|AT2G38470|AT3G06490|AT4G18880|AT4G11360|AT1G14540
	GO:0006334	nucleosome assembly	3 out of 49 genes, 6.1%	58 out of 12802 genes, 0.5%	0.05	AT4G40030|AT1G06760|AT4G40040
	GO:0034728	nucleosome organization	3 out of 49 genes, 6.1%	58 out of 12802 genes, 0.5%	0.05	AT4G40030|AT1G06760|AT4G40040
	GO:0050896	response to stimulus	23 out of 49 genes, 46.9%	3396 out of 12802 genes, 26.5%	0.05	AT2G35980|AT1G80820|AT2G46140|AT3G02880|AT3G24550|AT5G01540|AT4G12720|AT4G39260|AT3G06490|AT1G73010|AT4G11360|AT4G37910|AT2G39660|AT5G37770|AT4G34150|AT2G17660|AT4G02380|AT1G14550|AT5G26030|AT2G38470|AT4G18880|AT5G47910|AT1G14540
	GO:0065004	protein-DNA complex assembly	3 out of 49 genes, 6.1%	60 out of 12802 genes, 0.5%	0.05	AT4G40030|AT1G06760|AT4G40040
	GO:0071824	protein-DNA complex subunit organization	3 out of 49 genes, 6.1%	60 out of 12802 genes, 0.5%	0.05	AT4G40030|AT1G06760|AT4G40040
ClassIIIA	GO:0009081	**branched chain family amino acid metabolic process**	6 out of 269 genes, 2.2%	27 out of 12802 genes, 0.2%	0.01	AT1G18270|AT1G10070|AT5G43430|AT1G10060|AT1G03090|AT2G43400
	GO:0009310	**amine catabolic process**	7 out of 269 genes, 2.6%	40 out of 12802 genes, 0.3%	0.01	AT4G33150|AT2G43400|AT1G08630|AT5G43430|AT1G03090|AT1G65840|AT5G54080
	GO:0016054	organic acid catabolic	9 out of 269 genes, 3.3%	79 out of 12802 genes,	0.01	AT2G43400|AT2G33150|AT5G43430|AT4G33150|AT3G51840|AT1G08630|AT5G65110|AT1G03090|AT5G54080

		process		0.6%		
	GO:00 42221	response to chemical stimulus	62 out of 269 genes, 23%	1763 out of 12802 genes, 13.8%	0.01	AT1G08720|AT1G08920|AT5G66400|AT2G40170|AT2G22080|AT4G13430|AT4G37790|AT2G34600|AT1G54100|AT5G37260|AT3G51860|AT5G61590|AT5G47390|AT5G16970|AT2G38750|AT4G37220|AT5G16960|AT1G04410|AT1G49670|AT3G11410|AT4G32320|AT5G67450|AT1G08090|AT5G54500|AT5G50200|AT1G08830|AT3G56240|AT1G55020|AT4G33420|AT1G20340|AT4G27260|AT5G59220|AT1G28130|AT2G19810|AT3G05200|AT2G46270|AT5G03720|AT3G23230|AT1G73260|AT1G08930|AT5G39040|AT5G44380|AT1G18330|AT5G13740|AT4G30170|AT4G35770|AT1G16150|AT1G15050|AT2G14170|AT1G80460|AT5G10450|AT4G39070|AT3G14050|AT4G21440|AT1G02860|AT5G18170|AT1G68850|AT4G34350|AT2G01570|AT3G60690|AT5G05340|AT1G17190
	GO:00 46395	carboxylic acid catabolic process	9 out of 269 genes, 3.3%	79 out of 12802 genes, 0.6%	0.01	AT2G43400|AT2G33150|AT5G43430|AT4G33150|AT3G51840|AT1G08630|AT5G65110|AT1G03090|AT5G54080
	GO:00 06552	leucine catabolic process	3 out of 269 genes, 1.1%	4 out of 12802 genes, 0%	0.03	AT2G43400|AT5G43430|AT1G03090
	GO:00 06979	response to oxidative stress	16 out of 269 genes, 5.9%	271 out of 12802 genes, 2.1%	0.03	AT2G19810|AT2G22080|AT1G73260|AT1G08830|AT3G56240|AT5G16970|AT1G68850|AT4G33420|AT5G44380|AT4G30170|AT5G16960|AT4G35770|AT5G05340|AT2G14170|AT1G49670|AT4G32320
	GO:00 09063	**cellular amino acid catabolic process**	6 out of 269 genes, 2.2%	38 out of 12802 genes, 0.3%	0.03	AT4G33150|AT2G43400|AT1G08630|AT5G43430|AT1G03090|AT5G54080
	GO:00 09083	**branched chain family amino acid catabolic process**	3 out of 269 genes, 1.1%	5 out of 12802 genes, 0%	0.03	AT2G43400|AT5G43430|AT1G03090
	GO:00 50896	response to stimulus	97 out of 269 genes, 36.1%	3396 out of 12802 genes, 26.5%	0.03	AT1G08920|AT2G43400|AT2G33150|AT2G40170|AT2G22080|AT4G13430|AT4G37790|AT1G54100|AT1G02670|AT5G61590|AT5G47390|AT3G54960|AT2G38750|AT4G37220|AT5G16960|AT1G04410|AT1G49670|AT3G11410|AT4G32320|AT1G08090|AT5G54500|AT1G08830|AT1G25275|AT3G15950|AT4G33420|AT4G27260|AT5G59220|AT1G28130|AT5G24470|AT2G46270|AT5G03720|AT3G23230|AT1G06520|AT5G67320|AT1G73260|AT5G39040|AT4G30170|AT4G35770|AT1G16150|AT1G31480|AT1G80460|AT5G24530|AT1G75800|AT2G39980|AT4G39070|AT3G14050|AT1G60940|AT5G06980|AT1G02860|AT3G47640|AT1G68850|AT2G26280|AT5G13750|AT3G45060|AT1G17190|AT5G67440|AT5G27350|AT1G08720|AT5G66400|AT5G47740|AT5G52250|AT4G24220|AT2G34600|AT5G37260|AT3G51860|AT5G16970|AT3G61060|AT3G27690|AT5G67450|AT5G47240|AT5G50200|AT4G01120|AT5G61510|AT3G56

						240|AT1G55020|AT1G20340|AT5G04770|AT2G19810|AT3G05200|AT1G08930|AT5G44380|AT1G18330|AT5G13740|AT1G15050|AT2G14170|AT1G13080|AT5G10450|AT5G20250|AT2G32660|AT4G21440|AT1G75230|AT5G18170|AT4G34350|AT2G01570|AT3G60690|AT5G05340|AT5G61600
ClassIIIB	GO:0006952	defense response	36 out of 234 genes, 15.4%	683 out of 12802 genes, 5.3%	1.43E-05	AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT4G23440|AT1G11000|AT1G57630|AT1G18570|AT5G41550|AT5G58120|AT2G34930|AT3G05360|AT3G11840|AT1G11310|AT3G11820|AT2G26380|AT1G74710|AT1G61560|AT2G26560|AT1G15890|AT3G48090|AT5G04720|AT2G16870|AT4G39030|AT5G44070|AT1G56510|AT5G22690|AT4G11170|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G13650|AT1G66090|AT4G33300
	GO:0050896	response to stimulus	100 out of 234 genes, 42.7%	3396 out of 12802 genes, 26.5%	3.02E-05	AT4G23440|AT3G52360|AT4G17230|AT4G16780|AT5G24620|AT4G17260|AT4G34180|AT3G11840|AT5G62390|AT1G61560|AT1G18890|AT4G02200|AT4G30080|AT5G44070|AT3G61850|AT1G11210|AT1G09940|AT2G01150|AT5G51190|AT1G13340|AT3G44720|AT2G17040|AT1G55920|AT1G20510|AT3G61900|AT4G33300|AT3G45640|AT2G38870|AT3G25070|AT1G57630|AT1G07520|AT2G34930|AT3G17020|AT3G50480|AT5G62680|AT1G80530|AT5G61210|AT5G44610|AT5G66070|AT2G26560|AT3G07390|AT2G40180|AT1G56510|AT5G63770|AT4G11170|AT2G41380|AT5G25190|AT5G65020|AT3G13650|AT2G06050|AT3G52430|AT1G11000|AT5G06720|AT5G66880|AT3G59900|AT5G48540|AT1G18570|AT2G04160|AT3G05360|AT1G72060|AT1G11310|AT1G15890|AT3G48090|AT5G04720|AT4G26120|AT4G39030|AT1G52560|AT1G05710|AT5G24540|AT5G22690|AT3G52400|AT1G05055|AT3G28740|AT2G19190|AT1G52200|AT1G17750|AT1G74430|AT1G05800|AT1G66090|AT3G17700|AT1G30040|AT4G14630|AT4G11850|AT5G09980|AT5G41550|AT5G58120|AT3G28580|AT1G19220|AT3G11820|AT2G26380|AT1G74710|AT2G16870|AT2G16500|AT1G57560|AT1G70940|AT1G02400|AT5G54170|AT2G46590|AT3G09270|AT5G49620
	GO:0031348	negative regulation of defense response	7 out of 234 genes, 3%	18 out of 12802 genes, 0.1%	4.84E-05	AT3G25070|AT1G11310|AT3G52400|AT3G11820|AT4G39030|AT1G74710|AT3G52430
	GO:0051707	response to other organism	27 out of 234 genes, 11.5%	533 out of 12802 genes, 4.2%	0.000515	AT3G45640|AT2G06050|AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT5G24620|AT1G18570|AT2G34930|AT3G50480|AT5G61210|AT1G11310|AT3G11820|AT1G74710|AT1G61560|AT2G26560|AT3G48090|AT4G39030|AT5G44070|AT1G56510|AT5G24540|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G17700
	GO:0002376	immune system process	18 out of 234 genes, 7.7%	277 out of 12802 genes, 2.2%	0.000657	AT3G48090|AT3G52430|AT2G16870|AT3G25070|AT4G11850|AT4G23440|AT1G57630|AT1G56510|AT5G41550|AT5G58120|AT5G22690|AT3G05360|AT3G11840|AT1G11310|AT1G74710|AT1G66090|AT1G61560|AT2G26560
	GO:0006950	response to stress	62 out of 234 genes,	1943 out of 12802	0.000657	AT4G23440|AT4G17260|AT4G34180|AT3G11840|AT5G62390|AT1G61560|AT4G02200|AT5G44070|AT1G11210|AT1G09940|AT1G13340|AT1

			26.5%	genes, 15.2%		G55920|AT1G20510|AT4G33300|AT3G45640|AT2G38870|AT3G25070|AT1G57630|AT2G34930|AT3G17020|AT5G44610|AT2G26560|AT1G56510|AT5G63770|AT4G11170|AT5G65020|AT3G13650|AT2G06050|AT3G52430|AT1G11000|AT5G66880|AT5G06720|AT1G18570|AT3G05360|AT1G72060|AT1G11310|AT1G15890|AT3G48090|AT5G04720|AT4G39030|AT1G52560|AT5G22690|AT3G52400|AT1G05055|AT3G28740|AT2G19190|AT1G52200|AT1G17750|AT1G05800|AT1G66090|AT4G14630|AT4G11850|AT5G41550|AT5G58120|AT3G11820|AT2G26380|AT1G74710|AT2G16870|AT2G16500|AT5G54170|AT2G46590|AT5G49620
	GO:0009607	response to biotic stimulus	28 out of 234 genes, 12%	582 out of 12802 genes, 4.5%	0.000657	AT3G45640|AT2G06050|AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT5G24620|AT1G18570|AT2G34930|AT3G50480|AT5G61210|AT5G62390|AT1G11310|AT3G11820|AT1G74710|AT1G61560|AT2G26560|AT3G48090|AT4G39030|AT5G44070|AT1G56510|AT5G24540|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G17700
	GO:0051704	multi-organism process	27 out of 234 genes, 11.5%	562 out of 12802 genes, 4.4%	0.000657	AT3G45640|AT2G06050|AT2G38870|AT3G52430|AT3G25070|AT4G11850|AT5G24620|AT1G18570|AT2G34930|AT3G50480|AT5G61210|AT1G11310|AT3G11820|AT1G74710|AT1G61560|AT2G26560|AT3G48090|AT4G39030|AT5G44070|AT1G56510|AT5G24540|AT3G52400|AT3G28740|AT2G19190|AT1G17750|AT1G05800|AT3G17700
	GO:0080134	regulation of response to stress	10 out of 234 genes, 4.3%	86 out of 12802 genes, 0.7%	0.000674	AT3G45640|AT1G11310|AT3G11820|AT2G31880|AT3G52430|AT3G25070|AT3G52400|AT4G39030|AT1G74710|AT3G05360
	GO:0031347	regulation of defense response	9 out of 234 genes, 3.8%	72 out of 12802 genes, 0.6%	0.00102	AT1G11310|AT3G11820|AT2G31880|AT3G52430|AT3G25070|AT3G52400|AT4G39030|AT1G74710|AT3G05360
	GO:0045087	innate immune response	16 out of 234 genes, 6.8%	241 out of 12802 genes, 1.9%	0.00106	AT3G48090|AT3G52430|AT2G16870|AT3G25070|AT4G11850|AT4G23440|AT1G57630|AT1G56510|AT5G41550|AT5G58120|AT5G22690|AT1G11310|AT1G74710|AT1G66090|AT1G61560|AT2G26560
	GO:0006955	immune response	16 out of 234 genes, 6.8%	245 out of 12802 genes, 1.9%	0.00118	AT3G48090|AT3G52430|AT2G16870|AT3G25070|AT4G11850|AT4G23440|AT1G57630|AT1G56510|AT5G41550|AT5G58120|AT5G22690|AT1G11310|AT1G74710|AT1G66090|AT1G61560|AT2G26560
	GO:0008219	cell death	15 out of 234 genes, 6.4%	221 out of 12802 genes, 1.7%	0.00121	AT5G22690|AT3G48090|AT5G04720|AT2G16870|AT3G25070|AT4G23440|AT1G11000|AT1G11310|AT1G66090|AT5G41550|AT1G61560|AT5G58120|AT4G33300|AT2G26560|AT1G15890
	GO:0016265	death	15 out of 234 genes, 6.4%	221 out of 12802 genes, 1.7%	0.00121	AT5G22690|AT3G48090|AT5G04720|AT2G16870|AT3G25070|AT4G23440|AT1G11000|AT1G11310|AT1G66090|AT5G41550|AT1G61560|AT5G58120|AT4G33300|AT2G26560|AT1G15890
	GO:0016310	phosphorylation	33 out of 234 genes, 14.1%	872 out of 12802 genes,	0.00364	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|

				6.8%		AT1G70530|AT1G53430|AT1G61370|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT2G39110|AT1G17750|AT1G53050|AT4G39940
	GO:0048583	regulation of response to stimulus	12 out of 234 genes, 5.1%	170 out of 12802 genes, 1.3%	0.00495	AT3G45640|AT3G52430|AT3G25070|AT3G52400|AT4G39030|AT3G05360|AT5G66880|AT4G09570|AT1G11310|AT3G11820|AT2G31880|AT1G74710
	GO:0006468	protein phosphorylation	32 out of 234 genes, 13.7%	856 out of 12802 genes, 6.7%	0.00519	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT1G70530|AT1G53430|AT1G61370|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT2G39110|AT1G17750|AT1G53050
	GO:0006793	phosphorus metabolic process	34 out of 234 genes, 14.5%	948 out of 12802 genes, 7.4%	0.00605	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT1G70530|AT1G53430|AT1G61370|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT3G02800|AT2G39110|AT1G17750|AT1G53050|AT4G39940
	GO:0006796	phosphate metabolic process	34 out of 234 genes, 14.5%	947 out of 12802 genes, 7.4%	0.00605	AT3G45640|AT5G40540|AT3G25070|AT1G55610|AT5G41680|AT2G17220|AT1G51940|AT4G09570|AT2G31880|AT4G28350|AT2G19130|AT5G38210|AT1G70130|AT3G55950|AT2G37840|AT3G16030|AT1G51620|AT1G70530|AT1G53430|AT1G61370|AT3G08760|AT2G11520|AT1G18890|AT4G21390|AT5G07620|AT1G53440|AT1G28390|AT5G65600|AT1G04440|AT3G02800|AT2G39110|AT1G17750|AT1G53050|AT4G39940
	GO:0012501	programmed cell death	12 out of 234 genes, 5.1%	185 out of 12802 genes, 1.4%	0.00793	AT5G22690|AT3G48090|AT5G04720|AT2G16870|AT3G25070|AT4G23440|AT1G66090|AT5G41550|AT5G58120|AT4G33300|AT2G26560|AT1G15890
	GO:0048585	negative regulation of response to stimulus	7 out of 234 genes, 3%	62 out of 12802 genes, 0.5%	0.00793	AT1G11310|AT3G11820|AT3G52430|AT3G25070|AT3G52400|AT4G39030|AT1G74710
	GO:0010033	response to organic substance	36 out of 234 genes, 15.4%	1059 out of 12802 genes, 8.3%	0.00907	AT3G52430|AT4G17230|AT5G66880|AT3G59900|AT4G16780|AT1G18570|AT2G04160|AT4G17260|AT3G11840|AT5G62390|AT3G48090|AT4G26120|AT1G18890|AT4G30080|AT1G05710|AT5G51190|AT3G52400|AT2G17040|AT1G17750|AT1G74430|AT3G61900|AT3G45640|AT3G25070|AT1G07520|AT5G09980|AT3G28580|AT1G19220|AT5G61210|AT5G44610|AT3G11820|AT5G66070|AT3G07390|AT1G57560|AT2G40180|AT5G25190|AT5G49620
	GO:0042221	response to chemical stimulus	52 out of 234 genes, 22.2%	1763 out of 12802 genes, 13.8%	0.01	AT2G06050|AT3G52430|AT4G17230|AT5G06720|AT5G66880|AT3G59900|AT4G16780|AT1G18570|AT2G04160|AT4G17260|AT1G72060|AT3G11840|AT5G62390|AT3G48090|AT4G26120|AT1G18890|AT4G02200|AT4G30080|AT5G44070|AT1G52560|AT1G11210|AT1G05710|AT1G09940|AT5G51190|AT3G52400|AT1G13340|AT1G52200|AT2G17040|AT1G17750|AT1G74430|AT3G61900|AT3G45640|AT3G25070|AT1G07520|

						AT5G09980|AT3G28580|AT1G19220|AT5G61210|AT5G44610|AT3G11820|AT5G66070|AT2G26560|AT3G07390|AT2G16500|AT1G57560|AT2G40180|AT4G11170|AT2G41380|AT5G25190|AT5G65020|AT3G09270|AT5G49620
	GO:0009814	defense response, incompatible interaction	8 out of 234 genes, 3.4%	94 out of 12802 genes, 0.7%	0.01	AT3G48090|AT1G56510|AT1G11310|AT3G52430|AT3G25070|AT4G11850|AT1G74710|AT1G61560
	GO:0080135	regulation of cellular response to stress	4 out of 234 genes, 1.7%	17 out of 12802 genes, 0.1%	0.01	AT3G45640|AT3G25070|AT3G52400|AT3G11820
	GO:0050832	defense response to fungus	9 out of 234 genes, 3.8%	124 out of 12802 genes, 1%	0.02	AT2G34930|AT2G38870|AT3G52400|AT1G56510|AT1G11310|AT3G11820|AT1G05800|AT1G74710|AT1G61560
	GO:0010363	regulation of plant-type hypersensitive response	3 out of 234 genes, 1.3%	8 out of 12802 genes, 0.1%	0.02	AT3G25070|AT3G52400|AT3G11820
	GO:0009620	response to fungus	10 out of 234 genes, 4.3%	159 out of 12802 genes, 1.2%	0.02	AT2G06050|AT2G34930|AT2G38870|AT3G52400|AT1G56510|AT1G11310|AT3G11820|AT1G05800|AT1G74710|AT1G61560
	GO:0006915	apoptosis	9 out of 234 genes, 3.8%	134 out of 12802 genes, 1%	0.03	AT5G22690|AT5G04720|AT2G16870|AT4G23440|AT1G66090|AT5G41550|AT5G58120|AT4G33300|AT1G15890
	GO:0009863	salicylic acid mediated signaling pathway	4 out of 234 genes, 1.7%	26 out of 12802 genes, 0.2%	0.04	AT3G52400|AT3G11820|AT3G48090|AT3G52430
	GO:0010200	response to chitin	8 out of 234 genes, 3.4%	116 out of 12802 genes, 0.9%	0.04	AT3G45640|AT2G17040|AT3G11840|AT1G07520|AT5G51190|AT4G26120|AT5G66070|AT4G17230
	GO:0051245	negative regulation of cellular defense response	2 out of 234 genes, 0.9%	2 out of 12802 genes, 0%	0.04	AT3G11820|AT3G52400
	GO:0071446	cellular response to salicylic acid	4 out of 234 genes, 1.7%	26 out of 12802 genes, 0.2%	0.04	AT3G52400|AT3G11820|AT3G48090|AT3G52430

		stimulus				
	GO:00 31408	oxylipin biosyntheti c process	4 out of 234 genes, 1.7%	27 out of 12802 genes, 0.2%	0.05	AT2G06050|AT1G05800|AT2G26560|AT1G20510

Table 22: bZIP1 primary targets in the N-assimilation pathway.

Gene	Pathway role	bZIP1 target class
At2g26690	Nitrate Transporter	Class I
At5g07440	GDH	Class IIA
At1g08090	Nitrate Transporter	ClassIIIA
At3g45060	Nitrate Transporter	ClassIIIA
At5g18170	GDH	ClassIIIA
At3g16150	Asparaginase	ClassIIIA
At5g11520	ASP	ClassIIIA
At5g50200	Nitrate Transporter	ClassIIIA

[00400] Lastly, Class III transient target genes are uniquely enriched in genes that respond early and transiently to the N-signal *in planta* (Fig. 29C). While all three classes of bZIP1 target genes have significant intersections with N-regulated genes *in planta* (*p-val*<0.001) (Krouk et al., 2010, Genome Biology 11(12):R123; Gutierrez et al., 2008, Proc. Natl. Acad. Sci. U.S.A. 105:4939-4944; Wang et al., 2003, Plant Physiol. 132(2):556-567; Wang et al., 2004, Plant physiology 136(1):2512-2522) (Fig. 29C, "Union" of N-response genes *in planta*), only Class IIIA transient targets have a significant overlap with genes induced *transiently* or *early* in response to a N-signal (within 3-6 minutes) (*p-val*<0.001), based on fine-scale kinetic studies of N-treatments performed *in planta* (Krouk et al., 2010, Genome Biology 11(12):R123) (Fig. 29C; Table 23). These transient bZIP1 targets include known early N-responders, such as the transcription factors LBD38 (At3g49940) and LBD39 (At4g37540), which respond to N-signals in as early as 3-6 min (Krouk et al., 2010, Genome Biology 11(12):R123), and are involved in regulating N-uptake and assimilation genes *in planta* (Rubin et al., 2009, The Plant Cell 21(11):3567-3584). Additionally, Class IIIA transient targets are uniquely enriched in rapid N-responders (Fig. 29C; Table 23), identified as genes induced within 20 min after a supply of 250uM nitrate to roots (Wang et al., 2003, Plant Physiol. 132(2):556-567), including the nitrate transporters, NRT3.1 and NRT2.1. This result

further supports the notion that the Class IIIA transient bZIP1 targets are specifically relevant to a rapid N-signaling response *in planta*.

Table 23. Class IIIA bZIP1 primary targets that transiently and rapidly up-regulated by N.

A. The 15 genes that are (1) ClassIIIA, i.e. no binding but activated and (2) transiently upregulated by N (Krouk et al., 2010).	
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1
At5g57655	xylose isomerase family protein
At3g14050	AT-RSH2, ATRSH2, RSH2, RELA/SPOT homolog 2
At3g28510	P-loop containing nucleoside triphosphate hydrolases superfamily protein
At1g15380	Lactoylglutathione lyase / glyoxalase I family protein
At5g56870	BGAL4, beta-galactosidase 4
At1g73260	ATKTI1, KTI1, kunitz trypsin inhibitor 1
At2g43400	ETFQO, electron-transfer flavoprotein:ubiquinone oxidoreductase
At1g80460	GLI1, NHO1, Actin-like ATPase superfamily protein
At1g22400	ATUGT85A1, UGT85A1, UDP-Glycosyltransferase superfamily protein
At4g38490	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).
At5g65110	ACX2, ATACX2, acyl-CoA oxidase 2
At5g04310	Pectin lyase-like superfamily protein
At3g16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein
At4g13430	ATLEUC1, IIL1, isopropyl malate isomerase large subunit 1
B. The 9 genes that are (1) ClassIIIA, i.e. no binding but activated and (2) rapidly (3-6min) upregulated by N (Krouk et al., 2010).	
At3g49940	LBD38, LOB domain-containing protein 38
At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).
At2g43400	ETFQO, electron-transfer flavoprotein:ubiquinone oxidoreductase
At1g22400	ATUGT85A1, UGT85A1, UDP-Glycosyltransferase superfamily protein
At4g38490	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).
At4g37540	LBD39, LOB domain-containing protein 39
At5g65110	ACX2, ATACX2, acyl-CoA oxidase 2
At5g04310	Pectin lyase-like superfamily protein
At4g39780	Integrase-type DNA-binding superfamily protein
C. The 37 genes that are (1) ClassIIIA, i.e. no binding but activated and (2) early responder (20min) upregulated by N (Wang et al., 2003)	
At5g28610	BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT5G28630.1); Has 1536 Blast hits to 1202 proteins in 136 species: Archae - 0; Bacteria - 8; Metazoa - 888; Fungi - 120; Plants - 71; Viruses - 39; Other Eukaryotes - 410 (source: NCBI BLink).
At5g50200	ATNRT3.1, NRT3.1, WR3, nitrate transmembrane transporters

At3g11410	AHG3, ATPP2CA, PP2CA, protein phosphatase 2CA
At5g46590	anac096, NAC096, NAC domain containing protein 96
At3g49940	LBD38, LOB domain-containing protein 38
At1g14340	RNA-binding (RRM/RBD/RNP motifs) family protein
At3g60690	SAUR-like auxin-responsive protein family
At1g71980	Protease-associated (PA) RING/U-box zinc finger family protein
At5g37260	CIR1, RVE2, Homeodomain-like superfamily protein
At1g23870	ATTPS9, TPS9, TPS9, trehalose-phosphatase/synthase 9
At4g18340	Glycosyl hydrolase superfamily protein
At4g03510	ATRMA1, RMA1, RING membrane-anchor 1
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1
At3g53150	UGT73D1, UDP-glucosyl transferase 73D1
At5g13750	ZIFL1, zinc induced facilitator-like 1
At5g67440	NPY3, Phototropic-responsive NPH3 family protein
At4g36670	Major facilitator superfamily protein
At5g20885	RING/U-box superfamily protein
At4g32950	Protein phosphatase 2C family protein
At4g32960	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32970.1); Has 106 Blast hits to 106 proteins in 39 species: Archae - 0; Bacteria - 0; Metazoa - 62; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).
At5g13110	G6PD2, glucose-6-phosphate dehydrogenase 2
At1g61740	Sulfite exporter TauE/SafE family protein
At4g29950	Ypt/Rab-GAP domain of gyp1p superfamily protein
At5g47740	Adenine nucleotide alpha hydrolases-like superfamily protein
At2g46270	GBF3, G-box binding factor 3
At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).
At5g47560	ATSDAT, ATTDT, TDT, tonoplast dicarboxylate transporter
At3g16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein
At4g38340	NLP3;Plant regulator RWP-RK family protein
At4g39780	Integrase-type DNA-binding superfamily protein
At3g15650	alpha/beta-Hydrolases superfamily protein
At3g24520	AT-HSFC1, HSFC1, heat shock transcription factor C1
At4g38470	ACT-like protein tyrosine kinase family protein
At1g15380	Lactoylglutathione lyase / glyoxalase I family protein
At4g37540	LBD39, LOB domain-containing protein 39
At1g61660	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
At3g05200	ATL6, RING/U-box superfamily protein

[00401] A transient mode of bZIP1 action invokes a "hit-and-run" model for N-signaling. The significant enrichment of N-relevant genes in Class III targets, links the transient mode-of-action of bZIP1 with early and transient aspects of N-nutrient signaling

(Fig. 29C & D). This transient mode-of-action could allow a small number of bZIP1 molecules to initiate and catalyze a large response to an N-signal in the GRN within minutes, without having to wait for a significant buildup of the bZIP1 protein. Two unique properties of Class III "transient" targets support this hypothesis. First, pioneer TFs have been shown to facilitate and/or initiate gene expression (Ni et al., 2009, Gene Dev 23(11):1351-1363; Magnani et al., 2011, Trends Genet 27(11):465-474). Accordingly, bZIP1 binding to the promoter of Class III transient targets should be detected at very early time-points after DEX-induced nuclear localization of the GR-bZIP1 fusion protein (e.g. within minutes). Second, cis-motif analysis of target genes of a pioneer TF in *Drosophila* highlighted the specific enrichment of other TF binding motifs in close proximity to the pioneer TF motif (Satija et al., 2012, Genome Res 22(4):656-665), suggesting either active recruitment or passive enabling of binding by additional TF partners. By this model, the promoters of Class III transient bZIP1 targets should show specific enrichment for binding sites of other TFs in addition to bZIP1. Indeed, we find bZIP1 shares both of these properties, as detailed below.

[00402] To experimentally determine if any of the Class III transient targets are bound by bZIP1 at very early time-points, ChIP-Seq analysis was performed on four additional time-points after the DEX-induced nuclear import of bZIP1. 41 genes were revealed from Class III transient targets that have detectable bZIP1 binding at one or more of the earlier time-points (1, 5, 30, 60 min) (Fig. 29D; Table 20), but are not bound by bZIP1 at the 5 hour time point of the original study (Fig. 29A). Crucially, these 41 transiently bound bZIP1 targets are significantly enriched in GO-terms related to the N-signal (e.g. amino acid metabolism, $p<0.05$). The validated bZIP1 binding site (hybrid "ACGT" motif) (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361-373; Dietrich et al., 2011, The Plant Cell 23:381-395) is enriched in the promoters of these 41 genes (E=2.7e-3), as well as in the remaining Class III *transient* targets (E=1e-26). These transiently bound bZIP1 targets include NLP3, a key early regulator of nitrate signaling in plants (Konishi et al., 2013, Nature Communications 4: 1617). In this study, NLP3 is bound by bZIP1 at very early time-points (1 and 5 min), but not at the later points (30 and 60 min) following TF perturbation (Fig. 29D). Similarly, the promoter of an early response gene encoding the high-affinity nitrate transporter NRT2.1 (Krouk et

al., 2010, Genome Biology 11(12):R123, is bound by bZIP1 as early as 1 and 5 min after the DEX-induced nuclear import of bZIP1, but binding is weakened at 30 min and disappears at 60 min (Fig. 29D). In summary, this time-course analysis provides physical evidence that some Class III targets are indeed transiently bound to bZIP1, only at very early time-points after bZIP1 nuclear import (1-5 min). We note that such transient TF-binding is difficult to capture, unless multiple early time-points are designed for ChIP-seq study. However, the cell-based *TARGET* system can identify primary targets based on the *outcome* of TF-binding (e.g. TF-induced gene regulation), even if TF binding is highly transient (e.g. within seconds), or is *never* bound stably enough to be detected at any time-point.

[00403] Finally, the hypothesis that bZIP1 acts as a "pioneer/catalyst" TF in N-signal propagation through a GRN, is further supported by *cis*-motif analysis. Specifically, the promoters of Class III "transient" bZIP1 target genes contained the largest number and most significant enrichment of *cis*-regulatory motifs, in addition to bZIP1-binding sites (Fig. 30). In particular, the Class IIIA transient activated genes contain the most significant enrichment of the known bZIP1 binding site (E=1.3e-52), and are specifically enriched in co-inherited *cis*-elements that belong to the bZIP, MYB, and GATA families (Yilmaz et al., 2011, Nucleic Acids Research 39:D1118-1122) (Fig. 30). These results support the hypothesis that bZIP1 is a pioneer TF that interacts and/or recruits other TFs, including other bZIPs and/or MYB/GATA binding factors, to temporally co-regulate target genes in response to a N-signal (Fig. 34). Indeed, bZIP1 has been reported to interact with other TFs *in vitro* (Ehlert et al., 2006, Plant J 46(5):890-900). (Table 24) and *in vivo* (Ehlert et al., 2006, Plant J 46(5):890-900; (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361-373). This list of bZIP1 interactors includes bZIP25, a gene in the Class III transient bZIP1 primary targets. In support of a collaborative relationship between bZIP1 and the GATA family TFs in mediating the N-response, one GATA TF was reported to be nitrate-inducible and involved in regulating energy metabolism, thus serving as a functional analog to bZIP1 (Bi et al., 2005, Plant Journal 44(4):680-692). Taken together, the transient binding of bZIP1 and enrichment of co-inherited binding sites for additional TFs specifically in Class III transient bZIP1 targets, supports a role for bZIP1 as a TF "pioneer/catalyst" (Satija et al., 2012, Genome

Res 22(4):656-665) and a model for "hit-and-run" transcription (Schaffner, 1988, Nature 336:427-428), as depicted in Fig. 34 and discussed below.

Table 24. bZIP1 protein-protein interaction partners.

At5g37780	ACAM-1, CAM1, TCH1, calmodulin 1
At1g66410	ACAM-4, CAM4, calmodulin 4
At5g21274	ACAM-6, CAM6, calmodulin 6
At2g41100	ATCAL4, TCH3, Calcium-binding EF hand family protein
At3g51920	ATCML9, CAM9, CML9, calmodulin 9
At2g41090	Calcium-binding EF-hand family protein
At3g43810	CAM7, calmodulin 7
At4g14640	CAM8, calmodulin 8
At5g41910	MED10A, Mediator complex, subunit Med10
At4g34590	ATB2, AtbZIP11, BZIP11, GBF6, G-box binding factor 6
At5g49450	AtbZIP1, bZIP1, basic leucine-zipper 1
At4g02640	ATBZIP10, BZO2H1, bZIP transcription factor family protein
At2g18160	ATBZIP2, bZIP2, GBF5, basic leucine-zipper 2
At3g54620	ATBZIP25, BZIP25, BZO2H4, basic leucine zipper 25
At1g59530	ATBZIP4, bZIP4, basic leucine-zipper 4
At3g30530	ATBZIP42, bZIP42, basic leucine-zipper 42
At1g75390	AtbZIP44, bZIP44, basic leucine-zipper 44
At3g62420	ATBZIP53, BZIP53, basic region/leucine zipper motif 53
At1g13600	AtbZIP58, bZIP58, basic leucine-zipper 58
At5g28770	AtbZIP63, BZO2H3, bZIP transcription factor family protein
At5g24800	ATBZIP9, BZIP9, BZO2H2, basic leucine zipper 9

10.4. DISCUSSION

[00404] The discovery of a large and typically overlooked class of transient primary targets of the master TF bZIP1, disclosed herein, introduces a novel perspective in the general field of dynamic GRNs. Dynamic TF-target binding studies across eukaryotes have captured many transient TF-targets (Ni *et al.*, 2009, *Gene Dev* 23(11):1351-1363; Chang *et al.*, 2013, *Elife* 2:e00675). However, even those fine-scale time-series ChIP studies likely miss highly temporal connections, as they require biochemically detectable TF binding in at least one time-point to identify primary TF targets. Key to the discovery of the transient targets of bZIP1 involved in rapid N-signaling, disclosed herein, is the ability to identify *primary* targets based on TF-induced changes in mRNA that can occur even in the absence of detectable TF binding. The cell-based system also enabled the detection of rapid and transient binding within 1 minute of

TF nuclear import, owing to rapid fixation of protein-DNA complexes in plant cells lacking a cell wall. Importantly, the *in planta* relevance of the cell-based *TARGET* studies disclosed herein (Fig. 29A), confirms and complements data from bZIP1 T-DNA mutants and transgenic plants (Kang et al., 2010, Molecular Plant 3:361-373) (Fig. 29B), which are unable to distinguish primary from secondary targets, or capture transient TF-target interactions. Therefore, the transient interactions between bZIP1 and its targets uncovered in the cell-based *TARGET* system disclosed herein help to refine an understanding of the *in planta* mechanism of bZIP1.

[00405] The discovery of these transient TF targets, disclosed herein, adds a new perspective to the field of dynamic GRNs. Recent time-series studies in yeast by Lickwar *et. al.* reported transitive TF-target binding described as a "tread-milling" mechanism, in which a TF exhibits weak and transitive binding to some of its targets, resulting in a lower level of gene activation (Lickwar et al., 2012, Nature 484(7393):251-255). The transient bZIP1targets detected in this study do not fit this "tread-milling" model, since there is no significant difference between the expression fold-change distributions of for Class III "transient" targets, versus Class II "stable" targets. Instead, the transient TF-target interactions uncovered herein are conceptualized to a classic, but largely forgotten, "hit-and-run" model of transcription proposed in the 1980's (Schaffner, 1988, Nature 336:427-428) (Fig. 34). This "hit-and-run" model posits that a TF can act as a trigger to organize a stable transcriptional complex, after which transcription by RNA polymerase II can continue without the TF being bound to the DNA (Schaffner, 1988, Nature 336:427-428).

[00406] In support of this "hit-and-run" transcription model, Class III "transient" targets include genes that are rapidly and transiently bound by bZIP1 at very early time-points (1-5 min) after TF nuclear import, and whose level of expression is maintained at a higher level, despite being no longer bound by bZIP1 at later time-points. Continued regulation of the bZIP1 targets (after bZIP1 is no longer bound) might be mediated by other TF partners recruited by the "trigger/pioneer" TF (Fig. 34). This model is supported by the enrichment of *cis*-motifs co-inherited with the known bZIP1 binding motif (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361-373; Dietrich et al., 2011, The Plant Cell 23:381-395) in the Class III transient targets (Fig.

30). This finding also supports other explanatory models for "continuous" TF networks (Biggin MD, 2011, Dev Cell 21(4):611-626; Walhout AJM, 2011, Genome Biol 12(4); Lickwar et al., 2012, Nature 484(7393):251-255), which converge on the idea that TF-binding data alone is insufficient to fully characterize regulatory networks, and that other factors (including chromatin and other TFs) may influence the action of a master TF. In this transient mode-of-action, bZIP1 can activate genes in response to a N-signal ("the hit"), while the *transient* nature of the TF-target association ("the run"), enables bZIP1 to act as a TF "catalyst" to rapidly induce a large set of genes needed for the N-response. In support of this "catalytic" TF model, the global targets of bZIP1 N-signaling are broad, covering 32% of the directly regulated targets of NLP7 related to the N-signal, a well-studied master regulator of the N-response (Marchive et al., 2013, Nature Communications 4). Importantly, the Class III transient bZIP1 targets play a unique role in mediating a rapid, early, and biologically relevant response to the N-signal *in planta*. This "hit-and-run" model, supported by the results for bZIP1, could represent a general mechanism for the deployment of an acute response to nutrient sensing, as well as other signals.

[00407] Importantly, these results have significance beyond bZIP1, N-signaling, and indeed transcend plants. Across eukaryotes, TFs are found to bind only to a small percentage of their regulated targets, as shown in plants (Monke et al., 2012, Nucleic Acids Research 40:8240l; Arenhart et al., 2014, Molecular plant 7(4):709-721; Bolduc et al., 2012, Gene Dev 26(15):1685-1690), yeast (Hughes et al., 2013, Genetics 195(1):9-36) and animals (Gorski et al., 2011, Nucleic Acids Research 39:9536; Bianco et al., 2014, Cancer research 74(7):2015-2025). The large number of TF-regulated but unbound genes, including the false negatives of ChIP-seq (Chen et al., 2012, Nat Methods 9(6):609), must be dismissed as putative *secondary* targets in approaches that can only identify primary targets based on TF-DNA binding. Instead, it is shown herein that these typically dismissed targets, which can be identified as primary TF targets by a functional read-out in this cell-based *TARGET* approach (e.g. TF-induced regulation), are crucial for rapid and dynamic signal propagation, thus uncovering the "dark matter" of signal transduction that has been missed. More broadly, the approach described herein is applicable across eukaryotes, and can also be adapted to studying cell-specific GRNs, by

using GFP-marked cell lines in the assay (Birnbaum K, *et al.*, 2003, *Science* 302(5652):1956-1960). Moreover, this approach can identify primary targets even in cases where TF binding can *never* be physically detected. The transient targets thus uncovered, will reveal the elusive temporal interactions that mediate rapid and dynamic responses of GRNs to external signals.

11. EXAMPLE 6

[00408] As described herein, using the cell-based TARGET system, a novel class of transient TF targets that are directly regulated by the bZIP1 TF, but not detectably bound by it were identified. This class of transient targets (Class III) suggests a "hit-and-run" mode-of-action for bZIP1, where bZIP1 "hits" its target, initiates transcription, then dissociates ("run"), leaving the transcription going on even without bZIP1 binding to the promoter.

[00409] To test the hypothesis that transcription of a gene initiated by "the Hit" continues after "the Run," an affinity-tagged UTP was used to label and capture newly synthesized mRNA. By adding this label at a time-point when the TF is not detectably bound, it can be determined whether a gene is still actively transcribed. Briefly, biosynthetic tagging of newly synthesized RNA performed using 4-thiouracil and uracil phosphoribosyltransferase (referred to as "4sU tagging" hereinafter) (Sidaway-Lee et al., 2014, Genome Biology 15 (3): R45; Zeiner et al., 2008, Methods in Molecular Biology 419: 135–46), was adapted for the cell based TARGET system in plants (Bargmann et al., 2013, Molecular Plant 6(3):978). Technically, 4sU is fed to plant protoplasts and incorporated into newly synthesized RNA. After that, total RNA is extracted from the protoplasts, and the newly synthesized RNA that is tagged with 4sU is isolated from the total RNA through biotinylation and Streptavidin magnetic beads. Next, the RNA is purified and used for transcriptomics profiling. The 4sU tagged RNA represents only the newly transcribed genes.

[00410] 4sU tagged RNA can be detected as early as in 20 min after feeding 4sU to isolated protoplasts (Fig. 35). Using this technique, it was shown here that Class III "transient" genes have incorporated UTP label. These transient bZIP1 target genes that are activated (Class IIIA: 121 genes) or repressed (Class IIIB 42 genes). These genes are actively transcribed by bZIP1, even when bZIP1 is not bound to these targets (Fig. 29B;

Table 25). These bZIP1 transient targets include the NIN-like protein 3 (NLP3; At4g38340), bound by bZIP1 at 1-5 min after the nuclear import of bZIP1 (Fig. 35C), but no longer bound by bZIP1 at 20min, 1hr, or 5hr after the nuclear import of bZIP1 (Fig. 35C). These 4sU RNA tagging results show that NLP3 is actively transcribed at a higher rate in the cells that express bZIP1, even when bZIP1 does not bind to the NLP3 promoter (i.e. 5hr after the nuclear import of bZIP1) (Fig. 35). The control in Fig. 35D is empty vector. This provides evidence for the "hit-and-run" model, which posit that bZIP1 can "hit" the target genes, and dissociate ("run"), while the induced transcription of target genes by bZIP1 can carry on even after the dissociation of bZIP1.

Table 25. Transient targets that are actively transcribed due to bZIP1 as validated by 4sU tagging.

A. bZIP1 Class IIIA transient targets that are transcribed higher (FC>2) in the bZIP1 over-expressed cells compared to empty vector controls 5hr after the bZIP1 nuclear import

Gene ID	Tair 10 annotation
At5g06980	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12320.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).
At4g30170	Peroxidase family protein
At3g27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3
At3g14780	CONTAINS InterPro DOMAIN/s: Transposase, Ptta/En/Spm, plant (InterPro:IPR004252); BEST Arabidopsis thaliana protein match is: glucan synthase-like 4 (TAIR:AT3G14570.2); Has 315 Blast hits to 313 proteins in 50 species: Archae - 2; Bacteria - 16; Metazoa - 11; Fungi - 7; Plants - 181; Viruses - 2; Other Eukaryotes - 96 (source: NCBI BLink).
At1g30820	CTP synthase family protein
At2g30600	BTB/POZ domain-containing protein
At2g19320	unknown protein; Has 9 Blast hits to 9 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At1g04410	Lactate/malate dehydrogenase family protein
At5g65110	ACX2, ATACX2, acyl-CoA oxidase 2
At4g18340	Glycosyl hydrolase superfamily protein
At4g03510	ATRMA1, RMA1, RING membrane-anchor 1
At2g19800	MIOX2, myo-inositol oxygenase 2
At3g51730	saposin B domain-containing protein
At1g56700	Peptidase C15, pyroglutamyl peptidase I-like
At2g33150	KAT2, PED1, PKT3, peroxisomal 3-ketoacyl-CoA thiolase 3
At1g67810	SUFE2, sulfur E2
At5g67440	NPY3, Phototropic-responsive NPH3 family protein
At5g16110	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02555.1); Has 133 Blast hits to 133 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).

At1g75220	Major facilitator superfamily protein
At1g30900	BP80-3;3, VSR3;3, VSR6, VACUOLAR SORTING RECEPTOR 6
At1g66890	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: 50S ribosomal protein-related (TAIR:AT5G16200.1); Has 36 Blast hits to 36 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At3g49060	U-box domain-containing protein kinase family protein
At3g16800	Protein phosphatase 2C family protein
At1g61740	Sulfite exporter TauE/SafE family protein
At5g13740	ZIF1, zinc induced facilitator 1
At5g43430	ETFBETA, electron transfer flavoprotein beta
At4g21440	ATM4, ATMYB102, MYB102, MYB102, MYB-like 102
At1g55020	ATLOX1, LOX1, lipoxygenase 1
At5g19090	Heavy metal transport/detoxification superfamily protein
At1g64010	Serine protease inhibitor (SERPIN) family protein
At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).
At1g75800	Pathogenesis-related thaumatin superfamily protein
At5g07080	HXXXD-type acyl-transferase family protein
At1g61810	BGLU45, beta-glucosidase 45
At1g67880	beta-1,4-N-acetylglucosaminyltransferase family protein
At5g03720	AT-HSFA3, HSFA3, heat shock transcription factor A3
At2g38820	Protein of unknown function (DUF506)
At1g65840	ATPAO4, PAO4, polyamine oxidase 4
At1g08630	THA1, threonine aldolase 1
At5g61600	ERF104, ethylene response factor 104
At1g76240	Arabidopsis protein of unknown function (DUF241)
At1g28130	GH3.17, Auxin-responsive GH3 family protein
At3g55150	ATEXO70H1, EXO70H1, exocyst subunit exo70 family protein H1
At3g16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein
At4g38340	Plant regulator RWP-RK family protein
At3g46690	UDP-Glycosyltransferase superfamily protein
At2g19350	Eukaryotic protein of unknown function (DUF872)
At1g10070	ATBCAT-2, BCAT-2, branched-chain amino acid transaminase 2
At3g43430	RING/U-box superfamily protein
At3g14770	Nodulin MtN3 family protein
At1g76990	ACR3, ACT domain repeat 3
At1g52240	ATROPGEF11, PIRF1, ROPGEF11, RHO guanyl-nucleotide exchange factor 11
At1g69570	Dof-type zinc finger DNA-binding family protein
At1g13080	CYP71B2, cytochrome P450, family 71, subfamily B, polypeptide 2
At1g15060	Uncharacterised conserved protein UCP031088, alpha/beta hydrolase

At2g14170	ALDH6B2, aldehyde dehydrogenase 6B2
At5g18650	CHY-type/CTCHY-type/RING-type Zinc finger protein
At3g20410	CPK9, calmodulin-domain protein kinase 9
At3g01270	Pectate lyase family protein
At2g10640	transposable element gene
At4g35780	ACT-like protein tyrosine kinase family protein
At3g06850	BCE2, DIN3, LTA1, 2-oxoacid dehydrogenases acyltransferase family protein
At5g49650	XK-2, XK2, xylulose kinase-2
At4g15620	Uncharacterised protein family (UPF0497)
At1g20340	DRT112, PETE2, Cupredoxin superfamily protein
At1g55510	BCDH BETA1, branched-chain alpha-keto acid decarboxylase E1 beta subunit
At2g39570	ACT domain-containing protein
At4g10840	Tetratricopeptide repeat (TPR)-like superfamily protein
At1g06520	ATGPAT1, GPAT1, glycerol-3-phosphate acyltransferase 1
At2g41190	Transmembrane amino acid transporter family protein
At2g43060	IBH1, ILI1 binding bHLH 1
At4g35770	ATSEN1, DIN1, SEN1, SEN1, Rhodanese/Cell cycle control phosphatase superfamily protein
At3g60690	SAUR-like auxin-responsive protein family
At3g14760	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: LP.04 four leaves visible, LP.02 two leaves visible; Has 63 Blast hits to 63 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 63; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At1g32460	unknown protein; Has 19 Blast hits to 19 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At2g35230	IKU1, IKU1, VQ motif-containing protein
At1g09460	Carbohydrate-binding X8 domain superfamily protein
At3g57420	Protein of unknown function (DUF288)
At1g15050	IAA34, indole-3-acetic acid inducible 34
At3g61260	Remorin family protein
At5g57655	xylose isomerase family protein
At3g54960	ATPDI1, ATPDIL1-3, PDI1, PDIL1-3, PDI-like 1-3
At3g54620	ATBZIP25, BZIP25, BZO2H4, basic leucine zipper 25
At5g41610	ATCHX18, CHX18, cation/H+ exchanger 18
At4g33150	LKR, LKR/SDH, SDH, lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme
At1g03870	FLA9, FASCICLIN-like arabinoogalactan 9
At4g32870	Polyketide cyclase/dehydrase and lipid transport superfamily protein
At5g01590	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 59 proteins in 31 species: Archae - 0; Bacteria - 20; Metazoa - 1; Fungi - 2; Plants - 33; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).
At4g32950	Protein phosphatase 2C family protein
At4g19810	Glycosyl hydrolase family protein with chitinase insertion domain

At2g38400	AGT3, alanine:glyoxylate aminotransferase 3
At3g13965	pseudogene, hypothetical protein
At5g28050	Cytidine/deoxycytidylate deaminase family protein
At2g39980	HXXXD-type acyl-transferase family protein
At5g66030	ATGRIP, GRIP, Golgi-localized GRIP domain-containing protein
At1g06560	NOL1/NOP2/sun family protein
At5g20250	DIN10, Raffinose synthase family protein
At1g03100	Pentatricopeptide repeat (PPR) superfamily protein
At1g67480	Galactose oxidase/kelch repeat superfamily protein
At5g08350	GRAM domain-containing protein / ABA-responsive protein-related
At3g23230	Integrase-type DNA-binding superfamily protein
At5g18850	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).
At4g28040	nodulin MtN21 /EamA-like transporter family protein
At5g04040	SDP1, Patatin-like phospholipase family protein
At3g30396	transposable element gene
At1g66550	ATWRKY67, WRKY67, WRKY DNA-binding protein 67
At1g79700	Integrase-type DNA-binding superfamily protein
At5g49360	ATBXL1, BXL1, beta-xylosidase 1
At4g38470	ACT-like protein tyrosine kinase family protein
At1g15380	Lactoylglutathione lyase / glyoxalase I family protein
At1g60940	SNRK2-10, SNRK2.10, SRK2B, SNF1-related protein kinase 2.10
At1g48840	Plant protein of unknown function (DUF639)
At1g03090	MCCA, methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA)
At3g19390	Granulin repeat cysteine protease family protein
At1g32200	ACT1, ATS1, phospholipid/glycerol acyltransferase family protein
At3g45300	ATIVD, IVD, IVDH, isovaleryl-CoA-dehydrogenase
At3g22920	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
At1g17190	ATGSTU26, GSTU26, glutathione S-transferase tau 26
At1g18270	ketose-bisphosphate aldolase class-II family protein
At4g39730	Lipase/lipooxygenase, PLAT/LH2 family protein
At4g14500	Polyketide cyclase/dehydrase and lipid transport superfamily protein

B. bZIP1 Class IIIB transient targets that are transcribed lower (FC<-2) in the bZIP1 over-expressed cells compared to empty vector controls 5hr after the bZIP1 nuclear import

Gene ID	**TAIR10 annotation**
At5g13870	EXGT-A4, XTH5, xyloglucan endotransglucosylase/hydrolase 5
At2g17040	anac036, NAC036, NAC domain containing protein 36
At3g50480	HR4, homolog of RPW8 4

At5g60350	unknown protein; Has 110 Blast hits to 97 proteins in 36 species: Archae - 0; Bacteria - 10; Metazoa - 39; Fungi - 2; Plants - 5; Viruses - 0; Other Eukaryotes - 54 (source: NCBI BLink).
At2g11520	CRCK3, calmodulin-binding receptor-like cytoplasmic kinase 3
At4g39840	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 20719 Blast hits to 6096 proteins in 607 species: Archae - 22; Bacteria - 3243; Metazoa - 4364; Fungi - 2270; Plants - 237; Viruses - 128; Other Eukaryotes - 10455 (source: NCBI BLink).
At4g37400	CYP81F3, cytochrome P450, family 81, subfamily F, polypeptide 3
At5g56760	ATSERAT1;1, SAT-52, SAT5, SERAT1;1, serine acetyltransferase 1;1
At5g24540	BGLU31, beta glucosidase 31
At3g05490	RALFL22, ralf-like 22
At3g18250	Putative membrane lipoprotein
At2g26480	UGT76D1, UDP-glucosyl transferase 76D1
At1g11000	ATMLO4, MLO4, Seven transmembrane MLO family protein
At5g43520	Cysteine/Histidine-rich C1 domain family protein
At4g28350	Concanavalin A-like lectin protein kinase family protein
At3g59900	ARGOS, auxin-regulated gene involved in organ size
At4g30080	ARF16, auxin response factor 16
At5g44610	MAP18, PCAP2, microtubule-associated protein 18
At1g24150	ATFH4, FH4, formin homologue 4
At5g41680	Protein kinase superfamily protein
At3g47380	Plant invertase/pectin methylesterase inhibitor superfamily protein
At5g24430	Calcium-dependent protein kinase (CDPK) family protein
At4g16780	ATHB-2, ATHB2, HAT4, HB-2, homeobox protein 2
At4g33960	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G15830.1); Has 32 Blast hits to 32 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At4g34320	Protein of unknown function (DUF677)
At5g65600	Concanavalin A-like lectin protein kinase family protein
At3g28740	CYP81D1, Cytochrome P450 superfamily protein
At2g39700	ATEXP4, ATEXPA4, ATHEXP ALPHA 1.6, EXPA4, expansin A4
At3g20900	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).
At3g54980	Pentatricopeptide repeat (PPR) superfamily protein
At1g53440	Leucine-rich repeat transmembrane protein kinase

At1g35200	60S ribosomal protein L4/L1 (RPL4B), pseudogene, similar to 60S ribosomal protein L4 (fragment) GB:P49691 from (Arabidopsis thaliana); blastp match of 50% identity and 6.3e-17 P-value to SP|Q9XF97|RL4_PRUAR 60S ribosomal protein L4 (L1). (Apricot) {Prunus armeniaca}
At2g43000	anac042, NAC042, NAC domain containing protein 42
At4g15120	VQ motif-containing protein
At3g48090	ATEDS1, EDS1, alpha/beta-Hydrolases superfamily protein
At1g44100	AAP5, amino acid permease 5
At1g70530	CRK3, cysteine-rich RLK (RECEPTOR-like protein kinase) 3
At1g68150	ATWRKY9, WRKY9, WRKY DNA-binding protein 9
At3g02790	zinc finger (C2H2 type) family protein
At1g53980	Ubiquitin-like superfamily protein
At2g19190	FRK1, FLG22-induced receptor-like kinase 1
At3g29670	HXXXD-type acyl-transferase family protein

12. EXAMPLE 7

[00411] Transient TF-targets detected in cells help to decipher dynamic N-regulatory networks operating in planta. The transient TF-targets detected specifically in the TARGET cell-based system make a unique contribution to understanding how signal transduction occurs *in planta.* First, as the *TARGET* cell-based system detects *only* primary TF targets, this data enables the identification of *direct* TF-targets in the *in planta* TF perturbation data, which on its own cannot distinguish primary vs. secondary targets. Second, the network inference studies described herein for the proof-of-principle example bZIP1 predict that the *transient bZIP1 targets* (detected *only* in cells) are TF2's predicted to regulate *secondary* bZIP1 targets (detected *only* in planta) (Fig. 36). In Fig 37 an approach called "Network Walking" is described to construct networks that link transient TF1→TF2 data from the TARGET cell-based system, with TF1 perturbation data in planta. The Network Walking approach uses N-response data from time-series, and Network Inference approaches including one called State-Space modeling, a form of Directed Factor Graph that was previously validated (Krouk et al., 2010, Genome Biology 11:R123; Krouk et al., 2013, Genome Biology 14(6):123). The TF2→target predictions can then be experimentally validated in the cell-based TARGET system, as described herein.

[00412] Transient TF1→T2 targets detected in TARGET cell-based system are predicted to regulate secondary targets of TF1 identified in planta. The hypothesis that "transient" targets of bZIP1 detected in the cell-based TARGET system mediate N-regulation of downstream bZIP1 targets in planta was developed by the preliminary implementation of the "Network Walking" pipeline outlined in Fig 37.

[00413] In Step 1, to identify genes potentially involved in bZIP1-mediated N-signaling *in planta*, bZIP1 targets identified using the cell-based TARGET system (primary targets), described herein, were combined with bZIP1 targets identified by TF perturbation in planta (primary and secondary targets) (Kang et al., 2010, Molecular Plant 3:361), and then this union of bZIP1 targets was intersected with the list of N-regulated genes from a time-course study of N-treatments performed *in planta*.

[00414] In Step 2, TF→target connections were inferred between the bZIP1 targets identified in the cell-based TARGET system with those identified by TF perturbation in planta, using the N-treatment time-series data and the network inference approach that was previously and validated *in silico* and experimentally (Directed Factor Graphs) (Krouk et al., 2010, Genome Biology 11:R123) (Step 2, Fig. 37).

[00415] The resulting network (shown in Fig. 36): The 22 TF's (depicted as triangles on the inner ring) which were identified in the cell-based TARGET system, are predicted to serve as intermediate TF2's linking bZIP1 and its downstream targets (gene Z) identified *in planta* (Kang et al., 2010, Molecular Plant 3:361).

[00416] Remarkably, 18/22 of these TF2's are Class III transient targets of bZIP1 detected only in the TARGET cell-based system, described herein (Inner ring of Fig. 37). As validation of their predicted role in N-signaling in planta, these transient TF2 targets of bZIP1 include TFs known to involved in N-signaling in plants (e.g. NLP3 (Konishi et al., 2013, Nature Communications 4: 1617), LBD38,39 (Rubin et al., 2009, The Plant Cell 21(11):3567-3584)). Moreover, the in planta targets of these TF2 include 7/9 N-regulated genes involved in primary assimilation of nitrate (Wang et al., 2003, Plant Physiol. 132(2):556-567). These are deemed to be secondary targets of bZIP1, as collectively they are not enriched in any of the known bZIP1 binding sites (Baena-Gonzalez et al., 2007, Nature 448:938; Kang et al., 2010, Molecular Plant 3:361; Dietrich et al., 2011, The Plant Cell 23:381-395). These lists of genes are show in Table 26.

[00417] This result supports the hypothesis that transient bZIP1 targets detected *only* in the TARGET cell-based system described herein, are intermediate effectors of secondary bZIP1 targets detected only *in planta* (Kang et al., 2010, Molecular Plant 3:361). This combined experimental and computational approach is called "Network Walking", because it enables a "walk" from pioneer TF1→ transient target (TF2)→effector target in planta (e.g. N-assimilation gene), as described below.

[00418] **The general "Network Walking" Pipeline (Fig. 37):**

[00419] Step 1A: Experimental: Perturb pioneer TF1 and identify symmetric difference between cell-based targets identified in TARGET ($TF_{2.1\text{-}j}$), and in planta targets defined by TF perturbation in planta ($Z_{1\text{-}j}$), as well as overlap.

[00420] Step 1B: Computational: Infer edges in network. This will infer edges between potential "transient" targets detected in the cell-based TARGET system ($TF_{2.1\text{-}j}$) and in planta targets ($Z_{1\text{-}j}$) of TF1 using time-series data and network inference approaches DFG (Krouk et al., 2010, Genome Biology 11:R123), Genie3 or Inferrelator (Krouk et al., 2013, Genome Biology 14(6):123).

[00421] Step 2A: Experimental: Perturb TF2 in cell-based TARGET system to validate primary TF2→gene Z edges and also identify new transient targets of TF2 (e.g. $TF_{3.1\text{-}j}$).

[00422] Step 2B: Computational: Rerun network inference (e.g. DFG) using time-series data from N-treated plants, this time using a *directed matrix* that starts with priors defined experimentally by TF2 target data (Step 3).

[00423] Outcome: This combined computational/experimental pipeline will result in a validated "Network Walk" from pioneer TF1→ transient TF2.1 (identified in TARGET) → target gene Z's in planta. Another outcome will be *new* transient TF2→$TF_{3i\text{-}j's}$ which may drive a new round of TF perturbation e.g. Step 3A, in a true systems biology cycle. Each iterative cycle of TF perturbation and network modeling, will build a new set of edges in the network out from the original TF1. The networks generated herein test the general hypothesis that transient targets detected only in the rapid and temporal cell based system, reveal "hidden steps" that mediate downstream responses in planta – but cannot be detected in planta. Thus, rather than merely using the *in planta* data to confirm TF-targets identified in the TARGET cell-based system, these network connections show that

the transient targets identified in the cell-based TARGET system add to and refine our understanding of how dynamic networks operate in vivo, but whose specific connections elude detection *in planta*.

Table 26. Genes in bZIP1 network

>bZIP1_innerRing (Transient targets of bZIP1 only identified in the TARGET cell-based system)		
At4g37180	Homeodomain-like superfamily protein	
At4g17230	SCL13, SCARECROW-like 13	
At5g46590	anac096, NAC096, NAC domain containing protein 96	
At3g49940	LBD38, LOB domain-containing protein 38	This transcription factor has been associated with N-signaling in plants (Rubin et al., 2009, The Plant Cell 21(11):3567-3584).
At2g17040	anac036, NAC036, NAC domain containing protein 36	
At5g57660	ATCOL5, COL5, CONSTANS-like 5	
At5g37260	CIR1, RVE2, Homeodomain-like superfamily protein	
At5g47390	myb-like transcription factor family protein	
At1g75540	STH2, salt tolerance homolog2	
At1g35560	TCP family transcription factor	
At4g39780	Integrase-type DNA-binding superfamily protein	
At4g38340	Plant regulator RWP-RK family protein (NLP3)	This transcription factor NLP3 has been associated with N-signaling in plants (Konishi et al., 2013, Nature Communications 4: 1617).
At1g19700	BEL10, BLH10, BEL1-like homeodomain 10	
At2g28200	C2H2-type zinc finger family protein	
At1g29860	ATWRKY71, WRKY71, WRKY DNA-binding protein 71	
At1g07520	GRAS family transcription factor	
At4g37540	LBD39, LOB domain-containing protein 39	This transcription factor has been associated with N-signaling in plants (Rubin et al., 2009, The Plant Cell 21(11):3567-3584).
At3g61850	DAG1, Dof-type zinc finger DNA-binding family protein	
>bZIP1_outerRing (bZIP1 targets only identified in planta (secondary targets) (Kang et al., 2010, Molecular Plant 3:361)		
At5g66360	Ribosomal RNA adenine dimethylase family protein	
At4g31920	ARR10, RR10, response regulator 10	
At3g18560	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49000.1); Has 95 Blast hits to 95 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants -	

	95; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
At4g36010	Pathogenesis-related thaumatin superfamily protein	
At5g62720	Integral membrane HPP family protein	
At1g80440	Galactose oxidase/kelch repeat superfamily protein	
At4g09620	Mitochondrial transcription termination factor family protein	
At5g04950	ATNAS1, NAS1, nicotianamine synthase 1	
At4g36540	BEE2, BR enhanced expression 2	
At1g78050	PGM, phosphoglycerate/bisphosphoglycerate mutase	
At1g63940	MDAR6, monodehydroascorbate reductase 6	
At2g26980	CIPK3, SnRK3.17, CBL-interacting protein kinase 3	
At4g27410	ANAC072, RD26, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	
At1g04770	Tetratricopeptide repeat (TPR)-like superfamily protein	
At1g32920	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to wounding; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G32928.1); Has 42 Blast hits to 42 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
At4g02380	AtLEA5, SAG21, senescence-associated gene 21	
At1g72050	TFIIIA, transcription factor IIIA	
At1g15550	ATGA3OX1, GA3OX1, GA4, gibberellin 3-oxidase 1	
At4g01410	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	
At5g54170	Polyketide cyclase/dehydrase and lipid transport superfamily protein	
At1g75280	NmrA-like negative transcriptional regulator family protein	
At1g77760	GNR1, NIA1, NR1, nitrate reductase 1	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At3g48360	ATBT2, BT2, BTB and TAZ domain protein 2	
At4g13510	AMT1;1, ATAMT1, ATAMT1;1, ammonium transporter 1;1	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).

At5g52050	MATE efflux family protein	
At5g40850	UPM1, urophorphyrin methylase 1	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At5g06570	alpha/beta-Hydrolases superfamily protein	
At4g30930	NFD1, Ribosomal protein L21	
At2g22540	AGL22, SVP, K-box region and MADS-box transcription factor family protein	
At4g15690	Thioredoxin superfamily protein	
At2g15620	ATHNIR, NIR, NIR1, nitrite reductase 1	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At1g30510	ATRFNR2, RFNR2, root FNR 2	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At1g66760	MATE efflux family protein	
At4g05390	ATRFNR1, RFNR1, root FNR 1	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At1g17170	ATGSTU24, GST, GSTU24, glutathione S-transferase TAU 24	
At1g67910	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G24577.1); Has 167 Blast hits to 167 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 167; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
At1g71030	ATMYBL2, MYBL2, MYB-like 2	
At1g16170	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G79660.1); Has 55 Blast hits to 55 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	
At5g41670	6-phosphogluconate dehydrogenase family protein	
At1g22500	RING/U-box superfamily protein	
At2g45050	GATA2, GATA transcription factor 2	
At5g65010	ASN2, asparagine synthetase 2	N-regulated gene involved in N-reduction

		/assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At1g24280	G6PD3, glucose-6-phosphate dehydrogenase 3	N-regulated gene involved in N-reduction /assimilation (Wang et al., 2003, Plant Physiol. 132(2):556-567).
At2g22500	ATPUMP5, DIC1, UCP5, uncoupling protein 5	
At3g16560	Protein phosphatase 2C family protein	
At1g73600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	
At4g15700	Thioredoxin superfamily protein	

13. EXAMPLE 8: Network Walking Identifies Feed-Forward Loops (FFLs) Involved in bZIP1 Mediated N-Signaling

[00424] This example relates to the discovery that the downstream TF targets of bZIP1 (e.g., LBD38, LBD39 and NLP7) identified in the cell-based TARGET system, described herein, function in a Feed-forward loop to regulate genes involved in N-uptake/assimilation, determined via the Network Walking approach. This approach is generally applicable to identify the intermediate mediators of any TF of interest by combining the targets identified in the cell-based TARGET system, with in planta targets using the Network Walking approach to network inference.

[00425] More particularly, this example relates to the discovery that *transient* targets of bZIP1 detected *specifically* in the cell-based *TARGET* system, described herein, include a set of "intermediate TF2s" controlled by bZIP1 (e.g, LBD38, LBD39 and NLP3) that mediate the downstream targets of bZIP1 *in planta*. This discovery was made using a novel network inference approach called Network Walking. This method uses time-series transcriptome data to predict regulatory connections between the TF targets identified in the cell-based *TARGET* system (direct and transient targets) with ones identified by *in planta* TF perturbation (primary, secondary targets and systemic effects).

[00426] **bZIP1 and its downstream targets (e.g., LBD38 and LBD39) act in a FFL involved in N-signaling**: The cell-based TARGET system described herein identified transient TF2 targets of bZIP1 which include ones previously associated with in N-signaling (e.g. NLP3, and LBD38, LBD 39). The Network Walking approach described herein further showed that these targets of bZIP1 (LBD38, LBD39 and NLP3), are predicted to act as downstream intermediates of bZIP1 in interlocking feed-forward loops (FFL) to control N-assimilation genes (Fig. 38 A-B and Fig. 39 A-C). Specifically, the

incoherent FFL (I1-FFL) between bZIP1 and LDB38 is predicted to mediate the early and rapid induction of the high-affinity nitrate transporter (NRT2.1), while the coherent FFL (C1-FFL) between bZIP1 and LDB39 is predicted to mediate the delayed but sustained expression of NRT2.1 (Fig. 38 A-B).

[00427] The Network Walking approach also predicts that these TF2s (NLP3, LBD38, and LBD39) function downstream of bZIP1 to mediate the N-regulation of an additional 7/9 genes in the N-assimilation pathway identified in Wang et al., 2003, Plant Physiol. 132(2):556-567, some of which are shown in Fig. 39. Importantly, five of the LDB38 *in planta* targets predicted by the Network Walking approach (NRT2.1, NRT2.2, NRT3.1, NIA1, FNR2), have been experimentally validated based on an LBD38 T-DNA mutant and over-expressor (Rubin et al., 2009, The Plant Cell 21(11):3567-3584).

13.1. METHOD: NETWORK WALKING

[00428] ***Overview***: The Network Walking method uses a time-series transcriptome data to infer a gene regulatory network (GRN) to link the TF targets identified in the cell-based *TARGET* system (direct and transient targets) with those identified by *in planta* TF perturbation experiments (secondary targets and systemic effects). The Network Walking approach uses N-response data from time-series transcriptome, and network inference approaches including State-Space modeling (a form of Dynamic Factor Graph (DFG) analysis) that was previously validated (Krouk et al., 2010, Genome Biology 11:R123; Krouk et al., 2013, Genome Biology 14(6): 123). The first implementation of this approach shows that transient bZIP1 targets detected specifically in the cell-based *TARGET* system reveal "hidden intermediate genes" that cannot be detected *in planta*, but that mediate downstream responses in N-signaling in vivo. bZIP1 was used as proof-of-principle, but the Network Walking approach extends to other TFs (see NLP7, in Fig. 39C), and can be applied to any species of interest.

[00429] **The *Network Walking* inference approach exploits time-series data**: The Network Walking pipeline uses N-treatment time-series data for predicting TF→target interactions for two reasons. First, the N-treatment time-series transcriptome, as in Krouk et al., 2010, Genome Biology 11:R123, measures the overall response of the GRN to a specific external signal (i.e., supply of Nitrogen) and thus provides the context within which the GRN is to be studied. Second, the temporal information can be exploited to

derive *causal relationships* between TFs and genes and to identify the direction of regulation for each interaction, again as in Krouk et al., 2010, Genome Biology 11:R123. The combined experimental and computational approach to integrating the cell-based and *in planta* data is called Network Walking, because it uses time-series data to "walk" from a "catalyst TF1"→ transient target (TF2) detected in isolated cells, to effector targets (gene Z) N-regulated *in planta,* as described below.

[00430] Transient targets of bZIP1 detected specifically in cells are predicted to mediate N-regulation of downstream targets *in planta.* The following protocol is the basis for the Network Walking approach (Fig. 40): In Step 1 **(**Fig. 40**)**, genes are identified involved in bZIP1-mediated N-signaling *in planta* as the set union of bZIP1 targets identified in the cell-based *TARGET* system (primary and transient targets) *and* bZIP1 targets identified by TF perturbation *in planta* (primary and secondary targets) (Kang et al., 2010, Molecular Plant 3:361), and then intersect this union with the N-regulated genes from a time-course study *in planta* (Krouk et al., 2010, Genome Biology 11:R123). In Step 2 **(**Fig. 40**)**, TF→target connections are conferred between the bZIP1 targets identified in the cell-based *TARGET* system (e.g. bZIP1→TF2) with genes identified by bZIP1 perturbation *in planta* (Kang et al., 2010, Molecular Plant 3:361), using the N-treatment time-series transcriptome data using a previously validated State-space modeling network inference approach (Krouk et al., 2010, Genome Biology 11:R123).

13.2. RESULTS

[00431] The resulting data and Network Walk for bZIP1 shown in Fig 39 A-C, reveals that the bZIP1 primary targets (18 genes) from the cell-based *TARGET* system (inner ring of TF triangles) are predicted to regulate downstream targets of bZIP1 validated *in planta* (gene Zs - Outer ring of 47 genes, Fig. 39 A) (Kang et al., 2010, Molecular Plant 3:361). Remarkably, all these 18 TF2s predicted to serve as intermediates to downstream bZIP1 responses, are Class III transient bZIP1 targets detected *only* in the *TARGET* cell-based system (Inner ring, Fig. 39 A).

[00432] This finding indicates that the rapid and transient TF2 targets of bZIP1, specifically detected in the cell-based TARGET system, mediate early and rapid events in N-signaling *in vivo* that cannot be captured *in planta.* These findings for bZIP1, may be a

general principle, based on preliminary studies on NLP7, a known master regulator of N-signaling in plants (Marchive et al., 2013, Nature Communications, 4:713). Specifically, Network Walking analysis for NLP7 also shows that targets of NLP7 identified in the cell-based *TARGET* system (inner ring TFs in Fig. 39 C), are predicted to regulate NLP7 targets identified *in planta* (Hughs et al, 2013, Genetics, 195(1):9-3) (outer ring, Fig. 39 C). These findings suggest that the TF targets identified in the cell-based *TARGET* system identifies the intermediates involved in downstream events in N-signaling *in planta*.

13.3. NETWORK WALKING PIPELINE

[00433] The generalized Network Walking Pipeline (Fig. 39 A-C), will identify potential "catalyst TF1s" involved in N-signaling, and their primary TF2 targets (Fig. 40) as follows:

[00434] **Step 1: Experimental: Perturb "catalyst TF1":** Perturb a candidate "catalyst TF1" in the cell-based *TARGET* system and *in planta* to identify: its transient primary targets (in cells) and secondary targets (*in planta*). While all genes are used in the network inference, the symmetric difference of these two sets yields: i) The TFs unique to cell-based *TARGET* system , which constitute the primary and transient TF2 target set ($TF_{2.1\text{-}j}$), and ii) the genes unique to the *in planta* set define the downstream secondary targets (gene $Z_{1\text{-}j}$).

[00435] **Step 2A: Computational: Perform a Network Walk between primary TF2 targets identified in cells and effector genes identified *in planta*.** Infer regulatory edges using the time-course N-transcriptome dataset using a combination of network inference tools (DFG, Inferelator etc.) (Krouk et al., 2013, Genome Biology, 14(5): 123) in an unbiased manner (i.e., no prior regulatory information is provided to the algorithm). This step will suggest edges between potential "transient" and primary TF2 targets detected in the cell-based *TARGET* system ($TF_{2.1\text{-}j}$) and downstream *in planta* targets (gene $Z_{1\text{-}j}$) of the catalyst TF1. several network inference approaches will be tested such as Dynamic Factor Graphs (Krouk et al., 2010, Genome Biology 11:R123), Genie3 (Huynh-Thu et al., 2010, PLoS, 5(9)) or Inferelator (Krouk et al., 2013, Genome Biology 14(6): 123; Bonneau et al, 2007, Cell 131:1354-1365). This step will identify a broad network that includes, but is not limited to, targets of catalyst TF1.

[00436] Step 2B: Computational: Identify catalyst TF1→TF2→*in planta* connections. Perform a network connectivity analysis of the dynamic network edges inferred in Step 2A using Cytoscape (Shannon et al., 2003, Genome Research 13:2498), to reveal the predicted connectivity of TF2s in the network and identify the most influential TF regulators of the N-signaling network, as in (Krouk et al., 2010, Genome Biology 11:R123). The TF2s validated to be directly targets of TF1 (e.g. bZIP1) are candidates to propagate the N-signal "kick-started" by the catalyst TF1 "Hit". In other words, the sub-graph of the overall N-signaling network (Step 2A) that is directly affected by catalyst TF1 is isolated.

[00437] Step 2C: Computational: Select candidate TF2s to initiate a new round of "Network Walking": Such TF2s (from Step 2B), will be further processed to identify redundant vs. non-redundant TF2s. TF2s that govern distinct but related sub-graphs of the network will be prioritized for further experimentation in the cell-based *TARGET* system.

[00438] Step 2D: Computational: Identify *new* "catalyst TF1" candidates. The remaining network graph not explained by catalyst TF1 (e.g. bZIP1) must constitute components crucial to the N-response, but not directly downstream of TF1. Such putative new "catalyst TF1s" derived from the current time-series inferred N-regulatory network include CRF3 and HRS1 (Fig. 41 A-B), for example. Such putative catalytic TF1s can provide secondary inputs to the N-signaling network, such as hormonal regulation (e.g via CRF3) (Cutcliffe et al., 2011, Journal of Experimental Botany, 62(14): 4995-5002), or the status of other macronutrients such as phosphate etc. (via HRS1) (Liu et al., 2009, J Integr Plant Biol. 51(4): 382-392) (Fig. 41).

[00439] Step 3A: Experimental: Perturb new "catalyst TF1": Perturb putative *new* "catalyst TF1s" in the cell-based *TARGET* system and *in planta,* to generate a detailed set of primary targets (in cells) and secondary targets *(in planta)*.

[00440] Step 3B: Experimental: Perturb new TF2s: Perturb TF2 in the cell-based *TARGET* system to validate primary TF2→gene Z edges, and also identify new primary and transient targets of TF2 (e.g. $TF_{3.1\text{-}j}$).

[00441] Step 4A: Computational: Reinitiate *de novo* network inference (e.g. DFG (Krouk et al., 2010, Genome Biology 11:R123)) using time-series data from N-treated plants, this time using a ***directed matrix*** that starts with priors defined experimentally by

TF2 and catalytic TF1 target data. The validated TF perturbations will provide informative prior biases for TF-gene relationships, thus *enhancing the accuracy* of network inference.

[00442] Step 4B: Computational: After each round of network inference, the next highly influential but non-redundant TF2 (Step 2B) and newly discovered transient targets, i.e., TF3s, are selected for experimental validation in the next round of experimentation. Steps 2B → 3B are repeated until a fine-scale N-signal network from the catalyst TF1s as roots to N-assimilation genes through the intermediate TF2s and TF3s is derived.

[00443] Step 5: Computational: Identify Feed-Forward loops. Feed-forward loops (FFLs) are especially important in rapid propagation of metabolite signals in *E. coli* and yeast (Alon et al., 2007, Nature Reviews. Genetics, 8(6): 450-461). For example, catalyst TF1→TF2→N-metabolism-gene network motifs that will be found in bZIP1 networks contain examples of a coherent feed-forward loop (C1-FFL) or incoherent feed-forward loop (I1-FFL) (Mangan et al., 2003, PNAS, 100(21):11980-11985) (Fig. 38 A-B). I1-FFLs (Incoherent FFLs) are postulated to accelerate the GRN's response to N-signal, while the C1-FFLs (Coherent FFLs) are time-delayed and employed to detect persistence of a N-signal. The occurrence of each FFL can be detected using NetMatch , a tool to detect and quantify network motifs that were previously developed (Ferro et al., 2007, Bioinformatics, 23(7): 910-912).

[00444] Transient TF2 targets for validation studies:

The transient TF2 targets of bZIP1 (e.g., NLP3, LBD38,39) will be perturbed in the cell-based *TARGET* system. These TFs are each implicated in mediating the N-response *in planta,* but their specific and direct network targets are unknown. They will first be tested in the cell-based *TARGET* system, described herein. The targets identified for each TF2 (poised, stable and transient) will serve to validate predictions that they serve as intermediates for bZIP1 (e.g. bZIP1→transient LBD39→gene Z (in planta) (Figs. 38A-B and 39 A-C). The network inference algorithm best suited for the Network Walking analysis will be re-evaluated after each iteration by evaluating Precision (correctly predicted causal edges/total predicted edges) and Recall (correctly predicted edges/all experimentally validated causal edges) for all TFs (catalyst TF's and TF2s) whose targets

are experimentally validated. Algorithms will be scored by combining Precision and Recall into a measure called Area Under the Precision Recall curve (AUPR). The greater the measure's value (maximum value is one), the greater the combined recall and precision.

[00445] This combined computational/experimental pipeline will result in a validated Network Walk from pioneer TF1 of interest (e.g. bZIP1)→ transient TF2.1 target (identified in cell-based *TARGET* system) → effector gene Z's *in planta* (Fig. 39A). This approach will identify novel "catalyst TF1s" that initiate the N-response and integrate it with secondary signals such as hormones and other nutrients (Fig. 41B). This approach will also identify key feed-forward loops that control rapid N-uptake and metabolism (Figs. 38A-B, 39B, and 41A-B).

[00446] In preliminary studies, a simple ordinary differential equation (ODE) based method called *Dynamic Factor Graphs* (DFG) was used to infer causal relationships among genes responding in the N-treatment time-series data (Krouk et al., 2010, Genome Biology 11:R123; Krouk et al., 2013, Genome Biology 14(6): 123). In the roll-out of this approach, several ODE based methods (DFG, Inferelator etc.), Mutual information based methods (Time-Delay ARACNE, tlCLR etc.) and dynamic Bayesian networks (BANJO etc.) as discussed in (Krouk et al., 2013, Genome Biology 14(6): 123) will be tested. The DFG method which was previously implemented (Krouk et al., 2010, Genome Biology 11:R123) is robust to variations in expression measures and is best suited for well-replicated time-course studies (Krouk et al., 2013, Genome Biology 14(6): 123), while the Inferelator algorithm uses a combination of steady-state perturbations and time-series data (Krouk et al., 2013, Genome Biology 14(6): 123; Bonneau et al., 2006, Genome Biology, 7(5): P36). Finally, Genie3 uses a regression tree based approach to infer potential regulators for each gene from a range of steady-state experiments (Krouk et al., 2013, Genome Biology 14(6): 123; Huynh-Thu et al., 2010, PLoS, 5(9)). DFG is best suited for the experimental design, as it works exclusively with time-series data (Krouk et al., 2010, Genome Biology 11:R123; Krouk et al., 2013, Genome Biology 14(6): 123). As more TF perturbation experiments are added through this iterative approach, the refined network will be inferred with each of DFG, Genie3, Inferelator and any others (for example mutual information and dynamic Bayesian approaches). The algorithm that

best fits the experimental profile will be selected using PR curves (i.e., Precision of predictions vs. Recall) on known true positives for multiple TFs from independent studies: e.g. NLP7, LBD38 and bZIP1.

14. EXAMPLE 9: N-regulated network modules conserved across species.

[00447] In this Example, a cross-species network approach was used to uncover nitrogen-regulated network modules conserved across a model and a crop species. By translating gene "network knowledge" from the data-rich model Arabidopsis (*Arabidopsis thaliana*) to a crop (*Oryza sativa*), evolutionarily conserved N-regulatory modules were discovered as targets for translational studies to improve N-use efficiency in transgenic plants. To uncover such conserved N-regulatory network modules, a N-regulatory network based was first generated solely on rice (*O. sativa*) transcriptome and gene interaction data. Next, the "network knowledge" was enhanced in the rice N-regulatory network using transcriptome and gene interaction data from Arabidopsis and new data from Arabidopsis and rice plants exposed to the same N-treatment conditions. This cross-species network analysis uncovered a set of N-regulated transcription factors (TFs) predicted to target the same genes and network modules in both species. Supernode analysis of the TFs and their targets in these conserved network modules uncovered genes directly related to nitrogen use (e.g. N-assimilation) and to other shared biological processes indirectly related to nitrogen. This cross-species network approach was validated with members of two TF families in the supernode network, bZIP-TGA and HRS1/HHO family, have recently been experimentally validated to mediate the N-response in Arabidopsis.

14.1. INTRODUCTION

[00448] The goal of this study is to translate "network knowledge" from Arabidopsis, a data-rich model species, to enhance the identification of nitrogen (N)-regulatory networks in rice, one of the most important crops in the world. With a significantly smaller genome size than other cereals (~430 Mb), the ability to perform genetic transformations (Hiei and Komari, 2008), and a finished genome sequence (Matsumoto T, 2005), rice is an excellent monocot model for genetic, molecular and genomic studies

(Gale and Devos, 1998; Sasaki and Sederoff, 2003). In this Example, N-regulatory gene networks in rice were constructed using "network knowledge" from Arabidopsis, a data-rich laboratory model for dicots. Thus, this cross-species network study exploits the best-characterized experimental models for dicot and monocot plants, respectively.

[00449] Nitrogen (N) is a rate-limiting element for plant growth. Rice plants absorb NH_4^+ at a higher rate than NO_3^- (Fried et al., 1965). Because NH_4^+ strongly inhibits NO_3^- uptake in agricultural soils where both NO_3^- and NH_4^+ are present (Kronzucker et al., 1999a), root NH_4^+ uptake may be favored as a result of the specific down-regulation of NO_3^- uptake systems (Kronzucker et al., 1999b). In rice, combinations of NO_3^- and NH_4^+ usually result in a greater vegetative growth than when either N form is supplied alone (Cramer and Lewis, 1993). Therefore, N-treatment experiments were designed in this study to include both NO_3^- and NH_4^+.

[00450] In previous studies of the Arabidopsis N-response, transcriptome data was analyzed in the context of gene interactions to identify and validate N-regulated gene networks *in planta* (Gifford et al., 2008; Gutiérrez et al., 2008; Krouk et al., 2010). In this study, the N-regulated genes and gene networks between Arabidopsis and rice were compared. This cross-species network analysis provides a unique opportunity to examine the conservation and divergence of N-regulated networks in the context of monocot and dicot transcriptomes. As rice and Arabidopsis are highly divergent phylogenetically, any evolutionarily conserved networks should be of special importance.

[00451] Establishing the architecture of gene regulatory networks requires gathering information on transcription factors (TFs), their targets in the genome, and their corresponding binding sites in gene promoter regions. Generation of N-responsive transcriptome data from rice and Arabidopsis enabled us to identify conserved N-regulatory gene network modules shared between dicots and monocots. The rice and Arabidopsis transcriptome (using Affymetrix GeneChips) were analyzed in response to N-treatments in roots and shoots. The VirtualPlant software platform (Katari et al., 2010) which is operational for both Arabidopsis and rice, was used to perform much of the analysis including homology mapping analysis and significance of overlap in gene lists using the Genesect tool (www.virtualplant.org).

[00452] The N-regulated gene network includes expression data generated in this study and metabolic and protein-protein interactions from publicly available rice data (Rohila et al., 2006; Ding et al., 2009; Rohila et al., 2009; Gu et al., 2011; Dharmawardhana et al., 2013). Despite the fact that much of genomic and systemic rice data has been generated over the past years, a lot of information is still missing. For example, Arabidopsis has much more experimental data with regard to cis-binding sites and protein-protein interaction. To fill these gaps in rice "network knowledge", orthology-based Arabidopsis interaction data was integrated (Palaniswamy et al., 2006; Yilmaz et al., 2009; Gu et al., 2011; Ho et al., 2012) and searched for functional Arabidopsis cis-binding sites in rice, to identify N-regulatory network modules and biological processes ("network biomodules") conserved between dicots and monocots.

[00453] An important issue in this analysis is orthology. Monocots and dicots are quite distantly related with divergence estimation of 140-150 MYA (Chaw et al., 2004). A naïve and crude method for identifying putative orthologs, is to use Reverse Blast Hit thresholds – the putative orthologs must map to each other with a Blast e-value less than some cut-off. The identification of putative orthologs between monocots and dicots is confounded by the presence of paralogs (homologous genes originating from gene duplication events). There are several algorithms, such as OrthoMCL (Fischer et al., 2011), that are designed to help distinguish an ortholog from a paralog, by comparing sequences within species in addition to between species. However, even if these algorithms can detect true orthologs with greater specificity, there is always a possibility that different gene family members in each species take on the responsibility of responding to nutrients, like nitrogen. Here, the performance of Reverse Blast Hit method and OrthoMCL was tested and compared in identifying genes and gene interactions whose *function* is conserved across species. From here on, the cross-species gene mapping based on BLASTP will be referred to as 'homologs', and the matches based on OrthoMCL will be called 'orthologs'.

[00454] Finally, this cross-species network study significantly contributes to two important areas: (i) studying N-regulated gene networks in rice, an important crop, and (ii) identifying conserved and distinct N-regulatory hubs controlling network "biomodules" which can be used to enhance translational discoveries between a model

plant and crops. The aim to identify N-regulated genes across a model dicot and a monocot crop, and to interpret it in a systems biology/network context, is essential to derive testable biological hypotheses. By applying network information, key regulators of these N-responsive gene networks and biomodules can be identified, which can be further manipulated to study N-use efficiency in transgenic plants. This approach has the potential to enhance translational discoveries from Arabidopsis to a crop (rice) with the goal of improving plant N-use efficiency, which will contribute to sustainable agricultural practices by diminishing the use of N fertilizers.

14.2. METHODS

14.2.1. Plant Growth and Treatment Conditions

[00455] Rice seeds (*Oryza sativa* ssp. *japonica*) were provided by Dale Bumpers of the National Rice Research Center (AR, USA). Seeds were surface-sterilized in 70% ethanol for 3 minutes followed by commercial H_2O_2 for 30 minutes with gently agitation, and washed with distilled water. Seeds were sown onto 1x Murashige and Skoog basal salts (custom-made; GIBCO) with 0.5 mM ammonium succinate and 3 mM sucrose, 0.8% BactoAgar at pH 5.5 for 3 days in dark conditions at 27°C. Following germination, embryos with developed root system and aerial tissue were dissected from the rest of the seed using a sterile blade and transferred to a hydroponic system (Phytatray II, Sigma Aldrich) containing basal MS salts (custom-made; GIBCO) with 0.5 mM ammonium succinate and 3 mM sucrose at pH 5.5. Fresh media was replaced every 3 days to maintain a steady nutritional state and optimal pH levels. After 12 days under long-day (16 h light: 8 h dark) growth conditions, at light intensity of 180 $\mu E.s^{-1}.m^{-2}$ and at 27°C, plants were transferred to fresh media containing custom basal MS salts for 24 h prior treatment. On day 13, plants were transiently treated for 2 h at the start of their light cycle by adding nitrogen (N) at a final concentration of 20 mM KNO_3 and 20 mM NH_4NO_3 (referred here as 1xN). Control plants were treated with KCl at a final concentration of 20 mM. After treatment, roots and shoots were harvested separately using a blade, and immediately submerged into liquid nitrogen and stored at -80°C prior to RNA extraction.

[00456] Arabidopsis seeds were placed for 2 days in the dark at 4°C to synchronize germination. Seeds were surface-sterilized and then transferred to a hydroponic system (Phytatray I, Sigma Aldrich) containing the same media previously described for rice (pH 5.7). Growth conditions were the same as in rice, except that plants were under 50 $\mu E.s^{-1}.m^{-2}$ light intensity at 22°C. N-starvation and treatments were done as described above.

14.2.2. RNA Isolation and RT-QPCR Analysis

[00457] RNA was isolated from roots and shoots with the TRIzol reagent following manufacturer´s protocols (Invitrogen Life Technologies. Carlsbad, CA, USA). Standard manufacturer's protocols were used to reverse-transcribe total RNA (1 to 2µg) to one-strand cDNA using Thermo™ script RT (Invitrogen). RT-PCR measurements were obtained for a set of selected genes using gene-specific primers (Table 35) and LightCycler FastStart DNA Master SYBR Green (Roche Diagnostics). Expression levels of tested genes were normalized to expression levels of the actin or clathrin gene as described in (Obertello et al., 2010).

14.2.3. Microarray Analysis and Experiments

[00458] cDNA synthesis, array hybridization and normalization of the signal intensities were performed according to the instructions provided by Affymetrix. Affymetrix Arabidopsis ATH1 Genome Array and Rice Genome Array were used for respective species. The Affymetrix microarray expression data has been deposited in the Gene Expression Omnibus (GEO) database (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE38102.

[00459] Gene expression values were transformed by taking the logarithm to the base 2 ($\log_2$) of the ratio of 1xN-treatment (experimental state) over KCl treatment (control state) to yield the magnitude of the deviations in up- and down-regulated genes symmetrically ($\log_2$ value of the ratio of 1-fold is 0). Data normalization was performed using the RMA (Robust Microarray Analysis) method in the Bioconductor package in R statistical environment.

[00460] A two-way Analysis of Variance (ANOVA) was performed using a custom-made function in R to identify probes that were differentially expressed following N

treatment. The *p*-values for the model were then corrected for multiple hypotheses testing using FDR correction at 5% (Benjamini and Hochberg, 1995). The probes passing the cut-off ($p \leq 0.05$) for the model and, N treatment or interaction of N treatment and tissue, were deemed significant. A Tukey's HSD post-hoc analysis was performed on significant probes to determine the tissue specificity of N-regulation at *p*-value cut-off ≤ 0.05 and |fold-change| $\geq$ 1.5-fold ($\log_2$ of 1.5 is 0.585). Probes mapping to more than one gene were disregarded. Finally, for the cases of multiple probe sets representing the same gene, the assumption was that the expression levels should be upregulated or down-regulated in all the probes representing the gene. Expression levels were combined for those that passed the criterion. A set of 451 N-regulated genes differentially expressed in Rice and 1,417 N-regulated genes differentially expressed in Arabidopsis were obtained.

[00461] For both species, Pearson correlation coefficient was calculated for probes that passed the 2-way ANOVA and FDR correction. Specifically, the Pearson correlation coefficient was computed between different pair of probe sets using the mean value of their expression data across the replicates using a custom script in R. Correlation was calculated separately for root genes and shoot genes in both species and the corresponding correlation edge was labeled accordingly.

14.2.4. Orthology analysis

[00462] Sequence and annotation data for the *Oryza sativa* ssp. *japonica* genome was downloaded from the TIGR Rice Genome Annotation Database, version 6.1 (http://rice.plantbiology.msu.edu/). Similarly, data for the *Arabidopsis thaliana* genome was obtained from The Arabidopsis Information Resource (TAIR) website, version 10 (Lamesch et al., 2012). Homologous N-regulated genes between Rice and Arabidopsis were obtained using Reverse BLAST (Camacho et al., 2009) with an e-value $\leq$ 1e-20, thereby allowing for multiple orthologous gene hits. Orthology was determined using the data provided on the OrthoMCL website (Fischer et al., 2011).

14.2.5. Network Analysis

[00463] For the gene network analysis (Figure 43), rice network interaction data was obtained as follows: For Rice Only N-response Network (RONN) (Figure 43, Step 1), metabolic interactions were obtained from RiceCyc, Gramene Pathways (Dharmawardhana et al., 2013) and experimentally determined protein-protein interactions were obtained from the PRIN database (Gu et al., 2011) and Rice Kinase database (Rohila et al., 2006; Ding et al., 2009; Rohila et al., 2009).

[00464] For Rice Predicted N-regulatory Network (RPNN-predicted interactions) (Figure 43, Step 2), computationally predicted protein-protein interactions were obtained from the PRIN database (Gu et al., 2011), and the Rice Journal database (Ho et al., 2012).

[00465] Additionally for RPNN-predicted interactions (Figure 43, Step 2), regulatory interactions were predicted between a TF and its putative target. TF family membership in Rice was obtained from PlantTFDB (Jin et al., 2014) and cis-regulatory motifs were obtained from AGRIS (Palaniswamy et al., 2006). The upstream promoter sequences (1kb) in rice were retrieved from the RAP-DB (http://rapdb.dna.affrc.go.jp/). Cis-motifs in promoter regions were searched using the DNA pattern matching tool from the RSA tools – Plants server with default parameters (van Helden, 2003). HRS1-HHO family member targets were predicted similarly and cis-motifs for the TF family members were obtained from Medici et al. (Medici et al., 2015).

[00466] For the Rice-Arabidopsis N-regulatory Network using BLASTP (RANN-BLAST) and Rice-Arabidopsis N-regulatory Network using OrthoMCL (RANN-OrthoMCL) (Figure 43, Step 3), a correlation edge was considered as a 'conserved correlation edge' when the correlation between N-regulated gene pair in rice was supported by a significant correlation edge between its respective Arabidopsis N-regulated orthologous gene pair, with correct directionality (both correlation edges (in each species) were either both positive or both negative) and tissue-specificity (both correlation edges (in each species) were either both root correlation edge or both shoot correlation edge).

14.2.6. Network Construction

[00467] In Step 1 (Figure 43), the 451 rice N-regulated genes were queried against the metabolic and experimentally determined protein-protein interaction databases, and all

the significant correlation edges between them ($p \leq 0.05$) were used to generate RONN. Querying against the predicted protein-protein interactions databases in Step 2 (Figure 43) further enriched this network. Additionally, the predicted regulatory interactions, obtained using cis-motifs from Arabidopsis, were restricted to those TF:target gene pairs where the two were also significantly correlated ($p \leq 0.05$). The resulting network, RPNN-predicted for Step 2 (Figure 43) had 451 rice genes with 36 TFs, and a total of 32,839 interactions between them.

[00468] The RPNN-predicted interactions network has reduced number of correlation-only edges compared to RONN because adding cis-motif information to the network resulted in some of the correlation-only edges to be reassigned as regulatory edges. This also increased the total number of regulatory (4,128) edges and correlation-only (28,265) edges in the network to 32,393 edges from 32,225 correlation-only edges (Figure 43). The 168 additional edges were a result of added directionality of regulation, accounting for cases where one TF (TF1) was targeting and was being targeted by another TF (TF2) in the network (Figure 43).

[00469] In Step 3 (Figure 43), Arabidopsis N-regulated experimental correlation data was introduced using BLASTP and OrthoMCL and individual networks were generated for each method following a similar workflow. Briefly, in both methods the rice experimental correlation data was filtered with Arabidopsis correlation data, inferred in rice using orthology, to yield conserved correlation edges. If the significant correlation edge between N-regulated gene pair in rice was also supported by a significant correlation edge between its respective Arabidopsis N-regulated orthologous gene pair, then it was considered a 'conserved correlation' edge. The resulting networks for Step 3 (Figure 43), RANN-BLAST and RANN-OrthoMCL comprised a total of 180 N-regulated rice genes with 2,212 total interactions, and 48 N-regulated rice genes with 383 total interactions, respectively.

[00470] Finally, the two networks RANN-BLAST and RANN-OrthoMCL were merged in Step 4 to yield the RANN-Union network, which had 182 N-regulated rice genes and 2,273 total interactions between them.

14.2.7. Network Visualization and Analysis

[00471] All network visualizations were created using Cytoscape (v2.8.3) software (Shannon et al., 2003). Custom-made script was used to analyze the total number of direct targets for a TF for each of the regulatory network. The summarized result for the analysis across all networks is presented in Table 30. The Wilcoxon signed-rank test was used in R to validate that the change in number of direct targets for the TFs is significant across the network generation process (Hollander et al., 2014).

14.2.8. Supernode Network Analysis

[00472] The supernode analysis merges the individual nodes (genes) into a single node, its size proportional to the number of nodes merged, based on the classification system selected. The transcription factor families (Plant TFDB, Jin et al., 2014) and PlantCyc (OryzaCyc v1.0, PMN) pathways were the two major classification groupings used, with level-3 subclass hierarchical classification (Figure 44). The individual gene pair interactions were merged appropriately for the supernodes and were similar interaction types as present in the gene network analysis.

14.2.9. Phylogenetic Analysis

[00473] The sequences coding for G2-like (HHO) and TGA proteins were retrieved from the AGRIS (Arabidopsis Gene Regulatory Information Server; http://arabidopsis.med.ohio-state.edu/) database and from the Rice Genome Annotation Project (http://rice.plantbiology.msu.edu/). The alignment of the full-length amino acid sequences was performed in ClustalW using standard settings. The phylogeny reconstruction was inferred by using the maximum likelihood method. The bootstrap values were obtained based on 500 replicates. Phylogenetic analysis was conducted in MEGA5 software (Tamura et al., 2011).

14.3. RESULTS

14.3.1. Equilibrating Nitrogen-Treatment Conditions for Arabadopsis and Rice

[00474] The goal of this study is to identify conserved N-response networks in two species by comparison. Thus, N-treatments and growth conditions of rice and Arabidopsis as comparable were made as possible. A hydroponic system was adapted for Arabidopsis (Gifford et al., 2008) to grow and treat *O. sativa (*rice*)* seedlings, with only the plant roots submerged in liquid media. For plants with minimal seed reserves such as Arabidopsis, an external N-supply is required to allow plant growth and development. By contrast, rice can grow for longer periods using N-nutrients stored in their seeds. In order to equilibrate growth conditions of these two species, and to eliminate the seed-nutrient effect during N-treatment, the nutritive rice seed tissue was dissected away from the rice seedlings once the cotyledon and roots emerged, and only the germinated embryo was placed in the hydroponic system. For both species, the N-source during this initial growth phase contained 0.5 mM ammonium succinate, which was renewed every 2-3 days with fresh media to avoid NH_4^+ depletion due to different consuming rates between species. This growth on a low level of a N-source (ammonium), was a background in which to observe effects of transient treatments with nitrate (as in (Wang et al., 2000; Wang et al., 2004)) and/or high ammonium. As the N-regulation of gene expression is largely dependent on carbon (C) resource provision in Arabidopsis (Krouk et al., 2009), 0.5% (w/v) sucrose was included in the growth media as a constant nutrient to eliminate C-signaling effects during transient N-treatments. After 12 days, plants were N-starved for 24 h. Finally, at the start of their light cycle plants were N-treated for 2hr with a combination of NO_3^- (40 mM) and NH_4^+ (20 mM), the amount of N in MS media (Murashige and Skoog, 1962), referred here as 1xN (for more details see Materials and Methods). Shoot and root RNA samples were hybridized to the Arabidopsis ATH1 and Rice Genome Arrays from Affymetrix to evaluate changes in global gene expression (see Materials and Methods) in response to N-treatments. The normalized microarray data for each species has been deposited in the Gene Expression Omnibus (GEO) database (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE38102.

14.3.2. The Effect of N-Treatment on Genome-Wide Expression in Rice

[00475] The first aim was to identify N-regulated genes and study their response in rice shoots and roots. Following RMA normalization, 2-way ANOVA analysis with FDR correction, and filtering of transcriptome data using 1.5 fold cut-off (Figure 42), a set of 451 genes in rice was found that were significantly regulated in rice by N-treatment (Table 27). In rice shoots, 103 genes were N-induced, and 39 genes were repressed in response to N-treatment. In rice roots, 234 genes were N-induced while 106 genes were repressed in N-treated samples, compared to control treatments. (Table 27; see Table S31 for a complete list of regulated genes and see Figure 45 for organ specific gene response). Rice roots appear to have a much larger response in terms of number of genes, which has also been previously observed in Arabidopsis (Wang et al., 2003). Additionally, these results from the rice microarray data were confirmed by RT-*q*PCR for a number of selected genes (Figure 46).

[00476] The 451 N-regulated rice genes included genes involved in nitrate uptake and metabolism, sugar biosynthesis and ammonium assimilation among others (Table 28). Specifically, some of the genes in these groups are involved in producing reductants for nitrite uptake and also include enzymes of the pentose phosphate pathway, which generates the NADPH necessary for nitrogen assimilation (Table 28). N-induction of a gene that encodes the pentose-phosphate enzymes in both tissues: *G6PDH* (LOC_Os07g22350) was also observed. Such genes involved in C-metabolism are related to the production of energy for nitrate or nitrite reduction. These types of genes have also been previously identified as N-responsive in Arabidopsis (Wang et al., 2003).

[00477] Finally, rice genes involved in ammonium assimilation were found to respond to N-treatments in this study (Table 28). NADH-GOGAT (LOC_Os01g48960) was N-induced in rice roots while *GLN* (LOC_Os04g56400) was found to be N-regulated (1.09 and 0.71 fold change respectively) in both roots and shoots (Table 28). The complete list of N-regulated genes in rice is shown in supplemental Table 31.

14.3.3. Genome-Wide Effects on Nitrogen Treatment in *Arabidopsis thaliana*

[00478] Arabidopsis seedlings were N-treated as described above for rice (for more details see the Methods Section and Figure 42) and following RNA extraction, gene responses to N-treatments were analyzed using microarrays. Following normalization, 2-way ANOVA analysis, FDR correction and filtering for 1.5 fold change, 1,417 Arabidopsis genes were identified to be N-responsive compared to control treatment. In Arabidopsis shoots, 166 genes were N-induced and 184 genes were repressed in response to N-treatments. In Arabidopsis roots, 757 genes were N-induced and 424 genes were repressed (Table 27; for the complete list of regulated genes see Table 32). The N-regulated genes in Arabidopsis included genes involved in nitrate uptake and metabolism, genes in the Pentose Phosphate pathway and ammonium assimilation among others (Table 29).

[00479] As observed for rice, the majority of N-regulated genes in Arabidopsis are root-specific (also found previously (Wang et al., 2004)). For example, 75% of genes were uniquely N-regulated in Arabidopsis roots versus shoots, while only 16% of N-regulated genes were expressed exclusively in shoots (Figure 47). Several known Arabidopsis N-induced genes were also responsive to the treatments with ammonium nitrate, including: NIA1, NIA2, NIR, NRT2:1, NRT1:2, NRT3:1, ferredoxin 3, G6PD2, G6PD3, GLT1, ASN2 and GDH2 among others (Table 29, for a complete list see Table 32) (Wang et al., 2003; Krouk et al., 2010). Additionally, the microarray data was confirmed by RT-*q*PCR results in a number of selected Arabidopsis genes (Figure 48).

[00480] To determine whether the overlap between the rice and Arabidopsis N-responsive genes was significant, a permutation test was performed. 1,417 genes were selected randomly from Arabidopsis genes present on the Affy chip, and similarly 451 rice genes were selected randomly from genes present on the rice Affy chip. Using BLASTP homology, the overlap was measured in terms of rice and Arabidopsis genes. This was done 10,000 times and then the number of times the overlap was greater than or equal to the observed was counted. The overlap obtained from random sampling was never greater than or equal to the observed, making the p-value <0.0001. These results suggest that despite the difference in number of responsive genes, rice and Arabidopsis respond very similarly to the nitrogen treatments provided.

14.3.4. Network Analysis Identifies Conserved Genes Involved in N-Signaling in Rice

[00481] It is known that the expression of many TFs is regulated by NO_3^-. However, to date, only a few of such NO_3^- regulated TFs have been shown to be involved in NO_3^- signaling in Arabidopsis (for review see (Castaings et al., 2011) and recent studies (Alvarez et al., 2014; Medici et al., 2015)).

Creation of a "Rice Arabidopsis N-regulatory Network" (RANN-Union).

[00482] To identify novel TFs that may play a global role in a N-regulatory network, network analysis was performed that exploited microarray datasets from Arabidopsis and rice (Figure 43). A network was generated using the limited knowledge of known rice interactions and then, to enrich the existing network in rice, predicted interaction data was introduced based on homology to the large amount of Arabidopsis' "network knowledge". For this purpose, a network analysis was started by creating a "Rice Only N-response Network" (RONN) (Figure 43, Step 1). In Step 1, the rice experimental data generated was used by looking at significant correlations among N-regulated rice genes (Pearson correlation coefficient with a *p*-value cut-off of 0.05), metabolic pathways from RiceCyc (Dharmawardhana et al., 2013), and experimentally determined protein-protein interactions in rice (Rohila et al., 2006; Ding et al., 2009; Rohila et al., 2009; Gu et al., 2011) for this network creation (for details see Materials and Methods). This "rice only" analysis resulted in a network of 451 N-regulated genes, with 36 TFs and 32,405 interactions among them (Figure 43, RONN).

[00483] Next, in Step 2 (Figure 43), predicted protein-protein interactions in rice and cis-binding site information from Arabidopsis were added to the RONN network. This generated a new predictive network: Rice Predicted N-regulatory Network (RPNN-predicted interactions). The RPNN-predicted interactions network included rice predicted regulatory interactions obtained from cis-binding site data in Arabidopsis, and transcription factor family information in rice from PlantTFDB. In the RPNN network, predicted regulatory edges are defined by the presence of a cis-binding site and a significant correlation between a transcription factor and target. In this analysis, 3,960 of the 32,225 correlation edges also contain cis-binding information, thus re-categorizing

them as regulatory edges. In the case where the target of one transcription factor (e.g. TF1) is another transcription factor (e.g. TF2), there is a possibility that TF1 is a target of TF2 (and vice versa), in which case one correlation edge between two TFs is converted to two regulatory edges. There are 168 such TF1-TF2 correlation edges, thus increasing the number of regulatory edges from 3,960 to 4,128 (Figure 43, RPNN). The RPNN-predicted interactions network had the same number of genes as the RONN network, however the addition of predicted protein-protein interactions along with regulatory data increases the total number of interactions to 32,839 in the RPNN-predicted interactions network (Figure 43).

[00484] Next, further filtering the RPNN network was of interest to identify the N-regulatory genes and network modules whose regulation is conserved across two species, Arabidopsis and rice. To this end, in Step 3 (Figure 43), the Arabidopsis experimental data of N-responsive genes generated was introduced into the RPNN-predicted interactions network. This was approached using two different orthology methods (BLASTP and OrthoMCL) to obtain two different Rice-Arabidopsis N-regulated Networks (RANN-BLAST and RANN-OrthoMCL, respectively). Both networks RANN-BLAST and RANN-OrthoMCL only contain rice genes where the rice gene and its putative ortholog in Arabidopsis is N-regulated in the experimental conditions. Additionally the correlation and regulatory edges between these conserved N-regulatory genes also had to be conserved (Figure 43).

[00485] The RANN-BLAST network comprised 180 rice N-regulated genes, of which 23 are TFs. By contrast, the RANN-OrthoMCL network had only 48 rice N-regulated genes, of which 3 genes are TFs. It is not surprising that RANN-OrthoMCL network is smaller than RANN-BLAST, since OrthoMCL differentiates between orthologs and paralogs. It is important to note that out of 48 genes from RANN-OrthoMCL, only 2 additional genes were present uniquely in the RANN-OrthoMCL network and not in the RANN-BLAST network. These genes comprise a glycoprotein, LOC_Os10g41250 and a protein of unknown function, LOC_Os05g46340. As discussed below, validated gene interactions were identified using RANN-BLAST, which would have been missed had only RANN-OrthoMCL been used. Therefore, a union of the two conserved cross-species networks, RANN-BLAST and RANN-OrthoMCL, was performed to generate the Rice-

Arabidopsis N-regulatory Network (RANN-Union), which contains 182 rice N-regulated genes of which 23 genes are TFs (Figure 43, Step 4).

[00486] Of the 182 genes in the RANN-Union network (Figure 43, Step 4), some of the genes are known to be directly involved in N-assimilation; for example, nitrate transporters, nitrate and nitrite reductase, glutamine synthetase and glutamate synthase, among others (for the complete list of regulated genes see Table 33). The RANN-Union network also contains ferredoxin reductase genes (LOC_Os03g57120, LOC_Os05g37140 and LOC_Os01g64120) whose encoded proteins are indirectly involved in nitrite reduction by providing reducing power as shown in Arabidopsis (Wang et al., 2000). Additionally, LOC_Os03g57120 is orthologous to ATRFNR1 in Arabidopsis (At4g05390, based on BLASTP and OrthoMCL), which has also been shown previously to be involved in supplying reduced ferredoxin for nitrate assimilation (Hanke et al., 2005). In addition, two calcineurin B-like (CBL)-interacting protein kinases (CIPK) are present in the group of 182 N-regulated genes in the RANN-Union network. LOC_Os03g03510 has Arabidopsis CIPK23 as its ortholog (based on OrthoMCL and BLASTP), while, LOC_Os03g22050 is homolog to Arabidopsis CIPK23 only based on BLASTP (but not OrthoMCL). Interestingly, CIPK23 has been identified as NO_3^- inducible protein kinase (Castaings et al., 2011). Additionally, both rice CIPK loci (LOC_Os03g22050 and LOC_Os03g03510) are homologous to KIN11 and to MEKK1 (based on BLASTP but not OrthoMCL). KIN11, which is a Snf1-related kinase proposed to be part of an "energy-sensing" mechanism in Arabidopsis (Baena-González et al., 2007), and also found to be related to N-assimilation (Gutiérrez et al., 2008). Also, MEKK1 is involved in glutamate signaling in root tips of Arabidopsis (Forde, 2014). Moreover, LBD39 (LOC_Os03g41330) (Lateral Organ Boundary Domain), a transcription factor present in the RANN-Union, was found to be regulated at the transcriptional level by NO_3^- and involved in N-signaling in Arabidopsis (Rubin et al., 2009).

[00487] To study how TF connectivity changed throughout the network analysis, and to identify putative regulators that control the expression of conserved network modules, the transcription factors N-regulated in these networks were ranked based on their "hubbiness", the number of regulatory connections (Table 30). As mentioned previously,

the number of connections found for TFs in the RPNN-predicted interactions (Step 2, Figure 43) decrease when the network was filtered with Arabidopsis N-regulatory genes and their correlations (Step 3, Figure 43). The TF with the highest number of connections in the RANN-Union network is LOC_Os03g55590 (Table 30), a gene that belongs to the G2-like Transcription factor family, and sub-group HHO (for HRS1 Homolog). The HHO family has another member conserved in RANN-Union network, LOC_Os07g02800. A naïve assumption of the network analysis, is that the TF with the most connections has the most influential regulatory role. In previous studies, the ranking of TF hubbiness was used to identify candidates for follow-up mutational studies in which they were validated (Gutierrez et al. 2008). To test the influence of orthology data, it was determined whether the rank of TFs based on hubbiness changed from the RPNN-predicted interactions network to the final network RANN-Union using the Wilcoxon test. A *p*-value of 1.423e-08 indicates that the connectivity rank presented in Table 30 has significantly changed through the network generation steps shown in Figure 43.

Creation of "Arabidopsis-Rice N-regulatory Network" (ARNN-Union).

[00488] Considering that there is more information available in Arabidopsis than in rice, a similar network analysis was performed as in Figure 43, but now using Arabidopsis N-regulated data as the starting point (Figure 51). The Arabidopsis network was filtered with rice experimental data generated in the study using BLASTP and OrthoMCL (see Figure 51). The resulting Arabidopsis-Rice N-regulatory Network (ARNN-Union) has 276 genes. By definition, the identities of the genes from the Arabidopsis-Rice N-regulatory Network (ARNN-Union, 276 genes) (Figure 51) are equal to the Rice-Arabidopsis N-regulatory Network (RANN-Union, 182 genes) (Figure 43). The number of genes is different however, because in most of the cases rice genes have more than one N-regulated ortholog in Arabidopsis. Following this rationale, the ARNN-Union contains 76 TFs (Figure 51), while the RANN-Union contains only 23 TFs (Figure 43) (For a list of ARNN-Union TFs see Table 34). It was also studied how TF connectivity changed throughout the steps of the network analysis in Figure 51, by ranking TF's based on the number of regulatory connections (Table 34). In the top 5 highly ranked TFs of the ARNN-Union network (Table 34), 3 members of the

HRS1/HHO family, including HHO5, and TGA1 were found, which were each validated to be involved in the nitrogen response in Arabidopsis (Alvarez et al., 2010; Medici et al., 2015), in addition to WRKY28, a novel finding of this study.

[00489] It was unexpectedly discovered in this study that HHO5 is involved in nitrogen response in Arabidopsis. This finding is surprising because in a previous study that examined nitrate-responsive genes, HHO5 was not found to be involved in the nitrate response (see Medici et al., 2015). In contrast, the present study, which utilized ammonium nitrate treatments (used in commercial fertilizers), did uncover HHO5 to be a nitrogen-regulated gene. This finding suggests that HHO5 is more broadly responsive to nitrogen treatments significant to field studies, and not just to one form of nitrogen, *i.e.*, nitrate.

[00490] In Arabidopsis, HHO5 is positively correlated with NIR1, NRT3.1, GLN2 and GLT1 among others (see ARNN-union list of genes). WRKY28 is positively correlated with NIR1, NRT3.1 and GLN2 among others (from ARNN-union list of genes). Thus, HHO5 and WRKY28 are positive regulators of genes involved in nitrogen uptake (e.g., NRT3.1), and nitrogen assimilation (e.g., NIR, GLN2). Accordingly, HHO5 and/or WRKY28 can be ectopically expressed or overexpressed in the transgenic plants in order to increase nitrogen use efficiency (NUE) of the transgenic plant. Improving NUE is desirable to improve crop yields, reduce cost of production, and maintaining environmental quality.

[00491] It was also investigated whether the rank of TFs based on connectivity changed from the AONN network, to the final network ARNN-Union, again using a Wilcoxon test. *A p*-value of 1.391e-10 denotes that the connectivity rank of TFs (e.g. numbers of connections) in Table 34 has changed significantly through the network generation process used in Figure 51.

Supernode analysis of Rice-Arabidopsis N-regulatory Network (RANN-Union).

[00492] The supernode analysis groups genes with the same biological processes, functional terms and annotations into a single node whose size is proportional to the number of genes in the supernode. To gain an understanding of how the conserved genes

were connected to each other when categorized with plant metabolic network pathways information, a supernode network analysis was performed using transcription factor families (PlantTFDB, (Jin et al., 2014)) and OryzaCyc pathways associations (OryzaCyc v1.0 (Dharmawardhana et al., 2013) for the 182 genes in the RANN-Union network (Figure 43). The resulting supernode network of the RANN-Union network identified several well-represented transcription factor families highly connected to major metabolic pathways (Figure 44). The supernode network analysis also revealed that the transcription factor families with the highest number of members in this network are bZIP and WRKY.

[00493] The RANN-Union top transcription factor hubs include four members of the bZIP TF family in rice (LOC_Os05g37170, LOC_Os01g64020, LOC_Os06g41100 and LOC_Os01g64000). Homologs of these family members have been validated to be involved in N-responses in Arabidopsis (Gutiérrez et al., 2008; Hanson et al., 2008; Jonassen et al., 2009; Obertello et al., 2010; Para et al., 2014) (Figure 44 and Table 34). Three members of the bZIP TF family belong to the subfamily TGA, which has been recently indicated to be involved in nitrogen regulation (see below, Alvarez et al., 2010). The supernode network analysis also shows that the TF families: bZIP, bHLH, WRKY and G2-like (HHO) are involved in the N-regulation of genes related to "Nitrogen compound metabolism", which contains genes involved in the N assimilation pathway.

[00494] OsWRKY23, the second in the rank of most connected TFs in the RANN-Union network (Table 34), is homologous to Arabidopsis WRKY75 (At5g13080) based on BLASTP only, which has been shown to be related to phosphate acquisition (Devaiah et al., 2007). Also, OS-WRKY23 is orthologous to Arabidopsis WRKY28 (At4g18170) based on BLASTP and OrthoMCL, which has been shown to be involved in activation of salicylic acid (SA) biosynthesis (van Verk et al., 2011).

Two predicted transcription factor families conserved in the Rice/Arabidopsis N-regulatory Network (RANN-Union) are biologically validated.

[00495] Among the list of 23 TFs present in the RANN-Union network, two TF families were found whose role in N-signaling has been experimentally validated. The HHO/HRS1 family was first investigated. This TF family has two N-regulated members

in rice and four homologs in Arabidopsis (Figure 49). To gain insights into the HHO/HRS family and their conserved N-regulation, a phylogenetic analysis was performed and it was found that the common N-responsive members of the HHO family from rice and Arabidopsis fall in the same clade (Figure 49). The phylogenetic tree was built by ClustalW alignment and maximum likelihood method. This group of HHO family members present in the same clade is also orthologous to each other using either OrthoMCL or BLASTP (Figure 49). This result is an *in-silico* validation of the cross-species network approach. Also, it has been recently validated that two members of this TF family, HRS1 and HHO1, have an important role in integrating nitrate signaling in the Arabidopsis root (Medici et al., 2015).

[00496] Based on supernode analysis, the bZIP family has 20 connections to biological processes making it the third most highly connected TF family in the RANN-Union network. The three N-regulated rice TGA family members (LOC_Os01g64020, LOC_Os05g37170 and LOC_Os06g41100) are putative homologs to the four N-regulated Arabidopsis TGA family members: At1g22070 (TGA3), At1g77920 (TGA7), At5g10030 (TGA4) and At5g65210 (TGA1) (Figure 50). Based on the supernode network analysis, discussed above, these TFs have connections with "Biosynthesis" and "Degradation/ Utilization and Assimilation" metabolic pathway processes (Figure 44). A phylogenetic tree analysis was performed using all TGA family members in Arabidopsis and rice identified by BLASTP. The phylogenetic tree (Figure 50) shows that the rice and Arabidopsis N-regulated members of the TGA family are paralogs, as confirmed by OrthoMCL. As shown in Figure 50, all N-regulated TGA family members in each species were identified by homology based on BLASTP. However, it is important to point out that two of the members of the TGA transcription factor family identified in the RANN-BLAST network (TGA1 and TGA4) were recently validated as important regulatory components of the nitrate response in Arabidopsis (Alvarez et al., 2014). A significant overlap (*p*-value 0.008) was also observed between the validated targets identified *in-planta* in *tga1/4* double mutants, available data from Alvarez el al. 2014, and the predicted targets from the RANN-Union network analysis (analysis done using Genesect tool on VirtualPlant) (www.virtualplant.org). These TGA1/TGA4 targets identified in the analysis of this Example and validated *in planta* include two proteins that

have been shown to be involved in N-signaling. These TGA1 targets include HRS1, a TF involved in N-signaling as mentioned earlier (Medici et al., 2015) and CIPK3, one of the several kinases identified to have a role in nitrogen signaling (Hu et al., 2009). The last gene present in this intersect set of validated HRS1 targets in the RANN network is a proteasome subunit, a potential gene hypothesis to be involved in nitrogen regulation (RPT5B), a potential new hypothesis for N-signaling via the proteasome that the analysis has uncovered. Thus, the conservation of function across rice and Arabidopsis implicated the role of TGA family in the N-response. It is noteworthy that this prediction, which is also supported by recent experimental data (Alvarez et al., 2014), would have been missed if only on orthology based on OrthoMCL was relied on. Importantly, the cross species network analysis has also opened new hypotheses for testing about N-regulatory mechanisms in plants.

14.4. DISCUSSION

[00497] This study provides a novel analysis of N-regulated gene networks conserved across two highly divergent species: *O. sativa* (a monocot) and Arabidopsis (a dicot). Despite their large phylogenetic distance, the analysis revealed a set of N-regulated genes, TFs and network modules conserved in rice and Arabidopsis, exposed to the same N-treatment conditions. The analysis shows a statistically significant overlap, indicating that rice and Arabidopsis respond very similarly to the N-treatments. The list of genes regulated by nitrogen treatments in rice includes many of the known nitrate/ammonium regulated genes previously identified in Arabidopsis, including, genes known to respond to nitrate (NR, NiR, Fd, FNR, G6PDH). These results are not surprising in hindsight, given that the former are important to reduce the plant's risk of nitrite toxicity. Selected genes from the N-responsive lists were corroborated by RT-*q*PCR analysis. One of the important aspects of this genomic analysis is that the N-treatment performed on rice and Arabidopsis were comparable, so that the gene responses could be directly compared. Genome profiling revealed that 1.32% of the rice genome is regulated in response to N-treatment, while 6.76% of the Arabidopsis genome responds to N-treatment, and in both cases, roots were more sensitive to N than shoots. The result of the permutation test, which was performed to determine whether the overlap between the rice and Arabidopsis

N-responsive genes was significant, suggests that despite the difference in number of N-responsive genes, rice and Arabidopsis respond very similarly to nitrogen treatment.

[00498] The rice genome size is more than three times that of Arabidopsis, and is estimated to have significantly more genes (Yu et al., 2005). According to that estimate, more N-regulated genes in rice would have been expected; however, the difference in total number of N-regulated genes between species might be mainly due to the fact that the N treatment used in this study affects these two plants differently. In support of that notion, it has long been known that rice can form natural associations with endophytic diazotrophs, which are responsible for supplying the plants with fixed N, increasing plant height, root length and dry-matter production. In rice and maize, associative nitrogen fixation can supply 20–25% of total N requirements (Santi et al., 2013). The experiments performed here were done on a sterile environment, so the difference in number of N-regulated genes might be due to the fact that N-response pathway in rice needs the bacterial association to be completely active.

[00499] The N-signaling network has gained new levels of complexity during very recent years and is as yet far from being completely understood (Vidal et al., 2010; Castaings et al., 2011; Bargmann et al., 2013; Medici et al., 2015). In addition, it is an open question how well gene networks derived from model dicots, such as Arabidopsis, might faithfully reconstruct pathways in a monocot, such as rice.

[00500] The hypothesis was that the conserved network nodes (genes) and edges (interactions) among species would provide an initial framework to understand the complex functional genomic and genetic knowledge of N-regulatory networks. To address this, a gene expression network based on co-expression and homologs based on BLASTP and orthologs based on OrthoMCL were generated to reveal conserved co-expression relationships between rice and Arabidopsis. The results herein suggest that using BLASTP homology produced a more complete core N-regulatory network between rice and Arabidopsis compared to OrthoMCL alone. When OrthoMCL was used to distinguish between orthologs and paralogs, promising candidates were lost from the network. For example, if on OrthoMCL was used to obtain orthology information, the TGA family members and their interaction to regulate N-responsive biological processes would have been missed. From the phylogenetic analysis, it is clear that the TGA family

members evolved in their function so much that different members of the family have taken on the responsibility to be N-responsive in each species. Since it is well accepted that different members of the TF family bind to the same binding site, this hypothesis is quite reasonable. As described in the results section, the predicted TGA1 and TGA4 target genes from the RANN-Union network overlap significantly with published and biologically validated *in planta* data in Arabidopsis (Alvarez et al., 2014).

[00501] In this cross-species network approach, known rice annotation and experimental data was used to generate a "rice-only" expression network (RONN, Step 1, Figure 43), to which known Arabidopsis annotation data was added (Step 2, Figure 43), and subsequently filtered it with the Arabidopsis N-treatment experimental data generated in this study (Step 3, Figure 43). This analysis identified a core N-regulatory network conserved between rice and Arabidopsis (RANN-Union). This cross-species network analysis enabled the identification of conserved N-regulated genes, network modules, TFs and biological process related to this essential nutrient. The list of potential N-responsive genes in rice is considerably reduced when the experimental data from Arabidopsis is integrated (Step 3, Figure 43). In addition, the supernode network analysis allowed the visualization of how N-responsive biological processes such as, "nitrogen compound metabolism" and "sugar biosynthesis", are related to each other and which transcription factor families are regulating them. The presence of metabolic pathways related to sugar metabolism and amino acid biosynthesis is important in this context since the production of reduced carbon is necessary to produce both the energy and carbon skeletons required for the incorporation of inorganic N into amino acids.

[00502] By starting with the experimental data from the model plant Arabidopsis, and subsequently filtering it with the rice experimental data generated in this study, a subset of conserved TFs potentially involved in nitrogen regulation was uncovered. However, compared to the N-regulated network information already known in Arabidopsis, it was concluded that while it did not significantly improve the knowledge of Arabidopsis interactions by integrating rice data, a smaller evolutionarily conserved network was indeed identified. On the other hand, when started with rice experimental data and then added predicted 'network knowledge' inferred from Arabidopsis, subsequently introducing Arabidopsis experimental data, the network connections were significantly

improved and TF-target connections were identified that have been experimentally validated in Arabidopsis. To summarize, using Arabidopsis "network knowledge" including gene interactions and experimental data highly refined the rice networks, enabled the identification of potential master TFs involved in the N-response, some of which have been biologically validated in Arabidopsis by independent experiments (e.g. members of the TGA and HHO transcription family members).

[00503] In plants, transcriptional regulation is mediated by a large number of transcription factors (TFs) controlling the expression of tens or hundreds of target genes in various signal transduction cascades. Interestingly, a recent transcriptome data analysis supports the predictions for the TFs controlling this core N-regulatory network uncovered in the analysis. Specifically, Canales et al. integrated publicly available root microarray data under contrasting nitrate conditions, and concluded that the most represented transcription factors families are AP2/ERF, MYB, bZIP and bHLH (Canales et al., 2014). In this Example, the TFs regulated by N-treatment were ordered by their network connectivity, under the premise that highly connected genes are more likely to be involved in biological processes. These transcription factor families are also present in the supernode analysis based on the Rice-Arabidopsis N-regulatory Network (RANN-Union). Additionally, the supernode analysis also revealed the G2-like (HHO) family in rice -based on orthology to Arabidopsis- as one of the most highly-connected TF families. In addition, there is recent experimental validation of several members of the HHO family being involved in the N-response in Arabidopsis (Medici et al., 2015). Another highly connected TF family obtained from the supernode analysis was the TGA family, three members of which were N-regulated and conserved in the RANN-BLAST network, but not in the RANN-OrthMCL network. With these results, the conclusion is that it is important to consider homologs based on BLASTP for retrieval of conserved network modules. The RANN-Union network was further validated by determining that the predicted targets of TGA1/4 significantly overlap (p-val 0.008) with validated targets identified *in planta* in *tga1/4* double mutants (Alvarez et al., 2014). Thus, this novel finding of transcription factors implicated in N-regulation of genes and network modules, conserved in both rice and Arabidopsis according to the predicted network, are strongly supported by the experimental study of *tga1* and *tga4* mutants (Alvarez et al., 2014).

[00504] Finally, this study addresses a major challenge of translational research, which is to transfer "network knowledge" from data-rich model species, such as Arabidopsis, to data poor crop species, such as rice. The results presented here describe the transfer of "network knowledge" from Arabidopsis to crops (e.g. Steps 2 and 3 of Figure 43), and how it can help develop effective and sustainable biotechnological solutions to enhance N acquisition by plants in natural or agricultural environments. Proper plant N nutrition in the environment will not only improve production but will also contribute to sustainable agricultural practices by diminishing the use of N fertilizers and thus reducing greenhouse gases, stratospheric ozone, acid rain, and nitrate pollution of surface and ground water.

Table 27. Number of nitrogen regulated genes in *O. sativa* and *A. thaliana*. Percentage of regulated genes for each type of regulation is in parentheses.

	Roots		**Shoots**	
	Induced	**Repressed**	**Induced**	**Repressed**
Rice 451 genes	234 (51.8%)	106 (23.5%)	103 (22.8%)	39 (8.6%)
Arabidopsis 1417 genes	757 (53.4%)	424 (29.9%)	166 (11.7%)	184 (12.9%)

Table 28. Selected rice genes regulated by nitrogen in shoots and roots (for more details see Materials and Methods). The fold change of nitrogen response genes were calculated as the ratio between N / KCl expression value. *p*-value cut-off ≤ 0.05 and fold-change ≥ 1.5-fold (shown on table is the $\log_2$ of values, fold-change cut-off $\log_2 1.5 = 0.585$). NC, no change.

Gene_ID	Gene description	Log2 Ratio	
		Root	Shoot
Nitrate uptake			
LOC_Os02g02170	high affinity nitrate transporter, putative, expressed	-0.93	NC
LOC_Os02g38230	component of high affinity nitrate transporter, putative, expressed	1.66	NC
Nitrate/nitrite assimilation			
LOC_Os02g53130	nitrate reductase, putative, expressed	2.15	3.32
LOC_Os01g25484	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed	2.37	2.67
Ferredixin Reduction			
LOC_Os01g64120	ferredoxin-6, chloroplast precursor, putative, expressed	3.28	4.22
LOC_Os05g37140	ferredoxin-6	1.33	0.89
LOC_Os03g57120	ferredoxin--NADP reductase, root isozyme, chloroplast precursor, putative, expressed	1.55	1.95
LOC_Os04g44650	ferredoxin-thioredoxin reductase	0.67	0.95
Pentose Phosphate Pathway			
LOC_Os08g08840	glucose-6-phosphate/phosphate translocator 2, chloroplast precursor, putative, expressed	0.84	NC
LOC_Os07g22350	glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor, putative, expressed	1.62	1.07
Ammonium assimilation			
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed	1.17	NC
LOC_Os04g56400	glutamine synthetase, chloroplast precursor, putative, expressed	1.09	0.71

Table 29. Selected Arabidopsis genes regulated by nitrogen in shoot and/or roots (for more details see Materials and Methods). The fold change of nitrogen response genes were calculated as the ratio between N / KCl expression value. *p*-value cut-off ≤ 0.05 and fold-change ≥ 1.5-fold (shown on table is the $\log_2$ of values, fold-change cut-off $\log_2 1.5 = 0.585$). NC, no change.

Gene_ID	Gene description	Log2 Ratio	
		Roots	Shoots
Nitrate uptake			
At1g69850	nitrate transporter 1:2; calcium ion binding / transporter (NRT1:2)	-0.62	-1.04
At5g50200	Nitrate transmembrane transporters (NRT3.1)	1.79	2.04
At1g08090	high affinity nitrate transporter 2.1 (NRT2:1)	2.76	2.35
Nitrate/Nitrite assimilation			
At1g37130	nitrate reductase 2 (NIA2)	NC	2.65
At1g77760	nitrate reductase 1 (NIA1)	3.69	5.85
At2g15620	nitrite reductase; ferredoxin-nitrate reductase (NIR1)	3.33	6.33
Ferredixin Reduction			
At2g27510	ferredoxin 3: electron carrier (ATFD3)	1.52	3.16
At4g05390	ROOT FNR 1; oxidoreductase (ATRFNR1)	2.49	3.99
At1g30510	ROOT FNR 2; oxidoreductase (ATRFNR)	2.75	4.43
Pentose Phosphate Pathway			
At1g24280	Glucose-6-phosphate dehydrogenase 3 (G6PD3)	3.34	4.78
At5g13110	Glucose-6-phosphate dehydrogenase 2 (G6PD2)	1.93	2.99
Ammonium assimilation			
At5g35630	glutamine synthetase 2 (GS-GLN2)	1.14	NC
At5g16570	Glutamine synthetase 1;4 (GLN1;4)	-1.20	NC
At5g53460	NADH-dependent glutamate synthase 1 gene (GLT1)	1.38	2.40
Glutamate biosynthesis/degradation			
At1g51720	glutamate dehydrogenase, putative	1.14	NC
At5g07440	glutamate dehydrogenase 2 (GDH2)	1.76	NC

Table 30. List of the transcription factors in the "Rice-Arabidopsis N-regulatory Network (RANN-Union)". For each step of the network construction (Figure 43), transcription factors were rank based on their number of connections in the network.

Rice Gene Locus	Rice Gene Description	Number of directed connections			
		Rice Predicted N-regulatory Network (RPNN-predicted interactions)	Rice-Arabidopsis N-regulatory Network (RANN-BLAST)	Rice-Arabidopsis N-regulatory Network (RANN-OrthoMCL)	Rice-Arabidopsis N-regulatory Network (RANN-Union)
LOC_Os03g55590	DNA binding protein, putative, expressed	180	45	17	46
LOC_Os01g53260	OsWRKY23 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	162	41		41
LOC_Os01g64000	ABA response element binding factor, putative, expressed	138	35		35
LOC_Os01g06640	DNA binding protein, putative, expressed	191	31		31
LOC_Os07g02800	myb-like DNA-binding domain, SHAQKYF class family protein, expressed	150	30	14	30
LOC_Os01g43650	OsWRKY11 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	166	26	10	29
LOC_Os11g47570	chitin-inducible gibberellin-responsive protein 2, putative, expressed	163	27		27
LOC_Os09g35030	sbCBF6, putative, expressed	229	16		16
LOC_Os09g25070	OsWRKY62 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	170	14		14
LOC_Os01g34060	DNA binding protein, putative, expressed	99	12		12
LOC_Os04g42950	DNA binding protein, putative, expressed	96	12		12
LOC_Os09g32260	ANAC079/ANAC080, putative, expressed	129	12		12
LOC_Os11g08210	NAC domain-containing protein 71, putative, expressed	99	11		11
LOC_Os02g15340	NAC domain-containing protein 76, putative, expressed	67	10		10
LOC_Os04g55970	DNA binding protein, putative, expressed	143	10		10
LOC_Os12g10660	salt tolerance-like protein, putative, expressed	50	10		10
LOC_Os03g04310	DNA binding protein, putative, expressed	84	7		7
LOC_Os10g42130	ANAC071, putative, expressed	78	6		6
LOC_Os01g64020	transcription factor HBF-1b, putative, expressed	219	5		5
LOC_Os08g42550	AP2 domain containing protein, expressed	61	5		5
LOC_Os06g41100	TGA10 transcription factor, putative, expressed	119	2		2
LOC_Os05g37170	transcription factor TGA6, putative, expressed	90	1		1
LOC_Os02g06910	auxin response factor 6, putative, expressed	163			
LOC_Os03g21710	WRKY DNA binding domain containing protein, expressed	79			
LOC_Os03g47730	knotted1-interacting protein, putative, expressed	61			
LOC_Os03g55220	helix-loop-helix DNA-binding, putative, expressed	175			
LOC_Os04g56990	trans factor, putative, expressed	200			
LOC_Os05g20930	transcriptional regulator RABBIT EARS, putative, expressed	195			
LOC_Os05g38140	bHLH transcription factor, putative, expressed	79			
LOC_Os06g07030	dehydration responsive element binding protein, putative, expressed	101			
LOC_Os09g26420	ethylene response factor, putative, expressed	69			
LOC_Os09g36160	SHI, putative, expressed	30			

Table 31. Genes regulated by nitrogen in rice shoots are sorted based on their regulation according to the ANOVA analysis (pval<0.05).

>N_roots_REPRESSED **log2 ratio**

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.50750.1.S1_at	LOC_Os03g02190	receptor protein kinase CRINKLY4 precursor, putative, expressed	9.965584	9.795376	9.331556	9.258631	9.570871	9.586334	9.605317	9.652262	NA	-0.58539
Os.19130.1.S1_at	LOC_Os06g15370	peptide transporter PTR2, putative, expressed	7.908604	7.92103	7.445328	7.198794	9.63436	9.406701	9.398552	9.237551	NA	-0.59276
Os.5616.1.S1_at	LOC_Os03g18740	sex determination protein tasselseed-2, putative, expressed	9.516033	9.704963	9.048269	8.987165	10.98419	11.07738	10.73496	10.77173	NA	-0.59278
Os.35288.1.S1_at	LOC_Os08g30340	PAS2, putative, expressed	6.513644	6.397395	5.770556	5.94547	7.884752	8.061469	8.235758	8.537061	NA	-0.59751
Os.55806.1.S1_at	LOC_Os05g20930	transcriptional regulator RABBIT EARS, putative, expressed	7.408246	7.266649	6.737693	6.737393	5.176223	5.153294	5.754617	5.726452	NA	-0.5999
Os.47290.1.S1_at	LOC_Os04g34240	histone H3, putative, expressed	8.166384	7.977163	7.392799	7.540414	8.013262	7.834731	7.312993	7.241465	-0.64677	-0.60517
Os.22793.1.S1_at	LOC_Os11g07940	expressed protein	7.860002	8.071209	7.339905	7.377602	7.822913	7.892168	7.98359	7.965557	NA	-0.60685
OsAffx.17516.1.S1_at	LOC_Os08g44940	LOB domain protein 16, putative	6.120716	5.85819	5.240369	5.496659	4.870185	4.821281	4.624168	4.517676	NA	-0.62094
Os.17173.1.S1_at	LOC_Os05g08640	10-deacetylbaccatin III 10-O-acetyltransferase, putative, expressed	7.893697	7.656451	7.030065	7.276453	10.32525	10.2795	10.03268	9.91817	NA	-0.62182
Os.48334.1.S1_at	LOC_Os08g43320	membrane protein, putative, expressed	8.983041	8.733243	8.177541	8.294007	10.23623	9.982715	9.696381	9.824769	NA	-0.62237
Os.7949.1.S1_at	LOC_Os03g24020	50S ribosomal protein L6, putative, expressed	8.578804	8.948942	8.103912	8.177079	11.34102	11.24326	11.42505	11.29906	NA	-0.62338
Os.34146.1.S1_at	LOC_Os03g61080	expressed protein	6.569163	6.644393	5.835821	6.12605	7.08319	6.936057	6.965366	6.75254	NA	-0.62584
Os.41468.1.S1_at	LOC_Os01g47050	kelch motif family protein, expressed	8.498061	8.475314	7.816289	7.896368	6.480585	6.305412	6.072904	6.267697	NA	-0.63036
Os.18598.1.S1_at	LOC_Os03g49260	lipoxygenase 1, putative, expressed	8.20591	8.531031	7.869637	7.599683	5.87474	5.843838	5.658581	5.633431	NA	-0.63381
Os.51847.2.S1_at	LOC_Os03g55220	helix-loop-helix DNA-binding, putative, expressed	6.790473	6.621657	6.028537	6.115553	5.178228	5.333863	5.001796	5.335478	NA	-0.63402
Os.8511.1.S1_s_at	LOC_Os04g01140	cytochrome P450 93A2, putative, expressed	7.65361	7.371272	6.886276	6.862705	8.547637	8.493496	8.167595	8.225956	NA	-0.63795
Os.55105.1.S1_at	LOC_Os07g38370	expressed protein	8.808817	8.970208	8.316888	8.180706	7.810996	7.805971	7.747497	7.723218	NA	-0.64072
Os.7344.1.S1_at	LOC_Os02g52000	phi-1-like phosphate-induced protein, putative, expressed	8.322752	8.178211	7.731605	7.487609	4.453979	4.306641	4.536757	4.292365	NA	-0.64087

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.54041.1.S1_at	LOC_Os01g48000	S-locus-like receptor protein kinase, putative, expressed	6.507414	6.389526	5.871386	5.742253	6.400494	6.274769	6.272372	6.397795	NA	-0.64165
Os.54226.1.S1_s_at	LOC_Os02g54974	expressed protein	8.585095	8.445461	8.014614	7.728852	9.188448	9.148699	9.060226	8.85355	NA	-0.64355
Os.10428.1.S1_at	LOC_Os02g14170	peroxidase precursor, putative, expressed	8.671223	8.499488	7.954177	7.92718	8.885073	8.721144	8.910373	8.799108	NA	-0.64468
Os.27254.1.S1_s_at	LOC_Os03g06680	plant-specific domain TIGR01615 family protein, expressed	8.220129	8.138342	7.626269	7.436301	10.04241	9.705168	9.654811	9.630291	NA	-0.64795
OsAffx.23913.3.S1_at	LOC_Os01g64400	hypothetical protein	8.990178	8.795748	8.121871	8.355189	7.60454	7.648176	7.491558	7.459838	NA	-0.65443
Os.54056.1.S1_at	LOC_Os09g29160	expressed protein	7.09284	6.83641	6.339071	6.275334	5.321555	5.595035	5.153336	5.299813	NA	-0.65742
Os.5053.1.S1_at	LOC_Os10g38580	glutathione S-transferase GSTU6, putative, expressed	9.294338	9.092164	8.522158	8.542455	10.51011	10.2376	10.47864	10.29517	NA	-0.66094
Os.54825.1.S1_at	LOC_Os05g33080	serine/threonine-protein kinase NAK, putative, expressed	5.592461	5.298562	4.637142	4.9282	7.205084	7.263582	6.742076	6.812178	NA	-0.66284
Os.9929.1.S1_at	LOC_Os03g60509	expressed protein	9.300244	9.280361	8.505455	8.726394	10.70099	10.65729	10.68672	10.60778	NA	-0.67438
Os.24613.1.S1_at	LOC_Os12g07160	viral A-type inclusion protein repeat containing protein, expressed	8.882049	8.702539	8.203587	8.02128	9.084547	9.035501	8.99869	8.916707	NA	-0.67986
Os.56054.1.S1_at	LOC_Os03g05700	expressed protein	8.017565	7.907102	7.130418	7.432451	6.629347	6.56911	6.980316	7.000441	NA	-0.6809
Os.48260.1.S2_at	LOC_Os02g52490	expressed protein	6.013101	6.150449	5.242369	5.547113	4.803738	4.913523	5.065802	4.997965	NA	-0.68703
Os.7989.1.S1_at	LOC_Os02g20360	tyrosine aminotransferase, putative, expressed	13.32886	13.12748	12.46726	12.61011	9.457838	9.511083	9.957244	10.01321	NA	-0.68948
OsAffx.6829.1.S1_at	LOC_Os10g31510	glycine-rich cell wall structural protein 2 precursor, putative, expressed	5.698532	5.438184	4.744487	5.010631	4.690544	4.767703	4.636063	4.563421	NA	-0.6908
Os.5213.1.S1_at	LOC_Os02g44720	expressed protein	7.838434	7.625708	6.95706	7.122874	7.175281	7.097525	6.336651	6.45741	-0.73937	-0.6921
Os.15987.1.S1_at	LOC_Os02g52450	regulator of ribonuclease activity A, putative, expressed	9.112071	9.432881	8.450319	8.699288	10.43565	10.26682	10.52508	10.54931	NA	-0.69767
Os.32739.1.S1_at	LOC_Os01g33040	kinesin heavy chain, putative, expressed	7.902636	7.701861	7.060993	7.127077	7.215877	7.147541	6.947394	6.844677	NA	-0.70821
Os.56014.1.S1_at	LOC_Os01g40190	expressed protein	10.41874	10.37254	9.616498	9.750039	8.738019	8.727179	8.754286	8.82182	NA	-0.71237
OsAffx.7566.1.S1_at	LOC_Os12g12470	NADP-dependent oxidoreductase P1, putative, expressed	7.733649	7.606648	7.078893	6.816097	9.070722	8.671223	8.393565	8.439374	NA	-0.72265
Os.52778.1.S1_at	LOC_Os02g50810	expressed protein	8.213415	8.092535	7.505799	7.352355	9.929472	9.781827	9.782411	9.910474	NA	-0.7239
Os.49605.1.A1_at	LOC_Os03g59200	expressed protein	8.576879	8.374649	7.847058	7.652143	8.656526	8.546636	8.261085	8.127156	NA	-0.72616

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.9277.1.S1_at	LOC_Os11g07680	dirigent-like protein pDIR7, putative, expressed	8.453943	8.283407	7.772095	7.510054	9.213558	9.115652	9.082736	9.279126	NA	-0.7276
Os.10099.1.S1_at	LOC_Os03g13870	expressed protein	9.73069	9.827804	9.028648	9.061669	7.352866	7.409975	7.885148	7.693732	NA	-0.73409
Os.2759.1.S1_s_at	LOC_Os10g42299	mitochondrial carnitine/acylcarnitine carrier-like protein, putative, expressed	9.654535	9.908975	8.899688	9.163619	11.90628	11.92378	11.85962	11.92613	NA	-0.7501
Os.8643.1.S1_at	LOC_Os03g14610	receptor expression-enhancing protein 3, putative, expressed	8.859947	8.820096	8.050096	8.125086	9.142476	8.988328	9.103462	8.844464	NA	-0.75243
OsAffx.19698.1.S1_at	LOC_Os12g15920	copper ion binding protein, putative, expressed	7.320277	6.914118	6.274282	6.436969	4.90381	5.019446	4.972781	4.896181	NA	-0.76157
Os.28213.1.S1_at	LOC_Os12g41600	OsSAUR57 - Auxin-responsive SAUR gene family member, expressed	6.733944	6.355747	5.906439	5.652449	8.274922	8.324238	8.300215	8.393235	NA	-0.7654
Os.20163.1.S1_at	LOC_Os03g02860	metal ion binding protein, putative, expressed	9.772929	9.549417	8.807285	8.97709	6.928124	6.998624	6.614873	6.504999	NA	-0.76899
OsAffx.27322.1.S1_s_at	LOC_Os05g45480	arabinogalactan protein, putative, expressed	9.401128	9.340763	8.497265	8.697959	7.055687	7.068839	6.793053	7.267469	NA	-0.77333
Os.5883.1.S1_at	LOC_Os04g01500	expressed protein	10.05482	9.890048	9.232456	9.153217	8.90786	8.751232	8.55464	8.230244	NA	-0.7796
OsAffx.28932.1.S1_at	LOC_Os07g46520	rhythmically expressed gene 2 protein, putative, expressed	10.03666	9.719693	9.2741	8.900616	10.87129	10.83867	11.02235	10.95572	NA	-0.79082
Os.8045.1.S1_at	LOC_Os01g08440	indole-3-acetate beta-glucosyltransferase, putative, expressed	12.1765	12.39075	11.4464	11.52987	13.27788	13.36058	13.50901	13.23605	NA	-0.79549
Os.51755.1.S1_at	LOC_Os04g51450	brassinosteroid-regulated protein BRU1 precursor, putative, expressed	7.44476	7.244701	6.406967	6.676541	5.776087	5.58125	5.409615	5.538161	NA	-0.80298
Os.28030.1.S1_s_at	LOC_Os06g48160	xyloglucan endotransglucosylase/hydrolase protein 23 precursor, putative, expressed	8.848355	8.461022	8.010563	7.681743	10.88039	10.32275	10.31223	9.901146	NA	-0.80854
Os.2019.1.S1_at	LOC_Os01g50460	seven-transmembrane-domain protein 1, putative, expressed	6.534268	6.556822	5.698815	5.774925	10.29581	10.57027	10.03961	10.23506	NA	-0.80868
Os.49283.1.S1_at	LOC_Os02g15540	expressed protein	10.18483	10.01294	9.179281	9.391051	11.10282	10.80297	11.0157	11.22181	NA	-0.81372
Os.37905.1.S1_at	LOC_Os01g45720	expressed protein	9.993204	10.41945	9.390783	9.392037	6.820889	7.083258	7.053945	7.002252	NA	-0.81492
Os.47955.1.S1_at	LOC_Os12g02640	cytochrome P450 72A1, putative, expressed	6.465806	6.178973	5.529917	5.474985	8.212003	8.140866	8.398723	8.286477	NA	-0.81994
Os.55786.1.S1_at	LOC_Os06g09270	hypro1, putative, expressed	7.640608	7.040926	6.765751	6.262621	4.946993	4.900996	4.556473	4.479625	NA	-0.82658
Os.11556.1.S1_at	LOC_Os07g48030	peroxidase 2 precursor, putative, expressed	11.37697	10.61511	10.2745	10.05737	6.22656	5.749426	5.240289	5.16273	NA	-0.83011

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.5757.1.S1_at	LOC_Os12g38360	expressed protein	8.402632	8.224115	7.374571	7.588543	9.327863	9.210702	9.266917	9.374386	NA	-0.83182
Os.6354.1.S1_at	LOC_Os12g02370	chalcone--flavonone isomerase, putative, expressed	8.067703	7.795224	6.892972	7.293843	10.52655	10.68053	10.52824	10.7669	NA	-0.83806
Os.7097.2.S1_a_at	LOC_Os02g48900	aspartic proteinase nepenthesin-1 precursor, putative, expressed	11.59096	11.45371	10.7399	10.60884	11.89302	12.0675	11.8617	11.82879	NA	-0.84796
Os.20341.1.S1_s_at	LOC_Os03g52040	serine carboxypeptidase 1 precursor, putative, expressed	6.95528	6.929197	6.081872	6.09449	7.76725	7.589076	7.578125	7.69444	NA	-0.85406
Os.47600.2.S1_x_at	LOC_Os02g54730	amino acid permease, putative, expressed	10.66457	10.67453	9.709303	9.912327	10.3357	10.30924	10.40774	10.41707	NA	-0.85874
Os.7801.1.S1_at	LOC_Os12g05050	stem-specific protein TSJT1, putative, expressed	11.27975	11.13176	10.67444	10.00859	12.12544	12.105	11.90988	11.64287	NA	-0.86424
Os.55284.1.S1_at	LOC_Os05g07140	RING-H2 finger protein ATL3F, putative, expressed	8.911903	8.853773	7.996794	8.030486	9.014298	9.393736	9.312679	9.317765	NA	-0.8692
Os.51835.1.S1_a_at	LOC_Os05g48700	gibberellin 2-beta-dioxygenase, putative, expressed	6.606134	6.812908	5.656439	6.016074	5.596763	5.744706	5.666067	5.797422	NA	-0.87326
Os.55890.1.S1_at	LOC_Os03g36650	serine/threonine kinase-like protein, putative, expressed	8.601631	8.501654	7.669542	7.669542	5.246461	5.30645	5.224318	5.301676	NA	-0.8821
Os.5850.1.S1_at	LOC_Os09g26420	ethylene response factor, putative, expressed	12.25521	12.72016	11.42641	11.77759	13.21057	13.28235	13.0255	12.94041	NA	-0.88568
Os.36919.2.S1_s_at	LOC_Os01g62010	monoglyceride lipase, putative, expressed	6.020432	6.213286	5.110355	5.347823	6.653831	6.458943	6.650778	6.55893	NA	-0.88777
Os.54472.1.S1_at	LOC_Os07g32060	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	5.758953	5.887979	4.891188	4.972762	4.662224	4.816829	4.825972	5.084846	NA	-0.89149
Os.50189.1.S1_at	LOC_Os06g46910	nucleic acid binding protein, putative, expressed	7.242171	7.244701	6.182887	6.512158	6.448885	6.21632	5.938235	5.967997	NA	-0.89591
Os.36708.1.S1_at	LOC_Os07g04960	verprolin, putative, expressed	8.613919	8.779158	7.865501	7.707689	9.473912	9.790609	9.204309	9.303589	NA	-0.90994
Os.5560.1.S1_at	LOC_Os01g62870	aldose reductase, putative, expressed	12.03038	12.15775	11.39602	10.96581	11.09158	11.23214	10.85373	10.74528	NA	-0.91315
Os.49093.1.S1_at	LOC_Os02g02170	high affinity nitrate transporter, putative, expressed	5.075712	4.743508	3.964223	3.998482	3.802061	3.842825	3.800181	3.845435	NA	-0.92826
Os.5860.1.S1_at	LOC_Os03g04310	DNA binding protein, putative, expressed	8.804856	8.697999	7.564418	8.079595	6.945932	6.366966	6.414662	6.139675	NA	-0.92942
Os.30135.1.S1_at	LOC_Os03g36960	expressed protein	6.980595	6.589822	5.866071	5.830443	8.16846	8.135554	7.869293	7.734354	NA	-0.93695
Os.10743.1.S1_at	LOC_Os06g33200	expressed protein	7.184584	7.235002	6.118295	6.374177	10.33437	10.63999	11.07895	10.69147	NA	-0.96356
Os.48986.1.S1_s_at	LOC_Os05g04000	expressed protein	8.412312	8.775002	7.782393	7.474533	9.612466	9.512223	9.215112	9.53399	NA	-0.96519

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.47997.1.A1_at	LOC_Os01g43950	expressed protein	7.800735	7.410294	6.735433	6.54058	6.3504	6.181228	5.97712	5.872074	NA	-0.96751
OsAffx.26434.1.S1_at	LOC_Os04g42740	serine/threonine-protein kinase receptor precursor, putative	6.645061	7.283472	5.898635	6.090539	4.717274	4.748085	4.685392	4.761494	NA	-0.96968
Os.53617.1.S1_at	LOC_Os11g47610	xylanase inhibitor protein 1 precursor, putative, expressed	6.298036	6.399239	5.229575	5.491024	5.171409	5.100418	5.051083	5.16161	NA	-0.98834
Os.37598.1.S1_at	LOC_Os01g20980	pectinesterase-1 precursor, putative, expressed	10.41299	10.00629	9.333378	9.081212	6.042835	6.277775	5.917623	6.075347	NA	-1.00234
Os.17921.1.S1_at	LOC_Os05g47540	phosphoethanolamine N-methyltransferase, putative, expressed	9.100175	8.990594	8.071462	7.990688	10.09716	9.717378	9.179686	9.539836	NA	-1.01431
Os.44937.1.S1_at	LOC_Os03g60810	lectin-like receptor kinase 7, putative, expressed	6.35143	6.045863	5.231439	5.131276	7.021742	6.967717	7.351689	6.983626	NA	-1.01729
Os.51831.1.S1_at	LOC_Os02g15340	NAC domain-containing protein 76, putative, expressed	7.825316	7.765906	6.448581	7.103593	5.01142	4.725031	4.673093	4.634158	NA	-1.01952
Os.55339.1.S1_at	LOC_Os01g57004	adhesive/proline-rich protein, putative, expressed	8.382776	8.527738	7.337257	7.504764	9.135371	9.257616	9.189633	8.988959	NA	-1.03425
Os.49571.1.S1_at	LOC_Os03g15530	expressed protein	8.10305	8.021491	6.729531	7.263937	9.657586	9.811626	9.721293	9.656331	NA	-1.06554
OsAffx.12089.1.S1_at	LOC_Os02g17620	expressed protein	9.623342	9.453343	8.27571	8.665897	6.847691	6.95651	7.138149	7.179736	NA	-1.06754
Os.11707.1.A1_at	LOC_Os03g54130	cysteine protease 1 precursor, putative, expressed	8.317457	8.863267	7.030259	8.007465	11.74402	12.37505	11.17142	11.01411	NA	-1.0715
Os.15799.1.S1_at	LOC_Os03g11420	non-cyanogenic beta-glucosidase precursor, putative, expressed	10.75458	10.9894	9.614265	9.97146	9.359321	9.138476	9.073175	8.774125	NA	-1.07913
Os.36346.2.S1_at	LOC_Os01g67030	dopamine beta-monooxygenase, putative, expressed	6.907297	6.881326	5.79068	5.808547	5.761886	5.658658	5.697862	5.897743	NA	-1.0947
Os.54354.1.S1_at	LOC_Os03g27480	retinoid-inducible serine carboxypeptidase precursor, putative, expressed	8.95784	9.131888	7.551164	8.272523	7.028174	7.031808	6.745376	7.034724	NA	-1.13302
Os.49844.1.S1_at	LOC_Os06g37750	S-locus-like receptor protein kinase, putative, expressed	8.767887	8.957937	8.00849	7.379684	4.585365	4.829207	4.813031	4.758107	NA	-1.16883
Os.11846.1.S1_at	LOC_Os05g34980	amino acid carrier, putative, expressed	9.627826	9.696232	8.494802	8.433927	7.856608	7.263958	6.744778	7.505102	NA	-1.19766
Os.20355.1.S1_at	LOC_Os01g72100	polcalcin Jun o 2, putative, expressed	10.91036	11.37576	9.918107	9.926458	11.26713	11.30935	11.18574	11.02145	NA	-1.22078
Os.53717.1.S1_at	LOC_Os06g01250	cytochrome P450 93A1, putative, expressed	8.742551	8.43633	7.095782	7.623743	10.65214	10.68993	10.53615	10.50717	NA	-1.22968
Os.54950.1.S1_at	LOC_Os03g11950	CRAL/TRIO domain containing protein, expressed	8.976741	8.336388	7.286359	7.493381	7.04617	6.821568	6.697761	6.455375	NA	-1.26669
OsAffx.18861.1.S1_at	LOC_Os11g15250	expressed protein	10.60967	10.82934	9.524648	9.066508	4.908551	4.66887	5.206599	4.850899	NA	-1.42393

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.41771.1.S1_at	LOC_Os01g47900	S-locus-like receptor protein kinase, putative, expressed	7.254515	7.765105	5.874328	6.155942	8.379223	8.5271	8.281884	8.565806	NA	-1.49468
Os.7086.1.S1_at	LOC_Os07g35520	glucan endo-1,3-beta-glucosidase 3 precursor, putative, expressed	17.89241	17.78851	16.08621	16.41426	14.23194	14.18827	13.53118	13.64949	NA	-1.59023
Os.28079.1.S1_x_at	LOC_Os07g04180	amino acid permease 6, putative, expressed	19.0802	18.44592	16.71823	17.28773	20.86422	20.73065	20.5494	20.65806	NA	-1.76008
Os.37330.1.S1_at	LOC_Os01g58860	auxin efflux carrier component 5, putative, expressed	8.549271	8.935017	6.816097	6.618034	5.705178	5.191952	5.216028	5.354545	NA	-2.02508
Os.7930.1.S1_x_at	LOC_Os08g37370	mitochondrial 2-oxoglutarate/malate carrier protein, putative, expressed	23.33384	22.94443	21.25389	20.90244	25.0734	25.21759	24.79129	24.90046	NA	-2.06097
Os.14078.1.S1_s_at	LOC_Os10g07210	hsp20/alpha crystallin family protein, expressed	20.10071	19.83493	17.69361	18.11912	19.39525	19.40743	18.97501	18.77882	NA	-2.06145
Os.5753.1.S1_at	LOC_Os04g56060	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	18.30953	18.25678	16.13964	16.14528	19.36096	18.48781	18.5776	18.13158	NA	-2.14069
Os.5037.1.S1_s_at	LOC_Os12g16010	sex determination protein tasselseed-2, putative, expressed	27.2843	26.86889	24.32704	23.19203	18.16986	18.39735	17.93043	18.07015	NA	-3.31706

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Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.14071.1.S1_at	LOC_Os09g29940	auxin-independent growth promoter, putative, expressed	7.848139	7.614543	8.250468	8.38618	7.326639	7.202493	7.74557	7.926036	NA	0.586982
Os.18663.1.S1_at	LOC_Os09g37230	ATP binding protein, putative, expressed	9.762426	10.10549	10.50753	10.53662	9.233896	9.166184	9.543072	9.420941	NA	0.588119
Os.27288.2.S1_x_at	LOC_Os01g73680	aspartyl aminopeptidase, putative, expressed	6.347104	6.378106	7.043439	6.858602	7.172045	7.305243	7.261732	7.441496	NA	0.588415
OsAffx.12721.1.S1_at	LOC_Os03g03510	CIPK-like protein 1, putative, expressed	9.32261	9.263732	9.705446	10.05797	10.11991	10.07214	10.43545	10.54442	NA	0.588536
Os.15360.1.S1_at	LOC_Os04g41320	nucleotide-sugar transporter/ sugar porter, putative, expressed	7.255016	7.177775	7.668175	7.941732	7.696599	7.797284	8.114062	8.059705	NA	0.588558
Os.26565.3.S1_at	LOC_Os01g10320	class III HD-Zip protein 8, putative, expressed	8.497529	8.156274	8.964783	8.873305	5.388097	5.536542	5.638855	5.784947	NA	0.592142
Os.4385.1.S1_at	LOC_Os11g08210	NAC domain-containing protein 71, putative, expressed	10.99203	10.84267	11.38621	11.63317	10.24199	10.29286	10.33942	10.49479	NA	0.592337
Os.27419.1.S1_at	LOC_Os11g47870	chitin-inducible gibberellin-responsive protein 2, putative, expressed	7.347495	7.189077	7.899665	7.824831	7.205983	7.341759	7.511947	7.59229	NA	0.593962

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Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.1660.1.S1_at	LOC_Os01g02200	ubiquitin-protein ligase, putative, expressed	8.911863	8.948773	9.491423	9.557382	8.834977	8.774064	9.047781	8.90133	NA	0.594085
Os.26490.1.S1_at	LOC_Os10g35644	expressed protein	8.515346	8.675858	9.083478	9.298094	7.860962	7.851517	7.961653	8.268003	NA	0.595184
OsAffx.30915.1.S1_at	LOC_Os11g10430	conserved hypothetical protein	4.945152	4.651416	5.254091	5.534563	4.422216	4.432903	4.415547	4.379441	NA	0.596043
OsAffx.26598.1.S1_x_at	LOC_Os04g54190	serine/threonine-protein kinase receptor precursor, putative, expressed	9.416902	9.422834	10.07745	9.960234	6.634636	6.628383	6.20353	6.547657	NA	0.598976
Os.10272.1.S1_at	LOC_Os08g20570	chloride channel-like protein CLC-g, putative, expressed	9.264805	9.01532	9.821842	9.65624	8.26461	8.390187	9.431899	9.250314	1.013708	0.598978
Os.38309.1.S1_at	LOC_Os06g36390	expressed protein	6.563046	6.715202	7.338356	7.142051	7.294209	7.587704	7.779565	7.866446	NA	0.60108
Os.55617.1.S1_at	LOC_Os05g50230	expressed protein	7.393562	7.400917	8.161483	7.839547	8.934185	8.770675	9.2735	9.175921	NA	0.603275
Os.35073.1.S1_x_at	LOC_Os07g18944	expressed protein	6.852893	6.88125	7.59889	7.349798	6.70628	6.547055	6.36311	6.347183	NA	0.607272
Os.54039.1.S1_at	LOC_Os02g03590	expressed protein	6.800738	6.819299	7.448407	7.389601	6.774156	6.849548	6.905815	6.654329	NA	0.608986
Os.15338.1.S1_a_at	LOC_Os01g34060	DNA binding protein, putative, expressed	8.497992	8.581333	9.295276	9.002574	9.924535	9.774811	9.895652	9.77834	NA	0.609262
Os.53784.1.S1_at	LOC_Os02g02000	cytochrome P450 74A4, putative, expressed	5.385652	5.415354	5.924029	6.101184	9.051638	9.029981	9.672156	9.605387	0.597962	0.612104
Os.54911.1.S1_at	LOC_Os05g31740	cytochrome P450 86A2, putative, expressed	6.907076	6.795917	7.548196	7.385131	5.652355	5.852406	6.223227	6.417756	0.568111	0.615167
Os.38447.1.S1_s_at	LOC_Os06g07030	dehydration responsive element binding protein, putative, expressed	9.814353	9.744052	10.54414	10.2453	8.98771	9.188676	8.948835	8.883142	NA	0.615513
Os.22969.1.S1_at	LOC_Os12g39120	catalytic/ protein phosphatase type 2C, putative, expressed	7.400344	7.280504	8.06041	7.852369	6.404302	6.131238	6.525855	6.482749	NA	0.615965
Os.57529.1.S1_at	LOC_Os04g53994	ATP binding protein, putative, expressed	5.946431	6.051019	6.677648	6.566868	6.800765	6.863275	6.816935	7.140425	NA	0.623533
Os.56019.1.S1_at	LOC_Os06g04480	expressed protein	6.883218	6.845267	7.476417	7.50282	8.022972	8.047175	8.279554	8.282923	NA	0.625376
Os.15440.1.S1_at	LOC_Os01g37050	endoribonuclease Dcr-1, putative, expressed	5.716329	5.962904	6.51619	6.416337	7.568828	7.916899	8.12159	8.522589	NA	0.626647
Os.11186.1.S1_at	LOC_Os03g10620	sigma factor sigB regulation protein rsbQ, putative, expressed	11.82879	11.90231	12.55051	12.44072	11.71284	11.80384	11.94415	11.86091	NA	0.630067
OsAffx.25828.1.S1_at	LOC_Os04g01890	lectin-like protein kinase, putative	5.414642	5.497713	6.199822	5.985318	4.985699	4.843766	4.871438	4.836214	NA	0.636392
Os.52223.1.S1_at	LOC_Os11g12000	NBS-LRR disease resistance protein, putative, expressed	8.782295	8.757622	9.487564	9.325637	8.403307	8.66523	8.575475	8.772843	NA	0.636643

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.27325.1.S1_at	LOC_Os03g31706	expressed protein	7.898748	7.971013	8.51864	8.629069	8.001032	8.130918	8.258903	8.193625	NA	0.638974
Os.1605.1.S1_at	LOC_Os04g37619	zeaxanthin epoxidase, chloroplast precursor, putative, expressed	7.822294	7.915594	8.420131	8.600498	10.19198	10.3841	10.41857	10.37035	NA	0.64137
Os.17762.1.S1_at	LOC_Os06g29844	transparent testa 12 protein, putative, expressed	8.696943	8.519346	9.234561	9.266814	10.77265	10.97006	11.06655	11.04589	NA	0.642543
Os.18839.1.S1_at	LOC_Os02g51910	cytokinin-O-glucosyltransferase 2, putative, expressed	9.457966	9.675045	10.09676	10.32803	7.251817	7.104984	7.574325	7.921576	NA	0.645891
Os.10742.1.S1_at	LOC_Os03g06390	expressed protein	9.538634	9.811318	10.23558	10.41126	11.29215	11.32639	11.38146	11.57778	NA	0.648442
Os.21932.1.S1_at	LOC_Os10g42130	ANAC071, putative, expressed	6.721865	6.711106	7.55664	7.174876	5.52869	5.579091	5.43208	5.340941	NA	0.649272
Os.286.1.S1_a_at	LOC_Os01g17390	cyclin-like F-box, putative, expressed	8.716713	8.51129	9.263149	9.27036	9.273472	9.280852	9.340689	9.262858	NA	0.652753
Os.46566.1.S1_at	LOC_Os10g17940	F-box domain containing protein, expressed	6.322342	6.50834	7.002735	7.136952	4.851251	4.738491	4.865493	5.004094	NA	0.654502
Os.57048.1.S1_at	LOC_Os08g06930	transposon protein, putative, unclassified, expressed	6.069359	5.958824	6.766437	6.574168	4.844919	4.636315	5.258365	5.03598	NA	0.656211
Os.52240.1.S1_at	LOC_Os11g39190	resistance protein CAN_RGA1, putative, expressed	8.638789	8.707058	9.423788	9.234628	10.19482	10.56033	10.47907	10.58807	NA	0.656284
Os.51941.1.S1_s_at	LOC_Os03g27760	expressed protein	8.504672	8.66329	9.228817	9.254362	7.551848	7.497745	6.981771	7.186281	NA	0.657608
Os.21831.1.S1_at	LOC_Os02g02540	glutamate receptor 3.3 precursor, putative, expressed	8.741905	8.491782	9.410337	9.141823	7.702347	7.497559	7.468948	7.398763	NA	0.659236
Os.27517.1.A1_s_at	LOC_Os11g14140	protein kinase Kelch repeat:Kelch, putative, expressed	11.99393	12.15432	12.77282	12.6949	11.34489	11.57621	11.51477	11.5841	NA	0.659735
Os.20697.1.S1_at	LOC_Os09g34070	FPA, putative, expressed	8.656892	8.677789	9.383607	9.270651	8.617952	8.624635	8.910405	8.847033	NA	0.659788
Os.34523.1.S1_at	LOC_Os11g30500	HVA22-like protein e, putative, expressed	9.637141	9.667618	10.24638	10.3785	6.628787	6.84143	7.313596	7.092015	NA	0.66006
Os.21415.1.S1_at	LOC_Os12g06100	TLD family protein, expressed	9.76698	9.817296	10.41607	10.48883	8.69205	8.881418	9.814007	9.799504	1.020021	0.660315
Os.52358.1.S1_at	LOC_Os06g28590	ubiquitin-protein ligase, putative, expressed	8.48086	8.481546	9.058179	9.225624	8.123483	8.342787	8.446712	8.36762	NA	0.660699
Os.54203.1.S1_at	LOC_Os09g32260	ANAC079/ANAC080, putative, expressed	8.768739	8.487404	9.276406	9.302078	6.615025	6.401873	6.667349	6.808901	NA	0.66117
Os.18983.1.S1_at	LOC_Os03g52180	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, putative, expressed	4.824921	4.570949	5.329849	5.393528	4.528813	4.402161	4.197375	4.238763	NA	0.663753
Os.16895.1.A1_at	LOC_Os03g17300	protein kinase, putative, expressed	6.577017	6.375451	7.027126	7.254098	7.204813	7.236872	7.208919	7.297275	NA	0.664378

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.34171.1.S1_at	LOC_Os01g38180	peptidyl-prolyl isomerase, putative, expressed	4.589704	4.707799	5.449389	5.178481	4.393826	4.186826	4.421181	4.542823	NA	0.665184
OsAffx.28181.1.S1_at	LOC_Os06g49130	TAZ zinc finger family protein, expressed	7.357666	7.298386	7.894772	8.095647	6.398968	6.311431	6.297689	6.396744	NA	0.667183
OsAffx.14098.1.S1_at	LOC_Os04g32590	expressed protein	4.946598	4.82285	5.64986	5.456747	5.842485	5.684755	6.023198	6.016768	NA	0.668579
Os.6411.2.S1_at	LOC_Os07g42250	strictosidine synthase 1 precursor, putative, expressed	6.260375	6.526233	6.945803	7.180382	10.72275	10.90185	11.02346	10.82407	NA	0.669788
Os.54904.1.S1_at	LOC_Os02g45010	expressed protein	7.74573	7.657225	8.263312	8.486102	5.375392	5.212739	5.318826	5.432385	NA	0.67323
Os.18193.1.S1_at	LOC_Os04g44650	ferredoxin-thioredoxin reductase, variable chain, putative, expressed	8.420201	8.288967	8.918802	9.137407	8.978586	8.787984	9.925563	9.737518	0.948256	0.67352
Os.49376.1.S1_at	LOC_Os02g44270	expressed protein	6.455243	6.494292	7.007462	7.291591	5.430696	5.523996	5.675594	5.964895	NA	0.674759
Os.17439.1.S1_at	LOC_Os12g36270	expressed protein	7.628886	7.686544	8.527095	8.138967	7.298057	7.182012	7.136715	7.281946	NA	0.675316
Os.11148.1.S1_at	LOC_Os01g70800	mitochondrial deoxynucleotide carrier, putative, expressed	8.89438	8.80118	9.429864	9.618974	8.590514	8.531104	9.151811	9.046408	NA	0.676639
Os.8233.1.S1_s_at	LOC_Os01g54480	serine/threonine-protein kinase TNNI3K, putative, expressed	9.295154	9.572414	9.994072	10.23031	8.592863	8.605147	8.734405	8.86791	NA	0.678406
Os.28994.1.S1_at	LOC_Os01g67390	extensin-1 precursor, putative, expressed	7.006868	7.118019	7.687785	7.803466	5.825454	5.928077	5.994537	5.788741	NA	0.683182
Os.50371.1.S1_x_at	LOC_Os05g05620	glutathione S-transferase GSTF1, putative, expressed	7.135395	7.168289	7.671999	7.998722	6.505246	6.520825	6.631932	6.626598	NA	0.683518
OsAffx.14853.1.S1_at	LOC_Os05g27580	wound-induced protein WI12 containing protein	6.515866	6.57897	7.211017	7.261488	5.983856	6.310127	6.355654	6.08375	NA	0.688834
Os.25071.1.A1_at	LOC_Os02g19890	stripe rust resistance protein Yr10, putative, expressed	8.038263	8.306168	8.771791	8.95111	6.437032	6.32631	6.561185	6.416587	NA	0.689235
Os.46050.1.A1_x_at	LOC_Os07g43604	expressed protein	5.792836	5.769163	6.369398	6.571762	5.335697	5.418583	5.490841	5.361346	NA	0.68958
Os.50548.1.S1_at	LOC_Os09g17610	protein binding protein, putative, expressed	8.062045	7.935869	8.71082	8.670369	7.940344	7.907102	8.090728	8.137821	NA	0.691638
Os.12048.1.S1_at	LOC_Os08g03350	LHT1, putative, expressed	12.36353	12.25359	13.00511	12.99601	11.92885	11.78466	11.88229	12.27125	NA	0.691996
Os.4281.1.S1_x_at	LOC_Os06g03830	retinol dehydrogenase 14, putative, expressed	8.730068	8.506758	9.179686	9.44309	6.859817	7.087624	6.715095	6.550785	NA	0.692975
OsAffx.29514.1.S1_at	LOC_Os08g34720	D-3-phosphoglycerate dehydrogenase, chloroplast precursor, putative, expressed	11.49833	11.52654	12.2075	12.20456	11.32045	10.95636	11.41294	11.57762	NA	0.693597
Os.6683.1.S1_at	LOC_Os01g58130	expressed protein	6.702885	7.014319	7.533413	7.573651	7.423105	7.656763	7.889056	8.057233	NA	0.69493

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.56653.1.S1_at	LOC_Os01g66250	S-locus-like receptor protein kinase, putative, expressed	7.30077	7.354764	8.084023	7.978912	6.826176	7.003153	6.816097	6.8725	NA	0.7037
Os.5216.1.S1_at	LOC_Os01g14514	expressed protein	7.825753	7.859698	8.610136	8.487931	8.668123	8.925288	8.959019	9.144618	NA	0.706308
OsAffx.14409.1.S1_at	LOC_Os04g54180	serine/threonine-protein kinase receptor precursor, putative	5.846707	5.797453	6.494905	6.567128	5.299855	5.58971	5.128075	5.250306	NA	0.708936
Os.26376.2.S1_at	LOC_Os03g01830	DEAD/DEAH box helicase, putative, expressed	6.603299	6.814876	7.520743	7.337941	8.637533	8.714796	9.109731	8.802411	NA	0.720255
Os.50583.1.S1_at	LOC_Os03g60260	ANT1, putative, expressed	8.921819	8.893647	9.532637	9.726485	10.29111	10.53008	10.39323	10.70107	NA	0.721828
Os.46451.1.S2_at	LOC_Os10g25487	NBS-LRR disease resistance protein, putative, expressed	6.571302	6.639293	7.197092	7.46066	5.663815	5.640549	5.727899	5.793357	NA	0.723578
Os.46876.1.S1_at	LOC_Os10g41250	glycoprotein, putative, expressed	7.340164	7.029873	7.949132	7.869375	6.592261	6.748726	6.692944	6.655753	NA	0.724235
Os.648.1.S1_at	LOC_Os01g43480	ATP binding protein, putative, expressed	8.883825	9.191114	9.749845	9.773785	8.90529	8.846277	9.179365	9.246782	NA	0.724345
Os.27438.1.S1_a_at	LOC_Os08g05320	expressed protein	7.670383	7.519211	8.36195	8.283324	7.150835	7.393693	7.157709	7.336178	NA	0.72784
Os.52147.1.S1_at	LOC_Os11g30760	expressed protein	9.95173	9.799189	10.68352	10.52488	8.957389	8.731746	8.900817	9.098016	NA	0.728743
Os.9764.1.S1_at	LOC_Os12g36940	calmodulin-binding protein, putative, expressed	7.813808	7.743482	8.543213	8.488847	7.654695	7.588978	7.979679	7.913726	NA	0.737385
Os.14835.2.S1_at	LOC_Os02g31080	expressed protein	7.606866	7.60115	8.278776	8.406129	7.299196	7.21835	7.157709	7.521133	NA	0.738445
Os.51235.1.S1_at	LOC_Os08g26120	expressed protein	7.36253	7.601917	8.294877	8.163998	6.179367	6.124312	5.738719	6.146344	NA	0.747214
Os.17211.1.S1_at	LOC_Os02g15360	expressed protein	5.6841	5.571301	6.555322	6.195796	4.7298	4.605213	4.696859	4.851068	NA	0.747858
OsAffx.16746.1.S1_at	LOC_Os07g47230	receptor-like serine-threonine protein kinase, putative, expressed	5.199831	4.869763	5.780084	5.786129	4.068145	4.028574	4.064528	4.296933	NA	0.748309
Os.33446.1.A1_at	LOC_Os03g13250	peptide transporter PTR2, putative, expressed	8.782834	9.077107	9.650967	9.713877	7.338242	7.479054	8.099701	8.220012	0.751209	0.752451
Os.50824.1.S1_x_at	LOC_Os08g26520	hypothetical protein	9.156849	9.447804	10.13381	9.983419	7.319727	7.829002	7.775618	8.22944	NA	0.75629
Os.51098.1.S1_x_at	LOC_Os12g05890	expressed protein	6.044054	5.979375	6.960477	6.575882	7.829709	7.682886	8.21285	8.503425	NA	0.756464
Os.8049.1.S1_a_at	LOC_Os01g70170	transaldolase 2, putative, expressed	12.25507	12.06239	12.89595	12.93724	11.44259	11.13357	11.61182	11.42365	NA	0.757866
Os.31858.3.S1_x_at	LOC_Os07g35340	receptor-like serine-threonine protein kinase, putative, expressed	5.478989	5.732695	6.487515	6.247586	5.221701	5.38806	5.220284	5.103678	NA	0.761708

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.20575.1.S1_at	LOC_Os03g62240	expressed protein	9.240738	9.615574	10.24267	10.1372	11.34466	11.39878	11.937	12.08739	0.640474	0.761775
Os.13051.1.S1_at	LOC_Os12g04980	meiotic recombination protein DMC1, putative, expressed	5.826759	5.605599	6.518853	6.447966	4.945324	5.30324	4.814066	4.860466	NA	0.767231
Os.27067.2.A1_at	LOC_Os08g02230	FAD binding domain containing protein, putative, expressed	9.143395	9.009815	9.917699	9.771196	11.39509	11.09212	11.53041	11.27959	NA	0.767843
Os.22940.1.S1_at	LOC_Os02g07010	expressed protein	9.5048	9.565914	10.27241	10.33879	8.586972	8.946395	8.896602	9.041861	NA	0.770241
Os.51742.1.S1_x_at	LOC_Os02g37480	glycine-rich cell wall structural protein precursor, putative, expressed	5.797466	5.568824	6.40829	6.508483	5.100863	4.875475	4.844086	4.71932	NA	0.775242
Os.49952.1.S1_at	LOC_Os08g42550	AP2 domain containing protein, expressed	4.79621	5.141747	5.940747	5.552793	4.174418	4.228388	4.116911	4.255125	NA	0.777791
Os.31883.1.A1_at	LOC_Os11g06010	helix-loop-helix DNA-binding, putative, expressed	8.939502	8.796205	9.668452	9.630391	8.730434	8.444294	8.438789	8.139315	NA	0.781568
OsAffx.19055.1.S1_at	LOC_Os11g28470	expressed protein	7.026661	6.750802	7.612628	7.72816	5.684395	5.465837	5.750734	5.974349	NA	0.781663
Os.14125.1.S1_at	LOC_Os09g35030	sbCBF6, putative, expressed	5.810865	5.906209	6.648228	6.63254	4.742427	5.173223	5.223417	5.357801	NA	0.781847
OsAffx.28946.1.S1_at	LOC_Os07g47660	expressed protein	6.82417	7.063445	7.854735	7.597747	6.043846	5.84128	5.757826	6.094058	NA	0.782434
Os.9829.1.S1_at	LOC_Os05g48930	OsGrx_S2 - glutaredoxin subgroup III, expressed	10.651	10.53799	11.34927	11.40509	9.960409	9.8701	9.969786	9.999286	NA	0.782685
Os.4844.1.S1_at	LOC_Os05g06970	peroxidase 1 precursor, putative, expressed	11.8459	11.72001	12.52528	12.61403	7.304771	7.996235	8.045345	8.341678	NA	0.786701
Os.10541.1.S1_at	LOC_Os01g64000	ABA response element binding factor, putative, expressed	6.18851	6.156787	6.80488	7.120757	5.08826	5.274938	5.437951	5.31762	NA	0.79017
Os.7668.1.S1_at	LOC_Os04g17479	expressed protein	5.99643	6.093688	6.935666	6.735317	8.126241	8.646825	8.666464	8.996446	NA	0.790432
Os.50864.1.S1_x_at	LOC_Os04g55970	DNA binding protein, putative, expressed	8.565236	8.36866	9.384051	9.133385	6.272796	6.42774	6.345813	6.49378	NA	0.79177
Os.9427.1.S1_at	LOC_Os10g05020	transposon protein, putative, unclassified, expressed	9.969617	10.17079	10.76096	10.96432	7.837499	7.827962	7.878267	8.002034	NA	0.792438
OsAffx.3463.1.S1_at	LOC_Os03g40770	expressed protein	6.062658	6.159805	6.957404	6.863174	5.791814	5.701268	5.375175	5.539837	NA	0.799057
Os.29815.1.S1_at	LOC_Os01g73110	expressed protein	7.791524	8.095891	8.721719	8.770568	7.503022	7.591472	8.087387	7.840335	NA	0.802436
OsAffx.27299.1.S1_at	LOC_Os05g44140	non-symbiotic hemoglobin 2, putative	5.540328	5.781465	6.264205	6.666741	5.048084	5.218522	5.325841	5.324715	NA	0.804576
Os.20541.1.S1_at	LOC_Os03g37840	potassium transporter 16, putative, expressed	8.450378	8.417294	9.185193	9.304542	9.53145	9.957162	10.12987	10.24953	NA	0.811031

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.38330.2.S1_at	LOC_Os01g56010	protein Z, putative, expressed	8.217098	8.150561	8.985776	9.029513	6.50725	6.226917	6.679031	6.212109	NA	0.823815
OsAffx.30135.1.S1_at	LOC_Os09g34160	resistance protein, putative, expressed	7.261539	6.799843	7.925153	7.789972	5.154479	5.624538	5.575834	6.301383	NA	0.826871
Os.25597.1.S1_at	LOC_Os02g06910	auxin response factor 6, putative, expressed	9.778868	10.03429	10.80331	10.67829	9.381927	8.894924	8.977503	8.877993	NA	0.834224
Os.47472.1.S1_at	LOC_Os09g39410	male sterility protein 2, putative, expressed	6.302907	6.59078	7.227792	7.336492	9.229933	8.959096	8.909843	8.711287	NA	0.835299
Os.30386.1.S1_at	LOC_Os01g53260	OsWRKY23 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	8.55109	8.831334	9.467823	9.588364	6.724938	6.995173	7.025482	6.696431	NA	0.836881
Os.55524.1.S1_at	LOC_Os05g36310	RING-H2 finger protein ATL3C, putative, expressed	9.384383	9.714287	10.36219	10.4171	6.464406	6.862995	7.019079	6.81472	NA	0.840311
Os.4078.1.S1_at	LOC_Os08g08840	glucose-6-phosphate/phosphate translocator 2, chloroplast precursor, putative, expressed	11.44988	11.28531	12.11777	12.30231	10.7623	10.54865	10.81804	10.86197	NA	0.842444
Os.15914.1.S1_at	LOC_Os09g23350	ATTPS6, putative, expressed	9.789591	10.0176	10.74437	10.76811	8.827856	8.849523	8.766646	8.650137	NA	0.852649
Os.17985.1.S1_s_at	LOC_Os03g56500	expressed protein	7.533604	7.193755	8.178596	8.272056	6.260391	6.699813	7.001213	6.789897	NA	0.861647
Os.24180.1.A1_s_at	LOC_Os12g36920	calmodulin-binding protein, putative, expressed	9.939063	9.292907	10.47988	10.49208	7.865224	7.707215	8.151475	8.708343	NA	0.869992
Os.52171.1.S1_at	LOC_Os06g38950	ATATH6, putative, expressed	9.316355	9.033654	10.10135	9.997533	6.416566	6.408458	6.41381	6.532829	NA	0.874435
Os.30512.1.S1_at	LOC_Os01g43650	OsWRKY11 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	7.035344	6.845732	7.896057	7.735429	6.280377	5.931619	6.405106	6.631169	NA	0.875205
Os.36767.1.S1_at	LOC_Os01g04330	calmodulin-related protein 2, touch-induced, putative, expressed	8.701379	8.573868	9.524681	9.506936	9.549523	9.429696	10.69188	10.68154	1.1971	0.878186
Os.9195.1.S1_at	LOC_Os01g43370	expressed protein	11.55045	11.59087	12.45144	12.44674	11.21692	11.32443	11.8683	11.81796	NA	0.878428
Os.27625.1.S1_at	LOC_Os12g24020	senescence-associated protein DIN1, putative, expressed	7.116558	7.525453	8.255591	8.160985	7.184363	7.066488	6.972233	7.05264	NA	0.887283
Os.8772.1.S1_at	LOC_Os08g30740	ATATH1, putative, expressed	9.927587	9.64076	10.7148	10.62877	7.744436	7.666411	7.955769	8.173853	NA	0.887615
Os.26810.1.A1_s_at	LOC_Os02g16940	peptidase/ subtilase, putative, expressed	5.411327	5.434996	6.031856	6.596638	7.746241	8.390996	8.818495	8.567789	NA	0.891085
Os.53706.1.S1_at	LOC_Os02g12420	receptor-like protein kinase precursor, putative, expressed	5.704048	5.687481	6.412452	6.767307	4.325871	4.472707	4.467445	4.713518	NA	0.894115
Os.16532.1.S1_at	LOC_Os03g52370	expressed protein	12.06535	12.04484	12.98506	12.91504	9.603692	10.26717	10.26319	10.37051	NA	0.894953

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.55882.1.S1_at	LOC_Os03g08720	agmatine coumaroyltransferase, putative, expressed	9.890946	9.843756	10.58344	10.94689	5.143846	4.794892	4.773698	4.622102	NA	0.897812
OsAffx.24953.1.S1_s_at	LOC_Os03g03370	beta-carotene hydroxylase, putative, expressed	7.117317	6.799092	7.888296	7.825573	7.194286	7.286653	7.384069	7.322118	NA	0.89873
Os.4604.1.S1_at	LOC_Os03g15460	expressed protein	6.885508	6.718797	7.782009	7.642692	6.678649	6.656916	6.592667	6.872316	NA	0.910198
Os.27963.1.A1_at	LOC_Os01g72900	abscisic stress ripening protein 1, putative, expressed	7.282751	6.966223	8.120243	7.95304	8.27019	8.552833	9.526561	9.424435	1.063987	0.912154
Os.54736.1.S1_at	LOC_Os02g52910	protein binding protein, putative, expressed	6.430858	6.442785	7.477252	7.223779	5.412312	5.631791	6.007737	5.985318	NA	0.913694
Os.4772.1.S1_at	LOC_Os06g35540	aspartate aminotransferase, mitochondrial precursor, putative, expressed	8.778007	8.957987	9.671912	9.892205	9.938375	9.931805	10.33987	10.2659	NA	0.914062
OsAffx.28287.1.S1_at	LOC_Os07g05380	ATPase, putative, expressed	6.687671	6.780158	7.75265	7.554905	5.467753	5.654936	5.483645	5.570846	NA	0.919863
OsAffx.12383.1.S1_at	LOC_Os02g37260	expressed protein	10.87562	10.71193	11.67533	11.75972	5.397204	5.21008	5.254291	4.821281	NA	0.923747
Os.32630.1.S1_at	LOC_Os10g32700	hypersensitive-induced response protein, putative, expressed	10.95636	10.65382	11.73126	11.73082	5.646941	6.183623	6.314262	6.676434	NA	0.92595
OsAffx.26592.1.S1_at	LOC_Os04g53830	leucoanthocyanidin reductase, putative, expressed	7.284168	7.514098	8.343399	8.308476	6.750802	6.908163	7.310933	6.957541	NA	0.926804
Os.32682.1.S1_at	LOC_Os07g02960	expressed protein	8.092816	8.063905	8.963571	9.058763	6.790217	6.75275	7.17037	7.183194	NA	0.932807
Os.11305.1.S1_at	LOC_Os12g29400	ABA-responsive protein, putative, expressed	7.446218	7.412659	8.223766	8.53009	7.553949	7.432956	7.689095	7.712677	NA	0.947489
Os.39087.1.S1_at	LOC_Os01g14550	pathogen-related protein, putative, expressed	8.835367	8.487189	9.695661	9.524001	6.137646	5.91052	6.105352	6.2447	NA	0.948553
Os.25453.1.A1_at	LOC_Os03g55590	DNA binding protein, putative, expressed	11.4161	11.67423	12.41775	12.57676	11.16279	11.32909	11.50949	11.48104	NA	0.952088
OsAffx.31373.1.S1_at	LOC_Os11g38780	calcium ion binding protein, putative	8.100642	7.968495	9.011091	8.977629	6.230032	6.206666	6.669177	6.906013	NA	0.959792
Os.31171.1.S1_at	LOC_Os01g40290	expressed protein	11.60987	11.05274	12.32969	12.25845	9.414495	9.65871	10.07759	10.66441	NA	0.962764
Os.22312.3.A1_a_at	LOC_Os05g28740	universal stress protein, putative, expressed	9.99632	10.27511	10.83547	11.37324	11.66982	12.01558	12.13851	12.21373	NA	0.968637
Os.30528.1.S1_at	LOC_Os08g31860	expressed protein	7.524097	7.096563	8.325007	8.247525	6.278298	5.823307	6.747469	7.118442	NA	0.975937
Os.19070.1.S1_at	LOC_Os11g09020	amino acid carrier, putative, expressed	5.247002	5.100666	5.890228	6.409948	9.220155	9.29535	9.443087	9.495129	NA	0.976254
Os.6288.1.S1_at	LOC_Os08g31850	expressed protein	10.54182	10.09363	11.27366	11.31872	6.423138	6.864263	7.093195	7.202024	NA	0.97847

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.26517.1.S1_at	LOC_Os02g44990	F-box domain containing protein, expressed	10.34189	10.58102	11.54834	11.33752	9.400254	9.772437	9.757623	9.709398	NA	0.981478
OsAffx.30533.1.S1_s_at	LOC_Os10g25830	mitochondrial carrier-like protein, putative, expressed	8.995574	9.084241	10.06995	10.00098	10.5249	10.81825	10.93798	10.7658	NA	0.995558
Os.54410.1.S1_at	LOC_Os06g13720	pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor, putative, expressed	5.820679	5.615098	6.778908	6.64865	5.653146	5.4505	5.444222	5.463899	NA	0.995891
Os.4757.1.S2_at	LOC_Os11g04409	expressed protein	11.75263	12.28629	13.02434	13.00771	10.05279	10.29897	10.22422	10.56829	NA	0.996567
Os.56930.1.S1_at	LOC_Os03g17220	dirigent-like protein, expressed	7.9131	7.43402	8.674758	8.668989	5.415031	5.547039	5.520563	5.683805	NA	0.998314
OsAffx.20242.2.S1_at	LOC_Os10g34040	nodulin, putative, expressed	6.006336	5.75908	6.723928	7.041047	4.937602	5.183898	5.256429	5.118322	NA	0.999779
OsAffx.31475.1.S1_at	LOC_Os11g44630	expressed protein	8.835465	8.50211	9.673695	9.667478	6.469585	6.249186	6.652657	7.370723	NA	1.001799
OsAffx.13338.1.S1_at	LOC_Os03g44100	hydrolase-like protein, putative, expressed	6.848069	6.869724	7.708549	8.013117	5.071477	5.129217	5.099	5.287444	NA	1.001937
Os.17889.1.S1_at	LOC_Os05g46340	expressed protein	6.214491	6.056953	7.006755	7.275081	7.497226	7.390393	7.770736	7.549418	NA	1.005196
Os.35433.1.S1_at	LOC_Os04g39320	expressed protein	5.372557	5.324143	6.572128	6.139381	4.269169	4.365531	4.241394	4.274504	NA	1.007404
Os.11897.1.S1_at	LOC_Os03g61150	expressed protein	10.37716	10.88022	11.58087	11.69448	7.523473	8.045803	8.160431	8.336756	NA	1.008985
Os.4999.1.S1_at	LOC_Os06g50230	expressed protein	8.772661	8.902316	9.926285	9.772416	9.740272	9.931581	9.939612	10.26472	NA	1.011862
Os.10333.1.S1_at	LOC_Os07g02800	myb-like DNA-binding domain, SHAQKYF class family protein, expressed	9.189361	9.599045	10.37494	10.44725	10.56176	10.86827	11.08728	10.97014	NA	1.016892
Os.50121.1.S1_at	LOC_Os06g41100	TGA10 transcription factor, putative, expressed	5.935376	5.648824	6.996963	6.624778	4.681881	4.835598	4.79217	4.87189	NA	1.018771
Os.12239.1.S1_at	LOC_Os09g31031	ubiquitin, putative, expressed	8.839576	8.209625	9.51545	9.572892	7.910202	7.692341	8.935042	9.080033	1.206266	1.01957
Os.50152.1.S1_at	LOC_Os03g59770	calcium-binding allergen Ole e 8, putative, expressed	9.532081	9.308913	10.25752	10.63668	7.745632	7.84654	8.125829	8.805903	NA	1.026605
Os.39617.1.S1_at	LOC_Os09g29660	ATP-binding cassette sub-family G member 2, putative, expressed	8.943659	8.887587	9.954601	9.969427	8.544158	8.776274	8.713893	8.648298	NA	1.046391
Os.11287.1.S1_at	LOC_Os06g50930	senescence-associated protein DIN1, putative, expressed	8.918052	9.200002	9.954555	10.26783	8.74937	8.728319	9.336786	9.3596	0.609349	1.052164
Os.56824.1.S1_at	LOC_Os06g47750	phytosulfokine receptor precursor, putative, expressed	7.854371	7.986907	8.915566	9.046649	4.16565	4.406738	4.377664	4.183072	NA	1.060469

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.49319.1.S1_at	LOC_Os02g52990	OsSAUR12 - Auxin-responsive SAUR gene family member, expressed	10.48964	10.04848	11.5398	11.13814	9.104464	9.038134	9.790409	9.529754	NA	1.069906
Os.17111.2.S1_x_at	LOC_Os04g48460	cytochrome P450 86A1, putative, expressed	7.647675	7.394198	8.627562	8.56904	7.922896	7.923843	8.05004	8.02209	NA	1.077364
Os.48082.1.S1_at	LOC_Os09g25070	OsWRKY62 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	8.6056	8.320395	9.600275	9.482584	7.216031	7.385162	6.553059	6.845522	NA	1.078432
OsAffx.5041.1.S1_at	LOC_Os06g38110	hypothetical protein	6.389064	6.282801	7.163668	7.671194	4.253102	4.528191	4.595301	4.711922	NA	1.081499
Os.6672.1.S1_at	LOC_Os01g18080	tyrosine-protein phosphatase non-receptor type 23, putative, expressed	11.31704	10.96809	12.05573	12.40853	10.46339	10.41358	10.62887	10.72935	NA	1.089563
Os.46559.1.S1_at	LOC_Os10g37670	actin-depolymerizing factor, putative, expressed	6.719378	6.561261	7.505695	7.955954	6.265724	5.953554	5.927721	5.95841	NA	1.090505
Os.7879.2.S1_at	LOC_Os04g56400	glutamine synthetase, chloroplast precursor, putative, expressed	5.388456	5.703371	6.530319	6.742922	8.793282	8.852736	9.54648	9.515282	0.707872	1.090706
Os.52573.1.S1_at	LOC_Os09g36580	pathogenesis-related protein 5 precursor, putative, expressed	8.942013	8.861259	10.0885	9.899647	8.292567	8.44414	8.180434	8.376192	NA	1.092439
Os.49475.1.S1_at	LOC_Os03g25790	glycosyl hydrolases family 17 protein, expressed	8.531565	8.372746	9.567524	9.5535	8.058647	8.023323	8.20544	7.908427	NA	1.108356
Os.28200.1.S1_x_at	LOC_Os03g61160	expressed protein	7.96093	8.156261	9.488526	8.88176	5.714016	5.694133	6.193371	5.858426	NA	1.126548
Os.54033.1.S1_at	LOC_Os08g37180	patatin T5 precursor, putative, expressed	6.537005	6.455663	7.461	7.80278	4.787271	4.9973	5.088301	5.050281	NA	1.135556
Os.36834.1.S1_at	LOC_Os04g54830	expressed protein	8.65511	8.630683	9.750336	9.813055	7.718913	7.477209	8.807066	8.766646	1.188794	1.1388
Os.38205.1.S1_at	LOC_Os01g57710	expressed protein	8.566649	8.214247	9.669243	9.436391	7.963183	7.967429	8.367036	8.324901	NA	1.162369
Os.12738.1.S2_a_at	LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed	11.35888	11.53596	12.47579	12.75941	10.13159	10.01107	10.41535	10.23171	NA	1.170178
Os.2329.1.S1_a_at	LOC_Os01g45274	carbonic anhydrase, chloroplast precursor, putative, expressed	11.26885	11.20125	12.25703	12.57765	13.9452	14.01112	13.94338	14.0759	NA	1.182285
Os.54291.1.S1_at	LOC_Os11g42200	laccase LAC2-1, putative, expressed	6.620724	6.723863	7.983008	7.74685	6.02539	6.076435	7.127347	7.209793	1.117657	1.192636
Os.21893.3.A1_at	LOC_Os08g31980	trehalose 6-phosphate synthase, putative, expressed	9.117754	9.666754	10.65988	10.54011	7.331233	7.333307	7.508677	7.419136	NA	1.207742
Os.36176.1.S1_at	LOC_Os03g52360	expressed protein	9.726549	9.481446	10.94613	10.7288	6.443177	6.225631	5.932192	6.098948	NA	1.233466
OsAffx.4277.1.S1_s_at	LOC_Os05g08750	cold-induced glucosyl transferase, putative, expressed	7.3886	7.311893	8.445571	8.725654	8.46673	8.33316	8.961534	8.60668	NA	1.235365
Os.26226.1.S1_at	LOC_Os02g02780	ATP binding protein, putative, expressed	10.10178	10.39934	11.13709	11.8697	6.657283	6.650929	6.633407	6.78141	NA	1.252838

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
OsAffx.14448.1.S1_at	LOC_Os04g56930	beta-fructofuranosidase, insoluble isoenzyme 5, putative, expressed	6.441273	6.879252	8.020089	7.834186	4.245269	4.743606	4.315439	4.764988	NA	1.266875
Os.10774.1.S1_at	LOC_Os08g05570	monodehydroascorbate reductase, chloroplast precursor, putative, expressed	11.18579	11.01473	12.43213	12.30669	9.841455	9.749128	11.00351	10.86315	1.138034	1.269153
Os.15045.1.S1_at	LOC_Os04g56790	TLD family protein, expressed	8.996372	8.923811	10.01575	10.48822	8.529125	8.388237	10.04098	9.804022	1.46382	1.291891
Os.33082.1.S1_at	LOC_Os06g06400	NBS-LRR disease resistance protein, putative, expressed	8.344641	8.435254	9.524668	9.842351	5.569344	5.483179	4.930013	5.226903	NA	1.293562
Os.12528.1.S1_x_at	LOC_Os03g31750	pyruvate, phosphate dikinase, chloroplast precursor, putative, expressed	9.326695	8.688258	10.28551	10.33366	6.724751	6.624116	6.80457	7.185956	NA	1.302108
OsAffx.13696.1.S1_at	LOC_Os04g06734	expressed protein	5.633206	6.045872	7.19687	7.16779	4.541621	4.495768	4.229723	4.579541	NA	1.34279
Os.1443.1.S1_a_at	LOC_Os01g06640	DNA binding protein, putative, expressed	8.052729	7.735322	9.231006	9.280592	8.338375	7.942033	8.787271	8.885484	NA	1.361774
Os.2371.1.S1_at	LOC_Os12g26290	alpha-DOX2, putative, expressed	8.419494	8.008626	9.484266	9.67166	10.81447	10.96012	11.00675	11.31555	NA	1.363903
Os.17419.1.S1_at	LOC_Os10g09850	EF-Hand containing protein, putative, expressed	6.636373	6.919353	8.034305	8.301781	7.28335	7.488075	7.851655	7.878023	NA	1.39018
Os.27232.1.S1_at	LOC_Os01g68650	plant-specific domain TIGR01615 family protein, expressed	9.23245	9.612526	10.81119	10.83627	8.175499	8.396072	9.517912	8.910836	NA	1.40124
Os.56210.1.S1_at	LOC_Os04g42950	DNA binding protein, putative, expressed	8.442566	7.81639	9.771788	9.349335	4.760235	4.393988	4.569328	4.303293	NA	1.431084
Os.36162.1.S1_at	LOC_Os01g61044	amino acid-polyamine transporter, putative, expressed	18.39696	18.1173	19.64223	19.74621	20.17354	20.55759	20.72029	20.18368	NA	1.437091
Os.8796.1.S2_s_at	LOC_Os01g04630	muconate cycloisomerase-like protein, putative, expressed	10.34049	10.24975	11.60015	11.86982	11.18755	10.77547	10.98546	10.98539	NA	1.439866
Os.32597.1.S1_at	LOC_Os01g47300	retrotransposon protein, putative, Ty3-gypsy subclass, expressed	4.840682	5.027236	6.504336	6.343395	4.33676	4.822459	4.576009	4.57675	NA	1.489907
Os.23469.1.S1_at	LOC_Os05g37170	transcription factor TGA6, putative, expressed	7.935313	8.664748	9.583187	10.04111	5.385657	5.130691	5.459419	5.723729	NA	1.512116
Os.1853.1.S1_at	LOC_Os08g08960	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8.56252	8.732129	10.22419	10.16719	7.209581	7.4933	7.215521	7.582797	NA	1.548369
Os.141.1.S1_at	LOC_Os03g57120	ferredoxin--NADP reductase, root isozyme, chloroplast precursor, putative, expressed	11.02392	11.09614	12.48838	12.73325	8.794005	8.336151	10.65295	10.38532	1.954057	1.550785
Os.46731.1.S1_x_at	LOC_Os10g04674	disease resistance protein RPM1, putative, expressed	15.36719	15.39883	16.74807	17.15091	13.56921	13.14717	13.58838	13.59106	NA	1.566479

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.7688.1.S1_at	LOC_Os10g31040	arsenite transport protein, putative, expressed	6.205284	5.497695	7.506733	7.334923	10.2487	10.26596	10.11194	10.28876	NA	1.569339
Os.27207.1.S1_at	LOC_Os12g25200	chloride channel protein CLC-a, putative, expressed	9.209539	9.667618	10.92251	11.19349	7.97881	8.541238	11.28383	11.00722	2.885497	1.619421
Os.19172.1.S1_at	LOC_Os05g47780	CHY zinc finger family protein, expressed	20.72896	21.24409	22.49926	22.7165	17.337	17.40427	17.6773	17.57833	NA	1.621359
Os.6847.1.S1_at	LOC_Os07g22350	glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor, putative, expressed	10.07168	10.03215	11.67527	11.67815	9.312112	9.070808	10.29341	10.22565	1.068067	1.624794
Os.40424.1.S1_at	LOC_Os01g54340	plant-specific domain TIGR01615 family protein, expressed	8.690239	8.616801	10.00017	10.58558	10.18274	10.58604	10.29783	10.3202	NA	1.639355
OsAffx.24629.1.S1_at	LOC_Os02g38230	component of high affinity nitrate transporter, putative, expressed	9.114529	9.085169	10.58853	10.93696	7.442007	7.646461	7.881545	7.503714	NA	1.662894
Os.7457.1.S1_a_at	LOC_Os04g42520	adenine phosphoribosyltransferase 2, putative, expressed	8.934261	8.507697	10.4264	10.38936	9.722722	9.362743	9.274358	9.541074	NA	1.686898
Os.15877.1.S1_at	LOC_Os11g29400	6-phosphogluconate dehydrogenase, decarboxylating, putative, expressed	10.2154	10.08668	11.80079	11.88227	8.801136	8.41022	10.56772	10.21	1.783184	1.690491
Os.31771.2.S1_at	LOC_Os03g51479	maf-like protein, expressed	12.28441	12.19547	13.84026	14.0506	9.51169	9.714422	9.982482	10.18194	NA	1.705487
Os.18559.1.S1_at	LOC_Os02g45520	beta-lactamase, class A, putative, expressed	12.05343	11.46892	13.7817	13.21756	18.39201	18.67221	19.19507	19.68983	NA	1.738454
Os.21801.1.S1_at	LOC_Os01g04620	expressed protein	8.939834	9.282711	10.64069	11.14637	6.643579	6.851012	7.056798	6.901209	NA	1.782257
OsAffx.27459.3.S1_at	LOC_Os06g05010	early nodulin 93, putative, expressed	12.35247	11.46182	14.26097	13.51008	10.19996	10.59951	11.27621	11.39245	NA	1.97838
Os.11961.1.S1_at	LOC_Os05g38040	expressed protein	10.63612	11.0665	12.85174	12.854	9.245688	9.383364	10.13182	10.65805	1.080408	2.001559
Os.18296.1.S1_x_at	LOC_Os01g10440	xylosyltransferase oxt, putative, expressed	13.88841	13.06448	15.44292	15.64916	11.08432	11.82334	11.78353	11.72099	NA	2.069599
Os.54146.1.S1_at	LOC_Os02g53130	nitrate reductase, putative, expressed	5.745572	5.448965	7.479655	8.024856	4.707005	4.799625	8.396755	7.757421	3.323774	2.154987
Os.6092.1.S1_at	LOC_Os02g44230	expressed protein	7.611285	7.714487	9.621655	10.23591	6.86064	6.392689	6.274287	6.536533	NA	2.265895
Os.142.2.A1_a_at	LOC_Os01g25484	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed	11.43015	11.32216	13.59342	13.90218	10.79963	11.35548	13.74172	13.76339	2.674998	2.371638
Os.7512.1.S1_at	LOC_Os04g56990	transfactor, putative, expressed	6.168921	6.579547	8.668597	8.89498	5.735239	6.00607	7.872122	7.644027	1.88742	2.407555
OsAffx.13282.1.S1_s_at	LOC_Os03g41330	seed specific protein Bn15D17A, putative, expressed	7.551337	7.39829	10.01491	10.12327	5.691804	5.796925	7.387635	7.537277	1.718091	2.594279

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.14520.1.S1_at	LOC_Os03g48030	HPP, putative, expressed	8.096609	8.55581	10.73844	11.16789	8.719772	8.735252	10.41134	10.98382	1.970072	2.626953
Os.321.1.S1_at	LOC_Os05g37140	ferredoxin-6, chloroplast precursor, putative, expressed	20.52768	20.2803	22.97931	23.16294	18.2915	18.11269	19.33953	19.56151	1.248422	2.667139
Os.49271.1.S1_at	LOC_Os03g13050	ACI19, putative, expressed	7.134339	7.405762	9.754946	10.48105	7.03184	6.946378	6.582263	6.730571	-0.33269	2.847949
Os.12163.1.S1_at	LOC_Os03g12510	non-symbiotic hemoglobin 2, putative, expressed	7.853378	8.127675	11.07765	10.9153	7.127072	6.929176	9.337126	9.57972	NA	3.005947
Os.170.3.S1_at	LOC_Os01g64120	ferredoxin-6, chloroplast precursor, putative, expressed	8.93964	8.946957	11.93435	12.52096	8.868671	9.197967	13.28101	13.2314	4.222882	3.28436
Os.25548.1.A1_at	LOC_Os01g64020	transcription factor HBP-1b, putative, expressed	21.52478	21.56772	24.61651	25.16064	13.3762	13.82626	14.30149	14.10759	NA	3.342325
Os.4863.1.S1_at	LOC_Os01g44050	siroheme synthase, putative, expressed	16.7331	16.6491	20.29666	20.7324	13.36758	13.97181	16.68782	17.11258	3.230512	3.823426
Os.12191.1.S1_at	LOC_Os03g13140	non-symbiotic hemoglobin 2, putative, expressed	18.02063	17.56711	22.93766	22.03343	12.8633	12.94502	16.19752	16.48756	3.438376	4.691672
Os.8095.1.S2_at	LOC_Os03g22050	CBL-interacting serine/threonine-protein kinase 15, putative, expressed	27.08732	28.98371	32.18288	33.51194	16.35228	15.88291	18.01268	17.57657	NA	4.811897
Os.49182.1.S1_at	LOC_Os02g36590	expressed protein	7.711264	7.598664	8.254092	8.491855	8.405823	8.543219	8.398834	8.457383	NA	0.71801
Os.27112.1.S1_at	LOC_Os01g09800	regulatory protein NPR1, putative, expressed	9.236701	9.401711	9.950987	10.06916	7.967429	8.119152	8.009437	8.196775	NA	0.69087

>N_shoots_REPRESSED

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.1153.1.S1_at	LOC_Os01g15830	peroxidase 72 precursor, putative, expressed	11.80828	11.70274	11.81273	11.65692	10.10281	9.962539	9.334073	9.480706	-0.62529	NA
Os.1564.1.S1_at	LOC_Os01g22380	expressed protein	7.493215	7.509699	6.866744	7.100981	9.440338	9.051739	8.723304	7.914955	-0.92691	NA
Os.18388.1.S1_at	LOC_Os01g49640	nonspecific lipid-transfer protein precursor, putative, expressed	9.014181	9.524288	8.211956	8.493602	6.895562	5.917069	5.301445	5.336768	-1.08721	NA
Os.28229.2.S1_x_at	LOC_Os01g52770	anther-specific proline-rich protein APG, putative, expressed	5.78287	5.981521	5.569887	5.787546	6.961053	6.991533	6.218673	6.509924	-0.61199	NA
Os.4644.1.S1_at	LOC_Os01g60770	alpha-expansin 10 precursor, putative, expressed	9.097312	9.016638	8.297278	8.88765	11.65244	11.2383	10.47357	10.71415	-0.85151	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.18429.1.S1_x_at	LOC_Os01g63580	glycerol-3-phosphate acyltransferase 8, putative, expressed	6.635548	6.872454	7.15041	7.307808	9.193912	8.803998	8.337452	8.206699	-0.72688	NA
Os.24972.1.S1_at	LOC_Os02g09930	CSLA1 - cellulose synthase-like family A; mannan synthase, expressed	9.918135	9.651518	9.233869	9.240921	8.696996	8.230708	7.952936	7.555468	-0.70965	NA
Os.8984.1.S1_at	LOC_Os02g13660	meiosis 5, putative, expressed	6.833765	6.723863	5.922951	6.774489	11.96784	11.3162	10.23274	10.52949	-1.26091	NA
Os.50613.1.S1_at	LOC_Os02g25230	expressed protein	7.566205	7.321319	6.955064	6.858602	6.686461	6.214197	5.830443	5.757009	-0.6566	NA
Os.10651.1.S1_at	LOC_Os02g41904	low-molecular-weight cysteine-rich protein LCR69 precursor, putative, expressed	10.75732	10.39984	10.14077	9.938466	12.00982	11.64018	11.28664	10.95626	-0.70355	NA
Os.5213.1.S1_at	LOC_Os02g44720	expressed protein	7.838434	7.625708	6.95706	7.122874	7.175281	7.097525	6.336651	6.45741	-0.73937	-0.6921
Os.4612.1.S1_at	LOC_Os03g07100	lipid transfer protein, putative, expressed	6.923832	6.740255	6.525253	6.612524	10.48921	10.15906	9.491218	9.178483	-0.98928	NA
Os.18597.1.S1_at	LOC_Os03g09930	sulfate transporter 2.1, putative, expressed	7.722121	7.510393	7.540174	7.673223	10.09009	10.02573	9.221016	9.44178	-0.72651	NA
Os.1376.1.S1_at	LOC_Os03g11540	replication protein A 70 kDa DNA-binding subunit, putative, expressed	8.509536	8.369066	7.894203	7.796085	8.244347	7.548363	6.530166	6.494312	-1.38412	NA
Os.10803.1.S1_at	LOC_Os03g18220	pyruvate decarboxylase isozyme 2, putative, expressed	8.769995	8.741838	8.568703	8.388048	8.100488	7.686198	7.215065	7.135443	-0.71809	NA
Os.12186.2.S1_x_at	LOC_Os03g21040	expressed protein	11.53922	11.40813	11.58646	11.72942	10.07834	9.832524	9.430932	9.213042	-0.63344	NA
Os.2367.1.S1_at	LOC_Os03g21820	alpha-expansin 10 precursor, putative, expressed	6.720794	6.788135	6.658431	6.374818	8.896984	8.589711	7.686661	7.047072	-1.37648	NA
Os.8039.1.S1_at	LOC_Os03g46640	deoxyuridine 5-triphosphate nucleotidohydrolase, putative, expressed	10.5165	10.52534	9.915225	10.09397	9.752153	9.03853	8.481985	8.023552	-1.14257	NA
Os.49163.1.S1_at	LOC_Os03g47730	knotted1-interacting protein, putative, expressed	4.84481	4.915516	4.561502	4.586803	5.80516	5.510684	4.86652	4.943408	-0.75296	NA
Os.3160.1.S1_at	LOC_Os03g50030	phospholipase A2, putative, expressed	9.948681	9.570321	9.221672	9.024393	8.633123	8.041504	7.878952	7.395276	-0.7002	NA
Os.57309.1.S1_at	LOC_Os04g19960	expressed protein	9.571651	9.394623	7.854309	8.95452	7.276592	6.943009	6.156712	5.713408	-1.17474	NA
Os.49553.1.S1_at	LOC_Os04g30720	kinesin motor domain containing protein, expressed	7.51717	7.161489	6.82853	6.851388	6.803759	6.841449	6.268268	6.147477	-0.61473	NA
Os.47290.1.S1_at	LOC_Os04g34240	histone H3, putative, expressed	8.166384	7.977163	7.392799	7.540414	8.013262	7.834731	7.312993	7.241465	-0.64677	-0.60517
Os.46435.1.S1_s_at	LOC_Os04g39110	gibberellin-regulated protein 1 precursor, putative, expressed	6.991967	7.106289	6.988857	6.825475	8.477395	8.092311	7.45329	7.499623	-0.8084	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.54479.1.S1_at	LOC_Os04g49560	metal ion binding protein, putative, expressed	8.323849	8.197774	8.049182	8.033572	7.667566	7.277025	6.780611	6.834712	-0.66463	NA
Os.5270.1.S1_at	LOC_Os05g44200	anther-specific proline-rich protein APG, putative, expressed	6.129471	6.051915	5.897013	5.975516	8.192327	7.843212	7.197752	6.799566	-1.01911	NA
Os.9327.1.S1_at	LOC_Os05g45460	pistil-specific extensin-like protein precursor, putative, expressed	13.08388	13.42405	12.0149	12.78431	9.857258	8.463194	7.321852	6.499205	-2.2497	NA
Os.4651.1.S1_at	LOC_Os07g48710	VQ motif family protein, expressed	6.628517	6.804843	6.511457	6.77511	6.074922	6.210366	5.424015	5.397051	-0.73211	NA
OsAffx.6144.1.S1_at	LOC_Os08g38970	expressed protein	6.450776	6.368267	5.75973	5.995917	5.358614	5.277282	4.677986	4.532507	-0.7127	NA
Os.55378.1.S1_at	LOC_Os09g34890	expressed protein	7.008931	7.140009	6.63825	6.729619	8.608385	8.422213	7.814508	8.02293	-0.59658	NA
OsAffx.30149.1.S1_s_at	LOC_Os09g36160	SHI, putative, expressed	8.611921	8.123567	7.538531	7.744308	7.212177	6.583013	6.110711	5.938236	-0.87312	NA
Os.46551.1.S1_at	LOC_Os10g17260	flavonoid 3-monooxygenase, putative, expressed	6.525627	6.546752	6.080321	5.990104	8.282939	8.559352	7.338091	8.137086	-0.68356	NA
Os.46576.1.S1_x_at	LOC_Os10g36100	nonspecific lipid-transfer protein precursor, putative, expressed	6.724595	6.603092	6.532072	6.559847	10.01971	9.769715	9.05415	8.816951	-0.95916	NA
Os.6838.1.S1_at	LOC_Os10g40510	cortical cell-delineating protein precursor, putative, expressed	12.64327	12.51642	11.6126	11.69019	9.00885	8.301075	7.789595	7.374259	-1.07304	NA
Os.15841.1.S1_a_at	LOC_Os11g05290	pop3 peptide, putative, expressed	7.149812	6.783951	6.53156	6.30258	10.67893	10.2328	10.04827	9.592783	-0.63534	NA
Os.18929.1.S1_s_at	LOC_Os11g38580	expressed protein	10.80361	10.58292	10.04532	10.31845	14.87691	14.51714	12.94727	13.45684	-1.49497	NA
Os.52605.1.S1_at	LOC_Os12g38120	thaumatin-like protein precursor, putative, expressed	11.56664	11.69003	10.99848	11.09407	10.30113	9.856185	9.541398	9.053689	-0.78112	NA
Os.11513.1.S1_at	LOC_Os12g38140	expressed protein	13.91008	13.65447	13.72134	13.50524	13.02516	12.53933	11.84754	11.92855	-0.8942	NA
OsAffx.27633.1.S1_at	LOC_Os06g14280	secretory protein-like, putative, expressed	8.55979	8.355695	8.053802	8.120046	6.862536	6.617998	6.19178	5.835486	-0.72663	NA

>N_shoots_INDUCED

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.24864.1.S1_at	LOC_Os05g10310	acid phosphatase, putative, expressed	3.813504	3.855844	3.704216	4.006116	4.9262	5.131862	5.642924	5.618489	0.601675	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.28394.2.S1_s_at	LOC_Os05g38680	plant-specific domain TIGR01589 family protein, expressed	4.05732	3.893381	3.62651	3.793592	8.032218	7.827926	8.609268	8.988075	0.868599	NA
Os.15043.1.S1_at	LOC_Os01g02560	Ser/Thr receptor-like kinase, putative, expressed	4.113568	4.184765	4.136702	4.081026	5.250172	5.294037	5.895709	6.30454	0.82802	NA
Os.52563.2.S1_x_at	LOC_Os02g40200	receptor-like protein kinase precursor, putative, expressed	4.163176	4.22029	4.073489	4.084605	4.629321	4.55894	5.03979	5.409673	0.630601	NA
Os.55776.1.S1_at	LOC_Os01g06876	Cf-2, putative, expressed	4.213262	4.443141	4.215946	4.392555	5.466582	4.959989	6.184606	6.252112	1.005074	NA
Os.53728.1.S1_at	LOC_Os09g30454	OsWAK87 - OsWAK receptor-like protein kinase, expressed	4.582526	4.349131	4.463951	4.526992	6.50438	6.043897	7.281813	7.43505	1.084293	NA
Os.26537.1.S1_a_at	LOC_Os01g70520	beta-glucosidase homolog precursor, putative, expressed	4.687863	4.724508	5.001143	4.811372	6.994912	7.4164	8.105292	7.946807	0.820394	NA
Os.12660.1.S2_at	LOC_Os07g38800	lectin-like receptor kinase 7, putative, expressed	4.735877	4.784016	5.124755	5.561349	6.289243	6.339156	6.604233	7.215878	0.595856	NA
Os.57171.1.S1_at	LOC_Os02g38740	expressed protein	4.737839	4.854016	5.135573	4.982442	7.5445	7.503387	8.483302	8.249673	0.842544	NA
Os.21240.2.S1_at	LOC_Os10g05250	protein kinase domain containing protein, expressed	4.744264	4.341023	5.116708	5.39592	7.473063	6.972952	7.7935	8.144437	0.745961	NA
Os.22681.1.S1_at	LOC_Os01g41810	cytochrome P450 72A1, putative, expressed	4.769477	4.51536	4.95924	5.466804	7.744928	7.654342	8.415063	8.427831	0.721812	NA
Os.45887.1.S1_at	LOC_Os01g12750	cytochrome P450 71A4, putative, expressed	4.834868	4.517434	4.635402	4.947735	8.840758	9.001058	9.799401	9.583986	0.770785	NA
OsAffx.19104.1.S1_at	LOC_Os11g31540	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	4.883621	5.362003	6.226917	6.048839	8.031551	6.759138	8.486398	8.481649	1.088679	NA
Os.34631.1.S1_at	LOC_Os07g02630	expressed protein	4.982518	5.182859	5.092412	5.277475	5.287967	5.130332	5.962232	6.071569	0.807751	NA
Os.25496.1.S1_at	LOC_Os11g07930	retinol dehydrogenase 13, putative, expressed	5.007602	4.883896	4.907907	5.122061	7.667628	7.687838	8.315055	8.499005	0.729297	NA
Os.13008.1.S1_at	LOC_Os08g39850	lipoxygenase 8, chloroplast precursor, putative, expressed	5.271228	5.427598	5.706467	5.830443	9.535715	9.687109	10.15781	10.51721	0.726097	NA
Os.26891.1.A1_x_at	LOC_Os01g41820	cytochrome P450 72A1, putative, expressed	5.346846	4.928667	5.26979	5.077729	7.148229	7.246844	8.201557	7.884865	0.845674	NA
Os.53784.1.S1_at	LOC_Os02g02000	cytochrome P450 74A4, putative, expressed	5.385652	5.415354	5.924029	6.101184	9.051638	9.029981	9.672156	9.605387	0.597962	0.612104
Os.7879.2.S1_at	LOC_Os04g56400	glutamine synthetase, chloroplast precursor, putative, expressed	5.388456	5.703371	6.530319	6.742922	8.793282	8.852736	9.54648	9.515282	0.707872	1.090706
Os.52538.1.S1_s_at	LOC_Os12g10660	salt tolerance-like protein, putative, expressed	5.425522	5.322714	5.641591	5.470932	5.90167	5.943582	6.57419	6.925791	0.827364	NA
Os.52699.1.S1_at	LOC_Os04g55420	protein binding protein, putative, expressed	5.619156	5.820939	5.754227	5.739835	6.509476	6.75501	7.201922	7.55003	0.743733	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.55402.1.S1_at	LOC_Os11g43520	OsGrx_C17 - glutaredoxin subgroup III, expressed	5.704053	5.704053	6.103699	5.857842	8.028468	8.457511	9.501393	10.23184	1.623626	NA
Os.54146.1.S1_at	LOC_Os02g53130	nitrate reductase, putative, expressed	5.745572	5.448965	7.479655	8.024856	4.707005	4.799625	8.396755	7.757421	3.323774	2.154987
Os.51460.1.S1_at	LOC_Os02g33380	pectinesterase inhibitor domain containing protein, expressed	5.930687	5.794473	5.751708	5.80952	10.37858	10.06798	11.17164	10.94984	0.837462	NA
Os.50175.2.S1_at	LOC_Os04g51820	cation transporter HKT4, putative, expressed	6.144759	5.999044	6.420196	6.226917	7.374522	7.536767	8.347363	8.001606	0.71884	NA
Os.8468.1.S1_s_at	LOC_Os12g25180	expressed protein	6.146369	6.282097	6.019373	6.256119	7.460507	7.588461	8.775196	8.549426	1.137827	NA
Os.51323.1.S1_at	LOC_Os12g14540	expressed protein	6.148188	6.096965	6.168035	6.580651	6.652263	6.824693	7.483414	7.886749	0.946603	NA
Os.7512.1.S1_at	LOC_Os04g56990	transfactor, putative, expressed	6.168921	6.579547	8.668597	8.89498	5.735239	6.00607	7.872122	7.644027	1.88742	2.407555
Os.1191.1.S1_at	LOC_Os03g04060	basic endochitinase C precursor, putative, expressed	6.172519	5.715064	6.697344	6.452886	10.0249	9.303751	10.71013	10.61018	0.995834	NA
Os.31870.1.S1_at	LOC_Os01g24010	PDR5-like ABC transporter, putative, expressed	6.22081	6.139075	6.163973	6.342832	6.079214	6.284881	6.792423	6.850824	0.639576	NA
OsAffx.12954.1.S1_at	LOC_Os03g20680	embryonic protein DC-8, putative, expressed	6.286554	6.028867	5.904238	6.035597	7.34413	7.320973	8.77957	8.224013	1.16924	NA
Os.50903.1.S1_at	LOC_Os09g08130	indole-3-glycerol phosphate synthase, chloroplast precursor, putative, expressed	6.297603	6.403171	6.934149	6.448122	8.989093	8.2944	9.760191	10.89616	1.68643	NA
Os.12106.1.S1_at	LOC_Os03g48780	oxalate oxidase 2 precursor, putative, expressed	6.309907	6.306442	6.255158	5.723942	8.599141	8.692649	9.457106	9.445585	0.805451	NA
Os.15815.1.S1_at	LOC_Os08g01490	cytochrome P450 71C4, putative, expressed	6.322769	6.618728	6.830564	6.980529	8.647541	8.479893	9.644695	9.55992	1.03859	NA
Os.31088.1.S1_at	LOC_Os01g27140	glutaredoxin, putative, expressed	6.368606	6.031282	6.074129	5.707782	10.75006	10.98306	11.72326	12.04539	1.017759	NA
Os.49803.1.S1_at	LOC_Os07g35690	CRK6, putative, expressed	6.38211	6.324033	6.203382	6.414986	6.390527	6.244172	6.994797	7.004108	0.682103	NA
Os.27513.1.A1_a_at	LOC_Os01g11054	phosphoenolpyruvate carboxylase 1, putative, expressed	6.415352	6.372656	6.800466	7.022856	6.932284	6.82217	7.830813	7.709046	0.892703	NA
Os.6129.1.S1_at	LOC_Os11g43990	expressed protein	6.542912	6.634475	6.795814	6.939711	7.194699	7.349685	7.926505	8.070549	0.726335	NA
Os.54291.1.S1_at	LOC_Os11g42200	laccase LAC2-1, putative, expressed	6.620724	6.723863	7.983008	7.74685	6.02539	6.076435	7.127347	7.209793	1.117657	1.192636
Os.27591.1.A1_at	LOC_Os04g12499	amino acid permease, putative	6.816097	6.644837	6.970362	7.005633	8.525169	8.335633	10.20869	9.737518	1.542702	NA
OsAffx.5702.1.S1_s_at	LOC_Os08g04560	aromatic-L-amino-acid decarboxylase, putative, expressed	7.054479	7.54325	8.126563	7.680544	9.138226	8.534517	9.81816	9.901542	1.02348	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.54109.1.S1_at	LOC_Os03g38800	mitochondrial protein, putative, expressed	7.067833	6.413262	7.384009	7.345989	5.67216	5.548761	6.330041	6.178566	0.643843	NA
Os.54467.1.S1_at	LOC_Os03g21710	WRKY DNA binding domain containing protein, expressed	7.081001	7.108489	7.681458	7.655389	5.624324	5.717717	6.624016	6.862716	1.072346	NA
Os.28823.1.S1_at	LOC_Os01g37750	glutathione S-transferase GSTU6, putative, expressed	7.235056	7.756905	7.60444	7.992899	8.337332	8.265793	9.374936	9.155105	0.963458	NA
Os.27963.1.A1_at	LOC_Os01g72900	abscisic stress ripening protein 1, putative, expressed	7.282751	6.966223	8.120243	7.95304	8.27019	8.552833	9.526561	9.424435	1.063987	0.912154
Os.405.1.S1_a_at	LOC_Os12g37260	lipoxygenase 2.1, chloroplast precursor, putative, expressed	7.31034	7.551018	7.232761	7.200861	10.93423	10.44699	11.61737	11.80081	1.018478	NA
OsAffx.19473.1.S1_at	LOC_Os12g03740	ATPP2-B10, putative, expressed	7.509512	7.826649	8.281437	8.115079	6.108562	5.842843	6.637821	6.913421	0.799919	NA
Os.49329.1.S1_at	LOC_Os02g35490	MLO-like protein 1, putative, expressed	7.512031	7.624139	8.292158	8.186689	6.183658	5.730152	6.732793	7.243977	1.03148	NA
OsAffx.13282.1.S1_s_at	LOC_Os03g41330	seed specific protein Bn15D17A, putative, expressed	7.551337	7.39829	10.01491	10.12327	5.691804	5.796925	7.387635	7.537277	1.718091	2.594279
Os.5242.1.S1_at	LOC_Os01g58240	peptidase/ subtilase, putative, expressed	7.615982	7.043247	8.204342	8.462361	5.621064	4.997089	6.711348	7.30161	1.697402	NA
Os.12163.1.S1_at	LOC_Os03g12510	non-symbiotic hemoglobin 2, putative, expressed	7.853378	8.127675	11.07765	10.9153	7.127072	6.929176	9.337126	9.57972	2.430299	3.005947
Os.51480.1.S1_at	LOC_Os01g62980	lipid binding protein, putative, expressed	7.918574	7.845687	7.840664	8.236736	9.076952	9.17523	9.842233	9.781174	0.685612	NA
Os.14520.1.S1_at	LOC_Os03g48030	HPP, putative, expressed	8.096609	8.55581	10.73844	11.16789	8.719772	8.735252	10.41134	10.98382	1.970072	2.626953
Os.34767.2.S1_s_at	LOC_Os03g12530	metal tolerance protein C3, putative, expressed	8.098355	7.873437	7.915427	7.833987	9.790473	9.765557	10.51296	10.37801	0.667468	NA
Os.53148.1.S1_at	LOC_Os03g52720	magnesium-dependent phosphatase 1, putative, expressed	8.161062	8.192281	8.093416	7.887435	6.806837	6.435575	7.394248	7.485602	0.818719	NA
Os.54420.1.S1_at	LOC_Os01g16980	expressed protein	8.207645	8.036037	8.72616	8.695754	8.777955	8.72668	9.541408	9.14685	0.591811	NA
Os.54481.2.S1_at	LOC_Os04g49460	ATP binding protein, putative, expressed	8.321931	8.623456	8.839524	9.211528	6.963738	6.756753	7.72801	8.083976	1.045748	NA
Os.17325.1.S1_at	LOC_Os03g03200	hydrolase, putative, expressed	8.335712	8.616916	9.081829	8.983885	7.51244	7.435041	8.15909	8.069767	0.640688	NA
Os.551.1.S1_at	LOC_Os01g08110	flavonol-3-O-glycoside-7-O-glucosyltransferase 1, putative, expressed	8.401481	8.742649	8.66768	8.747431	6.50626	6.682802	7.412514	7.156446	0.689949	NA
Os.11851.1.S1_at	LOC_Os03g11900	sugar transport protein 8, putative, expressed	8.401563	8.492138	8.813652	9.155553	10.15873	9.618194	10.71036	10.86441	0.898921	NA
Os.18193.1.S1_at	LOC_Os04g44650	ferredoxin-thioredoxin reductase, variable chain, putative, expressed	8.420201	8.288967	8.918802	9.137407	8.978586	8.787984	9.925563	9.737518	0.948256	0.67352

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.7372.1.S1_at	LOC_Os01g72910	abscisic stress ripening protein 2, putative, expressed	8.434205	8.187732	8.615925	8.82768	9.015979	9.348883	9.775185	10.10873	0.759525	NA
Os.12119.1.S1_at	LOC_Os01g64470	YLS9, putative, expressed	8.471124	8.356067	8.878945	8.961539	8.612199	8.785906	9.27203	9.545478	0.709701	NA
Os.36834.1.S1_at	LOC_Os04g54830	expressed protein	8.65511	8.630683	9.750336	9.813055	7.718913	7.477209	8.807066	8.766646	1.188794	1.1388
Os.36767.1.S1_at	LOC_Os01g04330	calmodulin-related protein 2, touch-induced, putative, expressed	8.701379	8.573868	9.524681	9.506936	9.549523	9.429696	10.69188	10.68154	1.1971	0.878186
Os.33446.1.A1_at	LOC_Os03g13250	peptide transporter PTR2, putative, expressed	8.782834	9.077107	9.650967	9.713877	7.338242	7.479054	8.099701	8.220012	0.751209	0.752451
Os.47891.1.S1_at	LOC_Os04g45280	aprataxin, putative, expressed	8.80128	8.612942	8.755239	8.609309	7.063061	7.126038	7.7746	7.644399	0.61495	NA
Os.8043.1.S1_at	LOC_Os03g51010	monoglyceride lipase, putative, expressed	8.805437	8.64054	9.074588	9.3181	9.149297	9.277096	10.18034	9.836402	0.795173	NA
Os.12239.1.S1_at	LOC_Os09g31031	ubiquitin, putative, expressed	8.839576	8.209625	9.51545	9.572892	7.910202	7.692341	8.935042	9.080033	1.206266	1.01957
Os.11287.1.S1_at	LOC_Os06g50930	senescence-associated protein DIN1, putative, expressed	8.918052	9.200002	9.954555	10.26783	8.74937	8.728319	9.336786	9.3596	0.609349	1.052164
Os.170.3.S1_at	LOC_Os01g64120	ferredoxin-6, chloroplast precursor, putative, expressed	8.93964	8.946957	11.93435	12.52096	8.868671	9.197967	13.28101	13.2314	4.222882	3.28436
Os.15045.1.S1_at	LOC_Os04g56790	TLD family protein, expressed	8.996372	8.923811	10.01575	10.48822	8.529125	8.388237	10.04098	9.804022	1.46382	1.291891
Os.49198.1.S1_at	LOC_Os04g58090	NHL25, putative, expressed	9.049435	9.339335	9.698893	9.850688	8.702295	8.47907	9.370402	9.38751	0.788274	NA
Os.27207.1.S1_at	LOC_Os12g25200	chloride channel protein CLC-a, putative, expressed	9.209539	9.667618	10.92251	11.19349	7.97881	8.541238	11.28383	11.00722	2.885497	1.619421
Os.8504.1.S1_at	LOC_Os04g42420	nodulin-like protein, putative, expressed	9.236638	9.036365	9.604971	9.73625	9.94481	10.15372	10.73246	10.69446	0.664195	NA
Os.20575.1.S1_at	LOC_Os03g62240	expressed protein	9.240738	9.615574	10.24267	10.1372	11.34466	11.39878	11.937	12.08739	0.640474	0.761775
Os.10272.1.S1_at	LOC_Os08g20570	chloride channel-like protein CLC-g, putative, expressed	9.264805	9.01532	9.821842	9.65624	8.26461	8.390187	9.431899	9.250314	1.013708	0.598978
Os.20204.3.S1_a_at	LOC_Os02g12380	histone deacetylase, putative, expressed	9.280996	9.557722	9.970934	10.06883	7.546814	7.699337	8.732201	8.335323	0.910687	NA
OsAffx.30403.1.S1_at	LOC_Os03g03680	major facilitator superfamily protein, expressed	9.5228	9.566864	9.49781	9.37932	10.06915	10.32823	11.50675	11.28619	1.197777	NA
Os.5562.1.S1_at	LOC_Os04g51150	transposon protein, putative, unclassified, expressed	9.589229	9.394806	9.585632	9.74863	8.374572	8.253509	9.011631	8.957608	0.670579	NA
Os.55600.1.S1_at	LOC_Os04g08550	NAD(P)H-dependent oxidoreductase, putative, expressed	9.591003	9.545349	9.948944	9.979096	8.466066	8.208023	9.247041	9.331748	0.95235	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.49482.1.S1_at	LOC_Os01g12920	thioesterase family protein, expressed	9.662954	10.03342	10.09231	10.31957	8.120397	8.319391	9.039636	9.02328	0.811564	NA
Os.21415.1.S1_at	LOC_Os12g06100	TLD family protein, expressed	9.76698	9.817296	10.41607	10.48883	8.69205	8.881418	9.814007	9.799504	1.020021	0.660315
Os.6847.1.S1_at	LOC_Os07g22350	glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor, putative, expressed	10.07168	10.03215	11.67527	11.67815	9.312112	9.070808	10.29341	10.22565	1.068067	1.624794
Os.15471.1.S1_at	LOC_Os07g44410	WD40-like Beta Propeller Repeat family protein, expressed	10.20317	10.19436	10.51786	10.64379	8.728465	8.552591	9.23418	9.425889	0.689506	NA
Os.15877.1.S1_at	LOC_Os11g29400	6-phosphogluconate dehydrogenase, decarboxylating, putative, expressed	10.2154	10.08668	11.80079	11.88227	8.801136	8.41022	10.56772	10.21	1.783184	1.690491
Os.13015.1.S1_at	LOC_Os10g38360	glutathione S-transferase GSTU6, putative, expressed	10.26169	10.56805	10.87156	10.92847	6.489724	6.670451	7.874305	8.037019	1.375575	NA
OsAffx.26317.1.S2_at	LOC_Os04g33920	lipid binding protein, putative, expressed	10.50805	10.54729	10.42348	10.99927	7.436873	7.652349	9.413215	8.920496	1.622245	NA
Os.11961.1.S1_at	LOC_Os05g38040	expressed protein	10.63612	11.0665	12.85174	12.854	9.245688	9.383364	10.13182	10.65805	1.080408	2.001559
Os.141.1.S1_at	LOC_Os03g57120	ferredoxin--NADP reductase, root isozyme, chloroplast precursor, putative, expressed	11.02392	11.09614	12.48838	12.73325	8.794005	8.336151	10.65295	10.38532	1.954057	1.550785
Os.159.1.S1_s_at	LOC_Os03g13210	peroxidase N precursor, putative, expressed	11.10879	10.73766	11.82676	11.29598	6.050393	5.163196	6.833642	6.441747	1.0309	NA
Os.10774.1.S1_at	LOC_Os08g05570	monodehydroascorbate reductase, chloroplast precursor, putative, expressed	11.18579	11.01473	12.43213	12.30669	9.841455	9.749128	11.00351	10.86315	1.138034	1.269153
Os.142.2.A1_a_at	LOC_Os01g25484	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed	11.43015	11.32216	13.59342	13.90218	10.79963	11.35548	13.74172	13.76339	2.674998	2.371638
Os.11195.1.S1_at	LOC_Os07g17330	B12D protein, expressed	11.57904	11.28071	11.5999	11.56276	10.16149	9.866649	10.68061	10.96229	0.807382	NA
Os.18707.1.S1_at	LOC_Os11g04020	major facilitator superfamily antiporter, putative, expressed	12.62145	12.85597	12.02529	12.4388	4.223189	4.348154	5.292359	5.102935	0.911976	NA
Os.49030.1.A1_s_at	LOC_Os09g20220	glutathione S-transferase, putative, expressed	12.7481	13.31765	12.72011	12.6913	6.267594	5.955992	8.251759	7.5734	1.800786	NA
Os.4863.1.S1_at	LOC_Os01g44050	siroheme synthase, putative, expressed	16.7331	16.6491	20.29666	20.7324	13.36758	13.97181	16.68782	17.11258	3.230512	3.823426
Os.7338.1.S1_at	LOC_Os07g28850	argonaute-like protein, putative, expressed	17.00625	16.34889	18.17648	17.91718	14.9087	14.42069	15.83019	16.3448	1.422801	NA
Os.11800.1.S1_at	LOC_Os01g50100	multidrug resistance protein 4, putative, expressed	17.98069	18.03889	19.07193	19.29711	22.19053	21.59891	24.11722	25.93754	3.132666	NA

Affy_ID	Gene ID		1.Os_root_control.CEL	2.Os_root_control.CEL	1.Os_root_N+.CEL	2.Os_root_N+.CEL	1.Os_shoot_control.CEL	2.Os_shoot_control.CEL	1.Os_shoot_N+.CEL	2.Os_shoot_N+.CEL	SHOOT	ROOT
Os.12191.1.S1_at	LOC_Os03g13140	non-symbiotic hemoglobin 2, putative, expressed	18.02063	17.56711	22.93766	22.03343	12.8633	12.94502	16.19752	16.48756	3.438376	4.691672
Os.6075.1.S1_at	LOC_Os04g06520	expressed protein	19.72222	19.40995	20.92157	20.42576	15.95862	15.4093	17.04805	16.78379	1.231962	NA
Os.49628.1.S1_at	LOC_Os05g38140	bHLH transcription factor, putative, expressed	22.34337	22.9677	23.52096	23.48282	19.40949	19.5851	21.02106	20.7993	1.412886	NA
Os.321.1.S1_at	LOC_Os05g37140	cytochrome P450 86A2, putative, expressed	20.52768	20.2803	22.97931	23.16294	18.2915	18.11269	19.33953	19.56151	1.248422	2.667139

Table 32. Genes regulated by nitrogen in roots and shoots of Arabidopsis are sorted based on their regulation according to the ANOVA

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At3g02750	Protein phosphatase 2C family protein	6.45782	6.40555	7.13413	7.14702	7.44663	7.52082	8.07272	7.6748	NA	0.70889	258602_at
At1g03600	PSB27, photosystem II family protein	5.38237	4.55579	6.5876	6.60586	11.3413	11.6943	11.2295	11.2838	NA	1.62765	264837_at
At1g14730	Cytochrome b561/ferric reductase transmembrane protein family	7.48379	7.20926	8.6953	8.5589	5.40494	5.39892	5.76703	5.36199	NA	1.28057	262831_at
At5g48000	CYP708 A2, CYP708A2, THAH, THAH1, cytochrome P450, family 708, subfamily A, polypeptide 2	6.16416	5.70783	6.87653	7.12615	4.88203	4.82456	4.83879	4.77373	NA	1.06535	248728_at
At5g60750	CAAX amino terminal protease family protein	6.64306	6.47032	7.50896	7.36129	7.47336	7.47741	7.73931	7.39162	NA	0.87844	247583_at
At2g01950	BRL2, VH1, BRI1-like 2	6.85961	6.93055	7.66881	8.1265	5.40689	5.59779	5.47311	6.13547	NA	1.00258	265250_at
At2g24550	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G31510.1); Has 219 Blast hits to 219 proteins in 33 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 2; Plants - 184; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).	9.35731	8.91651	10.2212	9.97427	7.27157	7.0794	7.752	7.23434	NA	0.96081	263799_at
At3g13730	CYP90D1, cytochrome P450, family 90, subfamily D, polypeptide 1	5.77582	6.7331	8.07565	8.72296	5.39719	5.54017	6.16309	6.25923	NA	2.14485	256788_at
At3g04530	ATPPCK2, PEPCK2, PPCK2, phosphoenolpyruvate carboxylase kinase 2	6.47859	6.43136	8.52251	8.03427	5.51781	5.22938	5.32902	5.54345	NA	1.82342	258570_at
At5g14940	Major facilitator superfamily protein	6.68955	7.27124	8.09835	8.11974	6.68992	6.63991	6.20147	6.49492	NA	1.12865	246566_at
At3g49430	SRp34a, SER/ARG-rich protein 34A	6.34125	6.44664	7.10037	7.22891	6.86535	7.04049	6.81892	6.87287	NA	0.77069	252256_at
At5g24120	ATSIG5, SIG5, SIGE, sigma factor E	6.34657	5.9068	7.18593	7.49402	8.69744	8.83568	9.37232	9.4249	NA	1.21329	249769_at

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Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g01040	ASU1, ATDCL1, CAF, DCL1, EMB60, EMB76, SIN1, SUS1, dicer-like 1	5.63114	5.809	6.85987	6.68803	6.27794	6.21252	6.40826	6.1915	NA	1.05387	261584_at
At1g64740	TUA1, alpha-1 tubulin	7.05517	6.82105	7.82129	7.68247	8.62482	8.88281	9.1725	9.37762	NA	0.81377	262885_at
At4g26130	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G56980.1); Has 121 Blast hits to 116 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 113; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	6.63956	6.70801	7.42702	7.59018	6.97048	6.92605	7.32364	7.49275	NA	0.83482	253989_at
At3g49060	U-box domain-containing protein kinase family protein	5.93931	5.91062	6.53362	6.73761	6.23736	6.43479	5.97226	5.98639	NA	0.71065	252298_at
At5g01340	Mitochondrial substrate carrier family protein	6.14594	6.18497	7.34137	7.77022	6.47859	6.31633	6.89611	7.14254	NA	1.39035	251090_at
At1g09740	Adenine nucleotide alpha hydrolases-like superfamily protein	8.64141	8.31714	9.34267	8.98161	7.70033	7.59672	8.119	8.27046	NA	0.68287	264708_at
At1g74660	MIF1, mini zinc finger 1	7.33291	6.47261	7.8875	8.0057	5.52748	5.40164	5.949	6.06616	NA	1.04384	260226_at
At1g63970	ISPF, MECPS, isoprenoid F	5.3777	5.7027	6.41011	6.53897	7.69233	7.48371	7.54902	7.46288	NA	0.93434	260324_at
At3g06410	Zinc finger C-x8-C-x5-C-x3-H type family protein	6.29659	6.20553	7.07228	7.33855	7.4306	7.49005	7.32746	7.29698	NA	0.95435	258903_at
At2g35800	mitochondrial substrate carrier family protein	5.35576	4.85616	6.74711	6.70384	7.17497	7.19461	6.98468	6.84525	NA	1.61951	263943_at
At3g16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	8.14574	8.20378	10.0735	9.46794	7.19886	7.36692	7.0905	6.93751	NA	1.59598	258338_at
At1g75440	UBC16, ubiquitin-conjugating enzyme 16	7.09963	7.06137	8.12929	8.45997	7.30805	7.53684	7.57253	7.44622	NA	1.21413	261110_at
At4g16370	ATOPT3, OPT3, OPT3, oligopeptide transporter	6.45687	6.35433	7.47974	7.82452	8.01324	8.03454	8.26788	8.40379	NA	1.24653	245296_at
At3g15710	Peptidase S24/S26A/S26B/S26C family protein	7.11606	7.07335	8.02353	8.22119	8.02398	7.7368	7.85122	7.78245	NA	1.02766	258276_at
At2g45220	Plant invertase/pectin methylesterase inhibitor superfamily	8.59775	8.75756	9.39407	9.27123	9.91903	9.58367	10.2285	10.2347	NA	0.655	245148_at
At5g59210	myosin heavy chain-related	5.97505	6.06282	6.87153	6.92332	6.65927	6.91065	6.77912	6.86062	NA	0.87849	247738_at
At3g27210	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40860.1); Has 133 Blast hits to 98 proteins in 25 species: Archae - 0; Bacteria - 6; Metazoa - 32; Fungi - 7; Plants - 70; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	7.19824	6.52962	7.45769	7.66151	5.17384	4.90325	5.46051	5.7268	NA	0.69567	257154_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At2g22475	GEM, GRAM domain family protein	5.38253	5.30334	6.17492	6.36452	5.49334	5.59307	6.02123	6.07359	NA	0.92678	264003_at
At1g07700	Thioredoxin superfamily protein	6.77559	5.93601	7.585	7.73958	8.5747	8.61415	8.78315	8.73811	NA	1.30649	261417_at
At1g02110	Protein of unknown function (DUF630 and DUF632)	4.04075	4.20399	5.08686	5.19777	5.01065	5.24905	5.03564	5.35344	NA	1.01994	264176_at
At5g58500	LSH5, Protein of unknown function (DUF640)	6.49555	6.45988	7.18655	7.37691	5.62698	5.62031	5.77084	5.87512	NA	0.80401	247827_at
At5g17700	MATE efflux family protein	4.23947	4.30814	5.15108	4.97229	5.45699	5.03494	5.48059	5.37914	NA	0.78788	250045_at
At1g52080	AR791, actin binding protein family	5.937	5.64465	6.87674	6.70913	5.97969	5.93513	5.74863	5.63545	NA	1.00211	265059_at
At4g37550	Acetamidase/Formamidase family protein	6.34015	5.294	7.03745	7.26186	9.20433	9.28688	9.75842	10.0078	NA	1.33258	253042_at
At3g52840	BGAL2, beta-galactosidase 2	4.8264	5.38461	6.29393	6.26718	7.21107	7.39916	6.79838	6.97394	NA	1.17505	251996_at
At5g49830	EXO84B, exocyst complex component 84B	7.21868	7.1978	8.22228	8.07806	7.82306	7.6319	8.14925	7.90323	NA	0.94193	248574_at
At5g41010	NRPB12, NRPD12, NRPE12, DNA directed RNA polymerase, 7 kDa subunit	7.64484	7.65397	8.28353	8.3445	7.25438	7.29836	7.45344	7.6472	NA	0.66461	249335_at
At5g35630	ATGSL1, GLN2, GS2, glutamine synthetase 2	8.04994	7.83496	8.94245	9.22455	11.2131	11.229	11.6148	11.6088	NA	1.14105	249710_at
At2g16890	UDP-Glycosyltransferase superfamily protein	6.10032	6.59367	7.23824	7.58635	4.68788	4.55932	5.22089	5.65723	NA	1.0653	266532_at
At1g09900	Pentatricopeptide repeat (PPR-like) superfamily protein	5.5383	5.46535	6.40798	6.44845	7.16491	6.92776	6.4381	6.62843	NA	0.92639	264689_at
At3g29160	AKIN11, ATKIN11, KIN11, SNRK1.2, SNF1 kinase homolog 11	7.56426	7.27924	8.2856	8.52648	7.151	7.02936	7.28391	7.24844	NA	0.98429	258221_at
At2g44520	COX10, cytochrome c oxidase 10	6.12998	6.08428	7.01045	7.02222	6.66441	6.72844	6.92184	6.69524	NA	0.9092	267342_at
At4g25080	CHLM, magnesium-protoporphyrin IX methyltransferase	5.95423	5.21434	7.52288	7.18739	10.1864	10.3598	9.95986	10.0433	NA	1.77085	254105_at
At1g68440	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G25400.2); Has 86 Blast hits to 86 proteins in 29 species: Archae - 0; Bacteria - 6; Metazoa - 27; Fungi - 11; Plants - 24; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	7.69829	7.15146	8.94835	9.09906	9.03698	8.97825	9.32546	8.78118	NA	1.59883	259856_at
At5g47740	Adenine nucleotide alpha hydrolases-like superfamily protein	5.27115	5.0279	6.69956	6.72665	4.69792	4.69842	4.65204	4.55977	NA	1.56359	248770_at
At4g17070	peptidyl-prolyl cis-trans isomerases	5.40237	5.34802	6.12323	6.24089	6.47344	6.57703	6.30913	6.46786	NA	0.80687	245266_at
At1g23390	Kelch repeat-containing F-box family protein	8.57304	8.21437	9.7275	9.4481	11.7676	11.5845	10.8408	11.3189	NA	1.19409	262986_at
At5g08350	GRAM domain-containing protein / ABA-responsive protein-related	7.60238	7.92369	8.69634	8.70934	6.61008	6.64492	7.22786	6.86616	NA	0.93981	246034_at
At3g13430	RING/U-box superfamily protein	6.12529	6.28692	7.30643	7.10856	6.10604	6.0168	6.13	5.96423	NA	1.00139	256958_at
At1g08430	ALMT1, ATALMT1, aluminum-activated malate transporter 1	4.76391	4.88303	5.92953	6.34144	4.25591	4.23929	4.36939	4.35016	NA	1.31202	257481_at
At5g08340	Nucleotidylyl transferase superfamily protein	4.22888	4.56194	5.1336	5.06789	5.43487	5.57048	5.60535	5.55343	NA	0.70534	246053_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g80020	transposable element gene	5.53788	5.56521	6.21494	6.33633	5.9714	6.07524	5.88659	5.99998	NA	0.72409	262052_at
At5g58700	ATPLC4, PLC4, phosphatidylinositol-speciwc phospholipase C4	6.24767	6.26023	7.86018	8.01639	5.24467	5.08057	5.60942	5.73738	NA	1.68433	247776_at
At2g46740	D-arabinono-1,4-lactone oxidase family protein	5.78384	5.62631	6.43403	6.93929	4.50986	4.34531	4.55336	4.32228	NA	0.98158	266711_at
At5g42630	ATS, KAN4, Homeodomain-like superfamily protein	5.63948	5.42152	6.13616	6.22786	4.12599	4.22837	4.21772	3.98795	NA	0.65151	249206_at
At4g27720	Major facilitator superfamily protein	6.04291	6.33122	6.94472	6.9786	7.22162	6.99139	7.24337	7.01232	NA	0.7746	253891_at
At3g12750	ZIP1, zinc transporter 1 precursor	6.58224	7.0184	7.65607	8.06831	5.89024	6.0207	6.10044	5.93024	NA	1.06187	257715_at
At4g31800	ATWRKY18, WRKY18, WRKY DNA-binding protein 18	5.17444	5.83733	6.47055	6.7429	6.61077	7.08839	7.63511	7.65566	NA	1.10084	253485_at
At5g38030	MATE efflux family protein	6.79557	6.52454	7.1788	7.42882	4.41916	4.40284	4.36	4.14979	NA	0.64375	249545_at
At2g44050	COS1, COS1, 6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase	7.20762	7.22265	7.88794	7.71256	7.96043	7.85751	8.04339	8.06774	NA	0.58511	267188_at
At5g48170	SLY2, F-box family protein	5.07644	4.9472	5.6824	5.58176	5.17963	4.91221	4.6947	4.64224	NA	0.62026	248741_at
At4g13360	ATP-dependent caseinolytic (Clp) protease/crotonase family protein	7.03607	7.10734	7.95091	7.85811	7.84049	7.93811	7.8611	7.9685	NA	0.8328	254776_at
At1g70410	ATBCA4, BCA4, CA4, beta carbonic anhydrase 4	9.1807	8.7091	9.63956	10.3402	10.4733	10.6129	11.305	11.1646	NA	1.04497	264313_at
At1g76970	Target of Myb protein 1	5.49796	5.7095	6.40177	6.35116	5.42966	5.62675	5.77877	5.63721	NA	0.77274	264951_at
At5g09690	ATMGT7, MGT7, MRS2-7, magnesium transporter 7	4.22971	4.25084	5.03141	5.06541	4.68607	4.51535	4.88446	4.73735	NA	0.80813	250487_at
At2g28120	Major facilitator superfamily protein	6.32509	5.92214	7.33419	7.0598	7.83676	7.74431	8.37457	7.95668	NA	1.07338	266140_at
At1g10390	Nucleoporin autopeptidase	6.66809	6.35754	7.8239	7.66198	7.47831	7.43223	7.40906	7.46924	NA	1.23012	264456_at
At3g55605	Mitochondrial glycoprotein family protein	5.47142	5.60598	6.39467	6.90911	5.2734	5.44052	5.4407	5.62268	NA	1.11319	251760_at
At5g17230	PSY, PHYTOENE SYNTHASE	6.03098	6.18084	6.83253	7.08338	9.84812	9.97319	9.64815	9.41555	NA	0.85204	250095_at
At3g02710	ARM repeat superfamily protein	5.60748	5.69484	6.4327	6.2372	6.01381	5.99566	6.03807	6.00562	NA	0.68379	258478_at
At5g63050	EMB2759, embryo defective 2759	5.95102	5.9376	7.00908	6.72792	7.52558	7.17988	7.45682	7.26753	NA	0.92419	247414_at
At4g04350	EMB2369, tRNA synthetase class I (I, L, M and V) family protein	5.05129	5.07142	5.68131	5.61938	6.52644	6.54856	6.12562	6.1322	NA	0.58898	255328_at
At5g17280	CONTAINS InterPro DOMAIN/s: Oxidoreductase-like, N-terminal (InterPro:IPR019180); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	6.52738	6.67807	7.36318	7.12479	7.85094	7.55682	7.89943	8.01598	NA	0.64127	250097_at
At5g61030	GR-RBP3, glycine-rich RNA-binding protein 3	6.58727	6.7946	7.70062	7.464	6.1355	5.86218	6.19522	6.04016	NA	0.89138	247575_at
At1g80630	RNI-like superfamily protein	5.02383	4.84956	5.65083	5.50439	6.02779	6.18401	5.9682	5.82433	NA	0.64091	259830_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g43190	Galactose oxidase/kelch repeat superfamily protein	6.48368	6.66406	7.21664	7.22516	7.52076	7.58187	7.53838	7.5863	NA	0.64703	249140_at
At2g39950	unknown protein; Has 978 Blast hits to 254 proteins in 81 species: Archae - 0; Bacteria - 8; Metazoa - 109; Fungi - 53; Plants - 41; Viruses - 0; Other Eukaryotes - 767 (source: NCBI BLink).	5.69541	5.79791	6.48771	6.63117	6.55422	6.54965	6.9802	6.64476	NA	0.81278	267347_at
At1g48790	AMSH1, associated molecule with the SH3 domain of STAM 1	8.05011	7.91581	8.7917	8.67408	8.51839	8.34269	8.64002	8.61077	NA	0.74993	256142_at
At2g03240	EXS (ERD1/XPR1/SYG1) family protein	7.11234	6.95673	8.07065	8.65337	6.80383	6.89347	6.72563	6.77189	NA	1.32748	266732_at
At5g14050	Transducin/WD40 repeat-like superfamily protein	7.062	7.00106	7.87928	7.95773	7.71959	7.70898	7.66689	7.86851	NA	0.88698	250222_at
At5g64680	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 114 Blast hits to 110 proteins in 37 species: Archae - 0; Bacteria - 0; Metazoa - 42; Fungi - 10; Plants - 37; Viruses - 0; Other Eukaryotes - 25 (source: NCBI BLink).	6.27602	6.35545	6.94385	6.88037	6.1515	6.03037	6.21413	6.31477	NA	0.59637	247241_at
At4g16265	NRPB9B, NRPD9B, NRPE9B, RNA polymerases M/15 Kd subunit	5.24203	5.38185	6.1592	6.41029	4.91496	4.8996	5.08977	4.97124	NA	0.97281	245367_at
At3g01350	Major facilitator superfamily protein	6.35853	5.69105	7.5669	7.54617	5.21273	5.23001	4.8964	5.21137	NA	1.53174	259116_at
At4g00560	NAD(P)-binding Rossmann-fold superfamily protein	5.86255	5.964	6.81554	6.5816	7.23504	7.01693	7.07025	7.13882	NA	0.78529	255682_at
At5g67240	SDN3, small RNA degrading nuclease 3	6.80888	6.55053	7.5476	7.83234	6.73877	6.77661	6.65821	6.77989	NA	1.01026	247032_at
At5g67290	FAD-dependent oxidoreductase family protein	6.03526	6.06848	6.84921	6.73191	7.64144	7.4778	7.48445	7.1737	NA	0.73869	246985_at
At5g40870	ATUK/UPRT1, UK/UPRT1, UKL1, uridine kinase/uracil phosphoribosyltransferase 1	5.62629	5.71386	6.82328	6.75356	6.05826	5.85684	5.8308	5.88096	NA	1.11834	249318_at
At3g18940	clast3-related	6.17961	6.49169	7.05388	7.10498	6.41337	6.33314	6.42187	6.39572	NA	0.74378	256921_at
At2g16980	Major facilitator superfamily protein	5.63382	5.66253	6.84987	6.77567	4.62548	4.73162	4.61051	4.53136	NA	1.16459	266526_at
At1g31020	ATO2, TO2, thioredoxin O2	5.3452	5.28897	6.42051	6.16725	5.96268	5.75382	5.97933	5.80376	NA	0.9768	265104_at
At5g09650	AtPPa6, PPa6, pyrophosphorylase 6	7.85713	7.67501	8.40826	8.65887	8.89996	8.79482	9.17569	9.51348	NA	0.76749	250496_at
At4g19600	CYCT1;4, Cyclin family protein	6.37816	6.13839	7.17472	6.99263	6.33968	6.34697	5.95924	6.10666	NA	0.8254	254526_at
At5g64850	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RPM1-interacting protein 4, defence response (InterPro:IPR008700); BEST Arabidopsis thaliana protein match is: unknown protein	5.13986	5.28336	5.97511	6.3521	7.36989	7.80695	6.85544	7.06736	NA	0.952	247214_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	(TAIR:AT5G09960.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).											
At5g65530	Protein kinase superfamily protein	5.82383	5.59302	7.12778	7.4085	4.66735	4.69334	4.77486	4.91448	NA	1.55972	247170_at
At3g14050	AT-RSH2, ATRSH2, RSH2, RELA/SPOT homolog 2	8.82398	8.31246	9.73804	9.51773	7.68949	7.74129	8.12467	7.62788	NA	1.05966	258207_at
At1g08350	Endomembrane protein 70 protein family	4.90004	5.11747	5.87036	5.91412	5.51008	5.5361	5.35711	5.33009	NA	0.88348	261747_at
At5g63860	UVR8, Regulator of chromosome condensation (RCC1) family protein	6.42677	5.95799	6.95795	6.97982	7.81516	8.02916	7.74376	7.8896	NA	0.77651	247307_at
At4g37760	SQE3, squalene epoxidase 3	5.80488	5.82955	6.59178	6.74512	9.23449	9.36219	9.4849	9.03837	NA	0.85124	253039_at
At3g62300	ATDUF7, DUF7, DOMAIN OF UNKNOWN FUNCTION 724 7	5.2348	5.56957	6.42764	6.23424	5.32719	5.4589	5.15234	5.32717	NA	0.92876	251256_at
At4g39675	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	10.9739	10.6643	12.2823	12.2139	7.19864	7.37212	8.01074	9.22546	NA	1.42903	252882_at
At5g56080	ATNAS2, NAS2, nicotianamine synthase 2	6.77984	6.76106	8.11102	8.92231	5.04755	4.97366	5.02678	5.04545	NA	1.74621	248048_at
At5g13610	Protein of unknown function (DUF155)	4.90538	4.861	5.88659	6.06065	5.68113	5.35925	5.54518	5.55508	NA	1.09043	250250_at
At4g22720	Actin-like ATPase superfamily protein	7.02756	7.27248	7.89345	7.96263	7.6006	7.66419	7.76274	7.84164	NA	0.77802	254273_at
At1g80510	Transmembrane amino acid transporter family protein	6.148	5.81106	7.06358	6.7172	7.45053	7.15536	7.31063	7.2223	NA	0.91085	260290_at
At3g26744	ATICE1, ICE1, SCRM, basic helix-loop-helix (bHLH) DNA-binding superfamily protein	5.26804	5.4642	6.21291	5.91126	8.45981	8.5235	8.17833	8.32279	NA	0.69597	258310_at
At1g23850	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23840.1); Has 47 Blast hits to 40 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.97977	6.39792	8.23684	8.26655	6.0724	5.77169	6.17497	5.87612	NA	1.56286	263032_at
At5g55380	MBOAT (membrane bound O-acyl transferase) family protein	4.9219	4.79326	5.628	5.41677	6.45561	6.12938	6.43952	6.33892	NA	0.66481	248080_at
At1g21360	GLTP2, glycolipid transfer protein 2	5.03776	4.89853	5.67272	5.65836	4.30981	4.19833	4.31211	4.29778	NA	0.6974	260926_at
At5g10510	AIL6, PLT3, AINTEGUMENTA-like 6	5.38519	6.35417	7.15383	7.15872	5.01403	4.69773	4.94149	5.07122	NA	1.2866	250426_at
At4g11090	TBL23, TRICHOME BIREFRINGENCE-LIKE 23	5.82186	5.96327	6.83832	6.64224	7.0255	6.79554	6.91684	6.73172	NA	0.84772	254965_at
At5g50410	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.92791	5.97326	6.65103	6.58311	6.45477	6.61978	6.48447	6.53049	NA	0.66648	248500_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At4g16442	Uncharacterised protein family (UPF0497)	5.32598	5.54948	6.61977	6.44484	7.07524	6.801	6.74292	6.91017	NA	1.09458	245338_at
At2g34180	ATWL2, CIPK13, SnRK3.7, WL2, CBL-interacting protein kinase 13	4.36743	4.42275	6.76392	6.72688	4.48409	4.43356	4.56858	4.46102	NA	2.35031	267045_at
At2g40900	nodulin MtN21 /EamA-like transporter family protein	8.2572	7.88291	9.24566	9.12438	6.49469	6.24393	6.2458	6.33327	NA	1.11497	245090_at
At1g61100	disease resistance protein (TIR class), putative	5.57152	5.20489	7.22153	6.80494	7.13998	6.62774	7.53104	7.30326	NA	1.62503	264910_at
At5g22950	VPS24.1, SNF7 family protein	7.91669	7.53497	8.62139	8.37991	7.29643	7.36964	7.56924	7.61807	NA	0.77482	249863_at
At3g56200	Transmembrane amino acid transporter family protein	5.71414	5.58731	6.92602	7.11521	6.77595	6.79157	6.6737	6.52806	NA	1.36989	251722_at
At5g04550	Protein of unknown function (DUF668)	6.49401	6.22563	7.17647	7.09834	7.76686	7.73418	7.98966	7.60399	NA	0.77759	250850_at
At3g53620	AtPPa4, PPa4, pyrophosphorylase 4	7.03134	6.36882	8.69997	8.57688	5.4087	5.47748	5.37326	5.50591	NA	1.93835	251961_at
At1g74055	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 6 growth stages; Has 24 Blast hits to 24 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.43567	5.85917	6.37472	6.58314	4.95574	4.8609	5.11464	4.99491	NA	0.83151	260389_at
At2g42520	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.58328	5.83656	6.86817	6.6831	6.21095	6.43596	6.80329	6.80107	NA	1.06571	263493_at
At1g33270	Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein	5.69109	5.96801	6.44244	6.51632	6.50889	6.55908	6.79731	7.0236	NA	0.64983	256534_at
At2g40650	PRP38 family protein	4.97103	4.93913	6.23414	6.07252	5.16623	5.17153	5.24233	5.18201	NA	1.19825	266055_at
At4g23410	TET5, tetraspanin5	5.93694	5.99062	7.52189	7.12092	5.5661	5.42982	5.64038	5.50835	NA	1.35763	254258_at
At4g13020	MHK, Protein kinase superfamily protein	6.19484	6.03954	7.11309	6.88445	7.25071	7.362	7.04259	6.90213	NA	0.88158	254747_at
At5g07440	GDH2, glutamate dehydrogenase 2	10.2178	9.9731	11.8318	11.8862	9.76212	9.99476	9.61261	10.2046	NA	1.76355	250580_at
At1g14330	Galactose oxidase/kelch repeat superfamily protein	7.64739	7.85489	8.55837	8.5737	7.95149	8.0608	8.11553	8.07158	NA	0.81489	261525_at
At5g54170	Polyketide cyclase/dehydrase and lipid transport superfamily protein	5.5979	5.8985	7.6997	7.8571	8.58706	8.59642	9.3926	8.97404	NA	2.0302	248199_at
At5g48175	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: hypocotyl, male gametophyte, root; BEST Arabidopsis thaliana protein match is: Glycosyl hydrolase superfamily protein (TAIR:AT3G09260.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.69326	5.86759	6.64124	6.38452	4.48553	4.50094	4.53956	4.55497	NA	0.73245	248717_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g17710	EMB1241, Co-chaperone GrpE family protein	5.63627	5.50997	6.34664	6.24815	7.06531	7.15395	7.10041	7.34061	NA	0.72428	250061_at
At3g47980	Integral membrane HPP family protein	10.6255	10.3987	12.1307	12.8449	9.50812	9.32848	9.62585	9.87639	NA	1.97573	252396_at 252397_at
At4g27350	Protein of unknown function (DUF1223)	4.83031	4.84659	5.49271	5.57168	5.21716	5.16114	5.34597	5.28741	NA	0.69374	253919_at
At4g35760	NAD(P)H dehydrogenase (quinone)s	5.62815	5.43668	6.96116	6.54786	8.02252	7.83973	8.02136	7.72592	NA	1.2221	253160_at
At5g19590	Protein of unknown function, DUF538	8.82065	8.67042	9.58158	9.45958	8.55651	8.44477	8.81094	8.7274	NA	0.77504	245957_at
At3g03890	FMN binding	5.56342	5.59415	6.74972	6.4205	7.34864	7.46553	7.40153	7.33063	NA	1.00633	259342_at
At2g36835	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.67214	6.58112	7.44393	7.65499	8.40881	8.69286	8.05052	8.41517	NA	0.92283	263842_at
At5g20550	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	5.48141	4.7668	6.50879	6.74284	4.28178	4.29634	4.4003	4.32843	NA	1.50171	246093_at
At1g66140	ZFP4, zinc finger protein 4	7.89238	7.83331	8.43738	8.82202	6.7448	6.80108	6.67592	6.97597	NA	0.76686	256528_at
At4g30580	ATS2, EMB1995, LPAT1, Phospholipid/glycerol acyltransferase family protein	6.37139	6.46347	7.27556	6.92124	8.19812	8.26681	8.05884	8.09747	NA	0.68097	253624_at
At4g20320	CTP synthase family protein	6.7058	6.25416	7.36005	7.28342	4.99388	4.88541	5.28315	5.07	NA	0.84175	254490_at
At2g19860	ATHXK2, HXK2, hexokinase 2	5.55487	5.76504	6.16844	6.43335	6.6401	6.80247	6.1616	6.23287	NA	0.64094	266702_at
At3g55370	OBP3, OBF-binding protein 3	4.99555	4.85056	5.70576	5.65194	4.77271	4.90852	5.00721	4.97725	NA	0.75579	251806_at
At5g08335	ATICMTB, ATSTE14B, ICMTB, Isoprenylcysteine carboxyl methyltransferase (ICMT) family	5.17076	5.31696	6.07909	6.23277	5.90877	6.08045	5.91199	6.07237	NA	0.91207	246009_at
At5g16000	NIK1, NSP-interacting kinase 1	5.75435	5.86927	7.00621	7.27047	6.39043	6.39744	6.2558	6.52423	NA	1.32653	246483_at
At4g18610	LSH9, Protein of unknown function (DUF640)	5.9674	6.27616	7.08079	7.45393	4.76545	4.91527	4.84119	4.82328	NA	1.14558	254631_at
At5g52550	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25670.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.34733	5.58453	6.11242	6.30136	5.15274	5.30185	5.30978	5.14057	NA	0.74096	248310_at
At1g78000	SEL1, SULTR1;2, sulfate transporter 1;2	8.34621	8.23907	9.56649	10.0393	7.29888	7.16088	7.5244	6.81165	NA	1.51023	262133_at
At4g16920	Disease resistance protein (TIR-NBS-LRR class) family	4.35791	4.21368	5.14295	5.01827	4.25857	4.20537	4.39245	4.283	NA	0.79481	245454_at

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At5g48630	Cyclin family protein	5.69875	5.70472	6.42253	6.27288	6.94638	6.81126	6.78194	6.60961	NA	0.64597	248666_at
At5g66650	Protein of unknown function (DUF607)	6.23622	6.07189	7.77566	7.20248	5.46967	5.55084	5.25856	5.56771	NA	1.33502	247047_at
At5g25160	ZFP3, zinc finger protein 3	7.81077	6.88043	8.80439	8.84752	4.74664	4.54499	4.75115	4.66139	NA	1.48036	246933_at
At1g53400	Ubiquitin domain-containing protein	6.6214	6.35572	7.20018	7.40395	7.64913	7.95645	7.84767	7.93267	NA	0.8135	260589_at
At3g12130	KH domain-containing protein / zinc finger (CCCH type) family protein	6.85552	6.80305	7.58301	7.32065	7.41322	7.2947	7.51379	7.55539	NA	0.62254	256278_at
At2g24860	DnaJ/Hsp40 cysteine-rich domain superfamily protein	4.72637	4.55806	6.00948	5.72348	8.12817	8.26374	8.09004	8.22328	NA	1.22426	263541_at
At5g53570	Ypt/Rab-GAP domain of gyp1p superfamily protein	6.66562	6.54729	7.4539	7.61453	7.38467	7.74277	7.42991	7.6315	NA	0.92776	248222_at
At2g02970	GDA1/CD39 nucleoside phosphatase family protein	6.39749	6.31996	7.28062	7.18887	7.51428	7.48324	7.29143	7.44718	NA	0.87602	266744_at
At2g35690	ACX5, acyl-CoA oxidase 5	5.41311	5.73565	6.1495	6.37086	6.57168	6.83233	6.69995	6.74991	NA	0.6858	265843_at
At2g27830	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22758.1); Has 131 Blast hits to 131 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 131; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.96877	7.83044	8.79998	8.68209	7.37676	7.4474	7.72157	7.53141	NA	0.84143	266259_at
At1g64200	VHA-E3, vacuolar H+-ATPase subunit E isoform 3	6.76164	6.95053	7.47645	7.45386	6.79241	6.54229	6.68178	6.46004	NA	0.60907	262354_at
At2g26180	IQD6, IQ-domain 6	4.8443	4.64169	5.45159	5.53121	5.28613	5.16922	5.31379	5.32947	NA	0.74841	267402_at
At4g04770	ABC1, ATABC1, ATNAP1, LAF6, ATP binding cassette protein 1	8.21648	7.85587	8.98247	8.90148	10.0099	9.917	10.3877	10.0685	NA	0.9058	255305_at
At1g80640	Protein kinase superfamily protein	5.38609	5.47187	6.27659	6.32251	7.94822	7.9837	7.44403	7.82761	NA	0.87058	259860_at
At3g11420	Protein of unknown function (DUF604)	7.4252	7.23051	8.37559	8.28035	6.25866	6.17813	6.25204	6.00344	NA	1.00011	259232_at
At5g16650	Chaperone DnaJ-domain superfamily protein	6.92213	6.54456	8.12164	7.78369	8.38694	8.56393	8.10146	8.52578	NA	1.21931	250079_at
At5g16010	3-oxo-5-alpha-steroid 4-dehydrogenase family protein	7.08646	7.94556	8.8831	9.18031	9.51557	9.71498	9.8093	9.80445	NA	1.5157	246488_at
At1g60860	AGD2, ARF-GAP domain 2	4.73449	5.0578	5.74047	5.85852	4.94537	4.75438	4.5306	4.68981	NA	0.90335	259907_at
At2g46270	GBF3, G-box binding factor 3	6.60157	6.37967	7.55178	7.60658	6.37675	6.71581	6.75255	6.75806	NA	1.08856	266555_at
At5g57150	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	5.67428	6.25007	6.95342	7.02397	5.80444	5.54746	5.46859	5.40759	NA	1.02652	247945_at
At3g01260	Galactose mutarotase-like superfamily protein	7.29092	7.23974	9.02169	8.01956	4.81935	4.71256	5.19624	4.88549	NA	1.25529	259264_at
At3g55320	PGP20, P-glycoprotein 20	5.04794	4.80046	5.51528	5.51653	5.43438	5.48864	5.27292	5.27262	NA	0.5917	251781_at
At2g23030	SNRK2-9, SNRK2.9, SNF1-related protein kinase 2.9	7.19333	6.46268	8.60901	8.40547	4.93234	5.1977	4.8591	4.95002	NA	1.67923	267254_at
At1g64510	Translation elongation factor EF1B/ribosomal protein S6 family protein	5.43865	5.16438	6.14829	6.02432	9.16262	9.50201	9.26585	9.52467	NA	0.78479	261954_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g69800	Cystathionine beta-synthase (CBS) protein	6.04395	6.03866	6.9016	6.66534	7.26497	7.00877	7.03773	6.88068	NA	0.74217	260413_at
At1g54520	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1517 (InterPro:IPR010903); Has 276 Blast hits to 275 proteins in 83 species: Archae - 0; Bacteria - 108; Metazoa - 6; Fungi - 0; Plants - 113; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink).	6.17718	5.88802	6.9883	6.65264	7.98233	8.15471	8.05422	7.84545	NA	0.78787	262955_at
At1g10760	GWD, GWD1, SEX1, SOP, SOP1, Pyruvate phosphate dikinase, PEP/pyruvate binding domain	6.14305	5.94591	6.73856	6.90331	8.57847	8.56966	8.25296	8.46882	NA	0.77646	262784_at
At1g62660	Glycosyl hydrolases family 32 protein	11.0618	10.3932	11.8708	12.028	8.05176	8.09293	8.38176	8.40282	NA	1.22189	265118_at
At5g58440	SNX2a, sorting nexin 2A	6.49889	6.2729	7.25128	7.29491	6.7009	6.89415	6.8766	6.99295	NA	0.8872	247822_at
At3g53400	BEST Arabidopsis thaliana protein match is: conserved peptide upstream open reading frame 47 (TAIR:AT5G03190.1); Has 285 Blast hits to 285 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 279; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	5.15924	5.11379	5.77135	5.85667	6.06043	6.2113	6.05351	6.20969	NA	0.6775	251937_at
At3g62970	zinc finger (C3HC4-type RING finger) family protein	5.32562	5.72042	6.39598	6.23556	6.5969	6.52059	6.4138	6.34429	NA	0.79275	251198_at
At3g49810	ARM repeat superfamily protein	5.45984	5.57882	7.17246	7.00011	5.87519	5.70159	5.76192	5.89638	NA	1.56695	252230_at
At3g28950	AIG2-like (avirulence induced gene) family protein	7.4513	6.92191	8.23162	7.9883	6.72705	6.79549	6.77594	6.85815	NA	0.92336	258001_at
At2g01110	APG2, PGA2, TATC, UNE3, Sec-independent periplasmic protein translocase	5.58369	5.44269	6.57125	6.4148	8.19718	8.00585	8.19333	7.69993	NA	0.97983	262202_at
At5g16320	FRL1, FRIGIDA like 1	4.8093	5.00454	5.46351	5.53299	5.40031	5.47543	5.57128	5.64241	NA	0.59133	250113_at
At3g17900	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 45 Blast hits to 44 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 2; Plants - 39; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	5.96466	5.85604	6.5964	6.83347	6.70273	6.83621	6.64079	6.77808	NA	0.80458	258165_at
At4g01430	nodulin MtN21 /EamA-like transporter family protein	7.26819	7.29497	8.88646	8.50216	5.94927	5.72775	6.03055	6.41681	NA	1.41273	255575_at
At4g37590	NPY5, Phototropic-responsive NPH3 family protein	6.69956	6.40426	7.52654	7.69139	7.58638	7.63901	7.82025	7.69307	NA	1.05705	253062_at
At1g11820	O-Glycosyl hydrolases family 17 protein	5.58134	5.98296	7.28479	7.05934	8.41596	8.29911	7.87439	7.81835	NA	1.38991	264397_at

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At5g43140	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	4.63209	5.10757	5.9807	5.87946	6.04411	5.93206	5.68832	5.731	NA	1.06025	249137_at
At3g06850	BCE2, DIN3, LTA1, 2-oxoacid dehydrogenases acyltransferase family protein	9.10659	8.61182	11.1011	10.7562	8.74288	8.67543	8.08534	8.21169	NA	2.06943	258527_at
At4g22260	IM, IM1, Alternative oxidase family protein	5.53004	5.65964	6.67133	6.47104	7.01434	7.07027	7.33847	6.98318	NA	0.97634	254335_at
At1g76410	ATL8, RING/U-box superfamily protein	6.29174	6.01572	8.20483	7.81976	7.35047	7.5411	7.4091	7.75384	NA	1.85856	259982_at
At5g56020	Got1/Sft2-like vescicle transport protein family	5.16814	5.17091	6.11012	6.17937	6.14716	6.20406	5.94225	5.74962	NA	0.97522	248044_at
At3g12670	emb2742, CTP synthase family protein	7.48941	7.50935	8.41122	8.33504	8.26059	8.18045	8.42713	8.70018	NA	0.87375	257702_at
At2g47600	ATMHX, ATMHX1, MHX, MHX1, magnesium/proton exchanger	5.57358	5.57295	6.54496	6.45927	6.92818	6.78678	6.59256	6.57109	NA	0.92885	245127_at
At4g14910	HISN5B, HISTIDINE BIOSYNTHESIS 5B	4.63863	4.9231	5.98731	5.57814	6.39263	6.23995	6.1798	5.94205	NA	1.00186	245287_at
At4g35770	ATSEN1, DIN1, SEN1, SEN1, Rhodanese/Cell cycle control phosphatase superfamily protein	8.98317	8.31046	11.1274	11.118	12.1707	12.4217	11.3424	12.0546	NA	2.47585	253161_at
At4g37400	CYP81F3, cytochrome P450, family 81, subfamily F, polypeptide 3	5.28283	5.52149	5.89702	6.2391	4.80569	4.85389	4.90481	4.98118	NA	0.6659	253100_at
At3g10970	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	6.48062	6.23312	7.32037	7.2376	8.68423	8.67008	8.51808	8.41053	NA	0.92211	256440_at
At5g63930	Leucine-rich repeat protein kinase family protein	6.48093	6.32003	7.04742	7.35626	5.70949	5.7806	6.13561	6.3127	NA	0.80136	247308_at
At1g63180	UGE3, UDP-D-glucose/UDP-D-galactose 4-epimerase 3	6.55103	6.84497	8.27821	7.8873	7.52902	7.46307	7.61433	7.41846	NA	1.38476	259694_at
At2g33845	Nucleic acid-binding, OB-fold-like protein	6.38308	6.30068	7.19244	7.24337	6.27183	6.41052	6.4955	6.38869	NA	0.87602	267463_at
At1g11000	ATMLO4, MLO4, Seven transmembrane MLO family protein	4.91498	4.81364	5.44968	5.62263	4.87209	5.03078	4.82688	4.94868	NA	0.67184	260483_at
At3g05170	Phosphoglycerate mutase family protein	4.62528	4.38298	5.40346	5.51964	4.53315	4.66861	4.47877	4.58263	NA	0.95742	259352_at
At1g25470	AP2 domain-containing transcription factor family protein	5.73488	5.73797	7.27749	6.87184	7.29191	7.27475	7.22378	6.84644	NA	1.33824	255729_at
At5g15170	TDP1, tyrosyl-DNA phosphodiesterase-related	4.48704	4.57612	5.52734	5.34037	5.15404	5.10418	5.00875	5.04234	NA	0.90227	250156_at
At5g06600	UBP12, ubiquitin-specific protease 12	6.20733	6.35746	7.12486	7.34301	7.09744	7.07758	7.18163	7.08671	NA	0.95154	250693_at
At4g30340	ATDGK7, DGK7, diacylglycerol kinase 7	4.98527	4.67535	5.68777	5.73172	6.05848	5.97815	6.52141	6.09261	NA	0.87944	253578_at
At3g61670	Protein of unknown function (DUF3133)	4.67817	4.97972	5.99936	5.87973	5.55294	5.57472	5.88385	5.92898	NA	1.1106	251332_at
At5g65685	UDP-Glycosyltransferase superfamily protein	5.90842	5.59531	6.87935	6.89054	7.73725	7.57533	7.7949	7.21028	NA	1.13308	247163_at
At4g36630	EMB2754, Vacuolar sorting protein 39	6.13961	6.12457	7.03762	7.08063	7.16236	7.12103	7.01996	6.95926	NA	0.92703	246232_at
At1g16280	AtRH36, RH36, SWA3, RNA helicase 36	4.71638	4.97319	6.08477	6.08528	5.39473	5.4078	5.9492	5.64634	NA	1.24024	262706_at
At1g78960	ATLUP2, LUP2, lupeol synthase 2	7.53651	7.60443	8.23056	8.20246	6.09702	6.20435	6.01516	5.78069	NA	0.64604	264137_at

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At4g38180	FRS5, FAR1-related sequence 5	4.69019	4.80842	5.38276	5.5184	5.41187	5.50682	5.48517	5.56672	NA	0.70128	253030_at
At1g58340	ZF14, MATE efflux family protein	6.08562	5.76143	8.63933	8.579	6.79515	6.92882	7.49219	7.07836	NA	2.68565	256024_at
At3g56360	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05250.1); Has 45 Blast hits to 45 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	9.07568	8.55231	9.73054	9.58022	7.60104	7.5463	8.1558	8.07476	NA	0.84138	251704_at
At2g25850	PAPS2, poly(A) polymerase 2	5.49775	5.37435	6.44316	6.28307	6.31975	6.43262	6.61725	6.88026	NA	0.92706	266659_at
At5g56380	F-box/RNI-like/FBD-like domains-containing protein	4.82157	4.85435	5.32935	5.5457	5.71255	5.56824	5.88458	5.58471	NA	0.59957	248016_at
At1g05410	Protein of unknown function (DUF1423)	4.61684	4.72393	5.61996	5.72256	5.49505	5.40376	5.30281	5.28758	NA	1.00088	261387_at
At3g61080	Protein kinase superfamily protein	4.39343	4.47548	5.15542	5.03781	7.05438	6.92664	6.93213	6.75532	NA	0.66216	251353_at
At5g07290	AML4, ML4, MEI2-like 4	4.79141	4.98068	5.85938	5.92624	5.49125	5.70719	5.65436	5.61248	NA	1.00677	250617_at
At1g14650	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein	5.91028	5.88436	6.47561	6.58175	6.43424	6.46895	6.55263	6.60006	NA	0.63136	260779_at
At1g11080	scpl31, serine carboxypeptidase-like 31	5.08225	4.748	8.53818	8.7016	4.41709	4.67078	4.78032	4.56782	NA	3.70476	260475_at
At5g46800	BOU, Mitochondrial substrate carrier family protein	7.79926	7.63237	8.41124	8.57173	9.32778	9.24573	8.97312	8.79916	NA	0.77567	248838_at
At5g40980	Protein of unknown function (DUF 3339)	4.88273	5.18242	6.16125	6.31738	4.66255	4.57811	4.64793	4.69252	NA	1.20674	249332_at
At3g19390	Granulin repeat cysteine protease family protein	10.3714	10.0933	10.7291	10.9749	6.45944	6.47624	6.32864	6.38156	NA	0.61963	258005_at
At3g27670	RST1, ARM repeat superfamily protein	4.92927	5.23064	6.56459	6.36352	6.36008	6.22066	6.54464	6.21727	NA	1.3841	258238_at
At1g32200	ACT1, ATS1, phospholipid/glycerol acyltransferase family protein	6.48517	6.32761	7.31379	7.33586	8.07403	8.09226	7.50237	7.64427	NA	0.91843	245790_at
At1g44800	nodulin MtN21 /EamA-like transporter family protein	11.2157	11.481	11.9615	11.9281	8.01541	8.11403	8.2978	8.45405	NA	0.59647	261335_at
At5g47990	CYP705A5, THAD, THAD1, cytochrome P450, family 705, subfamily A, polypeptide 5	5.22979	4.74793	7.20174	7.34575	4.04165	4.2544	4.22284	4.29729	NA	2.28489	248727_at
At5g35450	Disease resistance protein (CC-NBS-LRR class) family	5.52634	5.29303	6.39283	6.13954	5.4264	5.30255	5.42996	5.39323	NA	0.8565	249724_at
At1g18270	ketose-bisphosphate aldolase class-II family protein	8.91652	8.50639	9.67395	9.38415	8.05902	8.13105	7.72478	7.54095	NA	0.81759	261674_at
At4g38440	LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: RNA polymerase II-associated protein 1, C-terminal (InterPro:IPR013929), RNA	4.87463	4.87842	5.84308	5.64523	5.53193	5.6738	5.73177	5.66001	NA	0.86763	252990_at

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	polymerase II-associated protein 1, N-terminal (InterPro:IPR013930); Has 276 Blast hits to 220 proteins in 102 species: Archae - 0; Bacteria - 2; Metazoa - 151; Fungi - 65; Plants - 41; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).											
At2g18780	F-box and associated interaction domains-containing protein	4.93433	5.05211	5.81742	5.79373	4.886	4.78803	4.73952	4.73521	NA	0.81236	266064_at
At5g38710	Methylenetetrahydrofolate reductase family protein	5.50038	6.27272	7.47203	8.07692	4.63556	4.63727	4.75926	5.08248	NA	1.88792	249527_at
At5g54800	ATGPT1, GPT1, glucose 6-phosphate/phosphate translocator 1	7.82661	7.58746	8.4648	8.71456	6.6183	6.66912	7.07027	6.952	NA	0.88264	248144_at
At1g28280	VQ motif-containing protein	7.03025	6.8743	7.59144	7.62111	7.31462	7.42873	7.29679	7.41312	NA	0.654	245666_at
At3g54220	SCR, SGR1, GRAS family transcription factor	5.43234	5.30402	6.55781	6.55662	7.24128	7.24603	7.23542	7.08979	NA	1.18903	251890_at
At1g36320	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37920.1); Has 93 Blast hits to 90 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 85; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).	6.23997	6.09567	7.16658	6.86405	8.41092	8.41621	8.55122	8.34815	NA	0.8475	260127_at
At2g45740	PEX11D, peroxin 11D	5.02483	5.23767	6.99304	6.55528	9.61794	9.40573	9.23809	8.89556	NA	1.64291	266925_at
At2g47180	AtGolS1, GolS1, galactinol synthase 1	7.20517	7.87014	8.65028	8.96913	6.90909	7.14247	7.04058	7.03397	NA	1.27205	263320_at
At3g13750	BGAL1, BGAL1, beta galactosidase 1	8.56898	8.18935	10.1884	9.66036	10.6575	10.9623	10.1847	9.90336	NA	1.54524	256772_at
At5g26740	Protein of unknown function (DUF300)	8.33017	7.82814	9.13681	9.22547	7.68748	7.70198	7.47205	7.57	NA	1.10198	246843_at
At3g53810	Concanavalin A-like lectin protein kinase family protein	4.97982	5.0832	5.90042	6.28161	6.38645	6.78391	7.07863	6.72228	NA	1.0595	251910_at
At2g31840	Thioredoxin superfamily protein	4.59074	4.42729	5.19149	5.11671	5.86668	6.01614	5.72688	5.4157	NA	0.64508	263488_at
At5g52250	Transducin/WD40 repeat-like superfamily protein	5.33226	5.79415	6.75826	6.50883	7.46274	7.31822	7.29454	7.13479	NA	1.07034	248347_at
At3g48070	RING/U-box superfamily protein	6.09952	5.91328	7.3678	7.27917	7.64481	7.51132	7.83203	7.65298	NA	1.31708	252371_at
At1g49890	Family of unknown function (DUF566)	5.03771	5.32185	5.9929	6.11919	6.2566	6.51252	6.40192	6.4631	NA	0.87627	259818_at
At1g26450	Carbohydrate-binding X8 domain superfamily protein	5.07598	5.27288	6.27223	6.12692	4.5696	4.75345	4.59047	4.7401	NA	1.02515	261004_at
At3g60750	Transketolase	9.02028	8.88297	11.067	11.7404	10.7066	10.8649	11.6805	12.0065	NA	2.45207	251396_at
At4g37610	BT5, BTB and TAZ domain protein 5	8.60994	8.40807	10.0999	10.2409	9.00533	9.06278	8.79046	8.6252	NA	1.66139	253061_at
At1g69760	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26920.1); Has 51 Blast hits to 51 proteins in 15 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 7; Plants - 29; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	6.01666	6.01854	7.29069	6.92472	7.90626	7.85264	7.62309	7.44198	NA	1.0901	260367_at

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At3g55030	PGPS2, phosphatidylglycerolphosphate synthase 2	5.60883	5.70413	6.84953	6.48433	6.59339	6.40283	6.6819	6.51369	NA	1.01045	251819_at
At1g50560	CYP705A25, cytochrome P450, family 705, subfamily A, polypeptide 25	5.86055	5.5747	6.89765	7.13083	4.67033	4.75988	4.585	4.84427	NA	1.29662	261878_at
At3g10330	Cyclin-like family protein	5.98207	5.96219	6.91819	6.91447	5.98438	6.14872	6.22984	6.05948	NA	0.9442	259155_at
At1g75180	Erythronate-4-phosphate dehydrogenase family protein	5.63819	5.29831	7.35723	7.11527	8.03927	7.6017	7.82092	8.05052	NA	1.768	256456_at
At5g51170	unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0406 (InterPro:IPR019146); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.3587	5.4142	6.11399	5.90062	6.12998	5.97399	6.00312	6.11728	NA	0.62085	248445_at
At1g04530	Tetratricopeptide repeat (TPR)-like superfamily protein	5.36077	5.66661	6.94857	6.67047	8.92746	8.82643	9.12695	8.51203	NA	1.29582	264609_at
At5g52440	HCF106, Bacterial sec-independent translocation protein mttA/Hcf106	6.11535	6.1004	7.04207	6.5875	8.47477	8.49485	8.3248	8.47964	NA	0.70691	248338_at
At3g15810	Protein of unknown function (DUF567)	8.81168	8.72114	9.23912	9.48057	8.55609	8.29513	8.52206	8.63422	NA	0.59344	258251_at
At3g13225	WW domain-containing protein	4.78075	4.95936	5.79853	5.60463	5.52065	5.56405	5.62918	5.4305	NA	0.83152	257653_at
At2g40400	Protein of unknown function (DUF399 and DUF3411)	4.62003	4.67402	5.45159	5.24103	6.7332	6.48313	7.03545	6.71364	NA	0.69929	263805_at
At1g33490	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2062 (InterPro:IPR018639); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10140.1); Has 88 Blast hits to 88 proteins in 29 species: Archae - 0; Bacteria - 28; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	5.41914	5.38122	6.75376	6.5974	6.98555	6.90786	6.99603	6.74468	NA	1.2754	256424_at
At5g08440	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23490.1); Has 141 Blast hits to 139 proteins in 35 species: Archae - 0; Bacteria - 9; Metazoa - 21; Fungi - 6; Plants - 94; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	4.97203	5.04271	5.74814	5.99477	5.88841	5.82191	6.07162	5.90933	NA	0.86409	246010_at
At3g02140	AFP4, TMAC2, AFP2 (ABI five-binding protein 2) family protein	6.0569	5.90703	6.57018	6.83821	5.42142	5.67714	5.13914	5.30471	NA	0.72223	259076_at
At3g18560	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49000.1); Has 95 Blast hits to 95 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 95; Viruses - 0; Other	7.15691	6.95107	8.94052	9.16243	7.09859	7.3022	7.24263	7.60207	NA	1.99748	256799_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	Eukaryotes - 0 (source: NCBI BLink).											
At2g01970	Endomembrane protein 70 protein family	7.11211	7.18208	8.0363	8.13083	7.48189	7.61912	7.88406	7.83233	NA	0.93647	265222_at
At4g38250	Transmembrane amino acid transporter family protein	8.33762	8.32756	9.02392	8.88584	9.65198	9.61468	9.90484	9.52625	NA	0.62229	253006_at
At4g29080	IAA27, PAP2, phytochrome-associated protein 2	8.06739	7.89368	8.89388	9.01902	7.38853	7.42673	7.19873	7.11397	NA	0.97592	253749_at
At1g23330	alpha/beta-Hydrolases superfamily protein	6.79398	6.48735	7.42892	7.43513	6.20648	6.53063	6.70559	6.67321	NA	0.79136	263010_at
At3g51450	Calcium-dependent phosphotriesterase superfamily protein	4.91898	4.75307	5.59045	5.67327	4.86291	4.85931	5.13778	5.25206	NA	0.79584	252114_at
At5g18840	Major facilitator superfamily protein	6.33099	5.8692	9.2127	9.25215	5.14863	4.76668	5.54807	5.1024	NA	3.13233	249955_at
At3g02600	ATLPP3, LPP3, lipid phosphate phosphatase 3	6.12164	5.64874	6.87311	6.6937	7.24185	7.08593	6.9805	6.84877	NA	0.89821	258481_at
At3g50280	HXXXD-type acyl-transferase family protein	4.75751	4.9563	5.63966	5.57056	4.65084	4.64593	4.69618	4.48494	NA	0.74821	252200_at
At1g08770	PRA1.E, prenylated RAB acceptor 1.E	6.5483	6.16031	7.19537	7.09685	7.01386	6.97485	7.51692	7.3574	NA	0.7918	264808_at
At4g32950	Protein phosphatase 2C family protein	8.63847	8.89082	9.59301	10.8758	5.72248	5.86561	6.14741	6.49492	NA	1.46976	253408_at
At5g13900	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	5.78734	5.60313	6.42444	6.34739	4.59433	4.3637	4.68157	4.57068	NA	0.69068	250230_at
At1g71720	Nucleic acid-binding proteins superfamily	5.10872	4.93133	5.70597	5.50439	7.48309	7.37894	6.9297	6.83558	NA	0.58515	261507_at
At5g53970	Tyrosine transaminase family protein	6.60339	7.04547	8.13112	7.9659	9.66016	9.70621	9.59809	9.53399	NA	1.22408	248207_at
At1g75710	C2H2-like zinc finger protein	5.79014	5.74564	6.33224	6.38292	6.11669	6.12013	5.86793	5.95037	NA	0.58969	262969_at
At5g22320	Leucine-rich repeat (LRR) family protein	4.66059	5.07986	6.02454	6.04642	5.61094	5.68631	5.51389	5.61539	NA	1.16525	249886_at
At1g15040	Class I glutamine amidotransferase-like superfamily protein	8.50655	7.61052	11.4133	11.2751	7.399	7.321	7.36759	7.79196	NA	3.28565	260741_at
At1g51720	Amino acid dehydrogenase family protein	7.09948	6.85736	8.12687	8.10227	7.63758	7.60767	7.67933	7.76529	NA	1.13615	256174_at
At2g21850	Cysteine/Histidine-rich C1 domain family protein	5.32828	5.27091	6.23353	6.11466	5.14398	5.28714	5.38212	5.08625	NA	0.8745	257432_at
At3g28510	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.62189	6.30064	7.68998	8.32801	4.27781	4.38196	4.28343	4.5364	NA	2.04773	256593_at
At4g21060	Galactosyltransferase family protein	5.34057	5.25744	5.98781	5.93132	5.35506	5.39888	5.28848	5.42182	NA	0.66056	254442_at
At5g11630	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17310.1); Has 90 Blast hits to 90 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.42008	6.2646	7.46683	7.6038	7.07475	6.98476	6.9621	6.79807	NA	1.19297	250353_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At3g61190	BAP1, BON association protein 1	4.89182	5.13998	6.91156	6.87086	4.94091	4.65961	5.65226	5.14429	NA	1.87531	251336_at
At2g14880	SWIB/MDM2 domain superfamily protein	5.73451	5.69803	6.26708	6.65867	7.38516	7.52017	7.29913	7.42154	NA	0.74661	266587_at
At5g20150	ATSPX1, SPX1, SPX domain gene 1	5.73497	7.09303	9.01654	9.06004	5.71518	5.67321	5.64671	5.04483	NA	2.62429	246071_at
At3g13000	Protein of unknown function, DUF547	4.71076	4.84445	5.43354	5.32808	5.92413	6.04069	5.96764	5.97606	NA	0.6032	257547_at
At2g40460	Major facilitator superfamily protein	6.19285	6.79606	7.95585	7.76296	5.27417	5.01566	5.02654	5.02303	NA	1.36495	255877_at
At4g29490	Metallopeptidase M24 family protein	5.78772	5.882	6.98102	6.83741	6.42425	6.48942	6.43653	6.60389	NA	1.07435	253719_at
At1g17190	ATGSTU26, GSTU26, glutathione S-transferase tau 26	5.64915	5.27161	6.41677	6.49755	4.54487	4.25196	4.44674	4.24977	NA	0.99678	262516_at
At5g05520	Outer membrane OMP85 family protein	7.13729	6.91754	7.7401	7.89115	7.01756	7.16514	7.14394	7.22015	NA	0.78821	250792_at
At3g18380	sequence-specific DNA binding transcription factors;sequence-specific DNA binding	6.42804	6.13961	6.91942	7.10366	7.01125	7.13147	7.08944	7.01925	NA	0.72772	257727_at
At3g25710	ATAIG1, BHLH32, TMO5, basic helix-loop-helix 32	5.45504	5.10445	6.25574	6.83088	4.3652	4.41111	4.64096	4.43657	NA	1.26357	257642_at
At3g10390	FLD, Flavin containing amine oxidoreductase family protein	4.84123	4.91025	5.54866	5.56842	5.18151	5.34399	5.59069	5.35895	NA	0.6828	258944_at
At3g56400	ATWRKY70, WRKY70, WRKY DNA-binding protein 70	7.14027	7.05329	7.81393	8.22421	6.204	6.08729	6.51301	6.53608	NA	0.92229	251705_at
At1g31050	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	5.77876	6.18781	7.24591	7.3965	4.8207	4.71879	4.85781	4.72847	NA	1.33792	265159_at
At4g31540	ATEXO70G1, EXO70G1, exocyst subunit exo70 family protein G1	6.24688	6.15974	6.93301	6.86711	7.24573	7.16187	7.36424	7.38265	NA	0.69675	253531_at
At1g16310	Cation efflux family protein	4.40502	4.6742	5.81255	6.25642	4.66346	4.67686	4.80342	4.77057	NA	1.49487	262751_at
At4g04880	adenosine/AMP deaminase family protein	5.23409	5.33915	6.28944	6.00507	6.39103	6.22221	6.47766	6.40563	NA	0.86063	255299_at
At3g63390	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.37334	5.3688	6.54798	6.48129	6.73464	6.8701	7.00578	6.98579	NA	1.14357	251117_at
At1g10150	Carbohydrate-binding protein	6.75351	6.12949	7.84988	7.84178	7.7571	7.61694	7.73418	7.88842	NA	1.40433	264463_at
At1g34210	ATSERK2, SERK2, somatic embryogenesis receptor-like kinase 2	5.33232	5.60358	6.9527	6.62028	7.04073	6.92291	6.83139	6.96912	NA	1.31854	262563_at
At1g08520	ALB-1V, ALB1, CHLD, PDE166, V157, ALBINA 1	5.69186	6.13571	6.88557	6.57653	8.93038	8.96357	8.74156	8.6444	NA	0.81727	261695_at
At5g52280	Myosin heavy chain-related protein	4.76788	4.8656	5.59889	6.12349	4.52438	4.57193	4.11436	4.33555	NA	1.04445	248344_at
At1g02860	BAH1, NLA, SPX (SYG1/Pho81/XPR1) domain-containing protein	6.89057	6.94616	8.09747	7.88154	6.51546	6.49374	6.59871	6.47839	NA	1.07115	262114_at
At4g26940	Galactosyltransferase family protein	6.96083	6.67813	7.68508	7.77182	7.40499	7.33522	7.6517	7.45641	NA	0.90897	253948_at
At4g27060	CN, SPR2, TOR1, ARM repeat superfamily protein	5.73274	5.53298	6.77477	6.98561	6.70111	6.53886	6.485	6.75525	NA	1.24733	253923_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At4g37790	HAT22, Homeobox-leucine zipper protein family	7.43028	7.213	8.62669	8.52589	7.85987	7.81015	8.41855	8.20638	NA	1.25465	253038_at
At1g79090	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Topoisomerase II-associated protein PAT1 (InterPro:IPR019167); BEST Arabidopsis thaliana protein match is: Topoisomerase II-associated protein PAT1 (TAIR:AT3G22270.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.51058	5.27967	6.87908	6.76431	6.75182	6.68386	7.11988	7.07525	NA	1.42657	264141_at
At2g48100	Exonuclease family protein	7.7765	7.66123	8.34712	8.28156	7.09087	7.19053	7.4877	7.75922	NA	0.59548	265770_at
At5g61440	ACHT5, atypical CYS HIS rich thioredoxin 5	5.28322	5.31698	6.86703	7.12344	5.31099	4.93859	5.54548	5.32177	NA	1.69513	247524_at
At5g16450	Ribonuclease E inhibitor RraA/Dimethylmenaquinone methyltransferase	7.85798	8.06159	8.67453	8.70961	7.14137	7.35806	7.28578	7.31073	NA	0.73228	250129_at
At2g18850	SET domain-containing protein	4.79508	4.81226	5.67937	5.6444	5.57602	5.71733	5.42375	5.45791	NA	0.85822	266948_at
At3g57560	NAGK, N-acetyl-l-glutamate kinase	6.74131	6.38273	7.15552	7.30718	7.78124	7.6691	7.43175	7.59784	NA	0.66933	251639_at
At3g63220	Galactose oxidase/kelch repeat superfamily protein	6.14322	6.17401	6.79506	6.7697	6.47229	6.70463	6.53986	6.53619	NA	0.62376	251171_at
At1g01940	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	6.19902	6.39648	7.21411	6.96175	5.53459	5.55792	5.71656	5.88517	NA	0.79018	261655_at
At4g15640	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21465.1); Has 38 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.91985	6.76714	7.66445	7.54882	6.76105	6.82267	6.76064	7.03736	NA	0.76314	245502_at
At5g10970	C2H2 and C2HC zinc fingers superfamily protein	4.91084	4.82497	6.78035	7.82698	4.83883	5.0962	4.74536	5.15451	NA	2.43576	250396_at
At1g12680	PEPKR2, phosphoenolpyruvate carboxylase-related kinase 2	5.89021	5.77072	6.86949	6.63518	7.07443	7.3291	7.09764	6.81717	NA	0.92187	255936_at
At2g31160	LSH3, Protein of unknown function (DUF640)	5.45257	5.73084	6.44298	6.36508	5.97024	6.08909	6.33429	6.51863	NA	0.81232	266479_at
At1g36390	Co-chaperone GrpE family protein	4.61914	4.46862	5.35043	5.34157	5.88459	5.64652	5.63774	5.83699	NA	0.80212	260125_at
At4g26470	Calcium-binding EF-hand family protein	6.3767	6.61672	7.18075	7.2454	4.9941	4.95441	5.04316	4.90676	NA	0.71637	253963_at
At5g58090	O-Glycosyl hydrolases family 17 protein	6.54048	6.70585	7.61662	7.83457	7.16704	7.4526	7.41178	7.2735	NA	1.10243	247845_at
At2g35450	catalytics;hydrolases	4.67	4.61959	5.41641	5.35853	6.15739	6.01197	6.22016	5.91002	NA	0.74268	266621_at
At1g63110	GPI transamidase subunit PIG-U	6.82973	6.82517	7.55422	7.47604	7.80188	7.61696	7.79479	7.60863	NA	0.68768	259687_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g72310	ATL3, RING/U-box superfamily protein	6.45	6.35627	7.11303	7.3408	7.06566	7.10081	7.32205	7.13347	NA	0.82378	260454_at
At4g01100	ADNT1, adenine nucleotide transporter 1	8.97926	8.69656	9.5064	9.4963	8.55854	8.42031	8.84738	9.07388	NA	0.66344	255570_at
At2g38810	HTA8, histone H2A 8	4.85891	5.01458	5.73467	6.10795	4.63722	4.38162	4.55567	4.67249	NA	0.98457	263264_at
At3g55910	unknown protein; Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.36114	5.67328	6.87264	6.299	4.46896	4.57366	4.76246	4.62216	NA	1.0686	251766_at
At5g48590	Protein of unknown function (DUF760)	6.19906	6.02293	8.01537	7.91713	8.9796	9.04377	8.42099	8.66842	NA	1.85526	248663_at
At5g40480	EMB3012, embryo defective 3012	5.56984	5.69343	6.27575	6.44269	5.38545	5.54696	5.28822	5.24547	NA	0.72759	249354_at
At5g04260	WCRKC2, WCRKC thioredoxin 2	5.55471	5.72331	6.65002	6.35669	6.8916	6.68848	6.67484	6.59848	NA	0.86434	245693_at
At5g06730	Peroxidase superfamily protein	5.70502	5.85264	6.80232	6.67973	4.79466	4.60919	4.58795	4.54901	NA	0.9622	250702_at
At2g47160	BOR1, HCO3- transporter family	6.33557	6.50894	8.86628	8.18026	6.58871	6.29309	6.24795	6.47495	NA	2.10101	263319_at
At1g80380	P-loop containing nucleoside triphosphate hydrolases superfamily protein	8.0986	7.38366	10.9764	10.8583	9.10563	9.22387	9.12684	9.58158	NA	3.17624	260284_at
At3g43430	RING/U-box superfamily protein	6.24766	6.41149	7.71368	7.50289	5.3459	5.55357	5.86286	5.91139	NA	1.27871	252751_at
At3g15760	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52565.1); Has 42 Blast hits to 42 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.66259	5.58016	6.50421	6.97563	7.39825	7.35104	7.94303	7.55356	NA	1.11855	258275_at
At3g50070	CYCD3;3, CYCLIN D3;3	6.54637	6.63292	7.62027	7.53361	7.72848	7.33478	7.29891	7.28976	NA	0.98729	252189_at
At4g12060	Double Clp-N motif protein	7.10614	7.33379	7.91154	7.85752	8.94872	8.81436	8.72347	8.82143	NA	0.66457	254859_at
At4g26260	MIOX4, myo-inositol oxygenase 4	4.8443	4.9073	6.85779	6.32655	4.86305	4.981	5.02295	4.845	NA	1.71637	254001_at
At2g25830	YebC-related	5.07852	5.44817	6.09537	6.22352	6.93718	6.5659	6.80584	6.60006	NA	0.89609	266662_at
At1g44920	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3054 (InterPro:IPR021414); Has 246 Blast hits to 246 proteins in 119 species: Archae - 14; Bacteria - 181; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	5.18638	4.85858	6.11008	5.94579	8.33765	8.23478	7.96615	8.02047	NA	1.00546	261338_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g09100	RPT5B, 26S proteasome AAA-ATPase subunit RPT5B	6.569	6.5603	7.5203	7.71931	6.01756	5.90557	6.38171	6.99268	NA	1.05516	264657_at
At5g51010	Rubredoxin-like superfamily protein	5.59186	5.3688	6.52415	6.37414	9.51559	9.17367	8.63907	8.92865	NA	0.96881	248491_at
At2g16500	ADC1, ARGDC, ARGDC1, SPE1, arginine decarboxylase 1	7.14283	7.55742	8.19365	8.37434	9.14482	9.40691	9.28827	8.98438	NA	0.93387	263241_at
At2g27900	CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2451, C-terminal (InterPro:IPR019514), Vacuolar protein sorting-associated protein 54 (InterPro:IPR019515); Has 316 Blast hits to 252 proteins in 92 species: Archae - 0; Bacteria - 2; Metazoa - 200; Fungi - 2; Plants - 68; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink).	5.87738	5.9104	6.68012	6.46012	6.2186	6.31154	6.20857	6.08224	NA	0.67623	264063_at
At3g22850	Aluminium induced protein with YGL and LRDR motifs	7.97655	8.56244	9.24728	9.14425	6.40712	6.35628	7.04152	7.32986	NA	0.92627	256829_at
At5g47980	HXXXD-type acyl-transferase family protein	4.34241	4.68219	6.14513	6.52061	4.97625	4.76339	4.8748	4.89115	NA	1.82057	248725_at
At3g14190	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12360.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.31667	5.49055	6.50407	6.87919	4.93725	5.35385	5.29758	5.62311	NA	1.28802	257005_at
At3g12640	RNA binding (RRM/RBD/RNP motifs) family protein	5.15366	4.84994	6.19946	6.1096	5.79288	5.85438	5.78272	5.91993	NA	1.15273	257703_at
At1g19800	TGD1, trigalactosyldiacylglycerol 1	5.29498	5.40673	6.63917	6.49693	7.29049	7.03464	7.07601	7.21991	NA	1.2172	261132_at
At3g04080	APY1, ATAPY1, apyrase 1	4.96534	4.89562	5.82049	5.88689	5.2891	5.33826	5.32617	5.38034	NA	0.92321	258567_at
At3g54720	AMP1, COP2, HPT, MFO1, PT, Peptidase M28 family protein	5.24443	5.50747	6.36842	6.46945	5.99048	5.80198	5.58668	5.68399	NA	1.04299	251856_at
At3g07350	Protein of unknown function (DUF506)	5.93885	5.25757	8.972	9.29288	6.86227	7.08959	7.88347	8.38015	NA	3.53423	259015_at
At1g33700	Beta-glucosidase, GBA2 type family protein	7.05655	7.15286	7.98457	8.18522	5.27326	5.85578	5.8305	5.70041	NA	0.98019	261991_at
At4g24040	ATTRE1, TRE1, trehalase 1	6.71275	5.9208	8.67571	8.65831	7.07324	7.42545	8.12723	8.29432	NA	2.35024	254197_at
At1g27980	ATDPL1, DPL1, dihydrosphingosine phosphate lyase	8.01358	7.76985	8.6229	8.37511	8.77466	8.80343	9.33272	9.34403	NA	0.60729	259598_at
At5g03900	Iron-sulphur cluster biosynthesis family protein	5.43962	4.76834	6.44052	6.27955	7.04565	7.03586	6.97445	6.94269	NA	1.25606	250865_at
At5g61910	DCD (Development and Cell Death) domain protein	5.0154	4.96739	5.98414	5.78762	5.66605	5.9631	6.00195	5.76279	NA	0.89448	247500_at
At5g59930	Cysteine/Histidine-rich C1 domain family protein	4.79766	4.40294	5.85564	6.02274	4.37098	4.31651	4.24815	4.14941	NA	1.33889	247674_at
At5g18100	CSD3, copper/zinc superoxide dismutase 3	5.82642	6.11951	6.7215	6.77292	7.10766	7.22819	7.02333	7.17364	NA	0.77424	250016_at
At4g08500	ARAKIN, ATMEKK1, MAPKKK8, MEKK1, MAPK/ERK kinase kinase 1	6.04772	6.14072	6.80954	6.70066	6.34739	6.33366	6.38761	6.25304	NA	0.66088	255095_at
At1g24100	UGT74B1, UDP-glucosyl transferase 74B1	6.66883	6.42064	8.35747	8.27605	6.75815	6.38894	6.8936	6.9304	NA	1.77203	264873_at

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At3g46500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	5.29821	4.68985	6.2658	6.21586	4.26941	4.30072	4.25917	4.1687	NA	1.24679	252530_at
At5g59080	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: chloroplast; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G46880.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	4.08897	4.33295	6.82477	6.38688	7.42099	7.45202	8.04139	8.28842	NA	2.39487	247754_at
At3g61400	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	6.68134	6.84861	7.85935	7.61851	5.4526	5.28537	5.14561	4.95576	NA	0.97396	251335_at
At5g47560	ATSDAT, ATTDT, TDT, tonoplast dicarboxylate transporter	8.13109	7.55281	9.60018	9.35154	10.6481	10.7552	11.0668	11.3492	NA	1.63391	248756_at
At1g67700	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 49 Blast hits to 49 proteins in 20 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	5.3131	5.17445	5.90698	5.9025	8.83185	8.82161	8.72574	8.90313	NA	0.66097	245198_at
At1g17350	NADH:ubiquinone oxidoreductase intermediate-associated protein 30	5.45558	5.44521	6.37677	6.30747	5.46003	5.46581	5.41615	5.70413	NA	0.89173	261087_at
At3g46200	aTNUDT9, NUDT9, nudix hydrolase homolog 9	4.86505	4.61327	5.41353	5.45	5.04025	5.05412	4.95753	4.99736	NA	0.6926	252507_at
At4g37410	CYP81F4, cytochrome P450, family 81, subfamily F, polypeptide 4	10.4677	9.86972	11.4277	11.7432	5.99746	6.09806	6.13973	6.01495	NA	1.41674	253073_at
At2g01830	AHK4, ATCRE1, CRE1, WOL, WOL1, CHASE domain containing histidine kinase protein	5.96508	5.51712	6.84655	6.80809	4.57623	4.70234	4.85681	4.69175	NA	1.08622	263599_at
At5g12880	proline-rich family protein	5.70304	5.33793	6.65152	6.82977	4.85511	4.74847	5.46261	4.83431	NA	1.22016	250323_at
At1g65700	Small nuclear ribonucleoprotein family protein	5.89537	6.13576	7.22386	6.97276	6.21126	6.12043	6.46274	6.27506	NA	1.08274	262931_at
At2g32760	unknown protein; Has 229 Blast hits to 229 proteins in 104 species: Archae - 0; Bacteria - 2; Metazoa - 79; Fungi - 90; Plants - 49; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	5.08492	4.95494	6.49843	6.6346	5.85456	6.12582	6.08464	6.22158	NA	1.54659	267540_at
At2g43400	ETFQO, electron-transfer flavoprotein:ubiquinone oxidoreductase	6.3674	5.8832	7.38088	7.29635	7.58542	7.62153	7.7251	7.31555	NA	1.21332	260536_at
At3g21540	transducin family protein / WD-40 repeat family protein	5.23074	4.9075	6.25546	6.27902	5.95799	5.82013	5.69691	5.87112	NA	1.19812	258166_at
At2g45430	AHL22, AT-hook motif nuclear-localized protein 22	7.16903	6.95569	8.36237	8.29699	4.83329	4.95557	4.87615	4.96099	NA	1.26731	245139_at

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At3g61850	DAG1, Dof-type zinc finger DNA-binding family protein	5.73237	6.10262	6.81547	6.58831	4.96755	4.83516	4.91181	4.90297	NA	0.7844	251290_at
At5g07890	myosin heavy chain-related	6.01558	6.30503	7.56853	7.76574	6.95215	6.64596	7.51345	7.33689	NA	1.50684	250552_at
At3g20800	Cell differentiation, Rcd1-like protein	7.15625	7.11439	8.05498	7.99065	7.70599	7.80362	8.15722	7.78769	NA	0.8875	257984_at
At5g60890	ATMYB34, ATR1, MYB34, myb domain protein 34	7.70471	7.63662	9.17614	9.11065	5.8484	5.74245	5.97431	6.30409	NA	1.47273	247600_at
At3g13450	DIN4, Transketolase family protein	5.87812	4.87798	7.85304	7.20669	8.1447	8.16723	8.09465	7.76592	NA	2.15181	256965_at
At1g67110	CYP735A2, cytochrome P450, family 735, subfamily A, polypeptide 2	4.78424	5.44912	8.23107	8.07474	5.01827	4.87256	5.48076	5.44313	NA	3.03622	264470_at
At3g20660	4-Oct, AtOCT4, organic cation/carnitine transporter4	6.413	6.16326	7.95471	7.99644	6.42236	5.97297	6.01404	5.39269	NA	1.68744	256697_at
At5g09230	AtSRT2, SRT2, sirtuin 2	5.87885	5.50039	6.58273	6.56582	6.78201	6.70245	6.48151	6.54735	NA	0.88465	245895_at
At1g18590	ATSOT17, ATST5C, SOT17, sulfotransferase 17	5.85905	5.90122	6.95637	6.96175	5.16793	5.00796	4.90171	5.54431	NA	1.07893	255773_at
At5g58730	pfkB-like carbohydrate kinase family protein	6.97292	6.6796	7.44268	7.46448	6.65238	6.6332	6.55848	6.49912	NA	0.62732	247788_at
At5g20040	ATIPT9, IPT9, isopentenyltransferase 9	4.81907	5.00088	5.49712	5.64475	5.84921	5.82209	5.58452	5.69724	NA	0.66096	246152_at
At1g08570	ACHT4, atypical CYS HIS rich thioredoxin 4	7.58474	7.96919	8.57777	8.62789	8.48094	8.52058	9.09328	8.96871	NA	0.82587	264779_at
At2g42300	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	4.9239	4.86817	5.43336	5.57282	6.09096	5.80557	5.86532	5.96038	NA	0.60706	265880_at
At1g79610	ATNHX6, NHX6, Na+/H+ antiporter 6	5.51795	5.33086	6.43122	6.18218	5.53834	5.28843	5.33262	5.23271	NA	0.8823	261398_at
At3g57170	N-acetylglucosaminyl transferase component family protein / Gpi1 family protein	5.27712	5.20823	6.28131	6.01027	6.15059	6.25186	6.16526	6.07005	NA	0.90312	251656_at
At3g54110	ATPUMP1, ATUCP1, PUMP1, UCP, UCP1, plant uncoupling mitochondrial protein 1	8.98803	8.71385	9.50332	9.62092	8.22147	8.34888	8.42294	8.69573	NA	0.71118	251902_at
At4g02510	ATTOC159, PPI2, TOC159, TOC160, TOC86, translocon at the outer envelope membrane of chloroplasts 159	7.12106	7.16616	7.82176	7.80008	9.05316	8.97956	8.90535	8.99757	NA	0.6673	255482_at
At5g48480	Lactoylglutathione lyase / glyoxalase I family protein	7.46357	7.43605	8.67404	8.32988	7.51056	7.48583	7.16931	7.17757	NA	1.05215	248710_at
At3g08950	electron transport SCO1/SenC family protein	5.3704	5.29143	6.42005	6.65399	5.65058	5.80276	5.77361	5.88532	NA	1.20611	258987_at
At3g55640	Mitochondrial substrate carrier family protein	5.42444	5.38976	6.63981	6.65448	6.65435	6.65589	6.97793	6.53996	NA	1.24004	251757_at
At1g35910	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	5.78466	5.88729	6.42839	6.75246	4.14091	3.98309	4.1392	4.07085	NA	0.75445	256319_at
At1g19740	ATP-dependent protease La (LON) domain protein	5.98263	5.82135	6.73168	6.52879	8.75768	8.81608	8.26136	8.65109	NA	0.72824	261141_at
At5g52830	ATWRKY27, WRKY27, WRKY DNA-binding protein 27	6.27893	6.02266	6.84463	7.03521	7.56858	7.74872	7.39947	7.4519	NA	0.78912	248306_at
At4g35450	AFT, AKR2, AKR2A, ankyrin repeat-containing protein 2	7.80408	7.50198	8.28992	8.24069	9.96547	9.94403	9.92881	9.90357	NA	0.61228	253139_at
At4g15330	CYP705A1, cytochrome P450, family 705, subfamily A, polypeptide 1	4.60486	4.67227	5.35758	5.27003	4.34157	4.33872	4.4611	4.3334	NA	0.67524	245550_at

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At1g79520	Cation efflux family protein	5.70086	5.78674	6.80238	7.2658	5.95752	6.21303	6.01471	6.06604	NA	1.29029	262940_at
At4g29950	Ypt/Rab-GAP domain of gyp1p superfamily protein	7.99176	7.35878	9.32525	9.18578	9.13795	9.21287	9.13158	9.183	NA	1.58025	253647_at
At5g67470	ATFH6, FH6, formin homolog 6	5.61318	5.52094	6.5727	6.63323	5.64439	5.60999	5.95567	5.79369	NA	1.0359	246995_at
At5g60460	Preprotein translocase Sec, Sec61-beta subunit protein	5.92348	5.76331	6.66258	6.8133	7.06897	7.06131	6.71487	6.74703	NA	0.89454	247632_at
At2g37450	nodulin MtN21 /EamA-like transporter family protein	4.39326	4.64798	5.78499	6.12879	7.28224	7.77329	6.56413	6.83558	NA	1.43627	265967_at
At2g44480	BGLU17, beta glucosidase 17	4.40949	4.7048	5.74251	5.8364	4.8359	4.85785	4.78104	4.84514	NA	1.23231	267391_at
At4g26750	hydroxyproline-rich glycoprotein family protein	6.64874	6.56879	7.20349	7.26277	6.60262	6.75687	7.00049	6.84245	NA	0.62437	253953_at
At2g46060	transmembrane protein-related	5.43569	5.46342	6.64984	6.49755	6.62553	6.58211	6.60589	6.35853	NA	1.12414	266601_at
At4g37190	LOCATED IN: cytosol, plasma membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Beta tubulin, autoregulation binding site (InterPro:IPR013838), Misato Segment II, myosin-like (InterPro:IPR019605), Tubulin/FtsZ, N-terminal (InterPro:IPR019746); Has 345 Blast hits to 341 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 131; Fungi - 140; Plants - 55; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink).	5.08728	5.1259	5.86243	6.05299	6.11216	6.23256	5.67064	5.71155	NA	0.85112	246278_at
At5g67030	ABA1, ATABA1, ATZEP, IBS3, LOS6, NPQ2, ZEP, zeaxanthin epoxidase (ZEP) (ABA1)	6.82449	6.80147	7.54806	7.43922	9.47752	9.44374	9.123	9.26713	NA	0.68066	247025_at
At1g78090	ATTPPB, TPPB, trehalose-6-phosphate phosphatase	5.3869	5.25817	6.15968	6.18368	4.40565	4.47756	4.41676	4.643	NA	0.84915	260059_at
At3g54980	Pentatricopeptide repeat (PPR) superfamily protein	5.13292	5.30616	6.71413	6.6789	6.14707	6.33591	6.45188	6.32945	NA	1.47697	251841_at
At3g11210	SGNH hydrolase-type esterase superfamily protein	5.38042	5.12677	6.26737	6.18009	7.16927	6.99356	6.84942	7.17053	NA	0.97013	256415_at
At5g11450	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	5.48542	5.75906	6.72242	6.39197	7.96638	7.69387	7.91666	7.78753	NA	0.93495	250371_at
At1g04260	MPI7, MPIP7, PRA1.D, CAMV movement protein interacting protein 7	6.53512	6.52074	7.36512	7.35382	7.23347	7.33566	7.24477	7.60666	NA	0.83154	263660_at
At3g16690	Nodulin MtN3 family protein	6.79509	6.27685	8.2666	7.98509	6.4623	6.11881	6.23163	5.88422	NA	1.58988	258421_at
At4g29700	Alkaline-phosphatase-like family protein	6.28434	5.46636	7.64242	8.79407	4.72597	4.67372	4.74087	4.95776	NA	2.34289	253697_at
At5g24270	ATSOS3, CBL4, SOS3, Calcium-binding EF-hand family protein	6.76071	6.63733	8.56092	7.9709	5.71467	5.92747	5.90451	5.42893	NA	1.56689	249783_at
At1g30840	ATPUP4, PUP4, purine permease 4	5.35675	4.95005	7.02795	6.9519	4.32037	4.54518	4.64979	4.52083	NA	1.83652	264497_at
At4g38810	Calcium-binding EF-hand family protein	7.24337	6.84329	8.3602	8.39292	7.27144	7.58007	8.01646	8.07997	NA	1.33323	252915_at
At1g50440	RING/FYVE/PHD zinc finger superfamily protein	5.53662	5.03987	6.42372	6.27295	6.49845	6.72382	6.46079	6.63193	NA	1.06009	261852_at

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At1g80410	EMB2753, tetratricopeptide repeat (TPR)-containing protein	7.23582	6.85617	8.0706	8.06188	7.9685	7.8146	7.92743	8.05861	NA	1.02024	260282_at
At2g43820	ATSAGT1, GT, SAGT1, SGT1, UGT74F2, UDP-glucosyltransferase 74F2	8.58356	8.3161	8.96352	9.14394	9.73358	9.77567	10.1322	9.93285	NA	0.6039	260567_at
At5g63940	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	6.71672	6.98528	7.39488	7.61872	6.47794	6.37802	6.61976	6.59226	NA	0.65581	247309_at
At2g25950	Protein of unknown function (DUF1000)	6.03149	5.99581	6.68845	6.78675	6.17561	6.15428	5.73979	5.87127	NA	0.72395	266848_at
At1g62480	Vacuolar calcium-binding protein-related	10.4778	10.3045	11.4427	11.3903	9.41294	9.8234	9.6399	9.86009	NA	1.02539	265116_at
At1g13300	HRS1, myb-like transcription factor family protein	5.03501	5.05884	8.13807	8.58609	4.40601	4.59012	4.62603	5.21286	NA	3.31515	259365_at
At1g11430	plastid developmental protein DAG, putative	6.24767	5.89851	7.28765	7.27413	8.45889	8.62571	8.2642	8.54252	NA	1.2078	261824_at
At3g24530	AAA-type ATPase family protein / ankyrin repeat family protein	4.76446	4.58598	5.33046	5.29553	4.58667	4.79407	5.00077	4.92681	NA	0.63778	258134_at
At3g56850	AREB3, DPBF3, ABA-responsive element binding protein 3	5.4361	5.47566	6.25559	6.29123	6.23148	6.05525	6.29057	6.28818	NA	0.81753	246314_at
At5g06810	Mitochondrial transcription termination factor family protein	4.44177	4.71522	5.4905	5.50302	5.261	5.24421	5.60051	5.40445	NA	0.91827	250698_at
At4g02400	U3 ribonucleoprotein (Utp) family protein	6.33957	6.3944	7.01238	7.17603	6.34131	6.33223	6.52559	6.47735	NA	0.72722	255501_at
At1g71740	unknown protein; Has 82 Blast hits to 82 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 82; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.59579	5.59918	6.84049	6.89332	6.1172	5.94155	5.89047	5.82612	NA	1.26942	261509_at
At1g72180	Leucine-rich receptor-like protein kinase family protein	4.96372	5.3759	6.69016	6.63272	6.91134	6.91299	6.46076	6.74413	NA	1.49163	259848_at
At5g24260	prolyl oligopeptidase family protein	6.30539	6.19238	7.1048	7.14254	6.49118	6.54856	6.60853	6.40303	NA	0.87478	249782_at
At1g31170	ATSRX, SRX, sulfiredoxin	6.12013	5.82763	6.6221	6.61043	7.46763	7.55252	7.27425	7.57981	NA	0.64239	263703_at
At3g59670	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G37440.2); Has 77 Blast hits to 77 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	5.92791	5.70129	6.52855	6.28277	5.27179	5.28338	5.33025	5.4595	NA	0.59106	251476_at
At4g02920	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G03340.1); Has 41 Blast hits to 41 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.36504	6.76259	8.62907	8.28179	9.51494	9.5415	10.1248	10.1606	NA	1.39162	255456_at
At1g63170	Zinc finger, C3HC4 type (RING finger) family protein	5.62694	5.659	6.56937	6.35961	7.19191	7.14265	7.6655	7.17066	NA	0.82152	259695_at
At1g17050	SPS2, solanesyl diphosphate synthase 2	5.46636	5.74639	6.7309	6.76287	7.51205	7.3952	7.79773	7.39938	NA	1.14051	262526_at
At3g15630	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown;	9.09927	8.26484	10.3937	10.4748	8.24687	8.36908	7.85147	8.37433	NA	1.75221	258225_at

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	LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52720.1); Has 61 Blast hits to 61 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 61; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).											
At3g57420	Protein of unknown function (DUF288)	5.52457	5.22322	6.30817	6.08851	6.67604	6.69026	6.80445	6.58932	NA	0.82444	251630_at
At3g50700	AtIDD2, IDD2, indeterminate(ID)-domain 2	5.67673	5.62977	7.10448	7.00122	6.39581	6.18044	6.51582	6.81711	NA	1.3996	252175_at
At1g68660	Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	6.21837	6.21102	7.16692	7.46823	8.43607	8.56723	8.35472	8.63816	NA	1.10287	262287_at
At3g06960	PDE320, TGD4, pigment defective 320	6.68339	6.57585	7.44761	7.40868	7.41161	7.50409	7.26098	7.4098	NA	0.79852	258553_at
At2g22080	unknown protein; Has 96314 Blast hits to 34847 proteins in 1702 species: Archae - 612; Bacteria - 27969; Metazoa - 24311; Fungi - 12153; Plants - 4409; Viruses - 1572; Other Eukaryotes - 25288 (source: NCBI BLink).	6.42308	6.09397	7.37975	7.10695	6.07137	5.93971	5.86614	5.69626	NA	0.98483	263352_at
At3g03300	ATDCL2, DCL2, dicer-like 2	5.63157	5.48399	6.37687	6.43075	5.68946	5.55102	5.8509	5.66897	NA	0.84603	258863_at
At1g78650	POLD3, DNA-directed DNA polymerases	4.50543	4.59047	5.15683	5.2419	4.46061	4.71869	4.41491	4.54549	NA	0.65142	263130_at
At4g29820	ATCFIM-25, CFIM-25, homolog of CFIM-25	4.77911	4.97302	5.54176	5.47025	5.60499	5.65826	5.85911	5.59552	NA	0.62994	253672_at
At3g33520	ARP6, ATARP6, ESD1, SUF3, actin-related protein 6	6.47007	6.70497	7.4322	7.5054	7.27982	7.46712	7.59605	7.64412	NA	0.88128	259242_at
At1g07570	APK1, APK1A, Protein kinase superfamily protein	5.67959	5.55725	6.39239	6.69464	9.66506	9.53695	9.34316	8.94432	NA	0.9251	261089_at
At5g04240	ELF6, Zinc finger (C2H2 type) family protein / transcription factor jumonji (jmj) family protein	5.79733	5.73434	6.554	6.46519	6.31683	6.29317	6.36691	6.39056	NA	0.74376	245691_at
At3g20870	ZTP29, ZIP metal ion transporter family	7.79035	7.58775	8.42973	8.21039	7.50459	7.33555	7.64378	7.51875	NA	0.63101	257988_at
At3g21390	Mitochondrial substrate carrier family protein	5.70791	5.96689	7.01522	6.83815	7.38901	7.25891	7.38156	7.16518	NA	1.08929	256819_at
At2g28250	NCRK, Protein kinase superfamily protein	5.15424	5.40179	6.03739	6.67235	4.77469	4.799	4.80096	4.73556	NA	1.07686	265545_at
At3g07100	ERMO2, SEC24A, Sec23/Sec24 protein transport family protein	7.45258	7.2007	8.31125	8.16691	8.10562	7.95151	7.97007	7.98519	NA	0.91244	258829_at
At3g51540	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G08670.1); Has 22744 Blast hits to 9965 proteins in 783 species: Archae - 64; Bacteria - 2760; Metazoa - 8515; Fungi - 3864; Plants - 499; Viruses - 702; Other Eukaryotes - 6340 (source: NCBI BLink).	4.88308	4.88561	6.24199	5.9792	4.82385	4.73973	4.78705	4.6174	NA	1.22625	252109_at
At2g39130	Transmembrane amino acid transporter family protein	5.17798	4.85497	6.61451	6.17893	5.26084	5.26001	5.36585	5.36433	NA	1.38025	267019_at
At1g28440	HSL1, HAESA-like 1	8.98421	8.94319	9.61491	9.76747	8.72864	8.78675	8.73275	8.84883	NA	0.72749	261498_at

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At3g06110	ATMKP2, DSPTP1B, MKP2, MAPK phosphatase 2	6.69576	6.52159	7.9534	7.82069	6.96982	6.95605	7.37829	7.20952	NA	1.27837	256397_at
At3g12480	NF-YC11, nuclear factor Y, subunit C11	5.74201	5.84443	6.99844	7.35487	6.91025	7.44794	7.26295	7.36423	NA	1.38344	256258_at
At4g15340	04C11, ATPEN1, PEN1, pentacyclic triterpene synthase 1	4.88837	5.08903	6.30995	6.55093	4.35299	4.46534	4.38806	4.50743	NA	1.44174	245258_at
At1g31770	ABCG14, ATP-binding cassette 14	8.65131	8.58146	9.83048	9.5849	6.99607	6.4915	7.82388	7.37109	NA	1.0913	246580_at
At2g06990	HEN2, RNA helicase, ATP-dependent, SK12/DOB1 protein	5.44346	5.53737	6.22011	6.28789	6.18549	6.0695	6.01432	6.12909	NA	0.76358	266501_at
At1g02020	nitroreductase family protein	4.84539	4.53244	5.49654	5.39863	6.08892	6.03593	6.09001	5.86668	NA	0.75867	264169_at
At1g02910	LPA1, tetratricopeptide repeat (TPR)-containing protein	4.26299	4.81115	5.5219	5.45902	7.09273	7.10304	7.0765	6.87711	NA	0.95339	262104_at
At4g36030	ARO3, armadillo repeat only 3	5.44457	5.24356	6.02179	6.01942	5.86629	5.94587	6.23326	6.11155	NA	0.67654	253124_at
At3g62150	PGP21, P-glycoprotein 21	5.40027	5.24333	6.4543	6.30612	6.54045	6.77438	7.39389	6.87693	NA	1.05841	251248_at
At3g26640	LWD2, Transducin/WD40 repeat-like superfamily protein	5.47841	5.22902	6.55419	6.52857	6.4954	6.70295	6.58232	6.56736	NA	1.18767	257833_at
At5g20880	transposable element gene	5.20427	5.11722	6.30206	6.48475	5.00096	4.98161	5.04942	5.40219	NA	1.23266	246193_at
At2g27970	CKS2, CDK-subunit 2	6.12474	6.18756	6.94598	7.18817	5.08479	5.15035	4.9276	5.27622	NA	0.91093	264061_at
At5g64300	ATGCH, ATRIBA1, GCH, RFD1, GTP cyclohydrolase II	5.78833	5.5482	6.89916	6.87115	7.82156	8.00158	8.70979	8.26886	NA	1.21689	247272_at
At5g40390	SIP1, Raffinose synthase family protein	8.12085	8.15841	8.87438	8.83629	8.00058	8.00412	8.35409	8.42649	NA	0.7157	249411_at
At5g46570	BSK2, BR-signaling kinase 2	4.78878	4.74743	5.7907	5.70699	5.24106	5.13232	5.21335	5.29552	NA	0.98074	248853_at
At1g10870	AGD4, ARF-GAP domain 4	5.53471	5.56875	6.45498	6.60086	6.46968	6.39948	6.11949	6.32169	NA	0.97619	260469_at
At5g16900	Leucine-rich repeat protein kinase family protein	4.51749	4.64692	5.12567	5.21911	4.58811	4.48589	4.52195	4.41931	NA	0.59018	246459_at
At1g19870	iqd32, IQ-domain 32	6.92251	6.85043	7.51144	7.75926	6.52546	6.85132	6.77606	6.83473	NA	0.74888	255783_at
At1g13260	EDF4, RAV1, related to ABI3/VP1 1	6.84523	6.74328	8.75606	8.47267	6.33401	6.15734	6.93794	6.62985	NA	1.82011	259364_at
At3g13226	regulatory protein RecX family protein	5.71003	5.7515	6.47451	6.42082	6.55301	6.84161	6.56025	6.43877	NA	0.7169	257659_at
At5g64050	ATERS, ERS, OVA3, glutamate tRNA synthetase	5.03497	5.17251	5.67958	5.86142	6.54203	6.38957	6.01604	6.31626	NA	0.66676	247319_at
At1g30820	CTP synthase family protein	8.42828	7.75443	10.5218	10.9037	6.88608	7.12819	6.98225	7.22596	NA	2.62135	264529_at
At2g03150	emb1579, ATP/GTP-binding protein family	5.59295	5.64301	6.18946	6.23718	6.04392	6.15052	6.04877	6.08157	NA	0.59534	266727_at
At1g30610	EMB2279, EMB88, pentatricopeptide (PPR) repeat-containing protein	6.10991	5.95383	6.80856	6.93077	6.90603	7.13296	6.88698	6.88326	NA	0.8378	263220_at
At4g32590	2Fe-2S ferredoxin-like superfamily protein	4.34076	4.11707	4.9322	4.77275	6.13687	6.36579	6.26355	6.19802	NA	0.62356	253391_at
At1g80440	Galactose oxidase/kelch repeat superfamily protein	8.62817	7.32776	10.5942	10.2978	11.2871	11.3714	11.3549	11.469	NA	2.46802	260287_at
At4g03550	ATGSL05, ATGSL5, GSL05, GSL05, GSL5, PMR4, glucan synthase-like 5	6.51788	6.18982	7.08821	7.14729	7.62191	7.26811	7.75101	7.54708	NA	0.7639	255378_at

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At2g32040	Major facilitator superfamily protein	5.81249	5.90087	7.14437	6.93608	7.11138	6.94132	6.91538	6.87977	NA	1.18355	265669_at
At3g52570	alpha/beta-Hydrolases superfamily protein	5.78584	5.88768	6.37412	6.50031	5.77171	5.48117	5.74858	5.6795	NA	0.60046	252051_at
At1g02370	Tetratricopeptide repeat (TPR)-like superfamily protein	4.74949	4.98266	5.53876	5.68709	5.18822	5.06531	4.89951	4.91956	NA	0.74686	259444_at
At4g15880	ATESD4, ESD4, Cysteine proteinases superfamily protein	5.46688	5.40584	6.49283	6.2542	5.81931	6.02573	6.28607	6.17385	NA	0.93716	245521_at
At1g22710	ATSUC2, SUC2, SUT1, sucrose-proton symporter 2	8.20108	7.91075	8.76775	8.81538	9.00687	9.14515	8.97929	8.95944	NA	0.73565	264204_at
At5g37680	ARLA1A, ATARLA1A, ADP-ribosylation factor-like A1A	5.25755	5.28334	6.27524	6.26951	6.56498	6.63362	6.45911	6.33892	NA	1.00193	249579_at
At3g07050	GTP-binding family protein	6.34066	6.1923	7.44615	7.27351	6.49571	6.39487	6.19756	6.35853	NA	1.09335	258545_at
At4g29140	MATE efflux family protein	4.89705	4.81148	6.29667	6.23799	5.92965	5.62196	6.15383	6.49103	NA	1.41306	253732_at
At5g17620	CONTAINS InterPro DOMAIN/s: Plant nuclear matrix 1 (InterPro:IPR010604); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.31506	5.67443	6.64238	6.52467	6.05823	6.15127	6.01558	5.95228	NA	1.08878	246443_at
At3g59050	ATPAO3, PAO3, polyamine oxidase 3	5.40329	5.58686	6.42939	6.4877	6.15802	6.21924	6.6672	6.71417	NA	0.96347	251505_at
At2g16990	Major facilitator superfamily protein	5.71325	5.40935	6.94152	6.54424	5.14484	5.10382	5.05981	5.02289	NA	1.18158	263574_at
At1g20090	ARAC4, ATRAC4, ATROP2, ROP2, RHO-related protein from plants 2	6.96452	6.97727	7.84576	7.93459	7.50689	7.33025	8.03291	7.94275	NA	0.91928	261229_at
At3g52360	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to karrikin; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G35850.1); Has 34 Blast hits to 34 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.10327	6.29522	8.09551	7.83067	6.36167	6.25519	6.7458	6.56407	NA	1.76385	256674_at
At1g13600	AtbZIP58, bZIP58, basic leucine-zipper 58	6.02386	5.04545	6.85176	7.13711	4.80484	4.62376	4.82736	4.76724	NA	1.45978	256131_at
At1g01790	ATKEA1, KEA1, K+ efflux antiporter 1	6.0274	5.73091	6.82004	6.67942	8.28665	8.14338	8.428	8.09086	NA	0.87058	261536_at
At5g62650	Tic22-like family protein	5.847	6.11368	6.83695	6.9091	7.13326	7.23001	7.10421	7.24363	NA	0.89268	247446_at
At1g22660	Polynucleotide adenylyltransferase family protein	5.16163	4.71264	6.00113	5.96936	5.87022	5.99645	5.98221	6.08609	NA	1.04811	264212_at
At1g02680	TAF13, TBP-associated factor 13	5.12894	4.96493	5.93695	6.09748	5.63561	5.63965	5.49739	5.69869	NA	0.97028	260929_at
At4g03610	Metallo-hydrolase/oxidoreductase superfamily protein	5.70603	5.49805	6.74504	6.61041	5.1527	5.07388	5.04115	5.05682	NA	1.07569	255385_at
At2g17370	HMG2, HMGR2, 3-hydroxy-3-methylglutaryl-CoA reductase 2	5.82884	6.09252	6.72087	6.75487	5.64461	5.72728	6.05888	5.74904	NA	0.77719	264856_at

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At1g23140	Calcium-dependent lipid-binding (CaLB domain) family protein	6.00604	5.87739	6.89076	7.12747	4.6006	4.53962	4.6483	4.47743	NA	1.0674	264893_at
At1g32640	ATMYC2, JAI1, JIN1, MYC2, RD22BP1, ZBF1, Basic helix-loop-helix (bHLH) DNA-binding family protein	7.28971	6.96491	8.20051	8.27212	6.47135	6.12634	7.18978	6.60219	NA	1.109	261713_at
At2g22360	DNAJ heat shock family protein	5.07588	4.94679	5.63777	5.672	6.15113	6.16081	6.36505	6.26113	NA	0.64355	264002_at
At5g53320	Leucine-rich repeat protein kinase family protein	6.49825	6.43575	7.11779	7.10878	4.67565	4.76382	4.70792	4.67848	NA	0.64628	248254_at
At3g16350	Homeodomain-like superfamily protein	5.64688	5.75102	7.44144	7.73614	5.69956	5.55564	5.5022	5.65151	NA	1.88984	259379_at
At4g32915	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of translational fidelity; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glu-tRNAGln amidotransferase, C subunit (InterPro:IPR003837); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.24944	5.01198	5.70299	5.8657	6.27941	6.02477	5.90232	6.08565	NA	0.65363	253384_at
At1g71430	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 64 Blast hits to 64 proteins in 28 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 6; Plants - 42; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	5.28586	5.20074	6.0655	6.25462	6.16139	6.09672	6.09088	6.34425	NA	0.91676	259894_at
At5g49970	ATPPOX, PDX3, PPOX, pyridoxin (pyrodoxamine) 5'-phosphate oxidase	6.58633	6.44107	7.38175	7.35994	7.80001	8.00579	8.0786	7.96462	NA	0.85715	248560_at
At4g01026	PYL7, RCAR2, PYR1-like 7	6.05824	6.03297	7.57363	7.17948	8.19242	7.99792	8.71488	8.69546	NA	1.33095	255602_at
At2g45810	DEA(D/H)-box RNA helicase family protein	7.15196	6.98758	8.125	7.97545	8.26264	8.18086	8.31857	8.20504	NA	0.98045	266896_at
At3g59940	Galactose oxidase/kelch repeat superfamily protein	5.75902	5.08185	8.35338	7.40149	9.29903	9.25838	9.01287	9.09773	NA	2.457	251443_at
At4g15110	CYP97B3, cytochrome P450, family 97, subfamily B, polypeptide 3	4.8443	4.92592	6.20547	6.08324	6.90169	7.00329	6.74752	6.77635	NA	1.25924	245532_at
At5g03380	Heavy metal transport/detoxification superfamily protein	10.0271	9.28621	10.5469	10.8149	8.28742	8.52816	9.33647	9.10556	NA	1.02426	250944_at
At1g55510	BCDH BETA1, branched-chain alpha-keto acid decarboxylase E1 beta subunit	7.91269	7.68464	9.25124	8.72817	7.87952	7.98554	7.60808	7.4219	NA	1.19104	265070_at
At5g10520	RBK1, ROP binding protein kinases 1	5.82792	5.86139	6.84051	6.72138	5.19179	5.25828	5.17827	5.15151	NA	0.93629	250443_at
At1g14720	ATXTH28, EXGT-A2, XTH28, XTR2, xyloglucan endotransglucosylase/hydrolase 28	5.47859	5.86466	6.97511	6.78511	7.64707	7.89008	7.68095	7.54835	NA	1.20849	262842_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At2g01270	AtQSOX2, QSOX2, quiescin-sulfhydryl oxidase 2	7.23267	7.05845	8.38436	8.15928	8.56224	8.43497	8.6768	8.36476	NA	1.12626	265739_at
At5g22875	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.81356	6.15271	6.69993	6.78681	6.87198	6.97775	6.85987	6.92861	NA	0.76023	249861_at
At1g18480	Calcineurin-like metallo-phosphoesterase superfamily protein	6.25944	6.53778	7.01607	7.01589	6.50115	6.61984	7.06764	7.02808	NA	0.61738	261676_at
At5g51340	Tetratricopeptide repeat (TPR)-like superfamily protein	6.215	6.08686	7.62905	7.44593	7.01468	6.94947	7.38686	7.05945	NA	1.38656	248453_at
At1g79450	ALIS5, ALA-interacting subunit 5	6.35853	6.2872	6.90015	7.05302	5.08581	5.07004	5.20938	5.24586	NA	0.65371	262942_at
At4g04830	ATMSRB5, MSRB5, methionine sulfoxide reductase B5	9.06162	8.96293	9.88898	10.3926	5.7659	5.31143	4.96224	5.02139	NA	1.12851	255302_at
At2g31940	unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19875.1); Has 227 Blast hits to 227 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 227; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.65753	4.77447	5.92094	6.268	4.80872	4.65483	4.9953	4.63629	NA	1.37847	263465_at
At2g31450	ATNTH1, DNA glycosylase superfamily protein	4.92815	5.1907	5.90544	6.02754	6.00075	6.0486	5.92008	5.75914	NA	0.90707	263248_at
At3g25660	Amidase family protein	5.37383	5.41967	6.67096	6.29608	7.55163	7.49768	7.96121	7.53178	NA	1.08677	256728_at
At5g24710	Transducin/WD40 repeat-like superfamily protein	4.56871	4.55158	5.32432	5.23354	5.14845	5.06883	5.21585	5.13892	NA	0.71879	246961_at
At5g18200	UTP:galactose-1-phosphate uridylyltransferases;ribose-5-phosphate adenylyltransferases	6.15824	6.41851	7.01067	7.01587	6.87457	6.80811	6.97501	6.83892	NA	0.7249	250029_at
At2g27590	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	7.23908	7.23656	7.87193	7.95137	7.39144	7.28736	7.28626	7.23434	NA	0.67383	266262_at
At3g29185	Domain of unknown function (DUF3598)	5.22772	5.12918	6.07643	6.02941	7.52614	7.52507	7.20386	7.22612	NA	0.87447	257773_at
At4g03030	Galactose oxidase/kelch repeat superfamily protein	6.58407	6.77388	7.67965	7.41596	8.5905	8.58508	8.51321	8.34321	NA	0.86883	255469_at
At5g08280	HEMC, hydroxymethylbilane synthase	5.54748	5.38875	6.54925	6.35448	8.587	8.64813	8.5144	8.47024	NA	0.98375	246033_at
At3g06750	hydroxyproline-rich glycoprotein family protein	5.81511	5.73698	7.25691	7.22887	8.07318	7.94763	8.31532	8.12408	NA	1.46685	258535_at
At1g24430	HXXXD-type acyl-transferase family protein	7.06975	6.91478	8.05048	7.69123	5.53732	5.33383	5.44566	5.40049	NA	0.87859	265014_at
At3g11945	ATHST, HST, PDS2, homogentisate prenyltransferase	5.95307	6.00901	6.85604	6.71395	7.59635	7.69398	7.844	7.54899	NA	0.80396	258755_at

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At4g24180	ATTLP1, TLP1, THAUMATIN-LIKE PROTEIN 1	5.80435	5.29755	6.45748	6.75154	5.11602	4.99706	5.00112	4.98879	NA	1.05356	254206_at
At3g25980	MAD2, DNA-binding HORMA family protein	5.36869	5.33091	6.17379	6.2384	5.00691	4.83905	4.88894	5.15295	NA	0.85629	258067_at
At1g54540	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	5.38641	5.37915	6.2	5.84223	4.23293	4.26464	4.19227	4.3007	NA	0.63834	263005_at
At2g24130	Leucine-rich receptor-like protein kinase family protein	5.66705	5.29421	7.29249	6.56043	4.78687	5.00755	4.77759	4.79111	NA	1.44583	265992_at
At5g04490	VTE5, vitamin E pathway gene 5	5.23424	5.10306	5.79859	5.81905	8.20351	8.26769	7.86552	7.90274	NA	0.64018	250842_at
At3g51140	Protein of unknown function (DUF3353)	6.05666	6.35299	7.22481	7.17226	8.07611	7.84891	7.90822	7.72365	NA	0.99371	252122_at
At5g66050	Wound-responsive family protein	6.05577	5.78468	7.40026	7.54882	6.22694	6.27379	6.13712	6.18569	NA	1.55432	247123_at
At5g11150	ATVAMP713, VAMP713, VAMP713, vesicle-associated membrane protein 713	5.42419	5.28398	6.11942	6.19088	6.00437	5.78004	5.88717	5.94258	NA	0.80106	250412_at
At5g19480	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G12230.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	6.37071	6.08054	6.97428	6.96277	6.3876	6.47977	6.36102	6.29823	NA	0.7429	246039_at
At2g25450	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	9.03302	9.55299	10.16	10.1939	10.9561	11.0056	11.0187	10.9538	NA	0.88398	265615_at
At5g61420	AtMYB28, HAG1, MYB28, PMG1, myb domain protein 28	5.72301	6.01215	6.83943	7.06203	6.78491	6.75424	7.09416	7.56758	NA	1.08315	247549_at
At4g39780	Integrase-type DNA-binding superfamily protein	6.74315	7.09923	8.23727	7.98023	8.24669	8.06408	8.42947	8.46277	NA	1.18756	252859_at
At4g36860	DAR1, LIM domain-containing protein	8.07388	7.84269	8.75565	8.98399	7.83982	8.06076	8.42684	8.55699	NA	0.91154	246283_at
At4g02440	EID1, F-box family protein	7.25829	7.11281	7.89088	7.9478	8.47003	8.28919	8.36333	8.29477	NA	0.73379	255478_at
At3g18035	HON4, winged-helix DNA-binding transcription factor family protein	7.68803	7.46472	8.45891	8.46122	7.7598	7.76786	7.24704	7.40058	NA	0.88369	258141_at
At3g01220	ATHB20, HB20, homeobox protein 20	5.23986	5.12135	6.38019	6.35822	4.69433	4.46951	4.65911	4.69231	NA	1.1886	259274_at
At5g07370	ATIPK2A, IPK2a, inositol polyphosphate kinase 2 alpha	7.10178	6.97123	7.61676	7.66529	7.80987	7.9159	7.90901	8.07083	NA	0.60452	250607_at
At3g02650	Tetratricopeptide repeat (TPR)-like superfamily protein	5.46212	5.40147	6.55174	6.62286	6.06723	5.9922	5.87286	5.83881	NA	1.1555	258474_at
At5g42030	ABIL4, ABL interactor-like protein 4	4.85161	4.93893	5.81874	5.45104	7.3387	7.49737	6.9814	6.92213	NA	0.73962	249231_at
At5g42970	ATS4, COP14, COP8, CSN4, EMB134, FUS4, FUS8, Proteasome component (PCI) domain protein	6.61879	6.58989	7.56512	7.518	6.68003	6.4772	7.07943	7.13451	NA	0.93722	249175_at
At2g46260	BTB/POZ/Kelch-associated protein	7.53155	7.38998	8.31793	8.08359	8.0448	7.99295	8.44261	8.3278	NA	0.74	266580_at
At3g53410	RING/U-box superfamily protein	5.62037	5.2648	6.12924	6.20202	5.77936	5.65369	5.18668	5.1951	NA	0.72304	251959_at
At1g47400	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G47395.1); Has 11 Blast hits to 11 proteins in 2 species: Archae - 0; Bacteria - 0;	5.35906	4.68096	6.84574	6.60192	4.7292	4.62442	4.97859	4.89265	NA	1.70382	261684_at

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	Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).											
At1g22850	SNARE associated Golgi protein family	5.26708	5.0358	6.44979	6.23884	8.39519	8.07088	8.37881	7.85845	NA	1.19288	264728_at
At1g03590	Protein phosphatase 2C family protein	6.32132	6.09734	6.75125	7.00711	8.21134	8.29775	7.8453	7.79373	NA	0.66985	264833_at
At1g20380	Prolyl oligopeptidase family protein	5.12229	5.04637	5.84061	5.79655	5.0459	5.01731	4.81026	5.0964	NA	0.73425	255940_at
At5g64290	DCT, DIT2.1, dicarboxylate transport 2.1	6.52355	6.29564	7.59223	7.51279	8.22981	8.26286	8.70365	8.15786	NA	1.14291	247289_at
At3g46790	CRR2, Tetratricopeptide repeat (TPR)-like superfamily protein	5.24289	5.18805	5.90439	5.78073	5.84259	5.63662	5.84355	5.8497	NA	0.62709	252496_at
At5g45160	Root hair defective 3 GTP-binding protein (RHD3)	5.93184	6.0029	6.6667	6.5883	6.24536	6.37048	6.14837	6.00269	NA	0.66013	248985_at
At5g14320	Ribosomal protein S13/S18 family	6.30859	6.20146	7.32865	7.03868	9.4463	9.46496	9.21713	9.54808	NA	0.92864	250190_at
At1g78210	alpha/beta-Hydrolases superfamily protein	6.51338	6.59781	7.47281	7.53924	6.88795	6.6155	6.8264	7.02528	NA	0.95043	260051_at
At5g65650	Protein of unknown function (DUF1195)	6.93168	6.47053	7.81259	7.67244	6.25178	6.22555	6.35458	6.52413	NA	1.04141	247150_at
At3g13910	Protein of unknown function (DUF3511)	5.89899	5.85938	6.64315	6.48143	5.30306	5.25391	5.51397	5.80781	NA	0.6831	258201_at
At5g15730	Protein kinase superfamily protein	6.43441	6.51998	7.30839	7.37279	6.60757	6.61035	6.47443	6.14152	NA	0.86339	246529_at
At3g57520	AtSIP2, SIP2, seed imbibition 2	9.32009	8.53622	10.9849	11.3254	6.81024	6.82705	7.0816	7.05597	NA	2.22699	251642_at
At3g16950	LPD1, ptlpd1, lipoamide dehydrogenase 1	6.03718	5.57079	7.08522	7.02051	7.86236	7.80011	8.30527	7.51272	NA	1.24888	257895_at
At5g44560	VPS2.2, SNF7 family protein	4.6325	4.90605	6.17169	5.97614	4.82214	4.66218	4.79436	5.05704	NA	1.30464	249060_at
At4g36010	Pathogenesis-related thaumatin superfamily protein	5.9377	5.27242	7.00425	6.54868	4.66304	4.54373	5.06346	5.22405	NA	1.17141	253104_at
At1g80160	Lactoylglutathione lyase / glyoxalase I family protein	5.94581	5.76489	7.68626	7.10881	7.55954	7.43356	7.2049	7.01026	NA	1.54219	262047_at
At2g30600	BTB/POZ domain-containing protein	6.65554	6.43007	8.79955	8.34512	7.33456	7.21532	7.37859	7.41081	NA	2.02953	267524_at
At4g16790	hydroxyproline-rich glycoprotein family protein	4.9163	5.06099	6.01818	6.10278	4.55943	4.77227	4.87341	4.9608	NA	1.07184	245384_at
At3g12150	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2048 (InterPro:IPR019149); Has 421 Blast hits to 334 proteins in 155 species: Archae - 2; Bacteria - 147; Metazoa - 215; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	5.27445	5.61067	6.28336	6.08958	6.62343	6.67315	6.84603	6.58117	NA	0.74391	256262_at
At1g63160	RFC2, replication factor C 2	6.60853	6.70181	7.20764	7.46012	6.54843	6.53639	6.32967	6.51923	NA	0.67871	259690_at
At1g55430	Cysteine/Histidine-rich C1 domain family protein	4.46921	4.39281	5.13732	5.44337	4.32748	4.32711	4.16853	4.29724	NA	0.85933	265124_at
At5g16520	unknown protein; Has 25 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.48688	5.55989	6.14753	6.13963	6.06025	6.06977	5.59733	5.43391	NA	0.62019	250122_at

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At4g22770	AT hook motif DNA-binding family protein	5.10104	5.38612	6.00246	6.05535	5.53278	5.36973	5.20854	5.2162	NA	0.78532	254274_at
At5g58030	Transport protein particle (TRAPP) component	6.87349	6.7331	7.70097	7.60304	6.85913	6.62558	7.11438	7.02087	NA	0.84871	247842_at
At5g60680	Protein of unknown function, DUF584	9.11737	8.82116	9.72907	9.94884	8.42498	8.66692	9.01331	9.04269	NA	0.86969	247585_at
At4g36670	Major facilitator superfamily protein	6.55577	5.08884	8.07842	7.75354	11.4148	11.332	11.4874	11.728	NA	2.09368	246238_at
At4g11080	HMG (high mobility group) box protein	4.82458	4.80529	5.62019	5.62189	4.36239	4.6128	4.44588	4.41011	NA	0.80611	254964_at
At5g02620	ANK1, ATANK1, ankyrin-like1	5.91914	5.77444	6.66315	6.41611	5.71746	5.83754	5.67126	5.72358	NA	0.69284	250998_at
At3g06080	TBL10, Plant protein of unknown function (DUF828)	5.32194	5.46985	6.30635	5.97298	8.9481	9.00922	8.47158	8.3171	NA	0.74377	258472_at
At1g73790	Protein of unknown function (DUF3743)	4.73681	4.71209	5.39926	5.2661	4.93128	4.75642	4.8995	4.77897	NA	0.60823	260078_at
At5g54530	Protein of unknown function, DUF538	5.38456	5.56091	6.1761	6.05449	5.99139	5.86886	6.10223	6.27419	NA	0.64256	248167_at
At4g19980	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: root, pedicel; EXPRESSED DURING: 4 anthesis; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	6.22502	5.90017	7.07797	7.66402	4.58012	4.87546	4.43955	4.75112	NA	1.3084	254522_at
At1g02750	Drought-responsive family protein	5.25223	5.53589	6.84753	6.34052	6.77443	6.57499	6.68976	6.81339	NA	1.19996	262107_at
At5g22760	PHD finger family protein	6.17147	5.94344	6.90663	6.81705	6.58306	6.82319	6.72681	6.82666	NA	0.80439	249908_at
At1g49450	Transducin/WD40 repeat-like superfamily protein	5.25451	5.34637	6.29173	6.5178	5.09065	4.97151	5.0192	4.875	NA	1.10432	262448_at
At3g62880	ATOEP16-4, Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	6.72063	6.65922	7.51857	7.27122	7.27142	7.33851	7.63353	7.39591	NA	0.70498	251208_at
At2g21340	MATE efflux family protein	5.09932	5.43156	6.1908	5.96868	6.89776	6.85269	6.58388	6.34202	NA	0.8143	263755_at
At1g20300	Pentatricopeptide repeat (PPR) superfamily protein	5.13334	5.25265	6.15822	6.01372	6.079	5.83954	6.27256	6.09332	NA	0.89298	255888_at
At2g29670	Tetratricopeptide repeat (TPR)-like superfamily protein	4.80262	4.86943	5.50969	5.6269	8.26534	8.19193	7.53533	7.75768	NA	0.73227	266617_at
At2g22090	UBA1A, RNA-binding (RRM/RBD/RNP motifs) family protein	5.28726	5.71005	6.93525	6.90243	6.69598	6.96175	7.05591	6.82746	NA	1.42019	263356_at
At5g43180	Protein of unknown function, DUF599	8.98505	8.91815	10.1706	9.78017	6.54295	6.1976	6.77424	6.3868	NA	1.02379	249136_at
At1g25580	ANAC008, SOG1, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	5.85801	5.76686	6.74328	6.72197	6.16288	5.96977	6.63578	6.41886	NA	0.92019	255739_at
At5g53800	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.43979	5.08963	6.25199	6.11841	5.20914	5.13697	5.38792	5.28222	NA	0.9205	248228_at

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At2g34610	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G30190.1); Has 342 Blast hits to 279 proteins in 74 species: Archae - 0; Bacteria - 7; Metazoa - 76; Fungi - 18; Plants - 51; Viruses - 0; Other Eukaryotes - 190 (source: NCBI BLink).	4.74468	4.56936	5.85264	6.53577	4.31768	4.3029	4.37036	4.28901	NA	1.53718	266900_at
At5g60760	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.00362	4.95494	7.22235	6.73067	4.46318	4.57985	4.4381	4.43552	NA	1.99723	247582_at
At1g18370	ATNACK1, HIK, NACK1, ATP binding microtubule motor family protein	4.82411	5.11391	5.77129	6.02941	4.76666	4.79243	4.65342	4.95002	NA	0.93134	261660_at
At2g03270	DNA-binding protein, putative	5.93814	5.72198	7.00871	6.81122	6.84505	6.88858	6.85165	6.95255	NA	1.0799	266679_at
At3g53340	NF-YB10, nuclear factor Y, subunit B10	6.31846	6.1437	6.91575	6.83511	6.60126	6.79341	6.78356	6.87633	NA	0.64435	251991_at
At4g22570	APT3, adenine phosphoribosyl transferase 3	6.18829	5.99418	7.76834	7.78581	6.12554	6.06898	6.5003	7.18881	NA	1.68584	254328_at
At5g56910	Proteinase inhibitor I25, cystatin, conserved region	5.29108	5.80804	6.42537	6.3669	6.79291	6.79535	6.58592	6.71364	NA	0.84657	247988_at
At4g19610	nucleotide binding;nucleic acid binding;RNA binding	5.24365	5.31894	6.13867	6.13524	5.78456	5.74468	5.62258	5.83503	NA	0.85566	254527_at
At3g58180	ARM repeat superfamily protein	6.07167	6.23585	7.18137	7.14382	7.5952	7.17532	7.36853	7.45482	NA	1.00884	251578_at
At3g54320	ASML1, ATWRI1, WRI, WRI1, Integrase-type DNA-binding superfamily protein	4.98591	4.76604	5.72655	5.70091	4.96442	4.90325	4.73157	4.63302	NA	0.83775	251892_at
At3g15360	ATHM4, ATM4, TRX-M4, thioredoxin M-type 4	6.56864	5.96238	7.47079	7.23577	10.2798	10.2668	9.89055	10.1204	NA	1.08777	258398_at
At5g28750	Bacterial sec-independent translocation protein mttA/Hcf106	5.61941	5.02686	6.44087	6.58379	8.30113	8.28071	8.11291	8.31214	NA	1.1892	245924_at
At5g57660	ATCOL5, COL5, CONSTANS-like 5	7.76582	6.96318	9.16267	9.19403	10.4345	10.4995	10.6313	10.9396	NA	1.81385	247921_at
At1g53090	SPA4, SPA1-related 4	4.978	5.31726	6.6406	6.21323	7.47938	7.38955	8.42494	7.76319	NA	1.27928	261319_at
At2g28550	RAP2.7, TOE1, related to AP2.7	7.06615	6.9684	7.94253	7.79613	7.19392	7.46876	7.73548	7.60597	NA	0.85206	264057_at
At3g19340	Protein of unknown function (DUF3754)	7.23787	7.21302	7.79796	7.87063	7.41313	7.25828	7.31985	7.39373	NA	0.60885	258015_at
At3g45780	JK224, NPH1, PHOT1, RPT1, phototropin 1	5.29145	4.59155	6.46864	6.30861	8.57902	8.57048	7.95884	8.07934	NA	1.44713	252543_at
At3g20970	ATNFU2, NFU4, NFU domain protein 4	5.98038	6.07571	7.41293	7.16138	7.16027	6.82653	7.20955	7.17331	NA	1.25911	256807_at
At3g14560	unknown protein; Has 6 Blast hits to 6 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.38299	6.89587	8.21304	7.75023	5.8118	5.7054	6.04036	5.84211	NA	1.34221	258091_at
At2g35710	Nucleotide-diphospho-sugar transferases superfamily protein	6.04501	5.65376	6.80394	6.9949	5.00387	5.0521	5.16336	5.05083	NA	1.05004	265841_at
At1g73130	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17780.2); Has 1447 Blast hits to 774 proteins in 215 species: Archae - 0; Bacteria - 679; Metazoa - 377; Fungi - 171; Plants - 42; Viruses - 6; Other Eukaryotes - 172 (source: NCBI BLink).	5.65641	5.70377	6.23823	6.41327	5.49089	5.31589	5.62954	5.5979	NA	0.64567	262372_at

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At5g43670	Sec23/Sec24 protein transport family protein	5.65814	5.57066	6.67165	6.4673	6.05986	6.01247	6.33419	6.10828	NA	0.95508	249106_at
At4g08330	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G17705.1); Has 98 Blast hits to 98 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 98; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.23086	6.28254	6.85209	7.06889	6.85915	6.66939	6.91072	6.90834	NA	0.7038	255134_at
At3g16030	CES101, lectin protein kinase family protein	5.08867	4.47363	6.06367	6.09	6.88313	6.49738	7.60361	6.94995	NA	1.29569	264223_s_at
At5g47580	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17250.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.65679	5.60828	6.60252	6.73818	6.36887	6.55965	6.71982	6.42803	NA	1.03781	248766_at
At1g76040	CPK29, calcium-dependent protein kinase 29	5.00999	4.58832	5.5467	5.45382	4.12069	4.08084	4.23521	4.27759	NA	0.70111	262671_at
At4g39660	AGT2, alanine:glyoxylate aminotransferase 2	9.19015	8.89574	10.2027	10.2657	7.76575	7.41685	7.5368	7.37279	NA	1.19124	252855_at
At2g17670	Tetratricopeptide repeat (TPR)-like superfamily protein	6.00143	6.25666	7.10304	7.2928	7.13446	6.94805	6.97347	7.26466	NA	1.06887	264591_at
At1g74100	ATSOT16, ATST5A, CORI-7, SOT16, sulfotransferase 16	9.23327	9.3379	10.0249	10.3887	8.56516	8.33221	8.56172	9.12316	NA	0.92122	260387_at
At3g25290	Auxin-responsive family protein	5.14783	5.36857	5.915	6.14266	4.75684	4.64141	5.12587	4.8999	NA	0.77063	257824_at
At1g52540	Protein kinase superfamily protein	4.98661	4.94942	6.48668	6.12434	5.19975	4.92923	5.29928	5.03626	NA	1.3375	262158_at
At5g27750	F-box/FBD-like domains containing protein	4.45097	4.7003	5.48403	5.53402	5.02787	5.05083	5.18728	5.02522	NA	0.93339	246743_at
At4g37180	Homeodomain-like superfamily protein	5.21614	5.00574	7.22912	7.12584	6.51849	6.54961	6.37544	6.65536	NA	2.06655	246215_at
At3g24350	ATSYP32, SYP32, syntaxin of plants 32	6.08634	6.31497	7.23182	7.19464	7.06574	6.86234	7.1141	7.27704	NA	1.01258	257157_at
At5g19180	ECR1, E1 C-terminal related 1	6.30869	6.28614	7.38052	7.40533	7.41027	7.36899	7.32669	7.28612	NA	1.09551	249926_at
At5g03940	54CP, CPSRP54, FFC, SRP54CP, chloroplast signal recognition particle 54 kDa subunit	5.44755	5.30405	6.09959	6.17715	7.67598	7.89778	7.335	7.65433	NA	0.76257	250884_at
At5g20270	HHP1, heptahelical transmembrane protein1	5.32477	5.48721	6.12038	6.15895	7.01944	6.75475	7.41871	7.33208	NA	0.73368	246097_at
At3g20570	AtENODL9, ENODL9, early nodulin-like protein 9	6.64621	6.76961	7.73428	7.42344	6.70581	6.69389	6.3505	6.55727	NA	0.87095	257093_at
At1g54290	Translation initiation factor SUI1 family protein	6.15423	6.26151	6.98171	6.85696	7.29756	7.4898	7.62111	7.20157	NA	0.71147	262959_at
At1g23410	Ribosomal protein S27a / Ubiquitin family protein	5.91865	5.51715	6.78932	6.45299	4.67564	4.60077	4.74083	4.73504	NA	0.90325	263016_at
At1g74640	alpha/beta-Hydrolases superfamily protein	5.65276	5.61497	6.72726	6.30133	7.37859	7.31538	7.50514	7.15819	NA	0.88043	260232_at

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At2g28930	APK1B, PK1B, protein kinase 1B	5.95561	5.97802	6.85715	6.64807	8.16674	7.86499	7.95063	7.77749	NA	0.7858	266803_at
At5g44000	Glutathione S-transferase family protein	5.7458	5.60521	6.52133	6.22061	7.41124	7.267	7.16782	7.05792	NA	0.69546	249075_at
At5g54390	AHL, ATAHL, HL, HAL2-like	6.7701	6.48536	7.29461	7.28541	9.24572	9.09312	9.37426	9.1145	NA	0.66227	248155_at
At5g53590	SAUR-like auxin-responsive protein family	7.87087	8.04467	8.86234	8.5634	6.10732	5.94579	5.94796	5.79246	NA	0.7551	248243_at
At4g15500	UGT84A4, UDP-Glycosyltransferase superfamily protein	5.63803	5.74995	6.36335	6.22136	5.74341	5.63702	5.64962	5.60256	NA	0.59837	245561_at
At1g31420	FEI1, Leucine-rich repeat protein kinase family protein	6.18477	6.36813	7.29922	7.15791	8.00783	7.98116	7.80108	7.76942	NA	0.95212	256482_at
At2g47260	ATWRKY23, WRKY23, WRKY DNA-binding protein 23	6.87604	6.86577	7.67535	7.35934	5.08608	4.87617	4.94672	4.75098	NA	0.64643	260528_at
At5g41080	PLC-like phosphodiesterases superfamily protein	5.54566	6.22313	7.82142	7.87216	4.60807	4.5311	4.46761	4.36208	NA	1.96239	249337_at
At5g49360	ATBXL1, BXL1, beta-xylosidase 1	8.70525	8.75818	10.148	9.96792	11.2017	11.333	10.167	10.3868	-0.99	1.32624	248622_at
At3g11670	DGD1, UDP-Glycosyltransferase superfamily protein	5.63203	5.90143	6.56688	6.50925	8.35015	8.61382	7.6919	7.52284	-0.87	0.77134	259070_at
At4g28290	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 45 Blast hits to 45 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.77387	4.55041	5.67086	5.42085	8.56276	8.42202	7.30084	7.46315	-1.11	0.88372	253814_at
At1g71880	ATSUC1, SUC1, sucrose-proton symporter 1	6.7575	6.53231	8.88143	8.61358	8.48208	8.34445	7.69127	7.57358	-0.78	2.1026	260143_at
At1g02640	ATBXL2, BXL2, beta-xylosidase 2	6.7737	6.95605	7.74199	7.87972	7.66116	7.90581	6.58377	6.77217	-1.11	0.94598	260914_at
At1g58180	ATBCA6, BCA6, beta carbonic anhydrase 6	8.5613	8.21431	9.26386	9.14873	8.66859	8.935	8.07758	7.92219	-0.8	0.81849	246396_at
At3g30775	AT-POX, ATPDH, ATPOX, ERD5, PRO1, PRODH, Methylenetetrahydrofolate reductase family protein	11.1435	10.8936	12.1451	12.3859	9.22831	9.24602	8.62996	8.55599	-0.64	1.24692	257315_at
At4g19420	Pectinacetylesterase family protein	5.08032	4.93335	5.78344	5.59777	7.27746	6.94272	5.51415	5.67125	-1.52	0.68377	254573_at
At5g47400	unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.55829	5.30506	6.48016	6.2901	6.04521	5.9543	5.25004	5.51091	-0.62	0.95346	248786_at
At1g66180	Eukaryotic aspartyl protease family protein	9.94513	9.87885	11.125	11.0085	10.6963	10.7429	9.36356	9.78237	-1.15	1.15474	256525_at
At5g62920	ARR6, response regulator 6	6.89608	6.67283	7.45594	7.62344	6.12278	6.06802	7.06976	7.25877	1.069	0.75524	247406_at
At4g34860	Plant neutral invertase family protein	7.26632	7.3395	8.21712	8.17574	6.82685	6.82426	7.52005	7.81047	0.84	0.89352	253224_at

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At3g58610	ketol-acid reductoisomerase	10.8777	10.9608	11.6853	11.7967	10.744	10.8339	11.7814	12.0319	1.118	0.82169	251536_at
At4g25835	P-loop containing nucleoside triphosphate hydrolases superfamily protein	4.60221	4.77366	5.83956	5.88709	5.22954	5.19033	6.18434	6.48512	1.125	1.17539	254027_at
At1g73920	alpha/beta-Hydrolases superfamily protein	7.88872	7.61572	9.55295	9.61569	8.57366	8.54526	10.2556	10.6402	1.888	1.8321	260393_at
At1g09780	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	9.69528	10.0741	10.4924	10.7308	8.51157	8.56712	10.7726	10.8198	2.257	0.72692	264668_at
At5g17380	Thiamine pyrophosphate dependent pyruvate decarboxylase family protein	9.02494	8.93523	9.58869	9.99416	9.15832	9.15863	9.81203	9.82754	0.661	0.81134	250094_at
At1g13740	AFP2, ABI five binding protein 2	6.98688	6.92169	8.13019	7.79394	6.65661	6.30317	7.31676	7.31441	0.836	1.00778	256069_at
At5g13420	Aldolase-type TIM barrel family protein	9.58985	9.70078	11.2498	11.78	9.30166	9.40799	10.5185	10.95	1.379	1.86959	250234_at
At5g66530	Galactose mutarotase-like superfamily protein	6.94803	7.2389	8.26707	8.47498	7.28105	7.35939	8.08644	8.55071	0.998	1.27756	247101_at
At5g39590	TLD-domain containing nucleolar protein	8.24323	7.94072	9.44505	9.60541	8.31589	8.62823	9.46795	9.6825	1.103	1.43325	249442_at
At3g03040	F-box/RNI-like superfamily protein	5.21778	5.71205	7.2735	6.83566	6.99277	6.48663	8.50235	8.24746	1.635	1.58967	257530_at
At1g49160	WNK7, Protein kinase superfamily protein	5.84633	5.49497	7.76843	8.63014	4.95808	5.65432	7.05131	7.38454	1.912	2.52864	260771_at
At5g04540	Myotubularin-like phosphatases II superfamily	5.97977	5.66383	6.91283	7.23977	6.1149	6.09984	7.21794	7.04359	1.023	1.2545	250833_at
At3g19030	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pyridoxine biosynthetic process, homoserine biosynthetic process; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49500.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	8.14587	6.86454	10.0516	10.3362	6.99728	6.89721	10.2107	10.4033	3.36	2.68871	256891_at
At1g48600	AtPMEAMT, PMEAMT, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	9.75247	9.8106	11.0724	11.4711	5.75538	6.10317	7.6874	8.44761	2.138	1.49021	261309_at
At5g20990	B73, CHL6, CNX, CNX1, SIR4, molybdopterin biosynthesis CNX1 protein / molybdenum cofactor biosynthesis enzyme CNX1 (CNX1)	7.84863	7.82916	8.77509	8.62551	7.94586	7.83059	8.74085	8.51871	0.742	0.8614	246131_at
At4g18010	5PTASE2, AT5PTASE2, IP5PII, myo-inositol polyphosphate 5-phosphatase 2	6.04943	5.79494	7.5076	7.30355	7.79804	7.98975	8.93063	8.5168	0.83	1.48339	254707_at
At2g39360	Protein kinase superfamily protein	4.69157	4.46456	5.44648	5.16873	5.37681	5.42448	6.12745	6.14735	0.737	0.72954	266968_at
At1g60140	ATTPS10, TPS10, TPS10, trehalose phosphate synthase	8.22953	7.58692	9.52815	9.42079	8.02961	8.10126	9.44726	9.75809	1.537	1.56624	264246_at
At3g48360	ATBT2, BT2, BTB and TAZ domain protein 2	5.28391	6.09065	10.6069	10.1718	4.82341	4.6103	10.5987	10.8078	5.986	4.70205	252367_at

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At5g12860	DiT1, dicarboxylate transporter 1	8.65152	8.35953	9.53617	9.92359	10.1558	10.1236	11.5197	11.4354	1.338	1.22435	250278_at
At5g42990	UBC18, ubiquitin-conjugating enzyme 18	7.08428	6.97626	7.89199	8.46713	7.16677	7.19361	8.47331	8.50263	1.308	1.14929	249183_at
At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	6.58564	5.91532	9.23094	9.45366	4.87024	4.57729	5.93088	6.64745	1.565	3.09183	250472_at
At2g15620	ATHNIR, NIR, NIR1, nitrite reductase 1	7.79853	7.72042	10.8234	11.3543	5.79816	5.96836	12.0575	12.3646	6.328	3.32936	265475_at
At4g26970	ACO2, aconitase 2	10.343	10.2422	11.2284	11.8238	9.96796	10.1752	11.1733	11.1941	1.112	1.23349	253954_at
At3g62930	Thioredoxin superfamily protein	4.47104	4.47363	6.98138	7.3533	4.62897	4.54036	5.62205	6.09625	1.274	2.695	251195_at
At4g05390	ATRFNR1, RFNR1, root FNR 1	6.26843	6.81159	8.79496	9.26916	5.89863	5.92941	9.56115	10.2417	3.987	2.49205	255230_at
At1g71010	FAB1C, FORMS APLOID AND BINUCLEATE CELLS 1C	8.43732	8.1949	9.20206	9.00446	7.69707	7.67922	8.37255	8.35431	0.675	0.78716	262308_at
At2g31380	STH, salt tolerance homologue	5.86169	6.02219	7.04769	7.39147	10.0473	10.1045	10.8402	10.9515	0.82	1.27763	263252_at
At5g14070	ROXY2, Thioredoxin superfamily protein	4.33233	4.33871	5.50827	5.40125	4.61016	4.52864	5.18204	5.12778	0.586	1.11924	250223_at
At1g49500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G19030.1); Has 24 Blast hits to 24 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.29953	5.69092	10.314	10.3911	6.66371	6.57563	10.2729	11.057	4.045	4.35733	262399_at
At5g17760	P-loop containing nucleoside triphosphate hydrolases superfamily protein	6.43507	6.61531	7.68549	7.81023	5.09776	4.97889	5.93509	5.69377	0.776	1.22267	250062_at
At4g37540	LBD39, LOB domain-containing protein 39	6.36564	5.67237	8.33066	8.21789	6.5385	6.37412	8.24112	8.31311	1.821	2.25527	253043_at
At5g53160	PYL8, RCAR3, regulatory components of ABA receptor 3	8.04892	8.18176	9.20623	9.11542	8.91659	8.66557	9.82764	9.70657	0.976	1.04549	248302_at
At1g24280	G6PD3, glucose-6-phosphate dehydrogenase 3	5.27825	5.27506	8.11335	9.12392	4.73266	4.72478	8.97006	10.0426	4.778	3.34198	264859_at
At5g54130	Calcium-binding endonuclease/exonuclease/phosphatase family	11.0168	12.0417	16.5215	16.4636	12.7682	12.183	14.8422	15.0024	2.447	4.96331	248190_at 248191_at
At5g50200	ATNRT3.1, NRT3.1, WR3, nitrate transmembrane transporters	10.5616	10.0081	11.779	12.3639	9.42821	9.77802	11.5772	11.709	2.04	1.78657	248551_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g14340	RNA-binding (RRM/RBD/RNP motifs) family protein	6.26235	6.33273	7.83786	8.05328	5.40274	5.44088	7.01397	7.21145	1.691	1.64803	261487_at
At5g37260	CIR1, RVE2, Homeodomain-like superfamily protein	5.03368	4.96095	6.62221	6.94693	4.99507	4.85511	6.26561	6.36445	1.39	1.78726	249606_at
At3g63110	ATIPT3, IPT3, isopentenyltransferase 3	5.61194	5.7799	6.3902	6.48501	5.69803	5.61181	6.78716	7.14101	1.309	0.74168	251154_at
At1g64190	6-phosphogluconate dehydrogenase family protein	9.84821	9.73758	11.1345	11.371	8.56238	8.62106	9.96481	10.5677	1.675	1.45984	262323_at
At5g65000	Nucleotide-sugar transporter family protein	7.24337	7.35378	7.89721	7.90712	7.33257	7.33968	7.94914	7.94191	0.609	0.60359	247207_at
At5g62720	Integral membrane HPP family protein	5.60954	5.09155	6.68108	6.50291	5.31794	5.1821	7.36982	7.71513	2.292	1.24145	247443_at
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1	8.67403	8.58488	11.1588	11.6121	5.545	6.19019	8.10102	8.33838	2.352	2.75597	260623_at
At5g10030	OBF4, TGA4, TGACG motif-binding factor 4	5.00949	5.50289	6.41994	6.45841	5.51985	5.54237	6.45187	6.45873	0.924	1.18299	250463_at
At2g41560	ACA4, autoinhibited Ca(2+)-ATPase, isoform 4	5.11281	5.53367	7.34014	7.46856	7.44208	7.55739	8.63711	9.07036	1.354	2.0811	245117_at
At1g63940	MDAR6, monodehydroascorbate reductase 6	8.81083	9.23554	10.6929	11.3715	7.52999	7.93811	11.3495	11.9044	3.893	2.00902	260325_at
At2g38170	ATCAX1, CAX1, RCI4, cation exchanger 1	6.87008	6.38684	7.92129	8.10031	9.29614	9.23266	11.2715	11.0473	1.895	1.38234	267093_at
At4g35260	IDH-I, IDH1, isocitrate dehydrogenase 1	8.31011	8.4808	9.36153	9.57015	7.49788	7.63091	8.61455	8.90603	1.196	1.07038	253196_at
At2g26980	CIPK3, SnRK3.17, CBL-interacting protein kinase 3	6.07435	6.32913	8.58444	8.79873	6.86193	6.729	10.2308	10.1576	3.399	2.48985	266313_at
At3g26090	ATRGS1, RGS1, G-protein coupled receptors;GTPase activators	7.15077	7.21367	8.04963	8.19731	6.84687	6.8557	7.69541	7.85746	0.925	0.94125	258072_at
At5g65210	TGA1, bZIP transcription factor family protein	10.2293	9.64646	11.2185	11.3691	7.33504	7.4943	8.29559	8.72416	1.095	1.35591	247199_at
At4g02380	AtLEA5, SAG21, senescence-associated gene 21	10.4131	9.14081	11.8623	12.0766	8.34905	8.62387	11.9117	12.4926	3.716	2.19245	255479_at
At5g40730	AGP24, ATAGP24, arabinogalactan protein 24	8.47777	8.55231	9.38276	9.43466	6.57098	6.27531	7.08487	7.35628	0.797	0.89367	249375_at
At2g27510	ATFD3, FD3, ferredoxin 3	9.89853	10.1759	11.2809	11.8281	8.47112	8.26665	11.2522	11.8026	3.159	1.51727	265649_at
At5g13110	G6PD2, glucose-6-phosphate dehydrogenase 2	6.79057	6.66063	8.3588	8.95847	6.42549	6.13461	8.83056	9.71606	2.993	1.93303	245977_at
At4g18170	ATWRKY28, WRKY28, WRKY DNA-binding protein 28	5.05468	4.89627	5.74052	5.75262	6.12531	6.1997	6.68155	6.87502	0.616	0.7711	254652_at
At1g77760	GNR1, NIA1, NR1, nitrate reductase 1	6.39261	6.98636	9.67103	11.0929	6.6691	6.91099	12.4174	12.8535	5.845	3.69248	259681_at
At1g70780	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0	8.81053	8.92502	11.1133	10.9972	9.08608	8.98679	11.2031	11.5246	2.327	2.18749	262262_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	(source: NCBI BLink).											
At1g49860	ATGSTF14, GSTF14, glutathione S-transferase (class phi) 14	10.0146	9.36535	11.8781	11.906	4.50831	4.28342	7.31731	7.90594	3.216	2.20208	259813_at
At3g13070	CBS domain-containing protein / transporter associated domain-containing protein	6.01231	6.29014	7.455	7.70075	7.23939	7.38937	8.43765	8.41843	1.114	1.42665	257178_at
At2g31955	CNX2, cofactor of nitrate reductase and xanthine dehydrogenase 2	7.07411	7.03034	7.77606	7.73442	7.07652	6.96248	8.36258	8.103	1.213	0.70301	263472_at
At2g30040	MAPKKK14, mitogen-activated protein kinase kinase kinase 14	5.68323	5.17352	6.9759	7.25325	5.58355	5.42076	7.67972	7.06499	1.87	1.6862	266832_at
At4g16000	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G15990.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	6.87146	6.86452	8.86834	8.54472	6.26489	6.18869	7.36449	7.36077	1.136	1.83854	245353_at
At5g53460	GLT1, NADH-dependent glutamate synthase 1	10.9544	10.6966	12.1603	12.2487	8.5974	9.20284	11.0853	11.5105	2.398	1.379	248267_at
At5g40850	UPM1, urophorphyrin methylase 1	6.61058	5.95696	9.21297	9.37054	6.1467	6.20915	10.5469	10.8962	4.544	3.00799	249325_at
At2g41310	ARR8, ATRR3, RR3, response regulator 3	5.38039	4.91755	6.39507	6.41347	4.9872	4.97113	5.85305	6.00201	0.948	1.2553	266372_at
At1g70810	Calcium-dependent lipid-binding (CaLB domain) family protein	7.22869	7.42427	7.95698	8.109	7.58338	7.62333	8.3801	8.34394	0.759	0.70651	262314_at
At3g48990	AMP-dependent synthetase and ligase family protein	10.3829	10.2739	11.8179	11.9043	10.8713	10.8673	12.0691	12.3818	1.356	1.53269	252293_at
At5g19970	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.97674	5.58897	7.67521	7.61511	5.06575	5.19033	7.6285	7.42888	2.401	1.8623	246142_at
At1g30510	ATRFNR2, RFNR2, root FNR 2	8.76956	8.765	11.2178	11.8101	6.0927	5.87588	9.8788	10.9453	4.428	2.74667	261806_at
At1g68670	myb-like transcription factor family protein	6.12999	6.3056	8.39817	9.043	6.60737	7.01582	8.26616	8.31402	1.479	2.50279	262284_at
At5g17020	ATCRM1, ATXPO1, HIT2, XPO1, XPO1A, exportin 1A	7.67847	7.79499	8.24997	8.42932	7.65466	7.82354	8.45466	8.30278	0.64	0.60291	246424_at
At4g00630	ATKEA2, KEA2, K+ efflux antiporter 2	6.42598	6.32964	7.84921	8.11171	6.90986	6.83126	7.752	7.50249	0.757	1.60265	255686_at
At1g16170	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G79660.1); Has 55 Blast hits to 55 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.11073	5.40731	7.14502	7.25332	5.66408	5.39409	7.39138	7.31023	1.822	1.94016	261791_at

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At5g41670	6-phosphogluconate dehydrogenase family protein	8.26333	8.66416	10.463	11.2961	7.87536	7.6397	10.772	11.5184	3.388	2.4158	249266_at
At1g03080	kinase interacting (KIP1-like) family protein	6.76302	6.48548	7.7208	7.6388	6.05405	6.06418	7.11598	6.65902	0.828	1.05555	263112_at
At1g30270	ATCIPK23, CIPK23, LKS1, SnRK3.23, CBL-interacting protein kinase 23	8.81523	8.81457	10.0938	9.80841	7.5548	7.12274	8.16653	8.29121	0.89	1.13622	245775_at
At3g16560	Protein phosphatase 2C family protein	6.00719	5.46885	8.94632	8.88435	7.35332	7.09853	9.31094	9.71708	2.288	3.17731	258437_at
At1g73600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	6.10215	5.94174	7.41075	7.98914	5.04829	4.89569	6.15259	6.48014	1.344	1.678	259842_at
At1g25550	myb-like transcription factor family protein	7.46777	7.31941	9.38172	10.0372	7.35636	7.71812	8.83306	9.37548	1.567	2.31587	255734_at
At5g26340	ATSTP13, MSS1, STP13, Major facilitator superfamily protein	7.10571	7.48265	8.23739	8.32238	8.74038	8.7813	9.65047	9.72133	0.925	0.98571	246831_at
At1g19050	ARR7, response regulator 7	5.96638	5.26446	8.24065	8.44435	7.68987	7.58566	8.79055	8.9432	1.229	2.72708	259466_at

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Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At3g23270	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	4.49941	4.4809	3.88993	3.87175	3.87371	3.91715	3.85653	3.96082	NA	-0.6093	257921_at
At4g15280	UGT71B5, UDP-glucosyl transferase 71B5	5.39915	5.65237	4.33645	4.57829	4.38808	4.59195	4.44549	4.54939	NA	-1.0684	245545_at
At5g34790	transposable element gene	5.5708	5.32192	4.57621	4.73462	4.95156	4.9947	4.73194	4.77625	NA	-0.7909	246691_at
At2g36885	unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 172 Blast hits to 172 proteins in 58 species: Archae - 0; Bacteria - 116; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 24 (source: NCBI BLink).	6.56924	6.71546	5.67352	5.79563	5.74218	5.93614	5.79901	6.08661	NA	-0.9078	263840_at
At4g13840	HXXXD-type acyl-transferase family protein	5.86535	5.75475	4.95168	4.64365	7.16144	7.28347	6.8765	7.11938	NA	-1.0124	254737_at
At1g63030	ddf2, Integrase-type DNA-binding superfamily protein	5.06605	4.93246	4.21055	4.38213	4.28307	4.40941	4.32266	4.33357	NA	-0.7029	261101_at
At2g19300	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 4 Blast hits to 4 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.38984	4.56756	3.79546	3.882	3.91378	4.01879	3.89414	4.0103	NA	-0.64	267320_at
At1g49380	cytochrome c biogenesis protein family	5.38967	5.73619	4.81141	4.89261	6.60706	6.47321	6.12682	6.32105	NA	-0.7109	262397_at

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At4g08410	Proline-rich extensin-like family protein	7.55744	7.91936	6.02073	6.08776	5.77279	5.70004	5.83314	6.06657	NA	-1.6842	255140_x_at
At5g19880	Peroxidase superfamily protein	5.29707	5.10881	4.3388	4.39692	4.36087	4.50063	4.25527	4.47363	NA	-0.8351	246145_at
At2g18060	ANAC037, VND1, vascular related NAC-domain protein 1	4.91333	5.16875	4.37684	4.31877	4.38988	4.40776	4.57871	4.4936	NA	-0.6932	265813_at
At1g51670	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G48180.1); Has 37 Blast hits to 37 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.09117	5.24459	4.28525	4.29988	4.40421	4.40762	4.59928	4.46332	NA	-0.8753	256175_at
At5g38960	RmlC-like cupins superfamily protein	5.78384	5.82821	4.99684	5.0107	4.9225	5.11522	4.65978	5.0007	NA	-0.8023	249479_at
At5g50780	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	6.32315	6.18508	5.60534	5.47904	5.22733	5.49333	5.22612	5.41097	NA	-0.7119	248495_at
At2g06960	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	5.02291	5.29023	4.48903	4.37554	4.56944	4.49985	4.47572	4.39447	NA	-0.7243	266498_at
At4g11930	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11940.1); Has 102 Blast hits to 102 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 2; Plants - 99; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.20698	5.6371	4.38757	4.35603	4.46574	4.34339	4.43592	4.45104	NA	-1.0502	254840_at
At1g41810	transposable element gene	5.95035	5.92096	5.0845	5.1426	5.05997	5.225	5.19446	5.29165	NA	-0.8221	260017_at
At4g23493	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	6.24237	6.82663	5.63033	5.61717	4.85052	5.06835	4.83879	4.89957	NA	-0.9107	254263_at
At3g52460	hydroxyproline-rich glycoprotein family protein	5.75154	5.41754	4.72514	4.60941	4.46364	4.48967	4.31877	4.51726	NA	-0.9173	252046_at
At1g28135	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 7 Blast hits to 7 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.86362	4.87666	4.029	4.12832	4.05941	4.29484	4.14052	4.23446	NA	-0.7915	259589_at
At3g24750	unknown protein; Has 25 Blast hits to 25 proteins in 12 species: Archae - 0; Bacteria - 8; Metazoa - 2; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.92478	4.81563	4.23611	4.22096	4.18402	4.12974	4.10305	4.12719	NA	-0.6417	257595_at
At1g76370	Protein kinase superfamily protein	5.66594	5.52357	4.44152	4.42284	4.45487	4.40844	4.40783	4.46891	NA	-1.1626	259886_at
At3g44510	alpha/beta-Hydrolases superfamily protein	5.1765	5.38532	4.50958	4.66059	4.25709	4.46917	4.1955	4.28784	NA	-0.6958	252635_at
At2g21830	Cysteine/Histidine-rich C1 domain family protein	4.93903	5.10709	4.37104	4.35012	4.89888	4.88484	4.76975	4.82187	NA	-0.6625	263883_at

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At1g16705	p300/CBP acetyltransferase-related protein-related	5.57878	5.42679	4.42924	4.48984	4.64329	4.79195	4.62766	4.51484	NA	-1.0432	255768_at
At5g45850	Protein of unknown function (DUF688)	4.71362	4.74351	4.15943	4.10485	4.10668	4.33741	4.23351	4.26181	NA	-0.5964	248917_at
At3g52540	ATOFP18, OFP18, ovate family protein 18	5.209	5.18562	4.60853	4.60016	4.93032	4.9271	4.97033	4.85213	NA	-0.593	252054_at
At3g03690	UNE7, Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	6.35837	6.85016	4.98429	5.15195	5.02952	5.35369	5.10079	4.9659	NA	-1.5361	259174_at
At5g64550	loricrin-related	7.67772	7.50103	6.77985	6.62526	6.58389	6.62531	6.65286	6.68994	NA	-0.8868	247265_at
At3g55800	SBPASE, sedoheptulose-bisphosphatase	6.68915	6.10945	4.98424	5.00899	10.207	10.6487	9.92343	10.2165	NA	-1.4027	251762_at
At1g36430	transposable element gene	4.73787	4.49507	3.9624	4.0328	4.01018	4.01249	4.0082	4.01744	NA	-0.6189	261963_at
At3g43080	transposable element gene	4.91998	4.79241	3.9395	3.94539	3.98014	4.12538	4.06659	4.11035	NA	-0.9137	252728_at
At1g52240	ATROPGEF11, PIRF1, ROPGEF11, RHO guanyl-nucleotide exchange factor 11	4.99106	5.22369	4.12162	4.2387	4.11804	4.24731	4.12337	4.12012	NA	-0.9272	259836_at
At5g02230	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	9.24679	8.65026	7.47511	7.1761	5.50479	5.7841	4.41292	4.75895	NA	-1.6229	251028_at
At5g58630	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.36557	5.1671	4.38111	4.51274	4.44589	4.57514	4.55387	4.65911	NA	-0.8194	247773_at
At1g62380	ACO2, ATACO2, ACC oxidase 2	11.0869	11.2336	10.6231	10.1894	12.0463	12.1678	11.8568	11.9133	NA	-0.754	260637_at
At3g19020	Leucine-rich repeat (LRR) family protein	5.18117	5.3657	4.10889	4.20339	4.26026	4.5528	4.22453	4.43083	NA	-1.1173	256945_at
At1g75590	SAUR-like auxin-responsive protein family	5.14429	5.5273	4.4007	4.42365	4.4232	4.51107	4.45904	4.47568	NA	-0.9236	262981_at
At1g02190	Fatty acid hydroxylase superfamily	5.46442	5.41935	4.39596	4.42978	4.46346	4.49359	4.50033	4.48734	NA	-1.029	264180_at
At3g25180	CYP82G1, cytochrome P450, family 82, subfamily G, polypeptide 1	6.77213	6.32903	5.14121	5.18725	5.47252	5.61657	5.50272	5.5979	NA	-1.3863	257835_at
At5g23790	AtGolS5, GolS5, galactinol synthase 5	4.87403	4.81609	4.1772	4.19249	4.26795	4.30107	4.31264	4.2726	NA	-0.6602	249804_at
At2g46870	NGA1, AP2/B3-like transcriptional factor family protein	5.42678	5.57579	4.79458	4.62661	5.50843	5.52852	5.26455	5.29771	NA	-0.7907	266760_at
At3g45090	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.86499	5.82789	4.81365	5.13739	4.55504	4.83806	4.50488	4.74021	NA	-0.8709	252608_at
At1g08270	CONTAINS InterPro DOMAIN/s: MIT (InterPro:IPR007330); BEST Arabidopsis thaliana protein match is: AAA-type ATPase family protein (TAIR:AT2G27600.1); Has 1133 Blast hits to 1133 proteins in 252 species: Archae - 47; Bacteria - 0; Metazoa - 540; Fungi - 145; Plants - 223; Viruses - 0; Other Eukaryotes - 178 (source: NCBI BLink).	5.02852	4.70635	4.11916	4.00777	4.02944	4.14036	4.03522	4.07285	NA	-0.804	261812_at
At3g49260	iqd21, IQ-domain 21	5.72173	5.82162	4.38263	4.75112	7.18754	7.39561	6.8136	7.03732	NA	-1.2048	252280_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g47280	ADR1-L3, ADR1-like 3	5.28514	5.10352	4.27329	4.37677	4.39413	4.44336	4.44862	4.38842	NA	-0.8693	248810_at
At2g06820	transposable element gene	5.59833	5.72342	4.46296	4.61987	4.64542	4.58715	4.76019	4.70044	NA	-1.1195	266211_at
At2g07760	Zinc knuckle (CCHC-type) family protein	5.81685	5.9274	4.51733	4.44124	4.50547	4.61632	4.48057	4.56573	NA	-1.3928	266933_at
At2g30890	Cytochrome b561/ferric reductase transmembrane protein family	5.47388	5.51356	4.74044	4.79353	5.09196	5.30423	5.00972	5.05407	NA	-0.7267	267192_at
At5g66700	ATHB53, HB-8, HB53, homeobox 53	9.01512	8.76574	7.18701	7.76291	5.13837	5.54181	5.05511	5.23259	NA	-1.4155	247052_at
At1g03320	unknown protein; Has 1038 Blast hits to 683 proteins in 112 species: Archae - 4; Bacteria - 14; Metazoa - 318; Fungi - 117; Plants - 86; Viruses - 8; Other Eukaryotes - 491 (source: NCBI BLink).	5.30624	5.38004	4.59553	4.66319	4.74766	4.80006	4.65691	4.81489	NA	-0.7138	264359_at
At3g23840	HXXXD-type acyl-transferase family protein	5.41151	5.74215	4.4022	4.4056	4.64019	4.61127	4.72353	4.8666	NA	-1.1729	256860_at
At3g10570	CYP77A6, cytochrome P450, family 77, subfamily A, polypeptide 6	5.14193	4.98015	4.24574	4.31795	4.34647	4.62055	4.58343	4.5947	NA	-0.7792	258962_at
At2g04160	AIR3, Subtilisin-like serine endopeptidase family protein	7.82089	7.2905	6.02941	6.78071	9.23941	9.38536	8.83187	9.22456	NA	-1.1506	263406_at
At2g38140	PSRP4, plastid-specific ribosomal protein 4	7.01015	6.76781	6.18964	6.18287	9.03464	9.0245	9.19957	9.09161	NA	-0.7027	267088_at
At2g28980	transposable element gene	5.23586	5.54696	4.33609	4.53409	4.47893	4.66096	4.54651	4.48667	NA	-0.9563	266786_at
At4g12500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	6.75269	7.08626	5.28302	4.98767	11.1957	11.3043	10.8351	11.0608	NA	-1.7841	254819_at
At2g12920	transposable element gene	4.85371	5.02231	4.22092	4.03429	4.1747	4.14646	4.09184	4.29806	NA	-0.8104	263992_at
At1g01280	CYP703, CYP703A2, cytochrome P450, family 703, subfamily A, polypeptide 2	4.65074	4.59269	3.97275	4.0264	3.9656	4.1112	4.04505	4.10859	NA	-0.6221	261051_at
At5g24160	SQE6, squalene monoxygenase 6	6.05812	6.75399	4.94166	5.02642	9.72089	9.59839	9.04297	9.36136	NA	-1.422	249775_at
At2g29320	NAD(P)-binding Rossmann-fold superfamily protein	5.49553	5.57661	5.06697	4.41586	7.89116	7.7829	7.12316	7.55604	NA	-0.7947	266291_at
At1g12150	Plant protein of unknown function (DUF827)	5.06656	4.79764	4.10589	4.09005	4.01103	4.15186	4.027	4.27409	NA	-0.8341	260992_at
At3g29780	RALFL27, ralf-like 27	4.88002	4.92185	4.21253	4.36857	4.11842	4.19532	4.01967	4.16987	NA	-0.6104	256563_at
At2g42980	Eukaryotic aspartyl protease family protein	4.96345	5.09182	4.44403	4.41643	4.34929	4.35668	4.43485	4.41365	NA	-0.5974	265262_at
At3g14670	unknown protein; Has 70811 Blast hits to 32163 proteins in 1591 species: Archae - 181; Bacteria - 15342; Metazoa - 24728; Fungi - 6779; Plants - 2998; Viruses - 578; Other Eukaryotes - 20205 (source: NCBI BLink).	5.49084	5.05604	4.13939	4.20872	4.15717	4.33808	4.14163	4.27624	NA	-1.0994	258115_at
At5g07130	LAC13, laccase 13	6.49034	6.90736	5.89049	5.56184	5.42837	5.3095	5.43108	5.34989	NA	-0.9727	250674_at
At5g19560	ATROPGEF10, ROPGEF10, ROP uanine nucleotide exchange factor 10	5.17098	5.34983	4.06724	4.21325	4.05698	4.17084	4.06432	4.12461	NA	-1.1202	245945_at
At5g60140	AP2/B3-like transcriptional factor family protein	4.89278	4.81196	4.01822	4.10083	4.02222	4.1542	4.03244	4.00838	NA	-0.7928	247666_at

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At3g61810	Glycosyl hydrolase family 17 protein	5.29052	5.28218	4.58448	4.33385	4.61501	4.51824	4.64267	4.44153	NA	-0.8272	251280_at
At4g03880	transposable element gene	4.57198	4.88825	3.88018	3.88439	3.90844	3.90977	3.90762	3.9537	NA	-0.8478	255354_at
At5g65130	Integrase-type DNA-binding superfamily protein	5.38964	5.45409	4.76035	4.88314	4.80391	4.97197	4.76235	4.62216	NA	-0.6001	247227_at
At3g49270	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: proline-rich family protein (TAIR:AT3G49300.1); Has 63 Blast hits to 43 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 28; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	5.45844	5.26298	3.90001	3.98059	3.94145	4.01824	3.89941	4.01927	NA	-1.4204	252306_at
At4g10380	NIP5;1, NLM6, NLM8, NOD26-like intrinsic protein 5;1	7.67801	7.85594	6.84508	6.66971	6.51246	6.72363	6.38201	6.12592	NA	-1.0096	254971_at
At1g64300	Protein kinase family protein	5.37217	5.3069	4.51181	4.44578	4.44292	4.57245	4.41864	4.51927	NA	-0.8607	259740_at
At2g28990	Leucine-rich repeat protein kinase family protein	6.02652	6.45991	5.5054	5.5359	4.85151	4.85702	4.81677	4.77214	NA	-0.7226	266787_at
At3g04170	RmlC-like cupins superfamily protein	5.30819	5.51434	4.62901	4.60762	4.61553	4.614	4.64311	4.5931	NA	-0.793	258580_at
At5g03210	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 7 growth stages; Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.82936	5.01991	4.00595	4.06008	4.05727	4.18752	4.16764	4.11885	NA	-0.8916	250956_at
At2g36090	F-box family protein	5.51933	5.43758	4.76234	4.95418	4.62663	4.59939	4.73175	4.71768	NA	-0.6202	263283_at
At2g19290	unknown protein; Has 1 Blast hits to 1 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 1; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.26231	5.03822	4.21879	4.11508	4.19011	4.25021	4.28215	4.2425	NA	-0.9833	267332_at
At2g28710	C2H2-type zinc finger family protein	6.53776	6.74774	6.06982	5.97051	5.69136	5.80426	5.7869	5.75587	NA	-0.6226	263411_at
At4g17660	Protein kinase superfamily protein	5.42955	5.46636	4.64036	4.80507	4.92812	5.05974	4.89457	4.98231	NA	-0.7252	245375_at
At2g36180	EF hand calcium-binding protein family	4.5764	4.86958	4.04291	3.95818	4.01842	3.9645	3.93931	3.94931	NA	-0.7224	263903_at
At2g47750	GH3.9, putative indole-3-acetic acid-amido synthetase GH3.9	4.88629	4.89477	4.20785	4.20599	4.36421	4.3568	4.22046	4.32265	NA	-0.6836	266465_at
At4g35190	Putative lysine decarboxylase family protein	6.71001	6.79213	6.08343	5.99545	5.8412	5.88768	5.90086	5.84885	NA	-0.7116	253182_at
At5g18560	PUCHI, Integrase-type DNA-binding superfamily protein	5.9684	6.12938	5.22076	5.12255	4.69889	4.89039	4.86065	4.63734	NA	-0.8772	249992_at

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At2g06170	transposable element gene	5.91859	6.09758	5.06071	5.02365	4.93206	5.08478	5.07119	5.04837	NA	-0.9659	265525_at
At3g12060	TBL1, Plant protein of unknown function (DUF828)	5.25657	4.95013	4.3607	4.34811	4.31925	4.34925	4.31497	4.28629	NA	-0.7489	256660_at
At1g13890	ATSNAP30, SNAP30, soluble N-ethylmaleimide-sensitive factor adaptor protein 30	5.27052	5.38362	4.10683	4.14759	4.12414	4.10909	4.21268	4.19781	NA	-1.1999	259451_at
At1g78990	HXXXD-type acyl-transferase family protein	6.61372	6.4224	5.38872	5.16714	4.45099	4.66745	4.61642	4.47363	NA	-1.2401	257428_at
At2g37070	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G53320.1); Has 1323 Blast hits to 775 proteins in 176 species: Archae - 0; Bacteria - 113; Metazoa - 351; Fungi - 175; Plants - 115; Viruses - 13; Other Eukaryotes - 556 (source: NCBI BLink).	6.42892	6.75081	5.64013	5.74051	5.59895	5.84014	5.67685	5.79966	NA	-0.8995	265465_at
At1g77330	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	9.40348	8.72988	7.75125	7.47675	5.53982	5.74418	5.60933	5.8146	NA	-1.4527	246390_at
At5g18470	Curculin-like (mannose-binding) lectin family protein	6.98918	6.91803	6.06676	5.73424	5.58892	5.45793	5.83191	5.30074	NA	-1.0531	249983_at
At2g46300	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	5.12	5.17618	4.55233	4.52184	4.66271	4.67793	4.73909	4.58131	NA	-0.611	266607_at
At1g66840	Plant protein of unknown function (DUF827)	5.18008	4.97788	4.16044	4.39904	5.17444	5.25285	5.01228	4.89115	NA	-0.7992	256379_at
At4g21050	Dof-type zinc finger domain-containing protein	4.87431	5.23634	4.10291	4.17008	4.3573	4.32945	4.28602	4.35347	NA	-0.9188	254441_at
At5g02420	unknown protein; Has 90 Blast hits to 90 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.44506	6.6248	5.32404	5.55576	4.73225	4.88245	4.6253	4.77769	NA	-1.095	251019_at
At3g31300	transposable element gene	4.70331	4.50616	3.85206	3.93482	3.90773	4.08434	3.8947	3.9718	NA	-0.7113	256558_at
At1g13680	PLC-like phosphodiesterases superfamily protein	4.98236	5.05358	4.1779	4.174	4.27406	4.22853	4.13993	4.24582	NA	-0.842	256102_at
At4g15870	ATTS1, TS1, terpene synthase 1	5.34975	5.16674	4.19888	4.18753	4.14327	4.24981	4.2351	4.21081	NA	-1.065	245520_at
At5g28780	PIF1 helicase	4.95468	5.15035	4.00491	4.02297	4.06351	4.02664	4.06042	4.03957	NA	-1.0386	245919_at
At4g18450	Integrase-type DNA-binding superfamily protein	6.21351	6.41687	4.66288	4.61891	4.73602	4.57874	4.54817	4.82255	NA	-1.6743	254674_at
At2g37610	unknown protein; Has 21 Blast hits to 21 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.86238	4.83389	4.00132	4.01548	4.16318	4.16257	4.04977	4.18968	NA	-0.8397	267156_at
At5g59900	Pentatricopeptide repeat (PPR) superfamily protein	5.85755	5.46381	4.43023	4.45623	4.49936	4.40121	4.35405	4.31967	NA	-1.2174	247701_at
At3g44540	FAR4, fatty acid reductase 4	8.38982	8.69538	7.19069	7.27632	4.86894	4.88061	4.80383	4.75134	NA	-1.3091	252638_at
At1g10880	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	5.0158	4.83038	4.36793	4.22551	4.41158	4.44755	4.45343	4.4522	NA	-0.6264	260473_at
At2g41860	CPK14, calcium-dependent protein kinase 14	4.71877	4.46563	3.98961	3.94472	4.10051	4.06762	4.07386	4.13736	NA	-0.625	267531_at

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At4g26790	GDSL-like Lipase/Acylhydrolase superfamily protein	6.52736	6.02802	4.88273	5.09438	4.32936	4.1912	4.20903	4.16201	NA	-1.2891	253946_at
At2g33290	ATSUVH2, SDG3, SUVH2, SU(VAR)3-9 homolog 2	5.81558	5.88795	5.20644	5.16994	5.0605	5.17127	5.01333	5.1109	NA	-0.6636	255796_at
At5g11400	Protein kinase superfamily protein	5.33148	5.03016	4.33669	4.39145	4.36345	4.49295	4.37988	4.48842	NA	-0.8168	250364_at
At1g65760	Protein of unknown function (DUF295)	5.20796	5.43932	4.49343	4.40176	4.45361	4.30452	4.49883	4.43142	NA	-0.876	262928_at
At5g24880	BEST Arabidopsis thaliana protein match is: calmodulin-binding protein-related (TAIR:AT5G10660.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.46348	5.27982	4.36394	4.3778	4.09873	4.12335	4.0155	4.15015	NA	-1.0008	246969_at
At1g73410	ATMYB54, MYB54, myb domain protein 54	5.9407	5.86673	5.03425	4.83777	4.35812	4.37451	4.22497	4.25849	NA	-0.9677	245735_at
At2g06630	transposable element gene	4.61201	4.62196	3.74906	3.84458	3.8733	3.89916	3.88904	3.85398	NA	-0.8202	265746_at
At1g33580	transposable element gene	4.90726	4.97173	4.14697	4.23763	4.28652	4.35588	4.18614	4.20959	NA	-0.7472	245766_at
At2g21740	Protein of unknown function (DUF1278)	5.38978	5.35774	4.21389	3.98892	4.12325	4.03844	4.14124	4.06911	NA	-1.2724	257434_at
At1g05630	5PTASE13, AT5PTASE13, Endonuclease/exonuclease/phosphatase family protein	5.79062	5.62388	4.50054	4.56649	4.55408	4.59671	4.45446	4.64436	NA	-1.1737	263202_at
At3g53470	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 35 Blast hits to 35 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.36517	6.3565	5.50487	5.66497	8.31491	8.04767	8.04456	7.92488	NA	-0.7759	251941_at
At5g60970	TCP5, TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 5	5.11356	5.09371	4.40909	4.30945	6.13014	6.18617	6.08178	6.14951	NA	-0.7444	247605_at
At3g29750	Eukaryotic aspartyl protease family protein	5.01241	5.33891	3.96363	4.10133	4.10336	4.23417	4.12279	4.10182	NA	-1.1432	257283_at
At2g24780	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.67358	4.77039	3.94121	3.99596	3.96081	3.99546	3.99656	4.0681	NA	-0.7534	263540_at
At2g34330	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G29540.1); Has 10 Blast hits to 10 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.28383	5.44939	4.27396	4.30745	4.48664	4.49359	4.41913	4.28142	NA	-1.0759	267043_at
At3g10310	P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain	5.4403	5.99805	4.66382	4.89203	4.3799	4.5192	4.25938	4.31178	NA	-0.9412	259151_at
At1g17460	TRFL3, TRF-like 3	5.42326	5.1144	4.6377	4.57293	4.34992	4.39724	4.3543	4.41682	NA	-0.6635	261086_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At4g15380	CYP705A4, cytochrome P450, family 705, subfamily A, polypeptide 4	6.51338	6.62471	5.9092	5.82874	4.25974	4.29556	4.348	4.2441	NA	-0.7001	245554_at
At5g45380	ATDUR3, DUR3, solute:sodium symporters;urea transmembrane transporters	10.621	10.7818	9.91723	10.1738	9.41598	9.63245	9.3601	9.15199	NA	-0.6559	248970_at
At1g68795	CLE12, CLAVATA3/ESR-RELATED 12	5.19166	5.52706	4.58417	4.60386	4.61596	4.73897	4.61962	4.62315	NA	-0.7653	260039_at
At2g24270	ALDH11A3, aldehyde dehydrogenase 11A3	5.46636	5.33949	4.64628	4.75403	10.7053	10.481	10.1981	9.72036	NA	-0.7028	265998_at
AtMg00140	ORF167, hypothetical protein	5.5363	5.35462	4.41243	4.43374	4.41916	4.42876	4.39999	4.41961	NA	-1.0224	244948_at
At1g21890	nodulin MtN21 /EamA-like transporter family protein	7.42644	8.68693	5.88246	5.14869	5.0371	4.75894	4.87176	4.6117	NA	-2.5411	260851_at
At3g49960	Peroxidase superfamily protein	5.84955	5.95017	4.60476	5.09204	4.50755	4.77144	4.49936	4.50245	NA	-1.0515	252238_at
At2g29070	Ubiquitin fusion degradation UFD1 family protein	6.11127	6.1537	5.29934	5.17164	4.83936	5.05452	4.73303	4.91911	NA	-0.897	266776_at
At5g05500	Pollen Ole e 1 allergen and extensin family protein	5.83608	6.15599	4.87047	5.30637	4.52661	4.54842	4.66304	4.67249	NA	-0.9076	250778_at
At2g33735	Chaperone DnaJ-domain superfamily protein	5.20347	5.28143	4.45328	4.6018	4.63378	4.55795	4.59238	4.27958	NA	-0.7149	267462_at
At5g26880	AGL26, AGAMOUS-like 26	4.95376	5.32592	3.93758	3.92585	3.89067	3.94636	3.85496	3.98243	NA	-1.2081	246851_at
At1g01450	Protein kinase superfamily protein	5.19279	5.59103	4.22322	4.32218	4.28969	4.3562	4.35886	4.33548	NA	-1.1192	259435_at
At1g23090	AST91, SULTR3;3, sulfate transporter 91	5.45724	6.01755	4.83323	4.60941	8.70569	8.60706	8.30994	8.1895	NA	-1.0161	264901_at
At5g19140	AILP1, ATAILP1, Aluminium induced protein with YGL and LRDR motifs	10.3186	10.572	9.21312	9.3751	11.6597	11.669	10.806	11.4005	NA	-1.1512	249922_at
At5g44670	Domain of unknown function (DUF23)	7.38702	7.63814	6.76167	6.94259	6.75813	6.7572	5.94057	6.31227	NA	-0.6604	249011_at
At4g31320	SAUR-like auxin-responsive protein family	5.39882	5.62584	4.51552	4.59046	4.30112	4.32603	4.247	4.18972	NA	-0.9593	253515_at
At5g07390	ATRBOHA, RBOHA, respiratory burst oxidase homolog A	7.11696	6.95234	6.37079	6.08018	4.71829	4.71767	4.62216	4.74693	NA	-0.8092	250629_at
At2g04330	transposable element gene	4.69991	4.74698	3.98554	3.92242	3.97763	3.91276	4.03466	3.97637	NA	-0.7695	263860_at
At5g30420	pseudogene, hypothetical protein	5.31799	5.72572	4.51737	4.48077	4.6034	4.74118	4.76871	4.71474	NA	-1.0228	246675_at
At4g12580	unknown protein; Has 24 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).	5.61063	5.70363	4.39912	4.35574	4.36986	4.36768	4.21039	4.35814	NA	-1.2797	254823_at
At1g55760	BTB/POZ domain-containing protein	8.19863	8.36123	6.9973	6.30474	5.70017	5.8362	5.38275	5.56329	NA	-1.6289	264562_at
At2g23630	sks16, SKU5 similar 16	6.04335	5.51571	4.5388	4.62771	4.35922	4.34107	4.35429	4.27391	NA	-1.1963	267287_at
At3g30530	ATBZIP42, bZIP42, basic leucine-zipper 42	5.6209	5.90571	4.43809	4.5549	4.60148	4.64713	4.43208	4.46081	NA	-1.2668	258306_at
At3g55060	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G39300.2); Has 61765 Blast hits to 33720 proteins in 2065 species: Archae - 846;	5.30425	5.23919	4.58965	4.51362	4.28065	4.3562	4.10782	4.50197	NA	-0.7201	251822_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	Bacteria - 6964; Metazoa - 31967; Fungi - 5247; Plants - 3104; Viruses - 205; Other Eukaryotes - 13432 (source: NCBI BLink).											
At3g06840	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G49170.1); Has 33 Blast hits to 33 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.63556	5.61334	4.78051	4.78829	5.50313	5.48847	5.07374	5.22796	NA	-0.84	258530_at
At5g32600	transposable element gene	6.00071	5.98164	4.36378	4.51078	4.31076	4.36068	4.37158	4.39424	NA	-1.5539	246163_at
At2g16040	hAT dimerisation domain-containing protein / transposase-related	4.53447	4.55378	3.98534	3.9246	3.98812	3.94602	4.03444	3.91913	NA	-0.5892	263095_at
At2g38830	Ubiquitin-conjugating enzyme/RWD-like protein	5.26164	4.87254	4.07582	4.05833	3.994	3.97871	4.04838	3.9782	NA	-1	263262_at
At3g01720	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25265.1); Has 374 Blast hits to 211 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 316; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink).	8.63791	8.23765	7.75739	7.81248	7.11846	7.11708	6.7884	6.78639	NA	-0.6528	259191_at
At1g23610	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23640.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.38946	5.07069	4.19139	4.214	4.20171	4.20562	4.16319	4.1632	NA	-1.0274	265165_at
At3g21760	HYR1, UDP-Glycosyltransferase superfamily protein	5.74771	5.86185	5.07446	5.28616	7.3612	7.47632	7.72761	7.4231	NA	-0.6245	257954_at
At2g10780	transposable element gene	5.18166	4.80524	4.02507	4.03792	3.98477	4.16792	4.04069	4.02333	NA	-0.962	264074_at
At4g19780	transposable element gene	4.8018	4.83062	3.98436	3.95535	4.07044	3.94777	3.88797	3.99176	NA	-0.8464	254541_at
At5g14330	unknown protein; Has 8 Blast hits to 8 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.03624	6.47696	5.02578	5.07758	5.02327	4.90227	4.95397	4.91892	NA	-1.7049	250172_at
At5g62330	BEST Arabidopsis thaliana protein match is: Plant invertase/pectin methylesterase inhibitor superfamily protein (TAIR:AT5G62340.1); Has 9 Blast hits to 9 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.00935	5.81269	4.70205	5.0057	4.67399	4.83139	4.7057	4.92253	NA	-1.0571	247476_at
At5g62500	ATEB1, ATEB1B, EB1B, end binding protein 1B	5.41453	5.11928	4.61175	4.56555	4.36542	4.51188	4.36611	4.49507	NA	-0.6783	247432_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At3g06230	ATMKK8, MKK8, MAP kinase kinase 8	5.37306	5.67286	4.34096	4.38098	4.3578	4.44509	4.45689	4.26992	NA	-1.162	256390_at
At4g16730	TPS02, terpene synthase 02	4.72725	4.99163	4.13294	4.02921	4.13576	4.20265	4.14298	4.26953	NA	-0.7784	245443_at
At4g23870	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11020.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.98689	5.14315	4.05523	4.21324	4.26966	4.44995	4.118	4.2421	NA	-0.9308	254193_at
At5g67400	RHS19, root hair specific 19	8.03665	8.48583	6.48655	7.23115	5.29223	5.82848	5.54928	5.4276	NA	-1.4024	246991_at
At2g10380	transposable element gene	4.72334	4.8599	4.04926	4.02367	4.02208	4.09298	4.02134	4.04195	NA	-0.7552	263308_at
At1g31690	Copper amine oxidase family protein	5.23334	5.06762	4.49043	4.43013	4.43539	4.44501	4.4432	4.43354	NA	-0.6902	246573_at
At4g39260	ATGRP8, CCR1, GR-RBP8, GRP8, cold, circadian rhythm, and RNA binding 1	10.0978	9.95085	9.34321	9.27927	7.80953	7.75064	7.2138	7.34382	NA	-0.7131	252885_at
At1g65940	pseudogene, similar to Dof zinc finger protein, blastp match of 61% identity and 1.7e-10 P-value to GP|4996646|dbj|BAA78575.1||AB028132 Dof zinc finger protein {Oryza sativa}	4.57532	4.317	3.80434	3.84204	3.87057	3.77455	3.86731	3.7445	NA	-0.623	261918_at
At5g20800	transposable element gene	4.62771	4.67047	4.02798	4.09179	4.13743	4.18283	4.14895	4.16201	NA	-0.5892	245996_at
At1g75690	DnaJ/Hsp40 cysteine-rich domain superfamily protein	5.36889	5.17613	4.53267	4.47899	8.97911	9.02485	8.31322	8.71915	NA	-0.7667	262970_at
At3g01250	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, C globular stage, petal differentiation and expansion stage; Has 50 Blast hits to 50 proteins in 23 species: Archae - 0; Bacteria - 28; Metazoa - 15; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	4.82137	4.78945	3.82957	3.77034	3.93128	3.88914	3.84584	3.87066	NA	-1.0055	259265_at
At3g30650	transposable element gene	4.6537	4.73572	4.03407	4.14522	4.07142	4.13421	4.05471	4.11251	NA	-0.6051	258305_at
At1g35320	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G30160.1); Has 9 Blast hits to 9 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 9; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.44811	5.91282	4.74942	4.93202	4.52001	4.50641	4.55241	4.45188	NA	-0.8397	259575_at
At1g35740	pseudogene, similar to putative beta-1,3-glucan synthase, blastp match of 57% identity and 2.1e-14 P-value to GP|23503034|gb|AAK49452.2|AF304372_1|AF304372 putative beta-1,3-glucan synthase {Nicotiana alata}	5.14432	5.82494	3.99871	4.07229	4.02456	4.10458	4.12344	4.04858	NA	-1.4491	261281_at
At5g10130	Pollen Ole e 1 allergen and extensin family protein	7.07922	6.40377	4.73821	5.21209	4.3953	4.72844	4.60404	4.68492	NA	-1.7663	250469_at

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At4g07700	transposable element gene	4.92856	4.85047	3.85729	3.80194	3.89074	3.84026	3.90001	3.75901	NA	-1.0599	255218_at
At1g73680	ALPHA DOX2, alpha dioxygenase	6.53943	5.74127	4.84112	4.95401	8.1798	8.22779	7.66468	7.09488	NA	-1.2428	260060_at
At5g28500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04550.1); Has 109 Blast hits to 109 proteins in 49 species: Archae - 0; Bacteria - 67; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	6.61222	6.56143	5.91049	5.8074	8.22342	8.07982	7.46591	7.86688	NA	-0.7279	245952_at
At1g75160	Protein of unknown function (DUF620)	4.90681	5.29659	4.16462	4.23378	4.28797	4.26926	4.26251	4.32761	NA	-0.9025	256506_at
At3g06895	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.55561	4.8039	3.95947	4.04855	3.99271	4.03498	4.00918	4.07015	NA	-0.6757	258547_at
At2g13230	transposable element gene	5.62901	5.60078	4.24653	4.43893	4.23748	4.53027	4.34067	4.4219	NA	-1.2722	265361_at
At1g68710	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	7.52027	7.09392	6.52426	5.90596	5.39448	5.14	5.23454	4.92134	NA	-1.092	262275_at
At2g22160	Cysteine proteinases superfamily protein	5.77765	5.23318	4.08224	4.18129	4.02253	4.19354	4.19517	4.19267	NA	-1.3737	263454_at
At1g03130	PSAD-2, photosystem I subunit D-2	6.54854	6.60291	6.01002	5.76221	11.4994	11.7073	11.0003	11.2752	NA	-0.6896	263114_at
At3g45670	Protein kinase superfamily protein	5.37778	5.33116	4.63154	4.66166	4.71389	4.659	4.75524	4.80794	NA	-0.7079	252590_at
At2g33690	Late embryogenesis abundant protein, group 6	5.31064	5.77776	3.92285	4.1056	4.05825	4.1106	4.00326	4.12601	NA	-1.53	267449_at
At5g32610	transposable element gene	4.86825	5.00762	4.14046	4.2371	4.25207	4.46943	4.26193	4.27659	NA	-0.7492	246164_at
At1g13290	DOT5, WIP6, C2H2-like zinc finger protein	6.00996	6.2084	5.43862	5.42862	5.32715	5.49783	5.45608	5.32177	NA	-0.6756	257515_at
At2g34790	EDA28, MEE23, FAD-binding Berberine family protein	5.72152	5.54431	5.16312	4.78193	4.65713	4.66826	4.54905	4.59594	NA	-0.6604	267414_at
At1g67865	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67860.1); Has 13 Blast hits to 13 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.24084	5.14032	4.32635	4.37586	4.48005	4.54361	4.48818	4.59535	NA	-0.8395	260012_at
At1g74930	ORA47, Integrase-type DNA-binding superfamily protein	5.36283	5.29368	4.6245	4.61643	4.72499	4.76574	4.80497	4.68104	NA	-0.7078	262211_at
At1g09310	Protein of unknown function, DUF538	7.4842	6.71126	5.74766	6.01638	10.3927	10.6717	9.91866	10.3437	NA	-1.2157	263709_at
At3g24715	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain	5.64833	5.43745	4.40093	4.69489	4.6401	4.78553	4.64049	4.71539	NA	-0.995	257618_at
At1g64355	unknown protein; FUNCTIONS IN: molecular_function	5.57059	5.96246	5.03192	5.07261	6.79781	6.80188	6.65624	6.39648	NA	-0.7143	259738_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3593 (InterPro:IPR021995); Has 301 Blast hits to 301 proteins in 96 species: Archae - 0; Bacteria - 143; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 114 (source: NCBI BLink).											
At1g76290	AMP-dependent synthetase and ligase family protein	5.0014	5.13289	4.46325	4.37335	4.60097	4.53197	4.76052	4.66142	NA	-0.6488	261752_at
At3g05390	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF248, methyltransferase putative (InterPro:IPR004159); BEST Arabidopsis thaliana protein match is: S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (TAIR:AT4G01240.1); Has 507 Blast hits to 498 proteins in 33 species: Archae - 4; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 493; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	5.68607	5.44899	4.95361	4.86789	4.80563	4.53666	4.41271	4.45363	NA	-0.6568	259134_at
At2g06090	Plant self-incompatibility protein S1 family	5.02289	4.77677	4.07044	4.03803	4.03833	4.05333	4.04173	4.08069	NA	-0.8456	265517_at
At5g65350	HTR11, histone 3 11	4.88029	4.756	4.17605	4.11508	4.04243	4.1046	4.15649	4.09335	NA	-0.6726	247180_at
At2g39040	Peroxidase superfamily protein	5.98182	5.73876	4.73259	4.86815	4.79633	5.18019	4.86381	4.90623	NA	-1.0599	266191_at
At1g67810	SUFE2, sulfur E2	8.87348	8.70279	6.36537	6.33396	7.42921	7.5732	7.08494	7.02588	NA	-2.4385	245193_at
At5g25620	YUC6, Flavin-binding monooxygenase family protein	6.15243	6.27993	5.68329	5.56158	5.396	5.51397	5.07372	5.26404	NA	-0.5937	246900_at
At3g53550	FBD-like domain family protein	4.76646	5.03357	4.27843	4.14964	4.30953	4.22334	4.30055	4.21602	NA	-0.686	251947_at
At1g16760	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	4.76818	4.75737	4.12743	4.04021	4.1639	4.09808	4.11462	4.18343	NA	-0.679	255765_at
At3g14210	ESM1, epithiospecifier modifier 1	6.49324	6.12248	4.9295	5.24434	11.0219	11.2116	10.1985	10.8671	NA	-1.2209	257008_at
At1g13590	ATPSK1, PSK1, phytosulfokine 1 precursor	5.75215	6.02762	5.09324	5.22213	4.59503	4.67239	5.20718	4.83777	NA	-0.7322	256158_at
At1g70950	TPX2 (targeting protein for Xklp2) protein family	5.22531	5.58004	4.70331	4.74392	4.62527	4.73926	4.44351	4.55731	NA	-0.6791	262305_at
At1g14100	FUT8, fucosyltransferase 8	5.20496	5.06313	4.43141	4.41163	4.50193	4.42106	4.48099	4.48428	NA	-0.7125	262651_at
At1g27790	transposable element gene	4.62789	4.62789	3.71651	3.70085	3.74958	3.75568	3.82641	3.73345	NA	-0.9192	261645_at
At1g23720	Proline-rich extensin-like family protein	8.12314	8.53592	7.50307	7.60391	7.09128	6.92977	6.94861	7.06519	NA	-0.776	265169_x_at

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At2g02580	CYP71B9, cytochrome P450, family 71, subfamily B, polypeptide 9	5.19027	5.72395	4.55993	4.56133	4.24268	4.17855	4.11489	4.09745	NA	-0.8965	267267_at
At5g15850	ATCOL1, COL1, CONSTANS-like 1	6.73975	6.73248	5.50549	5.88025	9.49988	9.66899	9.69223	9.78454	NA	-1.0432	246523_at
At5g01190	LAC10, laccase 10	5.21998	5.14306	4.24067	4.37042	4.35831	4.42253	4.38928	4.38019	NA	-0.876	251131_at
At2g27870	transposable element gene	5.65622	5.78459	4.57311	4.41134	4.71861	4.43068	4.68351	4.58851	NA	-1.2282	266250_at
At3g26150	CYP71B16, cytochrome P450, family 71, subfamily B, polypeptide 16	5.32317	5.43107	4.00976	4.12336	4.02762	4.11281	3.98334	4.09837	NA	-1.3106	257630_at
At3g09620	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.12521	4.93483	4.29478	4.39671	4.40648	4.42114	4.29946	4.35774	NA	-0.6843	258725_at
At2g25230	AtMYB100, MYB100, myb domain protein 100	4.61174	4.603	3.9207	3.93262	3.92022	3.9383	3.89073	4.01482	NA	-0.6807	263615_at
At1g54570	Esterase/lipase/thioesterase family protein	5.81968	5.71111	5.05827	5.11379	4.87004	5.05501	4.93555	4.98142	NA	-0.6794	264186_at
At3g14280	unknown protein; Has 51 Blast hits to 51 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	10.0986	9.87615	9.30478	8.80344	6.04192	5.87718	5.16899	5.31955	NA	-0.9333	258362_at
At1g45230	Protein of unknown function (DUF3223)	6.55923	7.28805	5.68924	5.81875	7.60887	7.49234	7.14657	7.12533	NA	-1.1696	245797_at
At5g66350	SHI, Lateral root primordium (LRP) protein-related	5.79642	5.68975	4.81931	4.9104	4.85403	5.18013	4.88888	4.92287	NA	-0.8782	247093_at
At2g30260	U2B", U2 small nuclear ribonucleoprotein B	8.52229	8.64194	7.986	7.99618	8.51757	8.7068	8.44216	8.46997	NA	-0.591	255871_at
At3g42250	transposable element gene	4.35446	4.38404	3.76057	3.75788	3.72384	3.79232	3.76572	3.77018	NA	-0.61	252793_at
At3g02100	UDP-Glycosyltransferase superfamily protein	5.21039	5.10294	4.45884	4.56713	4.51439	4.41372	4.7807	4.61645	NA	-0.6437	258854_at
At5g24100	Leucine-rich repeat protein kinase family protein	5.83865	5.50035	4.70219	4.9583	4.5823	4.60974	4.45227	4.63539	NA	-0.8393	249768_at
At5g17150	Cystatin/monellin superfamily protein	4.73563	4.93534	4.0491	4.0139	4.02393	4.08277	4.04037	4.10859	NA	-0.804	246474_at
At4g13390	Proline-rich extensin-like family protein	4.59917	4.5274	3.90019	3.98024	3.90782	3.92965	3.93708	3.91888	NA	-0.6231	254772_at
At3g46680	UDP-Glycosyltransferase superfamily protein	5.32368	5.08573	4.54567	4.58082	4.55569	4.55484	4.50488	4.44352	NA	-0.6415	252477_at
At1g77780	Glycosyl hydrolase superfamily protein	5.3653	5.51799	4.49396	4.49695	4.46354	4.3999	4.53162	4.4969	NA	-0.9462	259702_at
At3g05690	ATHAP2B, HAP2B, NF-YA2, UNE8, nuclear factor Y, subunit A2	9.73397	9.55708	8.84448	8.83446	7.99782	8.2458	7.92316	7.7998	NA	-0.8061	258890_at
At3g42080	transposable element gene	4.93878	4.7427	3.84113	3.90449	3.88929	3.86757	3.85171	3.89392	NA	-0.9679	252837_at
At5g17260	anac086, NAC086, NAC domain containing protein 86	4.94122	5.08699	4.35832	4.32973	4.22131	4.27994	4.24867	4.28554	NA	-0.6701	250086_at
At1g73220	1-Oct, AtOCT1, organic cation/carnitine transporter1	9.10207	10.4188	6.96708	7.6129	5.75166	5.97656	4.67788	4.42554	NA	-2.4705	260097_at
At2g21990	Protein of unknown function, DUF617	5.64909	5.86119	4.03837	4.2759	4.17658	4.30445	4.23012	4.41895	NA	-1.598	257433_at
At5g52300	LTI65, RD29B, CAP160 protein	5.53092	5.62825	4.7654	4.82533	4.84121	4.96248	5.03084	4.85408	NA	-0.7842	248352_at

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At5g42580	CYP705A12, cytochrome P450, family 705, subfamily A, polypeptide 12	5.1956	5.05195	4.35179	4.12474	4.27635	4.22291	4.3105	4.24262	NA	-0.8855	249202_at
At5g40590	Cysteine/Histidine-rich C1 domain family protein	9.15796	8.64685	7.73905	8.34815	5.53705	5.29646	4.8513	4.48023	NA	-0.8588	249364_at
At2g10920	unknown protein; Has 5 Blast hits to 5 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.24815	5.54986	4.31329	4.2308	4.39126	4.22884	4.40471	4.43147	NA	-1.127	263291_at
At1g65680	ATEXPB2, ATHEXP BETA 1.4, EXPB2, expansin B2	6.14782	6.1887	4.96948	5.17657	5.05083	5.1588	4.97885	5.03472	NA	-1.0952	264640_at
At5g40030	Protein kinase superfamily protein	5.37324	5.58709	4.69247	4.959	4.68779	4.71831	4.58302	4.5605	NA	-0.6544	249440_at
At5g47240	atnudt8, NUDT8, nudix hydrolase homolog 8	8.16296	7.98282	7.41611	6.66592	5.61111	4.976	4.92614	4.5324	NA	-1.0319	248793_at
At1g65210	Galactose-binding protein	4.69915	4.93272	4.095	4.12807	4.10679	4.10871	4.16871	4.24121	NA	-0.7044	263141_at
At5g07510	ATGRP-4, ATGRP14, GRP-4, GRP14, glycine-rich protein 14	5.25226	5.42439	4.25245	4.26938	4.31796	4.28683	4.23166	4.30152	NA	-1.0774	250635_at
At3g14510	Polyprenyl synthetase family protein	4.97248	4.85281	4.28661	4.29406	4.24556	4.21583	4.0909	4.37679	NA	-0.6223	257274_at
At1g25460	NAD(P)-binding Rossmann-fold superfamily protein	5.64501	5.63674	4.80418	4.64206	4.37804	4.36489	4.40199	4.25308	NA	-0.9178	255730_at
At4g00020	BRCA2(IV), BRCA2A, EDA20, MEE43, BREAST CANCER 2 like 2A	5.03997	4.72159	4.27545	4.29543	4.12871	4.17666	4.24142	4.16511	NA	-0.5953	255724_at
At2g12870	transposable element gene	5.3017	5.41448	4.37148	4.52884	4.57979	4.82497	4.59705	4.72488	NA	-0.9079	263965_at
At4g37160	sks15, SKU5 similar 15	4.66198	4.8565	4.13522	4.17445	4.21105	4.19311	4.10067	4.19362	NA	-0.6044	246229_at
At1g67290	glyoxal oxidase-related protein	5.50144	5.51768	4.93675	4.76712	4.98576	5.03381	5.05294	4.97472	NA	-0.6576	264993_at
At1g79320	AtMC6, MC6, metacaspase 6	7.56503	6.59601	5.27009	5.42784	4.3741	4.81884	4.53051	4.59971	NA	-1.7316	264144_at
At3g31380	transposable element gene	4.91108	5.17206	4.10808	4.24877	4.1716	4.22822	4.17025	4.2766	NA	-0.8631	256554_at
At3g10680	HSP20-like chaperones superfamily protein	5.50684	5.09378	4.50897	4.36749	4.337	4.2424	4.37143	4.1975	NA	-0.8621	258969_at
At4g04420	transposable element gene	4.92466	4.78931	3.94269	4.05993	4.00324	4.05183	3.98128	4.08882	NA	-0.8557	255334_at
At2g20570	ATGLK1, GLK1, GPRI1, GBF's pro-rich region-interacting factor 1	6.67672	6.29984	5.48271	5.42013	8.48001	8.85027	8.51348	8.67205	NA	-1.0369	263715_at
At5g19790	RAP2.11, related to AP2 11	7.16594	6.98451	5.33429	5.35593	5.25067	5.18616	5.63389	5.11373	NA	-1.7301	245966_at
At4g31900	PKR2, chromatin remodeling factor, putative	5.60829	5.68653	4.32909	4.56582	4.52414	4.59079	4.63994	4.54297	NA	-1.2	253499_at
At2g44810	DAD1, alpha/beta-Hydrolases superfamily protein	6.01381	6.00553	5.20364	5.25363	5.29821	5.33898	5.26653	5.2988	NA	-0.781	266883_at
At1g19230	Riboflavin synthase-like superfamily protein	6.64132	6.4032	5.39582	5.62189	4.41406	4.56296	4.23119	4.67926	NA	-1.0134	256011_at
At5g10260	AtRABH1e, RABH1e, RAB GTPase homolog H1E	4.82475	4.97903	4.15257	4.23993	4.17681	4.1016	4.02265	4.15821	NA	-0.7056	250479_at
At2g32860	BGLU33, beta glucosidase 33	4.67927	4.69723	3.97806	4.0501	4.86649	4.67723	4.96885	4.99574	NA	-0.6742	267645_at

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At3g21770	Peroxidase superfamily protein	10.4849	11.093	9.83285	10.0123	6.36819	6.15666	5.61729	6.18426	NA	-0.8664	257952_at
At3g23720	transposable element gene	4.66441	4.56777	3.75398	3.81709	3.73015	3.78253	3.75155	3.79768	NA	-0.8306	257200_at
At5g62730	Major facilitator superfamily protein	4.98281	5.12895	4.46252	4.35244	4.56761	4.49649	4.56717	4.40279	NA	-0.6484	247447_at
At4g15100	scpl30, serine carboxypeptidase-like 30	5.02456	5.02759	4.38599	4.48393	4.23246	4.34075	4.09503	4.33914	NA	-0.5911	245531_at
At5g03840	TFL-1, TFL1, PEBP (phosphatidylethanolamine-binding protein) family protein	5.31675	5.56693	4.76409	4.65084	4.79768	4.70738	4.73648	4.81663	NA	-0.7344	250869_at
At2g15610	Protein of unknown function (DUF1685)	5.28938	4.97816	4.3727	4.3811	4.40951	4.53832	4.43079	4.40771	NA	-0.7569	265488_at
At1g07550	Leucine-rich repeat protein kinase family protein	5.68207	5.9492	5.03844	4.37188	4.17144	4.10907	4.24967	4.1168	NA	-1.1105	261091_at
At2g12900	Basic-leucine zipper (bZIP) transcription factor family protein	4.97988	5.08483	4.18909	4.33798	4.36028	4.39769	4.2619	4.4109	NA	-0.7688	263994_at
At1g75520	SRS5, SHI-related sequence 5	7.59462	7.12068	6.3298	6.44626	5.5857	5.7106	5.82693	5.93635	NA	-0.9696	262976_at
At2g16910	AMS, basic helix-loop-helix (bHLH) DNA-binding superfamily protein	4.83841	4.69563	4.09532	4.14037	4.0696	4.23901	4.12025	4.03997	NA	-0.6492	266530_at
At3g51680	NAD(P)-binding Rossmann-fold superfamily protein	4.95084	5.00199	4.26667	4.32747	4.16314	4.27806	4.23817	4.2345	NA	-0.6793	252070_at
At1g68510	LBD42, LOB domain-containing protein 42	4.93008	4.98071	4.20447	4.28993	4.21267	4.22486	4.26022	4.22728	NA	-0.7082	260265_at
At2g45630	D-isomer specific 2-hydroxyacid dehydrogenase family protein	5.77053	6.14451	5.07384	5.12058	6.07185	6.17948	6.04883	6.01972	NA	-0.8603	267514_at
At1g15180	MATE efflux family protein	5.56409	4.84147	3.95465	3.99859	7.0941	7.32529	6.82627	7.18823	NA	-1.2262	262569_at
At5g10120	Ethylene insensitive 3 family protein	4.62631	4.71171	3.9899	3.94599	4.05805	3.94499	4.02454	3.97068	NA	-0.7011	250468_at
At3g29570	unknown protein; Has 271 Blast hits to 164 proteins in 59 species: Archae - 0; Bacteria - 19; Metazoa - 88; Fungi - 42; Plants - 45; Viruses - 9; Other Eukaryotes - 68 (source: NCBI BLink).	4.77682	4.82976	4.07263	4.02328	4.0064	4.05165	3.94576	4.04671	NA	-0.7553	255722_at
At2g04675	unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.88966	4.9439	4.20386	4.06966	4.15629	4.05525	4.15746	4.16196	NA	-0.78	263627_at
At4g08740	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.15116	5.36103	4.52326	4.63054	4.72771	4.60449	4.61937	4.70547	NA	-0.6792	255108_at
At5g52460	EDA41, FBD, F-box and Leucine Rich Repeat domains containing protein	5.40046	5.11257	4.51264	4.47148	4.64571	4.63613	4.66738	4.53777	NA	-0.7645	248361_at
At5g54040	Cysteine/Histidine-rich C1 domain family protein	8.67039	8.38607	7.79537	7.86711	4.73728	4.95114	4.70136	4.89115	NA	-0.697	248183_at
At5g51930	Glucose-methanol-choline (GMC) oxidoreductase family protein	5.43992	5.1759	4.13525	4.1549	4.22687	4.63234	4.21784	4.29724	NA	-1.1628	248384_at
At5g28130	transposable element gene	5.2113	5.40799	4.31515	4.27096	4.27368	4.26035	4.21339	4.37205	NA	-1.0166	246706_at

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At1g42550	PMI1, plastid movement impaired1	5.29769	5.5962	4.58852	4.79545	8.69959	9.05286	8.53828	8.54514	NA	-0.755	256542_at
At2g43000	anac042, NAC042, NAC domain containing protein 42	6.05419	5.89762	4.97153	5.20054	4.77556	4.99232	4.57327	4.93104	NA	-0.8899	265260_at
At5g67430	Acyl-CoA N-acyltransferases (NAT) superfamily protein	7.15795	7.84432	5.32935	5.65988	4.62737	4.88283	4.40896	4.482	NA	-2.0065	246992_at
At1g60980	ATGA20OX4, GA20OX4, gibberellin 20-oxidase 4	4.80542	4.92061	4.25924	4.25164	4.24952	4.34675	4.28761	4.32709	NA	-0.6076	259714_at
At5g05840	Protein of unknown function (DUF620)	4.89022	5.13778	4.29404	4.37652	4.1786	4.32155	4.35068	4.19844	NA	-0.6787	250744_at
At3g28330	F-box family protein-related	6.36391	6.20337	5.23877	5.36212	5.19814	5.40595	5.26264	5.30533	NA	-0.9832	256632_at
At1g38340	transposable element gene	5.09287	5.38907	4.55766	4.52788	4.5878	4.5362	4.59129	4.46209	NA	-0.6982	245217_at
At5g40020	Pathogenesis-related thaumatin superfamily protein	5.80262	6.03307	5.23569	5.03141	4.49282	4.82866	4.69007	4.93565	NA	-0.7843	249439_at
At5g16160	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	4.94807	4.86415	4.28529	4.13048	4.14386	4.23239	4.22494	4.18729	NA	-0.6982	246504_at
At3g13370	unknown protein; Has 84 Blast hits to 50 proteins in 21 species: Archae - 0; Bacteria - 2; Metazoa - 51; Fungi - 6; Plants - 20; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	4.5016	4.72834	3.80576	3.86304	3.86261	3.95626	3.9403	3.90076	NA	-0.7806	257681_at
At2g05090	transposable element gene	5.09173	4.81235	4.00529	3.99195	4.03069	4.09873	4.10813	4.01666	NA	-0.9534	263343_at
At3g25060	Tetratricopeptide repeat (TPR)-like superfamily protein	4.87892	4.62491	4.16011	4.15961	4.08923	4.11782	4.18112	4.22066	NA	-0.5921	257103_at
At3g12540	Protein of unknown function, DUF547	5.20296	5.35118	4.476	4.52604	4.44014	4.43393	4.35544	4.3235	NA	-0.7761	256283_at
At3g54580	Proline-rich extensin-like family protein	6.9555	6.97207	4.80451	5.20851	4.83188	5.20921	4.79294	5.10047	NA	-1.9573	251842_at
At5g26660	ATMYB86, MYB86, myb domain protein 86	6.22863	5.99443	5.16191	5.52902	4.86691	4.84359	4.73579	4.93277	NA	-0.7661	246844_at
At2g09910	transposable element gene	5.88146	5.8588	4.77985	4.63635	4.80597	4.73818	4.80742	4.68137	NA	-1.162	263820_at
At1g72870	Disease resistance protein (TIR-NBS class)	5.74717	5.7909	5.22759	5.11598	5.11206	4.91259	4.93205	4.81548	NA	-0.5973	262365_at
At5g06640	Proline-rich extensin-like family protein	7.70771	8.10572	7.00984	6.93072	6.6071	6.66074	6.72883	6.47221	NA	-0.9364	250683_x_at
At2g06220	transposable element gene	4.72308	4.6824	4.0685	4.07776	4.14334	4.07482	4.20688	4.16795	NA	-0.6296	265528_at
At5g51720	2 iron, 2 sulfur cluster binding	5.60695	6.17567	4.61136	4.28206	7.35747	7.2776	7.34948	7.35592	NA	-1.4446	248377_at
At4g07730	transposable element gene	4.892	4.89036	4.19329	4.22132	4.33355	4.55986	4.26044	4.44205	NA	-0.6839	255184_at
At2g28030	Eukaryotic aspartyl protease family protein	4.49536	4.70123	3.97464	4.0383	4.03115	4.05485	4.0387	3.98423	NA	-0.5918	266159_at
At2g26380	Leucine-rich repeat (LRR) family protein	5.76703	6.17975	4.48017	4.4902	4.68269	4.56751	4.54393	4.62263	NA	-1.4882	245033_at
At4g20220	Reverse transcriptase (RNA-dependent DNA polymerase)	5.13686	5.28145	4.15472	4.20324	4.18347	4.34336	4.13875	4.21912	NA	-1.0302	254511_at

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At2g34120	Cytochrome C oxidase polypeptide VIB family protein	5.63107	5.11811	3.79252	3.93437	3.7733	3.99891	3.84828	3.98916	NA	-1.5111	256718_at
At3g46520	ACT12, actin-12	5.00636	4.72955	4.23095	4.2711	4.2107	4.21284	4.21295	4.28129	NA	-0.6169	252531_at
At2g19570	AT-CDA1, CDA1, DESZ, cytidine deaminase 1	9.35557	9.54833	8.41775	8.84604	7.31159	7.33269	7.13072	7.16414	NA	-0.8201	265943_at
At3g24360	ATP-dependent caseinolytic (Clp) protease/crotonase family protein	5.07513	5.00631	4.50452	4.37374	4.37148	4.41478	4.44244	4.2387	NA	-0.6016	257158_at
At2g32680	AtRLP23, RLP23, receptor like protein 23	5.49325	5.48286	4.75779	4.9059	5.30852	5.40638	5.8544	5.86149	NA	-0.6562	267546_at
At2g17960	unknown protein; Has 1 Blast hits to 1 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 1; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.08095	5.01458	4.13441	4.28637	4.31539	4.28541	4.22269	4.38288	NA	-0.8374	265808_at
At3g21680	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: root, flower, stamen; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; Has 34 Blast hits to 34 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.80913	5.17295	4.19663	4.2977	3.91549	4.02385	3.99884	4.01187	NA	-0.7439	258178_at
At3g12190	BEST Arabidopsis thaliana protein match is: Frigida-like protein (TAIR:AT5G27220.1); Has 43637 Blast hits to 24906 proteins in 1566 species: Archae - 743; Bacteria - 4122; Metazoa - 22377; Fungi - 2585; Plants - 1803; Viruses - 158; Other Eukaryotes - 11849 (source: NCBI BLink).	4.41923	4.54282	3.85929	3.91825	3.84006	4.01519	3.92043	4.03817	NA	-0.5923	256287_at
At3g06220	AP2/B3-like transcriptional factor family protein	4.82824	5.08229	4.28758	4.22337	4.5106	4.39047	4.3965	4.35975	NA	-0.6998	256389_at
At3g20090	CYP705A18, cytochrome P450, family 705, subfamily A, polypeptide 18	5.77909	5.26037	4.64459	4.64613	4.11357	4.25063	4.07788	4.05233	NA	-0.8744	257142_at
At3g04210	Disease resistance protein (TIR-NBS class)	5.47159	5.15554	4.46378	4.3392	5.45896	5.72964	5.20513	5.35173	NA	-0.9121	258537_at
At5g53680	RNA-binding (RRM/RBD/RNP motifs) family protein	4.82132	4.68856	4.13853	4.11807	4.19809	4.31253	4.26627	4.26947	NA	-0.6266	248215_at
At1g22070	TGA3, TGA1A-related gene 3	7.74369	7.56992	7.0322	6.89187	6.71905	6.90074	6.2253	6.49125	NA	-0.6948	255953_at
At4g09560	Protease-associated (PA) RING/U-box zinc finger family protein	6.35853	6.36928	5.80912	5.5833	6.6152	6.60717	6.20521	6.31282	NA	-0.6677	255036_at
At5g26900	Transducin family protein / WD-40 repeat family protein	5.01253	4.96855	3.83294	3.84131	3.82701	3.89655	3.88796	3.84894	NA	-1.1534	246819_at
At4g18540	unknown protein; Has 209 Blast hits to 205 proteins in 54 species: Archae - 0; Bacteria - 17; Metazoa - 2; Fungi - 150; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.82978	5.59991	4.84071	4.73256	4.90137	4.81472	4.79469	4.74137	NA	-0.9282	254647_at
At5g25750	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi -	4.75845	4.87399	3.8718	4.03555	3.92146	4.03139	3.85801	4.01793	NA	-0.8625	246903_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).											
At1g30710	FAD-binding Berberine family protein	5.26327	5.76061	4.06534	4.16987	4.0839	4.21803	4.14923	4.19683	NA	-1.3943	263215_at
At1g43590	transposable element gene	5.66594	5.22768	4.37853	4.41584	5.19185	5.31036	5.44858	5.34559	NA	-1.0496	262719_at
At4g07970	transposable element gene	4.5307	4.73806	3.96429	3.91521	3.96821	3.97624	3.99101	3.94983	NA	-0.6946	255170_at
At5g25840	Protein of unknown function (DUF1677)	4.9927	5.34267	4.25456	4.37058	7.32434	7.4896	7.17539	6.86616	NA	-0.8551	246860_at
At1g63730	Disease resistance protein (TIR-NBS-LRR class) family	5.78831	5.64632	4.8923	4.81141	4.84915	5.1929	4.78916	4.90436	NA	-0.8655	260270_at
At4g15360	CYP705A3, cytochrome P450, family 705, subfamily A, polypeptide 3	5.08937	4.77789	4.2078	4.27687	4.10082	4.04505	4.16695	4.03082	NA	-0.6913	245552_at
At5g60520	Late embryogenesis abundant (LEA) protein-related	6.0366	5.92341	4.77337	4.87461	4.56233	4.67713	4.55188	4.39415	NA	-1.156	247634_at
At1g10690	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G60783.1); Has 59 Blast hits to 59 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 59; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.19944	7.20313	5.62019	6.00138	5.54463	5.8238	5.28937	5.71618	NA	-1.3905	262788_at
At1g06310	ACX6, acyl-CoA oxidase 6	5.22916	4.98071	4.48762	4.42022	4.41366	4.40959	4.44244	4.46608	NA	-0.651	259419_at
At1g21210	WAK4, wall associated kinase 4	5.69709	5.69813	4.77569	4.85468	4.07581	4.18309	4.03897	4.04862	NA	-0.8824	259557_at
At1g77920	bZIP transcription factor family protein	9.27562	9.57663	8.43305	8.68347	7.66209	7.62336	6.63841	7.31041	NA	-0.8679	262137_at
At5g28880	transposable element gene	4.62513	4.83597	4.08495	4.08718	4.21406	4.14953	4.0546	4.22212	NA	-0.6445	246048_at
At1g44120	Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein	5.0902	5.2098	4.39346	4.4003	4.53032	4.61426	4.49805	4.55672	NA	-0.7531	245741_at
At1g35820	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G30520.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	4.83419	4.93052	4.21772	4.31338	4.22985	4.27135	4.26152	4.38019	NA	-0.6168	256312_x_at
At5g22960	alpha/beta-Hydrolases superfamily protein	4.9596	5.03851	4.37482	4.41024	4.42339	4.29328	4.44364	4.47363	NA	-0.6065	249854_at
At3g26300	CYP71B34, cytochrome P450, family 71, subfamily B, polypeptide 34	5.72337	5.44953	4.62792	4.2611	7.71743	7.21178	6.65664	6.65173	NA	-1.1419	256870_at
At1g59630	F-box associated ubiquitination effector family protein	5.1819	4.98386	4.1145	4.19365	4.26072	4.07877	4.16763	4.07988	NA	-0.9288	262123_at
At3g61340	F-box and associated interaction domains-containing protein	4.82744	4.61988	4.10106	4.13094	4.32457	4.34253	4.26891	4.12463	NA	-0.6077	251366_at
At2g04370	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.51076	5.74452	4.37249	4.49508	4.62833	4.7594	4.42699	4.4935	NA	-1.1939	263858_at
At1g65740	Protein of unknown function (DUF295)	5.17804	5.04778	4.37845	4.14211	4.32809	4.19532	4.37977	4.16486	NA	-0.8526	257462_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g23580	Domain of unknown function DUF220	4.58763	4.81117	4.05609	4.07975	4.16306	4.17962	4.09388	4.12547	NA	-0.6315	265163_at
At5g32590	myosin heavy chain-related	4.68268	4.7584	3.93864	3.98576	4.02073	4.15611	4.00554	4.10336	NA	-0.7583	246102_at
At1g04330	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23170.1); Has 74 Blast hits to 74 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 74; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.01503	5.0215	4.13957	4.22124	4.17565	4.27885	4.15861	4.23518	NA	-0.8379	263652_at
At5g45950	GDSL-like Lipase/Acylhydrolase superfamily protein	6.21524	5.73085	4.83362	4.83651	7.04645	6.66131	6.6094	6.92754	NA	-1.138	248921_at
At5g46240	KAT1, potassium channel in Arabidopsis thaliana 1	4.73761	4.61484	3.95148	4.12125	4.81799	4.88751	4.59181	4.6286	NA	-0.6399	248888_at
At2g18720	Translation elongation factor EF1A/initiation factor IF2gamma family protein	5.16075	5.2265	4.52025	4.53572	4.61418	4.63275	4.71455	4.64742	NA	-0.6656	266061_at
At1g48100	Pectin lyase-like superfamily protein	5.9803	6.02952	4.87086	4.90819	6.33301	6.48862	5.84976	6.12385	NA	-1.1154	260727_at
At2g10400	transposable element gene	4.6645	4.45224	3.92483	3.91268	3.92387	4.06297	3.86065	3.91538	NA	-0.6396	257341_at
At1g36105	transposable element gene	4.82677	4.57886	3.96583	4.02366	4.00626	4.05525	3.97144	4.00022	NA	-0.7081	263190_at
At1g78410	VQ motif-containing protein	5.17574	5.07034	4.06929	4.19963	4.17431	4.288	4.22601	4.31416	NA	-0.9886	260804_at
At3g18700	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: autoinhibited Ca2+/ATPase II (TAIR:AT1G13210.1); Has 223 Blast hits to 223 proteins in 38 species: Archae - 0; Bacteria - 0; Metazoa - 92; Fungi - 0; Plants - 126; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	4.62627	4.60862	3.93182	3.98749	4.07763	4.15278	4.09634	4.07487	NA	-0.6578	257747_at
At1g54820	Protein kinase superfamily protein	4.8065	5.58037	4.44943	4.46344	6.72587	6.45269	5.91195	5.8015	NA	-0.737	264240_at
At1g29200	O-fucosyltransferase family protein	5.47658	5.7544	4.42188	4.33643	4.5352	4.41678	4.48242	4.48108	NA	-1.2363	260886_at
At5g44120	ATCRA1, CRA1, CRU1, RmlC-like cupins superfamily protein	5.26564	5.02175	4.13316	4.22636	4.1901	4.46896	4.29259	4.29724	NA	-0.9639	249082_at
At5g66740	Protein of unknown function (DUF620)	4.74465	4.87592	4.22424	4.21427	4.35891	4.35185	4.25632	4.16015	NA	-0.591	247055_at
At1g78940	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	5.25564	5.11632	4.18221	4.1717	4.09707	4.16924	4.1558	4.10003	NA	-1.009	264139_at
At2g22620	Rhamnogalacturonate lyase family protein	5.70342	5.80212	4.95494	5.0304	4.19975	4.35137	4.23106	4.29455	NA	-0.7601	265350_at
At2g48150	ATGPX4, GPX4, glutathione peroxidase 4	5.35201	5.55452	4.29767	4.5391	4.21027	4.42409	4.45178	4.36587	NA	-1.0349	262350_at
At5g41610	ATCHX18, CHX18, cation/H+ exchanger 18	5.3397	5.47501	4.70054	4.88382	4.50057	4.59177	4.42545	4.46936	NA	-0.6152	249255_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g05490	chr31, chromatin remodeling 31	4.82691	4.90325	4.28018	4.25869	4.22058	4.22994	4.28386	4.19854	NA	-0.5956	263204_at
At4g30040	Eukaryotic aspartyl protease family protein	4.78147	4.97298	4.16867	4.08282	4.28081	4.23292	4.25288	4.25375	NA	-0.7515	253652_at
At1g51060	HTA10, histone H2A 10	9.36712	9.76137	8.84214	8.97716	7.21701	7.26091	7.4767	7.50477	NA	-0.6546	245750_at
At1g01460	ATPIPK11, PIPK11, Phosphatidylinositol-4-phosphate 5-kinase, core	4.88581	4.97402	4.30352	4.3021	4.45218	4.42168	4.35775	4.42586	NA	-0.6271	259425_at
At5g38080	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G38090.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.3516	5.48593	4.50686	4.36663	4.53897	4.40728	4.5477	4.35468	NA	-0.982	249570_at
At3g44080	F-box family protein	4.6432	4.88129	4.0973	4.05649	4.13465	4.14763	4.08839	4.08746	NA	-0.6853	252664_at
At5g02120	OHP, one helix protein	5.95874	5.67655	5.16981	5.21988	9.31679	9.30827	9.11079	8.98379	NA	-0.6228	251031_at
At5g16570	GLN1;4, glutamine synthetase 1;4	7.99158	8.61157	6.78281	7.42439	5.39315	5.51184	5.34895	5.10804	NA	-1.198	250100_at
At1g24420	HXXXD-type acyl-transferase family protein	6.19937	5.81017	4.80812	4.7066	4.49846	4.57282	4.43675	4.42413	NA	-1.2474	265016_at
At2g01940	ATIDD15, SGR5, C2H2-like zinc finger protein	5.32783	5.26616	4.41096	4.62955	6.20797	6.26775	6.15746	6.51674	NA	-0.7767	265249_at
At4g03750	transposable element gene	5.63665	5.20899	4.04272	4.15907	4.20024	4.12121	4.17129	4.18092	NA	-1.3219	255399_at
At1g76420	ANAC031, CUC3, NAC368, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	5.12807	5.35285	4.23076	4.3433	4.47001	4.53467	4.43369	4.41646	NA	-0.9534	259972_at
At2g02830	transposable element gene	5.33626	5.09324	4.6264	4.48666	4.62662	4.61942	4.64509	4.63605	NA	-0.6582	267480_at
At4g38590	BGAL14, beta-galactosidase 14	6.0988	6.32706	5.1182	5.23732	5.28574	5.5477	5.42882	5.31494	NA	-1.0352	252978_at
At4g13760	Pectin lyase-like superfamily protein	4.86881	4.6299	4.07652	4.05776	4.07133	4.04154	4.03477	4.04696	NA	-0.6822	254733_at
At2g18930	unknown protein; Has 3 Blast hits to 3 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.75764	4.60765	3.90169	3.98302	3.98646	3.9386	4.00918	4.01815	NA	-0.7403	266937_at
At3g45810	ferric reductase-like transmembrane component family protein	4.92607	4.94684	4.29592	4.21805	4.30971	4.16188	4.24083	4.26551	NA	-0.6795	252544_at
At3g27510	Cysteine/Histidine-rich C1 domain family protein	4.84231	4.92431	4.11799	4.19723	4.1022	4.17099	4.09842	4.1059	NA	-0.7257	257998_at
At3g02910	AIG2-like (avirulence induced gene) family protein	10.4341	10.561	8.94057	9.42707	8.84574	8.93049	8.16427	8.78398	NA	-1.3137	258609_at
At1g13370	Histone superfamily protein	5.16923	4.91534	4.23367	4.26188	4.22376	4.27607	4.15546	4.22581	NA	-0.7945	259387_at
At1g64220	TOM7-2, translocase of outer membrane 7 kDa subunit 2	5.20186	5.17974	4.10224	4.09301	3.9164	3.98996	3.96434	3.9985	NA	-1.0932	262336_at
At1g62450	Immunoglobulin E-set superfamily protein	5.35739	5.35426	4.56493	4.64206	4.7219	4.70693	4.77283	4.83271	NA	-0.7523	265115_at
At2g15740	C2H2-like zinc finger protein	4.64063	4.65791	4.01356	3.96203	4.12494	3.96028	4.07896	4.02287	NA	-0.6615	265498_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g21100	Plant L-ascorbate oxidase	5.61855	5.91297	4.80913	5.0875	6.4102	6.38265	5.76667	6.01051	NA	-0.8174	246021_at
At3g28580	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.22455	5.02867	4.56624	4.37364	4.16274	4.19186	4.25597	4.31424	NA	-0.6567	256989_at
At1g48010	Plant invertase/pectin methylesterase inhibitor superfamily protein	4.70163	4.52044	3.91702	3.8699	3.89927	3.95863	3.88989	3.81686	NA	-0.7176	259613_at
At2g46600	Calcium-binding EF-hand family protein	9.64571	9.56596	8.5142	8.8065	8.77439	8.91572	8.83654	8.64103	NA	-0.9455	265460_at
At4g01480	AtPPa5, PPa5, pyrophosphorylase 5	9.29199	9.38293	8.36952	8.62307	7.19837	7.03142	6.48665	6.80447	NA	-0.8412	255587_at
At4g34220	Leucine-rich repeat protein kinase family protein	6.5813	6.88707	6.02079	6.04892	7.45529	7.28206	7.39023	7.3135	NA	-0.6993	253278_at
At2g14230	transposable element gene	4.44596	4.62741	3.88225	3.87845	3.90899	3.8256	3.78389	3.90636	NA	-0.6563	265600_at
At2g04670	transposable element gene	4.87496	4.99414	4.19993	4.21199	4.23786	4.27868	4.2575	4.31123	NA	-0.7286	263617_at
At5g48280	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	4.68051	4.7675	3.99368	3.93089	4.0103	3.9798	3.97921	4.04544	NA	-0.7617	248712_at
At5g24080	Protein kinase superfamily protein	5.37502	5.21954	4.69027	4.53715	4.63333	4.65483	4.64958	4.5651	NA	-0.6836	249771_at
At1g04500	CCT motif family protein	5.05266	4.9816	4.17502	4.27279	4.34913	4.45162	4.30376	4.42566	NA	-0.7932	263655_at
At3g62020	GLP10, germin-like protein 10	6.17594	6.04936	4.92763	4.96462	4.90558	5.20097	4.78829	4.9956	NA	-1.1665	251297_at
At3g20840	PLT1, Integrase-type DNA-binding superfamily protein	5.58856	5.56476	5.05999	4.88711	4.66121	4.55799	4.60271	4.47372	NA	-0.6031	257976_at
At2g40180	ATHPP2C5, PP2C5, phosphatase 2C5	5.72875	5.45895	4.80187	4.77874	4.67069	4.73221	4.86044	4.60796	NA	-0.8035	263378_at
At1g41795	transposable element gene	4.43764	4.72804	3.90618	3.94268	3.84781	3.94696	3.92768	3.95768	NA	-0.6584	260016_at
At1g04670	unknown protein; Has 40 Blast hits to 40 proteins in 14 species: Archae - 2; Bacteria - 5; Metazoa - 1; Fungi - 2; Plants - 30; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.04447	4.89398	4.17221	4.2387	4.23832	4.24274	4.20763	4.23832	NA	-0.7638	264603_at
At3g23650	protein kinase-related	5.02267	4.92101	3.882	3.86866	3.88413	3.91987	3.92948	3.89846	NA	-1.0965	258096_at
At2g33180	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 57 Blast hits to 57 proteins in 22 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	5.6735	6.03207	4.88541	4.86321	7.00819	6.95605	6.95321	6.64954	NA	-0.9785	245165_at
At3g45510	RING/U-box protein	5.01499	4.87621	4.27291	4.23444	4.31075	4.39845	4.26741	4.38921	NA	-0.6919	252579_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g27480	alpha/beta-Hydrolases superfamily protein	5.75653	5.1333	4.62892	4.68983	6.99576	7.14542	5.9754	6.67516	NA	-0.7855	264442_at
At4g14670	CLPB2, casein lytic proteinase B2	5.02205	5.10539	4.34918	4.38497	4.36156	4.52416	4.26744	4.40806	NA	-0.6966	245570_at
At5g01820	ATCIPK14, ATSR1, CIPK14, SnRK3.15, SR1, serine/threonine protein kinase 1	8.87355	9.18606	7.73014	7.91999	7.80359	7.89222	6.6431	7.06977	-0.99	-1.2047	251060_at
At5g54190	PORA, protochlorophyllide oxidoreductase A	5.38217	5.78847	4.43067	4.34129	6.88849	7.23482	5.7323	5.51581	-1.44	-1.1993	248197_at
At2g32560	F-box family protein	10.2106	10.3211	9.26023	9.04853	10.4277	10.3151	9.29061	8.92357	-1.26	-1.1115	267116_at 267117_at
At4g19170	CCD4, NCED4, nine-cis-epoxycarotenoid dioxygenase 4	5.49883	5.70756	4.70535	4.58924	8.55104	8.41622	5.4781	6.04728	-2.72	-0.9559	254564_at
At1g69850	ATNRT1:2, NRT1:2, NTL1, nitrate transporter 1:2	8.45353	8.51591	7.97198	7.76124	8.82494	8.93803	7.80256	7.88185	-1.04	-0.6181	260414_at
At3g13672	TRAF-like superfamily protein	5.44435	5.13562	4.50539	4.42821	5.19949	5.10066	4.36107	4.38992	-0.77	-0.8232	256789_at
At5g15410	ATCNGC2, CNGC2, DND1, Cyclic nucleotide-regulated ion channel family protein	5.29759	5.68141	4.44271	4.5226	8.54827	8.57011	7.93565	7.74715	-0.72	-1.0068	246510_at
At1g68190	B-box zinc finger family protein	5.50504	5.30657	4.72822	4.62108	6.33847	6.37452	5.60825	5.91659	-0.59	-0.7312	260431_at
At5g64410	ATOPT4, OPT4, oligopeptide transporter 4	9.36981	9.25133	8.6055	8.65891	9.58989	9.51921	7.80807	7.64456	-1.83	-0.6784	247284_at
At1g01140	CIPK9, PKS6, SnRK3.12, CBL-interacting protein kinase 9	5.1044	4.75942	4.31661	4.23164	8.43541	8.54721	7.17378	7.28696	-1.26	-0.6578	261581_at
At2g40970	MYBC1, Homeodomain-like superfamily protein	9.25396	9.60199	8.7001	8.73525	8.22952	8.2699	7.27341	6.98719	-1.12	-0.7103	267077_at
At4g19160	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	10.6742	10.6359	9.70465	9.11845	9.46615	9.41378	7.87558	7.26821	-1.87	-1.2435	254561_at
At4g28350	Concanavalin A-like lectin protein kinase family protein	5.68226	5.34204	4.92318	4.53836	6.4752	6.40706	4.72376	4.59462	-1.78	-0.7814	253819_at
At4g23700	ATCHX17, CHX17, cation/H+ exchanger 17	10.8726	10.4411	9.14387	9.11454	8.5447	8.58393	6.84093	7.49667	-1.4	-1.5276	254215_at
At4g17670	Protein of unknown function (DUF581)	8.2283	8.77232	6.22268	5.68125	6.49966	6.15932	4.65378	4.63828	-1.68	-2.5483	245401_at
At3g62550	Adenine nucleotide alpha hydrolases-like superfamily protein	5.47867	5.51224	4.92812	4.80331	7.16986	7.45728	6.1726	6.0823	-1.19	-0.6297	251221_at
At3g19450	ATCAD4, CAD, CAD-C, CAD4, GroES-like zinc-binding alcohol dehydrogenase family protein	9.50891	9.58377	8.92518	8.9086	10.4782	10.4803	9.34584	9.73797	-0.94	-0.6295	258023_at
At1g20640	Plant regulator RWP-RK family protein	8.35509	7.98079	7.07653	7.0539	6.96213	7.0485	5.73221	5.905	-1.19	-1.1027	259540_at
At1g76350	Plant regulator RWP-RK family protein	6.01076	5.85192	4.86468	4.61708	5.31261	5.32527	4.62523	4.49482	-0.76	-1.1905	259888_at
At1g64590	NAD(P)-binding Rossmann-fold superfamily protein	12.2825	12.2259	10.3895	9.90895	7.26668	7.51596	5.67939	5.19756	-1.95	-2.105	261956_at

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Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g54300	Protein of unknown function (DUF761)	6.55426	6.51008	6.47581	6.89089	6.82769	7.20497	8.08825	8.33106	1.193	NA	248205_at
At5g18600	Thioredoxin superfamily protein	4.53306	4.89627	5.12777	4.93749	8.43248	8.40546	9.5429	9.36847	1.037	NA	249996_at
At4g15920	Nodulin MtN3 family protein	7.31051	6.78837	7.85602	8.10532	5.31926	4.88206	5.98555	6.12361	0.954	NA	245524_at
At3g14990	Class I glutamine amidotransferase-like superfamily protein	11.727	11.5954	11.8864	11.7809	10.637	10.5433	11.2705	11.1157	0.603	NA	257216_at
At2g42070	ATNUDT23, ATNUDX23, NUDX23, nudix hydrolase homolog 23	6.81511	5.89009	7.62125	7.61628	7.36853	7.25855	8.68193	8.90691	1.481	NA	267533_at
At4g09620	Mitochondrial transcription termination factor family protein	5.79767	5.4365	6.38138	6.28456	6.31189	6.09825	7.44275	7.94795	1.49	NA	255041_at
At1g19440	KCS4, 3-ketoacyl-CoA synthase 4	5.37883	5.31276	5.76414	6.06849	5.09417	5.06852	5.8195	5.79873	0.728	NA	260667_at
At1g37130	ATNR2, B29, CHL3, NIA2, NIA2-1, NR, NR2, nitrate reductase 2	8.99481	10.058	10.7339	10.9382	10.1894	10.286	13.0079	12.7677	2.65	NA	261979_at
At5g22270	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11600.1); Has 136 Blast hits to 136 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 136; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.54529	7.65621	7.36931	7.39113	8.77956	8.66014	9.49953	9.35108	0.705	NA	249941_at
At4g00700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein	7.56658	7.47048	8.13574	7.95683	5.99319	5.58711	6.45112	6.65332	0.762	NA	255630_at
At1g07610	MT1C, metallothionein 1C	12.2699	12.0484	12.8091	12.3671	9.06967	8.25513	11.6868	11.411	2.887	NA	261410_at
At1g74030	ENO1, enolase 1	8.54489	8.55577	9.24687	10.0052	6.99436	6.75936	8.69567	9.26057	2.101	NA	260392_at
At1g24180	IAR4, Thiamin diphosphate-binding fold (THDP-binding) superfamily protein	8.05486	8.07834	8.49854	8.64371	6.89737	7.00252	8.08107	8.50927	1.345	NA	264871_at
At1g43710	emb1075, Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	8.91646	9.08211	9.84022	10.2679	8.71803	8.92228	10.186	10.8034	1.675	NA	260814_at
At5g65660	hydroxyproline-rich glycoprotein family protein	11.1607	11.0035	11.5685	11.5921	8.36451	8.60762	10.2898	10.7725	2.045	NA	247149_at
At1g07640	OBP2, Dof-type zinc finger DNA-binding family protein	7.58332	7.48407	7.90302	7.91365	6.94313	6.99072	7.53023	7.70449	0.65	NA	261409_at
At4g35720	Arabidopsis protein of unknown function (DUF241)	4.94157	4.39073	4.69922	4.53565	4.74859	4.61007	5.92649	5.8922	1.23	NA	253155_at
At1g05680	UGT74E2, Uridine diphosphate glycosyltransferase 74E2	4.50972	4.45364	4.59663	4.50817	5.9492	6.04474	9.1356	7.85629	2.499	NA	263231_at
At4g14480	Protein kinase superfamily protein	4.23643	4.37347	4.3334	4.54124	5.27484	5.03477	7.08453	6.43638	1.606	NA	245616_at
At2g42600	ATPPC2, PPC2, phosphoenolpyruvate carboxylase 2	7.88588	7.57565	7.79578	7.71319	9.47967	9.70659	10.3997	10.6824	0.948	NA	263491_at
At1g12580	PEPKR1, phosphoenolpyruvate carboxylase-related kinase 1	6.30899	6.1727	6.63825	6.85538	6.95596	6.8582	7.62823	7.43863	0.626	NA	259484_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At2g41660	MIZ1, Protein of unknown function, DUF617	6.61724	6.13888	6.58119	6.81374	5.2407	5.19186	6.13536	6.14061	0.922	NA	245113_at
At1g27970	NTF2B, nuclear transport factor 2B	8.00026	7.99417	8.1288	8.37589	8.87696	9.02925	9.61656	9.71331	0.712	NA	259593_at
At3g22160	VQ motif-containing protein	7.31253	7.46133	7.10404	7.08594	6.89552	7.02377	7.91415	7.73303	0.864	NA	256793_at
At1g68680	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 16 growth stages; Has 20 Blast hits to 20 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.61076	6.90315	7.13015	7.11868	6.39519	6.3772	7.04243	7.03817	0.654	NA	262285_at
At4g14400	ACD6, ankyrin repeat family protein	4.44906	4.7788	4.5598	4.14964	6.57947	6.57035	7.84897	7.46357	1.081	NA	245265_at
At3g17910	SURF1, Surfeit locus 1 cytochrome c oxidase biogenesis protein	6.52682	6.66315	6.61557	6.75042	5.78651	5.81841	6.73174	6.60694	0.867	NA	258164_at
At3g28050	nodulin MtN21 /EamA-like transporter family protein	8.05674	8.07007	8.49124	8.17471	8.3343	8.12428	8.94574	9.06212	0.775	NA	257299_at
At3g10910	RING/U-box superfamily protein	8.04843	7.80836	8.20802	8.75745	6.06855	6.47535	6.919	7.15219	0.764	NA	258757_at
At4g19960	ATKUP9, HAK9, KT9, KUP9, K+ uptake permease 9	5.06439	5.21047	5.15911	5.38077	6.22064	6.29993	7.03362	7.02782	0.77	NA	254520_at
At2g38640	Protein of unknown function (DUF567)	7.11354	6.9494	7.50672	7.54239	5.76513	5.76835	6.2995	6.41494	0.59	NA	257375_at
At1g65870	Disease resistance-responsive (dirigent-like protein) family protein	4.40251	4.7389	4.4475	4.16566	4.95541	4.78898	5.85964	5.77383	0.945	NA	261914_at
At2g21210	SAUR-like auxin-responsive protein family	4.14043	4.30832	4.21816	4.36591	4.44416	4.48675	7.67713	8.44501	3.596	NA	264014_at
At5g03290	IDH-V, isocitrate dehydrogenase V	9.33066	9.0076	9.7263	9.95952	8.52541	8.7362	9.62329	9.79069	1.076	NA	250929_at
At4g27520	AtENODL2, ENODL2, early nodulin-like protein 2	5.50676	5.08193	6.07714	6.69272	7.89699	8.15214	9.2157	9.56173	1.364	NA	253875_at
At2g17130	IDH-II, IDH2, isocitrate dehydrogenase subunit 2	8.50495	8.37142	8.48763	8.74789	7.55308	7.73631	8.30649	8.39857	0.708	NA	263583_at
At2g21320	B-box zinc finger family protein	5.8952	5.93584	6.01592	6.14596	8.18065	8.26527	9.18649	9.1843	0.962	NA	263739_at
At2g41730	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.89424	5.01063	4.64765	4.84742	5.63969	5.79899	8.75844	9.66369	3.492	NA	260522_x_at
At2g15080	AtRLP19, RLP19, receptor like protein 19	4.89245	4.48808	4.43804	4.45666	5.87409	6.21244	8.34076	8.45771	2.356	NA	265917_at
At4g37370	CYP81D8, cytochrome P450, family 81, subfamily D, polypeptide 8	5.24931	4.92654	4.99714	5.1155	5.83794	6.04152	10.4156	8.70927	3.623	NA	253046_at
At2g41100	ATCAL4, TCH3, Calcium-binding EF hand family protein	8.42814	9.13093	9.1115	9.52306	10.2734	10.1361	11.4697	10.8983	0.979	NA	267083_at
At1g09970	LRR XI-23, RLK7, Leucine-rich receptor-like protein kinase	10.0233	10.2096	10.3417	10.4941	9.33851	9.42844	10.0939	9.85632	0.592	NA	264663_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	family protein											
At5g26200	Mitochondrial substrate carrier family protein	5.39513	5.21917	5.2324	5.37856	5.10498	5.16135	6.62208	6.66932	1.513	NA	246854_at
At2g41290	SSL2, strictosidine synthase-like 2	5.92272	5.8157	5.84844	5.70044	7.63599	7.67783	8.32246	8.67151	0.84	NA	266391_at
At2g04040	ATDTX1, TX1, MATE efflux family protein	5.09624	4.96626	5.28658	5.13432	7.82782	7.9303	9.00323	8.68421	0.965	NA	263403_at
At5g50850	MAB1, Transketolase family protein	9.86594	9.91667	10.2436	10.6247	9.07154	9.13633	9.94166	10.2538	0.994	NA	248474_at
At1g18400	BEE1, BR enhanced expression 1	5.06411	5.28771	4.94154	4.8644	5.35476	5.12331	5.81075	5.84248	0.588	NA	261717_at
At5g50210	OLD5, QS, SUFE3, quinolinate synthase	6.93733	6.79259	7.44406	7.33506	7.18949	7.25714	8.96749	8.66619	1.594	NA	248550_at
At1g26580	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: ELM2 domain-containing protein (TAIR:AT2G03470.1); Has 161 Blast hits to 161 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 4; Plants - 156; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.16831	7.0169	7.54079	7.4967	6.44786	6.56753	7.13733	7.05943	0.591	NA	260999_at
At4g21410	CRK29, cysteine-rich RLK (RECEPTOR-like protein kinase) 29	7.11325	7.00981	7.70066	7.36782	8.19795	8.34981	8.8219	9.01476	0.644	NA	254410_at
At1g79660	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G16170.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	7.77119	7.83645	8.29755	8.43125	7.49127	7.46175	8.12675	8.43456	0.804	NA	261356_at
At5g56980	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G26130.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	8.89787	8.33131	8.77687	8.9913	6.59255	7.03192	7.89239	8.18296	1.225	NA	247933_at
At3g14940	ATPPC3, PPC3, phosphoenolpyruvate carboxylase 3	9.72235	10.6937	10.4566	11.0803	5.37381	5.76702	6.81482	7.34659	1.51	NA	257217_at
At1g26770	AT-EXP10, ATEXP10, ATEXPA10, ATHEXP ALPHA 1.1, EXP10, EXPA10, expansin A10	4.87336	5.93994	5.46588	5.52724	6.05997	6.24699	8.37137	8.53121	2.298	NA	261266_at
At5g54940	Translation initiation factor SUI1 family protein	11.1093	10.9612	11.5875	11.31	10.1596	10.3352	10.9771	10.8465	0.664	NA	248146_at
At5g46330	FLS2, Leucine-rich receptor-like protein kinase family protein	4.90702	4.83925	4.21131	4.46343	6.2033	5.90333	7.44524	6.98967	1.164	NA	248895_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At4g16860	RPP4, Disease resistance protein (TIR-NBS-LRR class) family	4.54096	4.3363	4.17522	4.02986	7.04162	6.45691	8.38483	7.83676	1.362	NA	245448_at
At3g44820	Phototropic-responsive NPH3 family protein	5.0966	5.41615	5.75022	5.89018	5.73123	5.76656	6.87064	6.7809	1.077	NA	246331_at
At4g11460	CRK30, cysteine-rich RLK (RECEPTOR-like protein kinase) 30	4.56987	4.5246	4.53315	4.36663	5.34658	5.37254	5.9258	6.37726	0.792	NA	254931_at
At2g03760	AtSOT1, AtSOT12, ATST1, RAR047, SOT12, ST, ST1, sulphotransferase 12	7.07381	6.71252	5.93323	6.19827	7.15492	7.21145	8.58303	9.14458	1.681	NA	264042_at
At3g05880	RCI2A, Low temperature and salt responsive protein family	9.90124	9.4251	10.2611	10.0046	8.26955	7.67179	8.59939	8.91289	0.785	NA	258735_at
At2g39980	HXXXD-type acyl-transferase family protein	4.69815	5.06554	4.97601	4.83375	7.85267	7.76725	8.53915	8.3674	0.643	NA	267337_at
At2g39010	PIP2;6, PIP2E, plasma membrane intrinsic protein 2E	6.80152	6.98779	6.86088	6.85893	9.64954	10.0289	10.5572	10.8049	0.842	NA	266172_at
At1g05000	Phosphotyrosine protein phosphatases superfamily protein	6.38847	6.52261	6.90029	7.4384	5.77587	6.08463	7.33997	7.32974	1.405	NA	265214_at
At1g76600	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: nucleolus, nucleus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21010.1); Has 220 Blast hits to 220 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 220; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	7.71339	7.39566	8.75941	8.83146	9.0929	9.11539	11.9969	10.6387	2.214	NA	259979_at
At1g77680	Ribonuclease II/R family protein	5.57746	5.83083	6.17962	6.16477	6.19193	6.15385	7.09849	7.00164	0.877	NA	259704_at
AtCg00730	PETD, photosynthetic electron transfer D	5.08044	5.14975	4.95152	4.79426	5.56169	5.31451	5.9369	6.11508	0.588	NA	244977_at
At4g15690	Thioredoxin superfamily protein	5.20938	4.95629	5.37219	5.068	4.68643	4.91098	7.37392	7.14691	2.462	NA	245505_at
At5g13080	ATWRKY75, WRKY75, WRKY DNA-binding protein 75	7.47817	7.10317	8.1351	7.85253	4.84079	4.68272	6.80769	5.7265	1.505	NA	245976_at
At4g30190	AHA2, HA2, PMA2, H(+)-ATPase 2	12.0061	11.9646	12.2922	12.4056	10.3828	10.6984	11.511	12.0743	1.252	NA	253609_at
At3g17860	JAI3, JAZ3, TIFY6B, jasmonate-zim-domain protein 3	7.52555	7.77163	7.62246	7.76463	6.17685	6.01233	6.72416	6.77952	0.657	NA	258189_at
At3g24520	AT-HSFC1, HSFC1, heat shock transcription factor C1	6.85914	6.13629	7.34475	7.68238	4.73266	4.92853	6.25237	5.8922	1.242	NA	258139_at
At1g69260	AFP1, ABI five binding protein	5.07002	5.30522	5.28707	5.58186	4.96569	5.00643	6.03919	6.15272	1.11	NA	260357_at
At2g22480	PFK5, phosphofructokinase 5	8.14239	8.10362	8.52468	8.73229	7.03154	6.99735	7.96909	8.22292	1.082	NA	264044_at
At4g34740	ASE2, ATASE2, ATPURF2, CIA1, GLN phosphoribosyl pyrophosphate amidotransferase 2	5.74017	6.09039	6.44836	6.43586	6.63373	6.56719	7.75499	7.83222	1.193	NA	253252_at
At4g11890	Protein kinase superfamily protein	5.52817	4.5346	4.47866	4.16751	5.55283	5.56543	7.92159	7.33156	2.067	NA	254869_at
At5g65010	ASN2, asparagine synthetase 2	6.35902	6.7908	7.80406	7.69662	6.31141	6.25689	10.9619	11.7362	5.065	NA	247218_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At2g46310	CRF5, cytokinin response factor 5	5.2661	5.54723	6.07315	5.89031	5.97859	5.69476	6.65256	6.73655	0.858	NA	266606_at
At4g25870	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	6.68606	6.44925	6.95771	7.21807	5.7073	5.74389	7.02649	7.2762	1.426	NA	254029_at
At1g55120	AtcwINV3, ATFRUCT5, FRUCT5, beta-fructofuranosidase 5	7.14215	7.3218	7.53314	8.18588	5.80763	5.77647	6.28596	6.73811	0.72	NA	256150_at
At1g26790	Dof-type zinc finger DNA-binding family protein	4.54423	4.41113	4.13012	4.17534	4.28968	4.54201	5.05701	5.01441	0.62	NA	261263_at
At2g22200	Integrase-type DNA-binding superfamily protein	5.25671	5.57762	5.30665	5.35806	5.43697	5.25968	6.21678	6.25582	0.888	NA	263486_at
At5g62920	ARR6, response regulator 6	6.89608	6.67283	7.45594	7.62344	6.12278	6.06802	7.06976	7.25877	1.069	0.75524	247406_at
At4g34860	Plant neutral invertase family protein	7.26632	7.3395	8.21712	8.17574	6.82685	6.82426	7.52005	7.81047	0.84	0.89352	253224_at
At3g58610	ketol-acid reductoisomerase	10.8777	10.9608	11.6853	11.7967	10.744	10.8339	11.7814	12.0319	1.118	0.82169	251536_at
At4g25835	P-loop containing nucleoside triphosphate hydrolases superfamily protein	4.60221	4.77366	5.83956	5.88709	5.22954	5.19033	6.18434	6.48512	1.125	1.17539	254027_at
At1g73920	alpha/beta-Hydrolases superfamily protein	7.88872	7.61572	9.55295	9.61569	8.57366	8.54526	10.2556	10.6402	1.888	1.8321	260393_at
At1g09780	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	9.69528	10.0741	10.4924	10.7308	8.51157	8.56712	10.7726	10.8198	2.257	0.72692	264668_at
At5g17380	Thiamine pyrophosphate dependent pyruvate decarboxylase family protein	9.02494	8.93523	9.58869	9.99416	9.15832	9.15863	9.81203	9.82754	0.661	0.81134	250094_at
At1g13740	AFP2, ABI five binding protein 2	6.98688	6.92169	8.13019	7.79394	6.65661	6.30317	7.31676	7.31441	0.836	1.00778	256069_at
At5g13420	Aldolase-type TIM barrel family protein	9.58985	9.70078	11.2498	11.78	9.30166	9.40799	10.5185	10.95	1.379	1.86959	250234_at
At5g66530	Galactose mutarotase-like superfamily protein	6.94803	7.2389	8.26707	8.47498	7.28105	7.35939	8.08644	8.55071	0.998	1.27756	247101_at
At5g39590	TLD-domain containing nucleolar protein	8.24323	7.94072	9.44505	9.60541	8.31589	8.62823	9.46795	9.6825	1.103	1.43325	249442_at
At3g03040	F-box/RNI-like superfamily protein	5.21778	5.71205	7.2735	6.83566	6.99277	6.48663	8.50235	8.24746	1.635	1.58967	257530_at
At1g49160	WNK7, Protein kinase superfamily protein	5.84633	5.49497	7.76843	8.63014	4.95808	5.65432	7.05131	7.38454	1.912	2.52864	260771_at
At5g04540	Myotubularin-like phosphatases II superfamily	5.97977	5.66383	6.91283	7.23977	6.1149	6.09984	7.21794	7.04359	1.023	1.2545	250833_at
At3g19030	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pyridoxine biosynthetic process, homoserine biosynthetic process; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G49500.1); Has 22 Blast hits to 22 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	8.14587	6.86454	10.0516	10.3362	6.99728	6.89721	10.2107	10.4033	3.36	2.68871	256891_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g48600	AtPMEAMT, PMEAMT, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	9.75247	9.8106	11.0724	11.4711	5.75538	6.10317	7.6874	8.44761	2.138	1.49021	261309_at
At5g20990	B73, CHL6, CNX, CNX1, SIR4, molybdopterin biosynthesis CNX1 protein / molybdenum cofactor biosynthesis enzyme CNX1 (CNX1)	7.84863	7.82916	8.77509	8.62551	7.94586	7.83059	8.74085	8.51871	0.742	0.8614	246131_at
At4g18010	5PTASE2, AT5PTASE2, IP5PII, myo-inositol polyphosphate 5-phosphatase 2	6.04943	5.79494	7.5076	7.30355	7.79804	7.98975	8.93063	8.5168	0.83	1.48339	254707_at
At2g39360	Protein kinase superfamily protein	4.69157	4.46456	5.44648	5.16873	5.37681	5.42448	6.12745	6.14735	0.737	0.72954	266968_at
At1g60140	ATTPS10, TPS10, TPS10, trehalose phosphate synthase	8.22953	7.58692	9.52815	9.42079	8.02961	8.10126	9.44726	9.75809	1.537	1.56624	264246_at
At3g48360	ATBT2, BT2, BTB and TAZ domain protein 2	5.28391	6.09065	10.6069	10.1718	4.82341	4.6103	10.5987	10.8078	5.986	4.70205	252367_at
At5g12860	DiT1, dicarboxylate transporter 1	8.65152	8.35953	9.53617	9.92359	10.1558	10.1236	11.5197	11.4354	1.338	1.22435	250278_at
At5g42990	UBC18, ubiquitin-conjugating enzyme 18	7.08428	6.97626	7.89199	8.46713	7.16677	7.19361	8.47331	8.50263	1.308	1.14929	249183_at
At5g10210	CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65030.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	6.58564	5.91532	9.23094	9.45366	4.87024	4.57729	5.93088	6.64745	1.565	3.09183	250472_at
At2g15620	ATHNIR, NIR, NIR1, nitrite reductase 1	7.79853	7.72042	10.8234	11.3543	5.79816	5.96836	12.0575	12.3646	6.328	3.32936	265475_at
At4g26970	ACO2, aconitase 2	10.343	10.2422	11.2284	11.8238	9.96796	10.1752	11.1733	11.1941	1.112	1.23349	253954_at
At3g62930	Thioredoxin superfamily protein	4.47104	4.47363	6.98138	7.3533	4.62897	4.54036	5.62205	6.09625	1.274	2.695	251195_at
At4g05390	ATRFNR1, RFNR1, root FNR 1	6.26843	6.81159	8.79496	9.26916	5.89863	5.92941	9.56115	10.2417	3.987	2.49205	255230_at
At1g71010	FAB1C, FORMS APLOID AND BINUCLEATE CELLS 1C	8.43732	8.1949	9.20206	9.00446	7.69707	7.67922	8.37255	8.35431	0.675	0.78716	262308_at
At2g31380	STH, salt tolerance homologue	5.86169	6.02219	7.04769	7.39147	10.0473	10.1045	10.8402	10.9515	0.82	1.27763	263252_at
At5g14070	ROXY2, Thioredoxin superfamily protein	4.33233	4.33871	5.50827	5.40125	4.61016	4.52864	5.18204	5.12778	0.586	1.11924	250223_at
At1g49500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G19030.1); Has 24 Blast hits to 24 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.29953	5.69092	10.314	10.3911	6.66371	6.57563	10.2729	11.057	4.045	4.35733	262399_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g17760	P-loop containing nucleoside triphosphate hydrolases superfamily protein	6.43507	6.61531	7.68549	7.81023	5.09776	4.97889	5.93509	5.69377	0.776	1.22267	250062_at
At4g37540	LBD39, LOB domain-containing protein 39	6.36564	5.67237	8.33066	8.21789	6.5385	6.37412	8.24112	8.31311	1.821	2.25527	253043_at
At5g53160	PYL8, RCAR3, regulatory components of ABA receptor 3	8.04892	8.18176	9.20623	9.11542	8.91659	8.66557	9.82764	9.70657	0.976	1.04549	248302_at
At1g24280	G6PD3, glucose-6-phosphate dehydrogenase 3	5.27825	5.27506	8.11335	9.12392	4.73266	4.72478	8.97006	10.0426	4.778	3.34198	264859_at
At5g54130	Calcium-binding endonuclease/exonuclease/phosphatase family	11.0168	12.0417	16.5215	16.4636	12.7682	12.183	14.8422	15.0024	2.447	4.96331	248190_at 248191_at
At5g50200	ATNRT3.1, NRT3.1, WR3, nitrate transmembrane transporters	10.5616	10.0081	11.779	12.3639	9.42821	9.77802	11.5772	11.709	2.04	1.78657	248551_at
At1g14340	RNA-binding (RRM/RBD/RNP motifs) family protein	6.26235	6.33273	7.83786	8.05328	5.40274	5.44088	7.01397	7.21145	1.691	1.64803	261487_at
At5g37260	CIR1, RVE2, Homeodomain-like superfamily protein	5.03368	4.96095	6.62221	6.94693	4.99507	4.85511	6.26561	6.36445	1.39	1.78726	249606_at
At3g63110	ATIPT3, IPT3, isopentenyltransferase 3	5.61194	5.7799	6.3902	6.48501	5.69803	5.61181	6.78716	7.14101	1.309	0.74168	251154_at
At1g64190	6-phosphogluconate dehydrogenase family protein	9.84821	9.73758	11.1345	11.371	8.56238	8.62106	9.96481	10.5677	1.675	1.45984	262323_at
At5g65000	Nucleotide-sugar transporter family protein	7.24337	7.35378	7.89721	7.90712	7.33257	7.33968	7.94914	7.94191	0.609	0.60359	247207_at
At5g62720	Integral membrane HPP family protein	5.60954	5.09155	6.68108	6.50291	5.31794	5.1821	7.36982	7.71513	2.292	1.24145	247443_at
At1g08090	ACH1, ATNRT2.1, ATNRT2:1, LIN1, NRT2, NRT2.1, NRT2:1, NRT2;1AT, nitrate transporter 2:1	8.67403	8.58488	11.1588	11.6121	5.545	6.19019	8.10102	8.33838	2.352	2.75597	260623_at
At5g10030	OBF4, TGA4, TGACG motif-binding factor 4	5.00949	5.50289	6.41994	6.45841	5.51985	5.54237	6.45187	6.45873	0.924	1.18299	250463_at
At2g41560	ACA4, autoinhibited Ca(2+)-ATPase, isoform 4	5.11281	5.53367	7.34014	7.46856	7.44208	7.55739	8.63711	9.07036	1.354	2.0811	245117_at
At1g63940	MDAR6, monodehydroascorbate reductase 6	8.81083	9.23554	10.6929	11.3715	7.52999	7.93811	11.3495	11.9044	3.893	2.00902	260325_at
At2g38170	ATCAX1, CAX1, RCI4, cation exchanger 1	6.87008	6.38684	7.92129	8.10031	9.29614	9.23266	11.2715	11.0473	1.895	1.38234	267093_at
At4g35260	IDH-I, IDH1, isocitrate dehydrogenase 1	8.31011	8.4808	9.36153	9.57015	7.49788	7.63091	8.61455	8.90603	1.196	1.07038	253196_at
At2g26980	CIPK3, SnRK3.17, CBL-interacting protein kinase 3	6.07435	6.32913	8.58444	8.79873	6.86193	6.729	10.2308	10.1576	3.399	2.48985	266313_at
At3g26090	ATRGS1, RGS1, G-protein coupled receptors;GTPase activators	7.15077	7.21367	8.04963	8.19731	6.84687	6.8557	7.69541	7.85746	0.925	0.94125	258072_at
At5g65210	TGA1, bZIP transcription factor family protein	10.2293	9.64646	11.2185	11.3691	7.33504	7.4943	8.29559	8.72416	1.095	1.35591	247199_at
At4g02380	AtLEA5, SAG21, senescence-associated gene 21	10.4131	9.14081	11.8623	12.0766	8.34905	8.62387	11.9117	12.4926	3.716	2.19245	255479_at
At5g40730	AGP24, ATAGP24, arabinogalactan protein 24	8.47777	8.55231	9.38276	9.43466	6.57098	6.27531	7.08487	7.35628	0.797	0.89367	249375_at
At2g27510	ATFD3, FD3, ferredoxin 3	9.89853	10.1759	11.2809	11.8281	8.47112	8.26665	11.2522	11.8026	3.159	1.51727	265649_at
At5g13110	G6PD2, glucose-6-phosphate dehydrogenase 2	6.79057	6.66063	8.3588	8.95847	6.42549	6.13461	8.83056	9.71606	2.993	1.93303	245977_at

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At4g18170	ATWRKY28, WRKY28, WRKY DNA-binding protein 28	5.05468	4.89627	5.74052	5.75262	6.12531	6.1997	6.68155	6.87502	0.616	0.7711	254652_at
At1g77760	GNR1, NIA1, NR1, nitrate reductase 1	6.39261	6.98636	9.67103	11.0929	6.6691	6.91099	12.4174	12.8535	5.845	3.69248	259681_at
At1g70780	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23150.1); Has 143 Blast hits to 143 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 143; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	8.81053	8.92502	11.1133	10.9972	9.08608	8.98679	11.2031	11.5246	2.327	2.18749	262262_at
At1g49860	ATGSTF14, GSTF14, glutathione S-transferase (class phi) 14	10.0146	9.36535	11.8781	11.906	4.50831	4.28342	7.31731	7.90594	3.216	2.20208	259813_at
At3g13070	CBS domain-containing protein / transporter associated domain-containing protein	6.01231	6.29014	7.455	7.70075	7.23939	7.38937	8.43765	8.41843	1.114	1.42665	257178_at
At2g31955	CNX2, cofactor of nitrate reductase and xanthine dehydrogenase 2	7.07411	7.03034	7.77606	7.73442	7.07652	6.96248	8.36258	8.103	1.213	0.70301	263472_at
At2g30040	MAPKKK14, mitogen-activated protein kinase kinase kinase 14	5.68323	5.17352	6.9759	7.25325	5.58355	5.42076	7.67972	7.06499	1.87	1.6862	266832_at
At4g16000	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G15990.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	6.87146	6.86452	8.86834	8.54472	6.26489	6.18869	7.36449	7.36077	1.136	1.83854	245353_at
At5g53460	GLT1, NADH-dependent glutamate synthase 1	10.9544	10.6966	12.1603	12.2487	8.5974	9.20284	11.0853	11.5105	2.398	1.379	248267_at
At5g40850	UPM1, urophorphyrin methylase 1	6.61058	5.95696	9.21297	9.37054	6.1467	6.20915	10.5469	10.8962	4.544	3.00799	249325_at
At2g41310	ARR8, ATRR3, RR3, response regulator 3	5.38039	4.91755	6.39507	6.41347	4.9872	4.97113	5.85305	6.00201	0.948	1.2553	266372_at
At1g70810	Calcium-dependent lipid-binding (CaLB domain) family protein	7.22869	7.42427	7.95698	8.109	7.58338	7.62333	8.3801	8.34394	0.759	0.70651	262314_at
At3g48990	AMP-dependent synthetase and ligase family protein	10.3829	10.2739	11.8179	11.9043	10.8713	10.8673	12.0691	12.3818	1.356	1.53269	252293_at
At5g19970	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.97674	5.58897	7.67521	7.61511	5.06575	5.19033	7.6285	7.42888	2.401	1.8623	246142_at
At1g30510	ATRFNR2, RFNR2, root FNR 2	8.76956	8.765	11.2178	11.8101	6.0927	5.87588	9.8788	10.9453	4.428	2.74667	261806_at
At1g68670	myb-like transcription factor family protein	6.12999	6.3056	8.39817	9.043	6.60737	7.01582	8.26616	8.31402	1.479	2.50279	262284_at
At5g17020	ATCRM1, ATXPO1, HIT2, XPO1, XPO1A, exportin 1A	7.67847	7.79499	8.24997	8.42932	7.65466	7.82354	8.45466	8.30278	0.64	0.60291	246424_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At4g00630	ATKEA2, KEA2, K+ efflux antiporter 2	6.42598	6.32964	7.84921	8.11171	6.90986	6.83126	7.752	7.50249	0.757	1.60265	255686_at
At1g16170	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G79660.1); Has 55 Blast hits to 55 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.11073	5.40731	7.14502	7.25332	5.66408	5.39409	7.39138	7.31023	1.822	1.94016	261791_at
At5g41670	6-phosphogluconate dehydrogenase family protein	8.26333	8.66416	10.463	11.2961	7.87536	7.6397	10.772	11.5184	3.388	2.4158	249266_at
At1g03080	kinase interacting (KIP1-like) family protein	6.76302	6.48548	7.7208	7.6388	6.05405	6.06418	7.11598	6.65902	0.828	1.05555	263112_at
At1g30270	ATCIPK23, CIPK23, LKS1, SnRK3.23, CBL-interacting protein kinase 23	8.81523	8.81457	10.0938	9.80841	7.5548	7.12274	8.16653	8.29121	0.89	1.13622	245775_at
At3g16560	Protein phosphatase 2C family protein	6.00719	5.46885	8.94632	8.88435	7.35332	7.09853	9.31094	9.71708	2.288	3.17731	258437_at
At1g73600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	6.10215	5.94174	7.41075	7.98914	5.04829	4.89569	6.15259	6.48014	1.344	1.678	259842_at
At1g25550	myb-like transcription factor family protein	7.46777	7.31941	9.38172	10.0372	7.35636	7.71812	8.83306	9.37548	1.567	2.31587	255734_at
At5g26340	ATSTP13, MSS1, STP13, Major facilitator superfamily protein	7.10571	7.48265	8.23739	8.32238	8.74038	8.7813	9.65047	9.72133	0.925	0.98571	246831_at
At1g19050	ARR7, response regulator 7	5.96638	5.26446	8.24065	8.44435	7.68987	7.58566	8.79055	8.9432	1.229	2.72708	259466_at

>N_shoots_REPRESSED

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g22570	Major facilitator superfamily protein	5.60278	5.80483	6.07863	6.12768	7.01885	7.05754	6.38083	6.50545	-0.6	NA	261937_at
At3g27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3	5.99592	5.89142	4.92188	5.49255	11.2492	11.3796	9.66229	9.73005	-1.62	NA	258239_at
At1g60550	DHNS, ECHID, enoyl-CoA hydratase/isomerase D	4.53286	4.27486	4.78759	4.92429	7.62218	7.87627	6.90998	7.12889	-0.73	NA	264920_at
At3g04550	unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28500.1); Has 110 Blast hits to 110 proteins in 51 species: Archae - 0;	4.99333	5.33496	5.48844	5.66688	6.67713	6.75576	5.84058	6.14665	-0.72	NA	258800_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	Bacteria - 67; Metazoa - 1; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).											
At3g19480	D-3-phosphoglycerate dehydrogenase	4.44948	4.40466	4.12256	4.13567	6.90465	6.91785	5.42855	6.01307	-1.19	NA	258025_at
At1g61820	BGLU46, beta glucosidase 46	9.21958	9.17033	8.93988	9.15768	6.46677	6.53855	5.57918	5.54304	-0.94	NA	264280_at
At2g24280	alpha/beta-Hydrolases superfamily protein	6.49649	6.67897	6.81721	7.07624	8.37833	8.50918	7.26785	7.64608	-0.99	NA	265990_at
At4g19530	disease resistance protein (TIR-NBS-LRR class) family	5.17239	4.95674	4.67839	4.67794	6.32367	6.23601	5.50901	5.4619	-0.79	NA	254553_at
At3g26510	Octicosapeptide/Phox/Bem1p family protein	8.64956	8.23226	8.12714	8.10439	10.8905	11.0052	8.2742	8.58263	-2.52	NA	257615_at
At1g60960	ATIRT3, IRT3, iron regulated transporter 3	9.8409	9.83886	9.65009	9.80901	8.95412	9.17534	7.83687	7.69597	-1.3	NA	259723_at
At1g80080	AtRLP17, TMM, Leucine-rich repeat (LRR) family protein	4.52778	4.78527	4.6024	4.46829	7.40563	7.30719	6.38038	6.78869	-0.77	NA	262040_at
At1g14780	MAC/Perforin domain-containing protein	8.26907	8.72439	7.39496	7.85093	7.59037	7.40427	6.1693	6.27634	-1.27	NA	262887_at
At5g45650	subtilase family protein	5.0241	5.33861	4.55964	4.67633	6.07533	6.48068	5.34257	5.36528	-0.92	NA	248961_at
At3g62700	ATMRP10, MRP10, multidrug resistance-associated protein 10	7.86039	7.83645	8.16175	7.99412	8.93462	8.90925	8.18847	8.40451	-0.63	NA	251227_at
At3g09580	FAD/NAD(P)-binding oxidoreductase family protein	4.59831	4.88681	4.70485	4.8226	7.44655	7.16822	6.49755	6.42863	-0.84	NA	258708_at
At5g55910	D6PK, D6 protein kinase	7.1167	7.15439	7.08301	7.06299	8.13879	8.20135	7.44115	7.47948	-0.71	NA	248034_at
At1g02300	Cysteine proteinases superfamily protein	4.74001	4.80186	4.95304	4.79231	6.31319	6.04474	5.03574	5.16145	-1.08	NA	259441_at
At5g55930	ATOPT1, OPT1, oligopeptide transporter 1	5.64292	5.72669	5.18806	5.42115	10.7078	10.7351	9.69223	9.02442	-1.36	NA	248037_at
At5g58140	NPL1, PHOT2, phototropin 2	5.97488	5.56154	5.19709	5.27213	8.85726	9.2079	8.13713	8.23545	-0.85	NA	247853_at
At3g61490	Pectin lyase-like superfamily protein	6.08414	6.09527	6.04953	5.84432	7.06487	7.03227	6.19597	6.49318	-0.7	NA	251317_at
At5g17860	CAX7, calcium exchanger 7	6.3045	7.01227	5.75067	5.76727	9.1063	9.08737	8.23104	7.46549	-1.25	NA	250054_at
At4g01460	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	4.70473	4.61902	4.33996	4.2701	7.00235	7.13247	5.29242	5.37705	-1.73	NA	255579_at
At1g02660	alpha/beta-Hydrolases superfamily protein	4.72215	5.00306	5.30582	5.06367	6.91627	6.83429	5.39839	5.84564	-1.25	NA	260915_at
At1g08230	ATGAT1, GAT1, Transmembrane amino acid transporter family protein	5.52626	5.79224	5.73056	5.42891	7.88262	7.783	6.92415	6.68632	-1.03	NA	261785_at
At1g55020	ATLOX1, LOX1, lipoxygenase 1	11.2375	10.9092	11.432	11.5064	7.9958	7.93612	7.36865	7.32719	-0.62	NA	256321_at
At1g14150	PQL1, PQL2, PsbQ-like 2	4.79893	5.05363	4.35701	4.38237	6.44662	7.16515	5.56299	6.19669	-0.93	NA	262612_at
At4g10120	ATSPS4F, Sucrose-phosphate synthase family protein	4.61623	4.92575	4.64589	4.72076	6.32723	6.65845	5.05575	5.19605	-1.37	NA	255016_at
At1g15690	ATAVP3, AtVHP1;1, AVP-3, AVP1, Inorganic H pyrophosphatase family protein	11.2164	11.4157	11.5032	11.574	11.2789	11.448	10.8509	10.7004	-0.59	NA	259504_at
At5g57180	CIA2, chloroplast import apparatus 2	5.84622	5.4408	5.52942	5.47297	7.33727	7.39972	6.20091	6.23043	-1.15	NA	247946_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g69160	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13980.1); Has 173 Blast hits to 172 proteins in 54 species: Archae - 0; Bacteria - 0; Metazoa - 25; Fungi - 33; Plants - 84; Viruses - 2; Other Eukaryotes - 29 (source: NCBI BLink).	4.90699	4.40394	4.50887	4.24997	7.60232	7.67512	6.32436	6.34433	-1.3	NA	259373_at
At2g41260	ATM17, M17, glycine-rich protein / late embryogenesis abundant protein (M17)	4.48602	4.65683	3.88362	4.05659	7.11884	6.96468	6.21726	6.54856	-0.66	NA	266393_at
At1g78180	Mitochondrial substrate carrier family protein	4.95462	5.0738	5.25726	5.17934	6.5214	6.57421	5.77193	5.75448	-0.78	NA	260082_at
At5g59430	ATTRP1, TRP1, telomeric repeat binding protein 1	6.46269	6.25711	6.77075	6.5673	7.35089	7.62844	6.76792	6.92055	-0.65	NA	247726_at
At1g66130	NAD(P)-binding Rossmann-fold superfamily protein	5.37459	5.19522	5.16811	5.07384	8.63855	8.53268	7.89206	8.05995	-0.61	NA	256514_at
At1g67830	ATFXG1, FXG1, alpha-fucosidase 1	4.81334	4.9578	4.95494	4.94892	8.06749	7.83947	7.21808	7.22979	-0.73	NA	245215_at
At4g12390	PME1, pectin methylesterase inhibitor 1	8.76087	8.71809	9.14508	9.08157	8.11755	8.222	7.35802	7.54803	-0.72	NA	254810_at
At4g33660	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	5.94113	6.15872	5.84669	5.92092	8.48732	8.06767	7.19153	7.39288	-0.99	NA	253302_at
At5g10310	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G13898.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	4.37663	4.3188	4.13807	4.17934	5.00518	5.44327	4.50972	4.43625	-0.75	NA	250481_at
At5g38980	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.51468	5.64356	5.2528	5.541	10.932	11.0036	10.0045	10.3045	-0.81	NA	249482_at
At1g05690	BT3, BTB and TAZ domain protein 3	5.02524	4.59064	4.8777	4.94759	6.41415	6.10397	5.50717	5.42041	-0.8	NA	257451_at
At4g03150	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants -	5.52006	5.53337	5.58976	5.56368	6.63272	6.68248	5.9782	6.10156	-0.62	NA	255436_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).											
At1g73870	B-box type zinc finger protein with CCT domain	5.26032	5.72917	4.74246	4.88605	8.0531	7.66874	7.12599	6.33562	-1.13	NA	260380_at
At2g42360	RING/U-box superfamily protein	5.35327	5.40426	5.16818	5.19247	7.74201	8.07329	5.97293	6.75457	-1.54	NA	265853_at
At3g52310	ABC-2 type transporter family protein	4.69408	5.00703	4.6414	4.64177	5.57119	5.55413	5.05695	4.88452	-0.59	NA	256672_at
At1g03630	POR C, PORC, protochlorophyllide oxidoreductase C	5.07119	5.1762	4.33385	4.60566	8.55834	8.60158	6.41216	7.31736	-1.72	NA	264839_at
At1g52220	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: photosystem I P subunit (TAIR:AT2G46820.2); Has 291 Blast hits to 291 proteins in 50 species: Archae - 0; Bacteria - 90; Metazoa - 0; Fungi - 0; Plants - 200; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	6.10616	5.46068	5.07267	5.29133	9.96441	9.82017	9.04821	9.42301	-0.66	NA	259838_at
At2g18360	alpha/beta-Hydrolases superfamily protein	9.04468	8.97328	8.58833	8.90442	6.46153	6.32827	5.33716	5.72099	-0.87	NA	265341_at
At1g13110	CYP71B7, cytochrome P450, family 71 subfamily B, polypeptide 7	10.8262	10.436	10.3137	10.2731	10.2715	10.3781	8.25122	8.7038	-1.85	NA	262793_at
At2g26710	BAS1, CYP72B1, CYP734A1, Cytochrome P450 superfamily protein	4.7287	4.90325	5.32078	5.19901	5.98603	6.35742	5.29573	5.15777	-0.94	NA	267614_at
At1g51805	Leucine-rich repeat protein kinase family protein	4.6504	4.55981	4.28525	4.04915	9.42276	9.31005	8.38476	7.67782	-1.34	NA	256168_at
At2g16430	ATPAP10, PAP10, purple acid phosphatase 10	6.20196	5.78159	6.30278	6.61614	8.88192	8.86888	7.86744	8.08141	-0.9	NA	263553_at
At3g18050	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28100.1); Has 67 Blast hits to 66 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	5.2712	4.94034	5.41145	5.26189	7.51032	7.60958	6.61017	6.96225	-0.77	NA	258156_at
At1g76110	HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain	5.3612	4.98606	4.66176	4.53732	6.44014	6.21685	5.22609	5.26064	-1.09	NA	261782_at
At1g62770	Plant invertase/pectin methylesterase inhibitor superfamily protein	6.93782	6.93911	6.86539	6.30661	5.0982	5.23847	4.42192	4.1784	-0.87	NA	262643_at
At5g13730	SIG4, SIGD, sigma factor 4	4.44476	4.27161	4.26646	4.29308	7.16176	7.11767	4.9243	4.97563	-2.19	NA	250255_at
At4g33000	ATCBL10, CBL10, SCABP8, calcineurin B-like protein 10	4.48154	4.30309	4.3479	4.31122	5.91693	5.69517	5.15198	5.27622	-0.59	NA	253412_at
At3g13610	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	11.0674	10.8998	10.3674	10.7479	7.14278	7.28182	5.40713	5.47519	-1.77	NA	256647_at
At1g70370	PG2, polygalacturonase 2	7.08994	7.50667	7.28634	7.2769	9.03369	8.71793	7.76714	8.07401	-0.96	NA	264315_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At5g52120	AtPP2-A14, PP2-A14, phloem protein 2-A14	6.15136	6.08647	6.54827	6.33974	5.99235	6.19966	4.86217	5.29572	-1.02	NA	248395_at
At5g48490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	5.10774	5.5497	4.67289	4.73126	10.856	11.055	9.43763	10.34	-1.07	NA	248683_at
At5g39210	CRR7, chlororespiratory reduction 7	4.15248	4.56192	4.19127	4.23207	5.65793	5.92287	4.9977	5.06192	-0.76	NA	249472_at
At4g24740	AFC2, AME1, FC2, FUS3-complementing gene 2	7.08858	6.9174	7.00785	6.92546	6.4453	6.48759	5.80082	5.79636	-0.67	NA	254131_at
At3g30180	BR6OX2, CYP85A2, brassinosteroid-6-oxidase 2	6.50173	6.73318	6.27107	6.49639	8.25606	7.91643	7.1718	7.24751	-0.88	NA	256598_at
At1g49010	Duplicated homeodomain-like superfamily protein	5.57473	5.336	5.21458	5.00234	7.56041	7.86502	6.73426	6.93881	-0.88	NA	260769_at
At4g02330	ATPMEPCRB, Plant invertase/pectin methylesterase inhibitor superfamily	5.33963	5.3475	5.04743	5.64483	7.31856	7.23127	6.23382	5.73278	-1.29	NA	255524_at
At3g23880	F-box and associated interaction domains-containing protein	5.42946	5.16464	5.16127	5.03662	7.74976	8.25659	5.95378	6.50853	-1.77	NA	256914_at
At4g28080	Tetratricopeptide repeat (TPR)-like superfamily protein	5.69639	5.49214	5.38408	5.63757	9.60705	9.92474	9.1024	8.99578	-0.72	NA	253849_at
At1g79700	Integrase-type DNA-binding superfamily protein	6.90967	6.77471	6.43439	6.60411	7.72292	8.25038	6.77867	6.54963	-1.32	NA	261395_at
At1g10640	Pectin lyase-like superfamily protein	4.73647	5.27506	4.40133	4.24815	6.21235	6.12181	5.11535	5.59309	-0.81	NA	261834_at
At3g22210	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	6.00009	5.38016	5.26169	4.92176	9.07444	8.79159	8.18476	8.48166	-0.6	NA	256796_at
At3g01660	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	4.76638	4.79461	4.84108	4.73646	6.66371	6.65332	5.86338	6.19121	-0.63	NA	259179_at
At3g19850	Phototropic-responsive NPH3 family protein	4.8443	5.2577	4.42077	4.43201	8.17393	7.7721	6.34055	7.03436	-1.29	NA	257964_at
At5g37540	Eukaryotic aspartyl protease family protein	5.19079	5.66157	6.02526	5.75683	7.13499	7.1672	5.82777	5.42583	-1.52	NA	249626_at
At4g01250	AtWRKY22, WRKY22, WRKY family transcription factor	5.30918	5.31947	5.25758	5.23142	8.22567	8.41833	7.40042	7.23902	-1	NA	255568_at
At3g50270	HXXXD-type acyl-transferase family protein	5.92924	5.78907	5.48576	5.76234	8.7419	8.93045	8.0595	8.25153	-0.68	NA	252199_at
At3g59400	GUN4, enzyme binding;tetrapyrrole binding	5.47158	5.02387	4.35358	4.88934	10.4437	10.6083	9.55764	10.035	-0.73	NA	251519_at
At3g61890	ATHB-12, ATHB12, HB-12, homeobox 12	4.92757	5.34601	4.98647	4.88324	7.78014	7.66281	5.09647	5.47009	-2.44	NA	251272_at
At3g19680	Protein of unknown function (DUF1005)	5.16163	5.61389	5.44668	5.68702	7.27666	7.35323	5.74515	6.00065	-1.44	NA	257076_at
At1g69490	ANAC029, ATNAP, NAP, NAC-like, activated by AP3/PI	10.4068	10.3347	10.844	10.8574	9.91814	10.0786	9.29471	9.19506	-0.75	NA	256300_at
At2g22980	SCPL13, serine carboxypeptidase-like 13	4.36559	4.42048	4.44147	4.43806	6.35433	6.33641	5.67259	5.06913	-0.97	NA	267265_at
At1g05300	ZIP5, zinc transporter 5 precursor	5.59941	5.43807	6.39926	5.93149	8.22338	7.8615	7.15181	6.74475	-1.09	NA	264574_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At3g06510	ATSFR2, SFR2, Glycosyl hydrolase superfamily protein	7.56175	7.27632	7.7163	8.00539	9.42305	9.75875	8.57995	8.85599	-0.87	NA	258512_at
At2g45340	Leucine-rich repeat protein kinase family protein	5.20082	5.22131	5.66316	5.436	7.33376	7.06296	5.69429	6.07595	-1.31	NA	245130_at
At4g23130	CRK5, RLK6, cysteine-rich RLK (RECEPTOR-like protein kinase) 5	4.39429	4.50598	4.42818	4.36635	6.12272	5.72831	4.94604	4.77761	-1.06	NA	254266_at
At5g58260	oxidoreductases, acting on NADH or NADPH, quinone or similar compound as acceptor	5.89704	5.91603	5.42854	5.22248	7.16568	7.09518	6.43906	6.18389	-0.82	NA	247816_at
At2g28630	KCS12, 3-ketoacyl-CoA synthase 12	5.0635	5.88373	5.95802	6.22365	9.93722	10.0627	8.5554	8.49748	-1.47	NA	263443_at
At3g21520	AtDMP1, DMP1, DUF679 domain membrane protein 1	8.03332	7.66024	7.44411	7.18431	5.86132	5.91071	5.46922	4.96504	-0.67	NA	257540_at
At2g17880	Chaperone DnaJ-domain superfamily protein	4.47871	5.01888	5.65657	5.92965	6.94134	7.51578	5.51753	5.86391	-1.54	NA	264788_at
At3g14067	Subtilase family protein	8.95405	8.8947	8.33395	8.45198	8.13382	8.39907	7.55557	7.78901	-0.59	NA	256997_at
At2g30390	ATFC-II, FC-II, FC2, ferrochelatase 2	5.4542	5.29172	5.75297	5.79999	8.0263	7.96717	7.46936	7.33742	-0.59	NA	267471_at
At3g53670	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37480.1); Has 176 Blast hits to 173 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 13; Plants - 154; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	8.78596	8.57979	8.46168	8.35282	7.57914	8.0032	6.78325	6.22467	-1.29	NA	251954_at
At2g45210	SAUR-like auxin-responsive protein family	8.72205	9.01231	9.46026	9.09506	8.63089	8.70029	7.88422	7.81647	-0.82	NA	245136_at
At3g53130	CYP97C1, LUT1, Cytochrome P450 superfamily protein	5.48403	5.26996	4.84114	4.85103	6.61462	6.9056	5.91713	6.21493	-0.69	NA	251969_at
At3g01480	ATCYP38, CYP38, cyclophilin 38	5.25897	5.29249	5.8986	5.70626	8.83546	8.88406	8.18305	8.29201	-0.62	NA	259193_at
At4g09900	ATMES12, MES12, methyl esterase 12	4.64859	4.80337	4.52758	4.41867	5.78526	5.8301	5.23902	5.17824	-0.6	NA	255025_at
At1g19510	ATRL5, RL5, RSM4, RAD-like 5	4.57715	5.16961	4.16058	4.23839	6.21267	6.15294	4.58774	4.44233	-1.67	NA	260664_at
At2g29290	NAD(P)-binding Rossmann-fold superfamily protein	4.57433	4.27415	4.41113	4.27334	9.06968	8.96391	7.08654	7.49864	-1.72	NA	266279_at
At3g06980	DEA(D/H)-box RNA helicase family protein	6.29498	6.08515	6.87287	6.59436	8.11873	8.15528	7.47284	7.52848	-0.64	NA	258554_at
At2g01620	MEE11, RNI-like superfamily protein	5.95374	5.95797	6.83732	6.4673	7.81578	8.15072	7.07943	7.12977	-0.88	NA	265867_at
At3g02040	SRG3, senescence-related gene 3	6.82946	6.77848	6.89084	6.97311	6.63528	6.80398	5.8499	5.94789	-0.82	NA	258856_at
At1g51500	ABCG12, ATWBC12, CER5, D3, WBC12, ABC-2 type transporter family protein	6.90738	6.97238	7.60082	7.39442	9.91331	9.81766	9.31688	9.24037	-0.59	NA	260490_at
At3g22640	PAP85, cupin family protein	4.71029	4.5279	4.23238	4.14091	6.71498	6.54088	5.18972	4.9988	-1.53	NA	258327_at
At1g33960	AIG1, P-loop containing nucleoside triphosphate hydrolases superfamily protein	4.90958	4.75329	4.18723	4.46973	6.16145	5.73854	4.69007	5.06095	-1.07	NA	260116_at
At1g01320	Tetratricopeptide repeat (TPR)-like superfamily protein	4.93822	4.7459	5.09749	5.14472	9.51616	9.68418	8.87532	9.12548	-0.6	NA	261053_at
At1g52760	LysoPL2, lysophospholipase 2	10.6556	10.8399	10.4709	10.5577	9.94875	10.0162	8.85377	9.27022	-0.92	NA	260153_at

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At5g52910	ATIM, timeless family protein	5.52366	5.78941	5.19352	5.3306	6.78319	6.96623	5.74861	5.75233	-1.12	NA	248279_at
At4g10910	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	4.86088	5.10218	4.34592	4.64881	6.33605	6.45958	4.9864	5.66497	-1.07	NA	254954_at
At4g23200	CRK12, cysteine-rich RLK (RECEPTOR-like protein kinase) 12	4.57455	4.89578	4.40936	4.54917	7.04695	7.12789	6.4634	5.60718	-1.05	NA	254242_at
At1g74940	Protein of unknown function (DUF581)	8.05597	7.51412	6.88487	6.81926	7.16383	7.32929	5.96557	6.32468	-1.1	NA	262170_at
At3g56060	Glucose-methanol-choline (GMC) oxidoreductase family protein	5.10901	4.70501	4.07016	4.50193	6.44542	6.86219	5.75107	5.86685	-0.84	NA	251746_at
At5g61560	U-box domain-containing protein kinase family protein	5.44932	4.94893	4.89205	4.7858	7.22157	7.30943	6.48531	6.14305	-0.95	NA	247532_at
At1g78290	SNRK2-8, SNRK2.8, SRK2C, Protein kinase superfamily protein	9.52999	8.77908	9.92566	9.42536	8.12351	8.17662	6.64321	6.91544	-1.37	NA	260774_at
At1g52190	Major facilitator superfamily protein	5.14751	4.97486	5.0789	5.0017	7.42931	7.3104	6.41897	6.7281	-0.8	NA	259839_at
At5g48370	Thioesterase/thiol ester dehydrase-isomerase superfamily protein	5.20539	5.1802	4.93954	5.22307	6.23073	6.51925	5.59492	5.40326	-0.88	NA	248697_at
At2g03550	alpha/beta-Hydrolases superfamily protein	4.81717	4.78226	4.3198	4.2387	7.58179	7.35444	5.9261	5.94917	-1.53	NA	265699_at
At1g75460	ATP-dependent protease La (LON) domain protein	5.50863	5.57903	4.55928	4.6481	8.22604	8.56803	6.81919	7.4252	-1.27	NA	261118_at
At4g14605	Mitochondrial transcription termination factor family protein	5.70373	5.62568	5.75433	6.16369	6.85086	7.04283	5.92334	6.21853	-0.88	NA	245565_at
At1g66820	glycine-rich protein	5.3688	5.13676	5.5567	5.57549	7.50347	7.22956	6.79424	6.72841	-0.61	NA	256383_at
At4g01390	TRAF-like family protein	8.97326	8.85321	8.73173	7.94597	6.84353	6.63057	6.12864	5.99507	-0.68	NA	255621_at
At3g50240	KICP-02, ATP binding microtubule motor family protein	4.67926	4.82761	4.79896	4.9946	5.3865	5.47239	4.76436	4.78151	-0.66	NA	252215_at
At5g62140	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 60 proteins in 24 species: Archae - 0; Bacteria - 14; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	5.00501	5.01287	4.67077	4.39543	6.08365	6.31354	5.12898	5.12256	-1.07	NA	247486_at
At5g23660	MTN3, homolog of Medicago truncatula MTN3	6.33178	6.46771	5.54616	5.89795	7.60488	8.02532	7.32708	6.84902	-0.73	NA	249800_at
At4g27730	ATOPT6, OPT6, oligopeptide transporter 1	5.87212	6.08822	5.8713	6.04327	8.38967	8.46834	7.66054	7.69572	-0.75	NA	253887_at
At5g10100	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	6.02134	6.07674	5.47894	5.79073	7.06349	7.08197	5.67385	5.45614	-1.51	NA	250467_at
At1g07180	ATNDI1, NDA1, alternative NAD(P)H dehydrogenase 1	4.43896	4.66225	4.41025	4.46184	7.83412	7.859	7.1473	7.24253	-0.65	NA	256057_at
At2g22990	SCPL8, SNG1, sinapoylglucose 1	4.58088	4.31656	4.75737	4.64284	10.1832	10.1737	9.55155	9.45096	-0.68	NA	267262_at

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At5g47610	RING/U-box superfamily protein	4.51676	4.69398	4.38263	4.20174	8.96335	9.21972	7.75613	7.85632	-1.29	NA	248759_at
At3g10420	P-loop containing nucleoside triphosphate hydrolases superfamily protein	7.94898	7.31521	6.91081	6.95921	9.68851	9.60898	8.98456	8.8939	-0.71	NA	258925_at
At1g55960	Polyketide cyclase/dehydrase and lipid transport superfamily protein	7.9302	7.92211	7.71334	7.45888	9.82055	10.0395	8.993	8.79992	-1.03	NA	260603_at
At2g44670	Protein of unknown function (DUF581)	10.2217	9.9226	9.40274	9.81307	8.91902	8.94418	8.10415	7.4831	-1.14	NA	266882_at
At1g64170	ATCHX16, CHX16, cation/H+ exchanger 16	6.16956	6.86459	5.92922	5.82899	9.09449	8.92768	7.46266	7.43732	-1.56	NA	262324_at
At5g50160	ATFRO8, FRO8, ferric reduction oxidase 8	4.377	4.45425	4.26318	4.12078	5.90257	5.81774	4.53837	4.52662	-1.33	NA	248540_at
At3g44970	Cytochrome P450 superfamily protein	4.55968	4.83342	4.38197	4.71387	6.21521	6.49268	5.65018	5.35764	-0.85	NA	252629_at
At3g18890	NAD(P)-binding Rossmann-fold superfamily protein	5.27716	5.60564	5.30037	5.30251	7.28241	7.50369	6.66936	6.72841	-0.69	NA	256655_at
At2g34620	Mitochondrial transcription termination factor family protein	5.47314	5.42456	4.70595	5.33588	8.60594	8.79348	7.09317	7.60137	-1.35	NA	266899_at
At5g66170	STR18, sulfurtransferase 18	10.6517	10.3633	9.96744	9.4291	8.08233	8.19446	7.32669	7.13056	-0.91	NA	247136_at
At5g18130	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03870.2); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	8.61931	8.93445	8.63672	8.52889	8.53397	8.76034	7.47575	7.31555	-1.25	NA	250028_at
At3g16250	NDF4, NDH-dependent cyclic electron flow 1	4.50912	4.84465	4.04702	4.393	5.92096	5.89959	4.75855	5.1977	-0.93	NA	258055_at
At2g22540	AGL22, SVP, K-box region and MADS-box transcription factor family protein	8.38029	8.06295	8.22089	8.10696	9.20732	9.07338	8.37482	8.29456	-0.81	NA	264054_at
At3g28270	Protein of unknown function (DUF677)	4.31449	4.85711	4.21272	3.99931	6.01073	5.91473	4.61269	4.38222	-1.47	NA	256603_at
At1g16390	3-Oct, ATOCT3, organic cation/carnitine transporter 3	4.42087	4.67035	4.67258	4.5226	5.58189	5.5312	4.8814	4.95528	-0.64	NA	262730_at
At5g58350	WNK4, ZIK2, with no lysine (K) kinase 4	8.94417	8.83787	8.53194	8.54446	9.86786	9.9584	9.18429	9.45243	-0.59	NA	247819_at
At5g62130	Per1-like family protein	6.50431	6.19564	6.14423	5.91911	7.55871	7.52746	6.52232	6.51934	-1.02	NA	247467_at
At2g17500	Auxin efflux carrier family protein	10.4651	9.88575	9.49866	9.59704	8.7201	8.7616	8.11371	7.74791	-0.81	NA	263073_at
At3g02380	ATCOL2, COL2, CONSTANS-like 2	5.8596	5.78318	5.04003	5.68	10.7875	11.1306	9.06789	10.056	-1.4	NA	258497_at
At1g09850	XBCP3, xylem bark cysteine peptidase 3	6.16379	6.21145	6.64333	6.59869	6.19428	6.10662	5.50467	5.2851	-0.76	NA	264687_at
At2g32150	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	10.847	10.2866	11.2463	10.9226	10.2169	10.3226	9.04313	8.63879	-1.43	NA	265680_at
At4g13220	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 27 Blast hits to 27 proteins in 10 species: Archae - 0;	5.14134	5.23907	5.5438	5.35537	7.47914	7.43933	6.8695	6.86617	-0.59	NA	254755_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
	Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).											
At1g18620	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74160.1); Has 1987 Blast hits to 1263 proteins in 207 species: Archae - 0; Bacteria - 172; Metazoa - 665; Fungi - 149; Plants - 271; Viruses - 6; Other Eukaryotes - 724 (source: NCBI BLink).	5.20205	5.02306	5.17386	5.28763	7.01303	7.07695	6.07196	5.94056	-1.04	NA	255774_at
At1g78995	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	4.78693	4.91974	5.29481	5.01765	7.10307	6.84211	5.77263	5.95331	-1.11	NA	264096_at
At3g02870	VTC4, Inositol monophosphatase family protein	6.15136	6.15794	6.55209	6.46172	7.46136	7.69562	6.77147	6.72031	-0.83	NA	258613_at
At4g33010	AtGLDP1, GLDP1, glycine decarboxylase P-protein 1	8.07257	7.61502	7.86725	7.73497	11.27	11.279	10.5887	10.3026	-0.83	NA	253387_at
At4g14630	GLP9, germin-like protein 9	11.1437	10.8606	10.6829	11.3577	7.2368	7.28176	5.63861	5.69408	-1.59	NA	245567_at
At5g25610	ATRD22, RD22, BURP domain-containing protein	7.72875	7.75064	7.16588	7.80523	9.12746	9.40858	8.21711	8.41281	-0.95	NA	246908_at
At5g49360	ATBXL1, BXL1, beta-xylosidase 1	8.70525	8.75818	10.148	9.96792	11.2017	11.333	10.167	10.3868	-0.99	1.32624	248622_at
At3g11670	DGD1, UDP-Glycosyltransferase superfamily protein	5.63203	5.90143	6.56688	6.50925	8.35015	8.61382	7.6919	7.52284	-0.87	0.77134	259070_at
At4g28290	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 45 Blast hits to 45 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	4.77387	4.55041	5.67086	5.42085	8.56276	8.42202	7.30084	7.46315	-1.11	0.88372	253814_at
At1g71880	ATSUC1, SUC1, sucrose-proton symporter 1	6.7575	6.53231	8.88143	8.61358	8.48208	8.34445	7.69127	7.57358	-0.78	2.1026	260143_at
At1g02640	ATBXL2, BXL2, beta-xylosidase 2	6.7737	6.95605	7.74199	7.87972	7.66116	7.90581	6.58377	6.77217	-1.11	0.94598	260914_at
At1g58180	ATBCA6, BCA6, beta carbonic anhydrase 6	8.5613	8.21431	9.26386	9.14873	8.66859	8.935	8.07758	7.92219	-0.8	0.81849	246396_at
At3g30775	AT-POX, ATPDH, ATPOX, ERD5, PRO1, PRODH, Methylenetetrahydrofolate reductase family protein	11.1435	10.8936	12.1451	12.3859	9.22831	9.24602	8.62996	8.55599	-0.64	1.24692	257315_at
At4g19420	Pectinacetylesterase family protein	5.08032	4.93335	5.78344	5.59777	7.27746	6.94272	5.51415	5.67125	-1.52	0.68377	254573_at
At5g47400	unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	5.55829	5.30506	6.48016	6.2901	6.04521	5.9543	5.25004	5.51091	-0.62	0.95346	248786_at

Gene_ID		1.At_root_control.CEL	2.At_root_control.CEL	1.At_root_N+.CEL	2.At_root_N+.CEL	1.At_shoot_control.CEL	2.At_shoot_control.CEL	1.At_shoot_N+.CEL	2.At_shoot_N+.CEL	SHOOT	ROOT	Affy_ID
At1g66180	Eukaryotic aspartyl protease family protein	9.94513	9.87885	11.125	11.0085	10.6963	10.7429	9.36356	9.78237	-1.15	1.15474	256525_at
At5g01820	ATCIPK14, ATSR1, CIPK14, SnRK3.15, SR1, serine/threonine protein kinase 1	8.87355	9.18606	7.73014	7.91999	7.80359	7.89222	6.6431	7.06977	-0.99	-1.2047	251060_at
At5g54190	PORA, protochlorophyllide oxidoreductase A	5.38217	5.78847	4.43067	4.34129	6.88849	7.23482	5.7323	5.51581	-1.44	-1.1993	248197_at
At2g32560	F-box family protein	10.2106	10.3211	9.26023	9.04853	10.4277	10.3151	9.29061	8.92357	-1.26	-1.1115	267116_at 267117_at
At4g19170	CCD4, NCED4, nine-cis-epoxycarotenoid dioxygenase 4	5.49883	5.70756	4.70535	4.58924	8.55104	8.41622	5.4781	6.04728	-2.72	-0.9559	254564_at
At1g69850	ATNRT1:2, NRT1:2, NTL1, nitrate transporter 1:2	8.45353	8.51591	7.97198	7.76124	8.82494	8.93803	7.80256	7.88185	-1.04	-0.6181	260414_at
At3g13672	TRAF-like superfamily protein	5.44435	5.13562	4.50539	4.42821	5.19949	5.10066	4.36107	4.38992	-0.77	-0.8232	256789_at
At5g15410	ATCNGC2, CNGC2, DND1, Cyclic nucleotide-regulated ion channel family protein	5.29759	5.68141	4.44271	4.5226	8.54827	8.57011	7.93565	7.74715	-0.72	-1.0068	246510_at
At1g68190	B-box zinc finger family protein	5.50504	5.30657	4.72822	4.62108	6.33847	6.37452	5.60825	5.91659	-0.59	-0.7312	260431_at
At5g64410	ATOPT4, OPT4, oligopeptide transporter 4	9.36981	9.25133	8.6055	8.65891	9.58989	9.51921	7.80807	7.64456	-1.83	-0.6784	247284_at
At1g01140	CIPK9, PKS6, SnRK3.12, CBL-interacting protein kinase 9	5.1044	4.75942	4.31661	4.23164	8.43541	8.54721	7.17378	7.28696	-1.26	-0.6578	261581_at
At2g40970	MYBC1, Homeodomain-like superfamily protein	9.25396	9.60199	8.7001	8.73525	8.22952	8.2699	7.27341	6.98719	-1.12	-0.7103	267077_at
At4g19160	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	10.6742	10.6359	9.70465	9.11845	9.46615	9.41378	7.87558	7.26821	-1.87	-1.2435	254561_at
At4g28350	Concanavalin A-like lectin protein kinase family protein	5.68226	5.34204	4.92318	4.53836	6.4752	6.40706	4.72376	4.59462	-1.78	-0.7814	253819_at
At4g23700	ATCHX17, CHX17, cation/H+ exchanger 17	10.8726	10.4411	9.14387	9.11454	8.5447	8.58393	6.84093	7.49667	-1.4	-1.5276	254215_at
At4g17670	Protein of unknown function (DUF581)	8.2283	8.77232	6.22268	5.68125	6.49966	6.15932	4.65378	4.63828	-1.68	-2.5483	245401_at
At3g62550	Adenine nucleotide alpha hydrolases-like superfamily protein	5.47867	5.51224	4.92812	4.80331	7.16986	7.45728	6.1726	6.0823	-1.19	-0.6297	251221_at
At3g19450	ATCAD4, CAD, CAD-C, CAD4, GroES-like zinc-binding alcohol dehydrogenase family protein	9.50891	9.58377	8.92518	8.9086	10.4782	10.4803	9.34584	9.73797	-0.94	-0.6295	258023_at
At1g20640	Plant regulator RWP-RK family protein	8.35509	7.98079	7.07653	7.0539	6.96213	7.0485	5.73221	5.905	-1.19	-1.1027	259540_at
At1g76350	Plant regulator RWP-RK family protein	6.01076	5.85192	4.86468	4.61708	5.31261	5.32527	4.62523	4.49482	-0.76	-1.1905	259888_at
At1g64590	NAD(P)-binding Rossmann-fold superfamily protein	12.2825	12.2259	10.3895	9.90895	7.26668	7.51596	5.67939	5.19756	-1.95	-2.105	261956_at

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Table 33. List of 182 genes in the "Rice-Arabidopsis N-regulatory Network" (RANN-Union).

LOC_Os11g47870	chitin-inducible gibberellin-responsive protein 2, putative, expressed
LOC_Os11g12000	NBS-LRR disease resistance protein, putative, expressed
LOC_Os03g48780	oxalate oxidase 2 precursor, putative, expressed
LOC_Os02g14170	peroxidase precursor, putative, expressed
LOC_Os01g52770	anther-specific proline-rich protein APG, putative, expressed
LOC_Os03g04310	DNA binding protein, putative, expressed
LOC_Os02g48900	aspartic proteinase nepenthesin-1 precursor, putative, expressed
LOC_Os02g02170	high affinity nitrate transporter, putative, expressed
LOC_Os12g05050	stem-specific protein TSJT1, putative, expressed
LOC_Os01g58240	peptidase/ subtilase, putative, expressed
LOC_Os01g44050	siroheme synthase, putative, expressed
LOC_Os01g33040	kinesin heavy chain, putative, expressed
LOC_Os07g35690	CRK6, putative, expressed
LOC_Os01g68650	plant-specific domain TIGR01615 family protein, expressed
LOC_Os06g46910	nucleic acid binding protein, putative, expressed
LOC_Os03g55590	DNA binding protein, putative, expressed
LOC_Os01g48960	glutamate synthase, chloroplast precursor, putative, expressed
LOC_Os09g36580	pathogenesis-related protein 5 precursor, putative, expressed
LOC_Os11g08210	NAC domain-containing protein 71, putative, expressed
LOC_Os01g72100	polcalcin Jun o 2, putative, expressed
LOC_Os04g55420	protein binding protein, putative, expressed
LOC_Os01g70170	transaldolase 2, putative, expressed
LOC_Os02g15340	NAC domain-containing protein 76, putative, expressed
LOC_Os09g37230	ATP binding protein, putative, expressed
LOC_Os03g01830	DEAD/DEAH box helicase, putative, expressed
LOC_Os03g11420	non-cyanogenic beta-glucosidase precursor, putative, expressed
LOC_Os07g22350	glucose-6-phosphate 1-dehydrogenase 2, chloroplast precursor, putative, expressed
LOC_Os06g29844	transparent testa 12 protein, putative, expressed
LOC_Os01g53260	OsWRKY23 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed
LOC_Os10g09850	EF-Hand containing protein, putative, expressed
LOC_Os01g02560	Ser/Thr receptor-like kinase, putative, expressed
LOC_Os02g52450	regulator of ribonuclease activity A, putative, expressed
LOC_Os01g20980	pectinesterase-1 precursor, putative, expressed
LOC_Os01g60770	alpha-expansin 10 precursor, putative, expressed
LOC_Os05g37140	ferredoxin-6, chloroplast precursor, putative, expressed
LOC_Os06g47750	phytosulfokine receptor precursor, putative, expressed
LOC_Os03g60260	ANT1, putative, expressed
LOC_Os02g40200	receptor-like protein kinase precursor, putative, expressed
LOC_Os03g13250	peptide transporter PTR2, putative, expressed
LOC_Os05g37170	transcription factor TGA6, putative, expressed
LOC_Os02g12420	receptor-like protein kinase precursor, putative, expressed

LOC_Os01g64020	transcription factor HBP-1b, putative, expressed
LOC_Os03g22050	CBL-interacting serine/threonine-protein kinase 15, putative, expressed
LOC_Os11g14140	protein kinase Kelch repeat:Kelch, putative, expressed
LOC_Os01g41820	cytochrome P450 72A1, putative, expressed
LOC_Os11g07930	retinol dehydrogenase 13, putative, expressed
LOC_Os08g01490	cytochrome P450 71C4, putative, expressed
LOC_Os04g42950	DNA binding protein, putative, expressed
LOC_Os12g15920	copper ion binding protein, putative, expressed
LOC_Os03g60810	lectin-like receptor kinase 7, putative, expressed
LOC_Os05g28740	universal stress protein, putative, expressed
LOC_Os03g44100	hydrolase-like protein, putative, expressed
LOC_Os09g31031	ubiquitin, putative, expressed
LOC_Os09g30454	OsWAK87 - OsWAK receptor-like protein kinase, expressed
LOC_Os08g08840	glucose-6-phosphate/phosphate translocator 2, chloroplast precursor, putative, expressed
LOC_Os01g34060	DNA binding protein, putative, expressed
LOC_Os01g11054	phosphoenolpyruvate carboxylase 1, putative, expressed
LOC_Os01g41810	cytochrome P450 72A1, putative, expressed
LOC_Os01g45274	carbonic anhydrase, chloroplast precursor, putative, expressed
LOC_Os08g39850	lipoxygenase 8, chloroplast precursor, putative, expressed
LOC_Os04g56790	TLD family protein, expressed
LOC_Os01g08110	flavonol-3-O-glycoside-7-O-glucosyltransferase 1, putative, expressed
LOC_Os03g51010	monoglyceride lipase, putative, expressed
LOC_Os12g29400	ABA-responsive protein, putative, expressed
LOC_Os01g04330	calmodulin-related protein 2, touch-induced, putative, expressed
LOC_Os05g46340	expressed protein
LOC_Os09g32260	ANAC079/ANAC080, putative, expressed
LOC_Os04g55970	DNA binding protein, putative, expressed
LOC_Os04g49460	ATP binding protein, putative, expressed
LOC_Os02g19890	stripe rust resistance protein Yr10, putative, expressed
LOC_Os04g37619	zeaxanthin epoxidase, chloroplast precursor, putative, expressed
LOC_Os01g12750	cytochrome P450 71A4, putative, expressed
LOC_Os04g56400	glutamine synthetase, chloroplast precursor, putative, expressed
LOC_Os03g03510	CIPK-like protein 1, putative, expressed
LOC_Os04g54830	expressed protein
LOC_Os01g24010	PDR5-like ABC transporter, putative, expressed
LOC_Os04g51450	brassinosteroid-regulated protein BRU1 precursor, putative, expressed
LOC_Os04g53830	leucoanthocyanidin reductase, putative, expressed
LOC_Os01g50460	seven-transmembrane-domain protein 1, putative, expressed
LOC_Os05g06970	peroxidase 1 precursor, putative, expressed
LOC_Os04g42520	adenine phosphoribosyltransferase 2, putative, expressed
LOC_Os04g01890	lectin-like protein kinase, putative
LOC_Os09g34160	resistance protein, putative, expressed

LOC_Os07g42250	strictosidine synthase 1 precursor, putative, expressed
LOC_Os01g43480	ATP binding protein, putative, expressed
LOC_Os06g50930	senescence-associated protein DIN1, putative, expressed
LOC_Os06g15370	peptide transporter PTR2, putative, expressed
LOC_Os03g11900	sugar transport protein 8, putative, expressed
LOC_Os09g39410	male sterility protein 2, putative, expressed
LOC_Os02g38230	component of high affinity nitrate transporter, putative, expressed
LOC_Os05g47540	phosphoethanolamine N-methyltransferase, putative, expressed
LOC_Os01g67030	dopamine beta-monooxygenase, putative, expressed
LOC_Os01g54340	plant-specific domain TIGR01615 family protein, expressed
LOC_Os03g21820	alpha-expansin 10 precursor, putative, expressed
LOC_Os05g47780	CHY zinc finger family protein, expressed
LOC_Os03g62240	expressed protein
LOC_Os01g70800	mitochondrial deoxynucleotide carrier, putative, expressed
LOC_Os01g48000	S-locus-like receptor protein kinase, putative, expressed
LOC_Os05g05620	glutathione S-transferase GSTF1, putative, expressed
LOC_Os01g47900	S-locus-like receptor protein kinase, putative, expressed
LOC_Os09g35030	sbCBF6, putative, expressed
LOC_Os01g43650	OsWRKY11 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed
LOC_Os08g06930	transposon protein, putative, unclassified, expressed
LOC_Os08g42550	AP2 domain containing protein, expressed
LOC_Os02g45010	expressed protein
LOC_Os02g02780	ATP binding protein, putative, expressed
LOC_Os04g48460	cytochrome P450 86A1, putative, expressed
LOC_Os03g25790	glycosyl hydrolases family 17 protein, expressed
LOC_Os03g18740	sex determination protein tasselseed-2, putative, expressed
LOC_Os09g29940	auxin-independent growth promoter, putative, expressed
LOC_Os01g54480	serine/threonine-protein kinase TNNI3K, putative, expressed
LOC_Os01g17390	cyclin-like F-box, putative, expressed
LOC_Os01g70520	beta-glucosidase homolog precursor, putative, expressed
LOC_Os10g42299	mitochondrial carnitine/acylcarnitine carrier-like protein, putative, expressed
LOC_Os07g35520	glucan endo-1,3-beta-glucosidase 3 precursor, putative, expressed
LOC_Os12g39120	catalytic/ protein phosphatase type 2C, putative, expressed
LOC_Os06g48160	xyloglucan endotransglucosylase/hydrolase protein 23 precursor, putative, expressed
LOC_Os02g16940	peptidase/ subtilase, putative, expressed
LOC_Os11g42200	laccase LAC2-1, putative, expressed
LOC_Os09g25070	OsWRKY62 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed
LOC_Os08g02230	FAD binding domain containing protein, putative, expressed
LOC_Os12g37260	lipoxygenase 2.1, chloroplast precursor, putative, expressed
LOC_Os01g61044	amino acid-polyamine transporter, putative, expressed
LOC_Os02g20360	tyrosine aminotransferase, putative, expressed
LOC_Os03g13050	ACI19, putative, expressed

LOC_Os04g54180	serine/threonine-protein kinase receptor precursor, putative
LOC_Os06g41100	TGA10 transcription factor, putative, expressed
LOC_Os01g25484	ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed
LOC_Os03g41330	seed specific protein Bn15D17A, putative, expressed
LOC_Os08g08960	germin-like protein subfamily 1 member 11 precursor, putative, expressed
LOC_Os04g53994	ATP binding protein, putative, expressed
LOC_Os02g44230	expressed protein
LOC_Os02g54730	amino acid permease, putative, expressed
LOC_Os01g64000	ABA response element binding factor, putative, expressed
LOC_Os10g42130	ANAC071, putative, expressed
LOC_Os10g38580	glutathione S-transferase GSTU6, putative, expressed
LOC_Os07g02800	myb-like DNA-binding domain, SHAQKYF class family protein, expressed
LOC_Os03g57120	ferredoxin--NADP reductase, root isozyme, chloroplast precursor, putative, expressed
LOC_Os01g66250	S-locus-like receptor protein kinase, putative, expressed
LOC_Os03g38800	mitochondrial protein, putative, expressed
LOC_Os04g56060	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed
LOC_Os12g02640	cytochrome P450 72A1, putative, expressed
LOC_Os02g36590	expressed protein
LOC_Os09g29660	ATP-binding cassette sub-family G member 2, putative, expressed
LOC_Os01g10440	xylosyltransferase oxt, putative, expressed
LOC_Os08g31980	trehalose 6-phosphate synthase, putative, expressed
LOC_Os03g52040	serine carboxypeptidase 1 precursor, putative, expressed
LOC_Os07g38800	lectin-like receptor kinase 7, putative, expressed
LOC_Os04g42740	serine/threonine-protein kinase receptor precursor, putative
LOC_Os01g50100	multidrug resistance protein 4, putative, expressed
LOC_Os04g56930	beta-fructofuranosidase, insoluble isoenzyme 5, putative, expressed
LOC_Os06g03830	retinol dehydrogenase 14, putative, expressed
LOC_Os07g32060	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
LOC_Os10g41250	glycoprotein, putative, expressed
LOC_Os07g35340	receptor-like serine-threonine protein kinase, putative, expressed
LOC_Os06g37750	S-locus-like receptor protein kinase, putative, expressed
LOC_Os04g34240	histone H3, putative, expressed
LOC_Os10g04674	disease resistance protein RPM1, putative, expressed
LOC_Os03g48030	HPP, putative, expressed
LOC_Os08g37370	mitochondrial 2-oxoglutarate/malate carrier protein, putative, expressed
LOC_Os05g31740	cytochrome P450 86A2, putative, expressed
LOC_Os02g53130	nitrate reductase, putative, expressed
LOC_Os01g06640	DNA binding protein, putative, expressed
LOC_Os11g43520	OsGrx_C17 - glutaredoxin subgroup III, expressed
LOC_Os05g08750	cold-induced glucosyl transferase, putative, expressed
LOC_Os05g48700	gibberellin 2-beta-dioxygenase, putative, expressed

LOC_Os01g64120	ferredoxin-6, chloroplast precursor, putative, expressed
LOC_Os03g17300	protein kinase, putative, expressed
LOC_Os08g05570	monodehydroascorbate reductase, chloroplast precursor, putative, expressed
LOC_Os04g54190	serine/threonine-protein kinase receptor precursor, putative, expressed
LOC_Os06g06400	NBS-LRR disease resistance protein, putative, expressed
LOC_Os12g16010	sex determination protein tasselseed-2, putative, expressed
LOC_Os03g06680	plant-specific domain TIGR01615 family protein, expressed
LOC_Os07g47230	receptor-like serine-threonine protein kinase, putative, expressed
LOC_Os01g27140	glutaredoxin, putative, expressed
LOC_Os11g29400	6-phosphogluconate dehydrogenase, decarboxylating, putative, expressed
LOC_Os01g43370	expressed protein
LOC_Os02g51910	cytokinin-O-glucosyltransferase 2, putative, expressed
LOC_Os12g26290	alpha-DOX2, putative, expressed
LOC_Os01g04620	expressed protein
LOC_Os12g10660	salt tolerance-like protein, putative, expressed
LOC_Os09g23350	ATTPS6, putative, expressed

Table 34. List of the transcription factors in the "Arabidopsis-Rice N-regulatory Network (ARNN-Union)" from Figure 51. For each step of the rice core translational network, transcription factors were rank based on their number of connections.

Arabidopsis Gene Locus	Arabidopsis Gene Description	Number of directed connections			
		Arabidopsis Only N-regulatory Network (AONN)	Arabidopsis-Rice N-regulatory Network (ARNN-BLAST)	Arabidopsis-Rice N-regulatory Network (ARNN-OrthoMCL)	Arabidopsis-Rice N-regulatory Network (ARNN-Union)
At4g37180	Homeodomain-like superfamily protein (HHO5)	940	65	20	75
At1g13300	HRS1, myb-like transcription factor family protein	896	45		45
At2g45210	TGA1, bZIP transcription factor family protein	591	41		41
At4g18170	ATWRKY28, WRKY28, WRKY DNA-binding protein 28	902	33	11	39
At1g68670	myb-like transcription factor family protein (HHO2)	934	36		36
At1g31050	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	524	35		35
At3g56850	AREB3, DPBF3, ABA-responsive element binding protein 3	721	31		31
At5g10030	OBF4, TGA4, TGACG motif-binding factor 4	613	25		25
At1g22070	TGA3, TGA1A-related gene 3	479	21		21
At1g54320	ASML1, ATWRI1, WRI, WRI1, Integrase-type DNA-binding superfamily protein	696	20		20
At1g25550	myb-like transcription factor family protein (HHO3)	861	19		19
At3g20840	PLT1, Integrase-type DNA-binding superfamily protein	590	18		18
At1g77920	bZIP transcription factor family protein (TGA7)	436	16		16
At2g43000	emc042, NAC042, NAC domain containing protein 42	317	16		16
At3g16150	Homeodomain-like superfamily protein	827	16		16
At3g25710	ATAIG1, BHLH32, TMO5, basic helix-loop-helix 32	287	16		16
At5g17260	emc086, NAC086, NAC domain containing protein 86	438	15		15
At5g60890	ATMYB34, ATR1, MYB34, myb domain protein 34	927	15		15
At1g63030	ddf2, Integrase-type DNA-binding superfamily protein	570	14		14
At2g28550	RAP2.7, TOE1, related to AP2.7	728	14		14
At1g76420	ANAC031, CUC3, NAC138, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	414	13		13
At2g47260	ATWRKY23, WRKY23, WRKY DNA-binding protein 23	305	12		12
At5g61420	AtMYB28, HAG1, MYB28, PMG1, myb domain protein 28	576	11		11
At2g18060	ANAC037, VND1, vascular related NAC-domain protein 1	335	10		10
At4g31800	ATWRKY18, WRKY18, WRKY DNA-binding protein 18	183	5		5
At1g26660	ATMYB86, MYB86, myb domain protein 86	238	3		3
At3g26744	ATICE1, ICE1, SCRM, basic helix-loop-helix (bHLH) DNA-binding superfamily protein	286	2		2
At1g10510	AIL6, PLT3, AINTEGUMENTA-like 6	123	2		2

Table 35. Quantitative real-time PCR primers used in this study.

Primer	**Sequence 5´- 3´**	**SEQ ID NO.**
OsActin-F	CCGCCAGAGAGGAAGTACAG	2
OsActin-R	AAGCACTTCCTGTGGACGAT	3
LOC_Os01g48960-F	TGGAGTGCCAAACATGAAGA	4
LOC_Os01g48960-R	AGGAACTCCATGGCAAAATG	5
LOC_Os03g57120-F	CTGAAACTGGCAAGGAGGAC	6
LOC_Os03g57120-R	GTAGGTAGCCACGGAATGGA	7
LOC_Os01g44050-F	TCAACACTGCCATCTCTTGC	8
LOC_Os01g44050-R	GAATCGATCCAAAAGGGTGA	9
LOC_Os02g53130-F	TACTGGTGCTGGTGCTTCTG	10
LOC_Os02g53130-R	ACCCTGAACCAGCAGTTGTT	11
AtClathrin-F	AGCATACACTGCGTGCAAAG	12
AtClathrin-R	TCGCCTGTGTCACATATCTC	13
At4g35770-F	CTAAGACAGGTCTCGTCCCA	14
At4g35770-R	AGCAGTGAGAAGATCAGTT	15
At5g50200-F	CAATCTCTTCAGCGTTCAGG	16
At5g50200-R	GACAAAGAAGACGACAAGAGC	17
At1g77760-F	GCCTATGATTCAGTTTGCG	18
At1g77760-R	AGCTCTGATAAACAACAACTAT	19
At5g53460-F	ACAGGGAAAAAGGTTGC	20
At5g53460-R	GTCATAAGATCAACCCGC	21

Table 36. Transcription factors that regulate the nitrogen-responsive gene network conserved in Arabidopsis and Maize. Orthology was determined using the one-to-many BLAST mapping function on VirtualPlant with an e-value cutoff of 1E-20.

Arabidopsis TF ID	Edge Count	Arabidopsis Alias	**Ortholog Mapping.** One-to-many (Respond to Nitrogen in Maize)
AT5G44190 (SEQ ID NO. 22)	118	ATGLK2, GLK2, GPRI2	GRMZM2G026833 (SEQ ID NO. 37) GRMZM2G087804 (SEQ ID NO. 38) GRMZM2G409974 (SEQ ID NO. 39)
AT2G20570 (SEQ ID NO. 23)	118	ATGLK1, GLK1, GPRI1	GRMZM2G026833 (SEQ ID NO. 37) GRMZM2G087804 (SEQ ID NO. 38)
AT1G01060 (SEQ ID NO. 24)	120	LHY, LHY1	GRMZM2G474769 (SEQ ID NO. 40) GRMZM2G145041 (SEQ ID NO. 41) GRMZM2G181030 (SEQ ID NO. 42) GRMZM2G014902 (SEQ ID NO. 43) GRMZM2G170148 (SEQ ID NO. 44)
AT2G46830 (SEQ ID NO. 25)	120	CCA1	
AT5G24800 (SEQ ID NO. 26)	82	ATBZIP9, BZIP9, BZO2H2	GRMZM2G103647 (SEQ ID NO. 45) GRMZM2G098904 (SEQ ID NO. 46)
AT2G22430 (SEQ ID NO. 27)	78	ATHB6, HB6	GRMZM2G122076 (SEQ ID NO. 47) GRMZM2G041127 (SEQ ID NO. 48)
AT1G68840 (SEQ ID NO. 28)	78	EDF2, RAP2.8, RAV2, TEM2	GRMZM2G018336 (SEQ ID NO. 49)
AT1G53910 (SEQ ID NO. 29)	78	RAP2.12	GRMZM2G110333 (SEQ ID NO. 50) GRMZM2G148333 (SEQ ID NO. 51)
AT1G80840 (SEQ ID NO. 30)	25	ATWRKY40, WRKY40	GRMZM2G120320 (SEQ ID NO. 52)
AT3G04070	23	ANAC047, NAC047	GRMZM2G176677 (SEQ ID

(SEQ ID NO. 31)			NO. 53) GRMZM2G031001 (SEQ ID NO. 54) GRMZM2G123667 (SEQ ID NO. 55) GRMZM2G054252 (SEQ ID NO. 56) GRMZM2G167018 (SEQ ID NO. 57) GRMZM2G127379 (SEQ ID NO. 58) GRMZM2G180328 (SEQ ID NO. 59) GRMZM2G159500 (SEQ ID NO. 60) GRMZM2G104400 (SEQ ID NO. 61)
AT1G77450 (SEQ ID NO. 32)	21	ANAC032, NAC032	
AT1G01720 (SEQ ID NO. 33)	18	ANAC002, ATAF1	
AT3G01560 (SEQ ID NO. 34)	11	TriHelix family TF	GRMZM2G025215 (SEQ ID NO. 62)
AT2G38470 (SEQ ID NO. 35)	22	ATWRKY33, WRKY33	GRMZM2G012724 (SEQ ID NO. 63) GRMZM2G054125 (SEQ ID NO. 64)
AT3G60030 (SEQ ID NO. 36)	19	SPL12	GRMZM2G169270 (SEQ ID NO. 65) GRMZM2G081127 (SEQ ID NO. 66) GRMZM2G133646 (SEQ ID NO. 67) GRMZM2G101499 (SEQ ID NO. 68)

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15. EXAMPLE 10

[00505] The study described in Example 9 herein of a cross-species N-regulated gene network conserved across Arabidopsis and Rice (ARNN), identified HHO5 (At4g37180) as the top regulatory transcription factor (TF) hub with the highest number of target genes in this network (Arabidopsis Rice Nitrogen Regulatory Network, ARNN) (see also Obertello et al., 2015, Plant Physiology, 168: 1830-1843). Among the predicted targets of HHO5 are key genes in N-assimilation (e.g. nitrate reductase (NR), nitrite reductase (NiR), glutamine synthetase (GLN) and glutamate synthtase (GLT). It was thus found that HHO5 is a key TF regulating N-assimilation and Nitrogen Use Efficiency (NUE) in plants. The present example experimentally proves this finding. It is shown that Arabidopsis hho5 mutant plants (CS876691) (see Fig. 53) are defective in N-assimilation and NUE based on three independent lines of evidence:

[00506] **1**) hho5 mutants are defective in the expression of HHO5, and in the regulation of the HHO5 targets predicted in the ARNN network, including key genes involved in the assimilation of nitrate into organic form (e.g., glutamine) (see Fig. 54).

[00507] **2**) hho5 mutants show a N-dependent defect in root growth and shoot biomass (see Figs. 56 and 57).

[00508] **3**) hho5 mutants have less nitrogen content in seeds, compared to wild type (see Fig. 58).

[00509] Together these results show that HHO5 plays an important role mediating NUE, including N assimilation, N-dependent root development and shoot biomass, and N storage in seed. These experimental findings for HHO5 confirm that the N-regulatory networks conserved between Arabidopsis and Rice, as described in Example 9 and Obertello et al., 2015, Plant Physiology, 168: 1830-1843, can be used to identify TFs of importance to N-use efficiency and accurately predict their network target.

15.1. MATERIALS AND METHODS

[00510] In order to test the role of HHO family members in mediating nitrogen use efficiency (NUE) in plants, T-DNA mutants obtained from the Arabidopsis Stock Center (Ohio) were analyzed in a N-treatment context. CS876991 has a T-DNA insertion in exon 5 of the HHO5 gene. SALK_077802 has a T-DNA insertion in exon 1 of the HHO5 gene (see Figure 53). *hho5* homozygous lines (CS876991) were obtained by self-fertilization after two backcrossing to wild-type plants (Col0) to eliminate potential undesired insertions. CS876991 mutant plants were tested in the present example. SALK_077802 mutant plants can also be tested suing the same or similar methodology.

[00511] Briefly, as described in Obertello et al., 2015, *Arabidopsis thaliana* and rice (*Oryza sativa* ssp. *japonica*) 13 days-old seedlings were transiently treated for 2 h at the start of their light cycle by adding nitrogen (N) at a final concentration of 20 mM KNO_3 and 20 mM NH_4NO_3. Control plants were treated with KCl at a final concentration of 20 mM. After treatment, roots and shoots were harvested separately using a blade, and immediately submerged into liquid nitrogen and stored at -80°C prior to RNA extraction. RNA was isolated from roots and shoots with the TRIzol reagent following

manufacturer´s protocols (Invitrogen Life Technologies. Carlsbad, CA, USA). cDNA synthesis and array hybridization were performed according to the instructions provided by Affymetrix. The Affymetrix microarray expression data has been deposited in the Gene Expression Omnibus (GEO) database under accession number GSE38102. Data normalization was performed using the RMA (Robust Microarray Analysis) method in the Bioconductor package in R statistical environment. A two-way Analysis of Variance (ANOVA) was performed using a custom-made function in R to identify probes that were differentially expressed following N treatment. The *p*-values for the model were then corrected for multiple hypotheses testing using FDR correction at 5% (Benjamini and Hochberg, 1995). The probes passing the cut-off ($p \leq 0.05$) for the model and, N treatment or interaction of N treatment and tissue, were deemed significant. A Tukey's HSD post-hoc analysis was performed on significant probes to determine the tissue specificity of N-regulation at *p*-value cut-off ≤ 0.05 and |fold-change| ≥ 1.5-fold ($\log_2$ of 1.5 is 0.585). Probes mapping to more than one gene were disregarded. Finally, a set of 451 N-regulated genes differentially expressed in Rice and 1,417 N-regulated genes differentially expressed in Arabidopsis were obtained.

[00512] RT-PCR measurements were obtained for HHO5 and a set of selected HHO5 target genes in the N-assimilation pathway in hho mutant plants (see Figures 54A-D). These experiments were done using gene-specific primers and 5x HOT FIREPol EvaGreen® qPCR Mix Plus (NO ROX) kit (Solis BioDyne, Estonia) (see Table 37 below). Relative expression levels of tested genes were normalized to expression levels of the housekeeping actin genes (At3g18780/At1g49240 (ACT2/8). Values are the mean ±SE from three biological replicates. Asterisks denote significant difference between Col0 and *hho5* mutant line according to 1 way-ANOVA (**p<0.001, *p<0.05).

[00513] Table 37: List of used primers

Gene ID	Right primer (seq. 5´ - 3´)	Left primer (seq. 5´ - 3´)
At1g77760 (NIA1)	GCCTATGATTCAGTTTGCG (SEQ ID NO: 74)	AGCTCTGATAAACAACAACTAT (SEQ ID NO: 75)
At5g53460 (GLT1)	ACAGGGAAAAAGGTTGC (SEQ ID NO: 76)	GTCATAAGATCAACCCGC (SEQ ID NO: 77)
At3g18780/At1g49240	AACGACCTTAATCTTCATGCTGC	GGTAACATTGTGCTCAGTGGTGG

(ACT2/8)	(SEQ ID NO: 78)	(SEQ ID NO: 79)
At2g15620 (NiR1)	TGTTCGTGTCACGGAG (SEQ ID NO: 80)	AAACCCAAAATTATGGGCA (SEQ ID NO: 81)
At4g37180 (HHO5)	TTGTCGGATGCAGCGGATGCTTAC (SEQ ID NO: 82)	TTGGAGGGCCACAAGTTGCTACAC (SEQ ID NO: 83)

Table 38: Genotyping primers

Gene ID	Genotyping primers (Seq 5'a 3')
CS876991 At4g37180 (HHO5)	RP : TGATGCTCTTCATAGGCTTGG (SEQ ID NO: 84)
	LP : G AACATGCAAATCTCGTGGAAG (SEQ ID NO: 85)
	LB3: TAGCATCTGAATTTCATAACCAATCTCGATACAC (SEQ ID NO: 86)

[00514] Regulatory interactions were predicted between a TF and its putative target as follows: Cis-motifs in promoter regions were searched using the DNA pattern matching tool from the RSA tools – Plants server with default parameters (van Helden, 2003) over the upstream promoter sequences (1kb) in Arabidopsis. HRS1-HHO family member targets were predicted similarly and cis-motifs for the TF family members were obtained from Medici et al. (Medici et al., 2015). Finally, nodes are connected with long arrows indicating positive correlation among TF-target expression data and the presence of HHO cis-motif in the promoter of their putative targets (see Figure 54E). Network visualization was created using Cytoscape (v2.8.3) software (Shannon et al., 2003) (see Figure 54E).

[00515] Experimentation was performed to test if hho5 mutant plants have altered growth when grown in the presence of increasing levels of N sources, compared to wild-type (Col-0) plants (see Figure 55). Briefly, wild-type (Col0) and *hho5* homozygous mutant (stock #CS876991 on the Arabidopsis Stock Center) plants (HHO5 absence-of-function) seeds were vernalized in the dark at 4°C for 2 days to synchronize germination. Seeds were surface-sterilized and then transferred to vertical Petri plates containing

sterile Murashige and Skoog basal salts with 3 mM sucrose, 0.8% BactoAgar at pH 5.7 supplemented with three different concentrations of N: KNO_3 or NH_4NO_3 (0.1, 1 or 10 mM). In addition, we included a control treatment where both plant lines were mock-treated on MS without any N source but supplemented with KCl in the same three concentrations. Plants were grown for 10 or 18 days under long-day (16 h light: 8 h dark) growth conditions, at light intensity of 50 $\mu E.s^{-1}.m^{-2}$ and at 22°C. Knowing that N is an essential macronutrient and that can modulate primary root growth, every three days primary root length was measured on the vertical plates.

[00516] Primary root growth was assayed over time when hho5 plants (compared to wild-type Col-0) were grown on MS supplemented with 0.1, 1 or 10 mM KNO_3 (see Figure 56A). Control plants were grown on MS supplemented with 0.1, 1 or 10 mM KCl. Primary root length was measured every three days. Primary root length of wild-type and *hho5* mutant plants was assessed at the end of the experiment (day 10) (see Figure 56B).

[00517] Primary root growth over time of Arabidopsis plants (hho5 mutants vs wild-type control Col-0) on MS supplemented with 0.1, 1 or 10 mM NH_4NO_3 was assayed over time (see Figure 57A). Control plants were grown on MS supplemented with 0.1, 1 or 10 mM KCl. Primary root length was measured every three days. Primary root length of wild-type and *hho5* mutant plants was assessed at the end of the experiment (day 10) (see Figure 57B).

[00518] Nitrogen assimilation was estimated comparing total N content in Col0 (wild-type) and *hho5* mutant seeds by the Kjeldahl method and expressed as mg N 100 mg^{-1} dry weight (performed by Laboratorio de Análisis Clínicos y Biología Molecular, Laboratorios Fox (Venado Tuerto, Santa Fe, Argentina) (see Figure 58).

[00519] To identify HHO5 orthologs across many more plant species, recent phylogenetic analysis of the 33 fully sequenced plant genomes was exploited (Delaux et al, 2014). The HHO5 orthology analysis was expanded to include 33 fully sequenced plant genomes (Delaux et al, 2014) and the orthologs of HHO5 across all these genomes were identified using BigPlant phylogenetic pipeline (Lee et al, 2011). The two Arabidopsis genes (HHO5 and HHO6) and three Rice genes (LOC_Os07g02800, LOC_Os03g55590 and LOC_Os12g39640) identified as orthologs in Example 9 (Obertello et al 2015), belong to a gene family that includes 104 genes across the 33

plant genomes (see Figure 59 and Table 39). Due to multiple gene and genome duplication events in the history of plant evolution, this gene family includes multiple orthologs of HHO5 in their genomes.

15.2. RESULTS

[00520] HHO5 is predicted to be the top TF hub in a N-regulatory network conserved between Arabidopsis and Rice (Obertello et al., 2015, Plant Physiology, 168: 1830-1843, Table S4). Moreover, the cross-species network predicted that HHO5 regulates key genes in the N-assimilatory pathway including; nitrate transporters (NRT3.1), nitrate reductase (NIA1), nitrite reductase (NiR), glutamine synthetase (GLN), and glutamate synthase (GLT). These network connections thus predict that HHO5 is a master transcription factor (TF) hub controlling genes involved in nitrogen use efficiency. To validate this finding, gene expression and N-use phenotype studies were peformed on hho5, a mutant defective in the expression of the HHO5 gene. The results described below confirm that an hho5 mutant is impaired in Nitrogen Use Efficiency.

15.2.1. Hho5 mutant is impaired in the regulation of genes involved in N-assimilation.

[00521] In order to test the role of HHO5 in mediating nitrogen use efficiency (NUE) in plants, it was determined whether a T-DNA mutant obtained from the Arabidopsis Stock Center (Ohio), has altered root growth or biomass when grown on various levels of nitrogen, compared to wild-type plants.

[00522] First, it was shown that the *hho5* mutant plants in the HHO5 gene (At4g37180), had no expression of HHO5 mRNA, thus hho5 (CS876691) is a bonafide mutant in HHO5 (Fig. 54A). Moreover, the expression of HHO5 gene targets predicted by the Arabidopsis-Rice conserved regulatory network (Fig. 54E), were also reduced in the hho5 mutants (Fig. 54 B-D). These misregulated HHO5 target genes in the hho5 mutant include key genes in N-assimilation, such as genes that reduce nitrate to ammonia (NIA1 (nitrate reductase), NiR (nitrite reductase), and genes that assimilate ammonia into glutamine (GLN (glutamine synthetase)/GLT1 (glutamate synthase), and

the organic-N products of N-assimilation that are used in all biosynthetic reactions including DNA, RNA, and chlorophyll (Fig. 54 B, C, D, E)).

15.2.2. The hho5 mutant shows an impairment in root growth and shoot biomass that is dependent on the N-concentration.

[00523] Since the hho5 mutant has lower expression of the N-assimilation genes (Fig. 54), it was next determined whether the hho5 mutant was impaired in nitrogen use efficiency. To do this, wild-type (Col0) and *hho5* homozygous mutant plants (HHO5 absence-of-function) were grown on vertical Petri plates for 15 days with MS media supplemented with three different concentrations of N: KNO_3 or NH_4NO_3 (0.1, 1 or 10 mM) (Fig. 55). In addition, a control treatment was included, in which both plant lines were mock-treated on MS without any N source but supplemented with KCl in the same three concentrations. Knowing that N is an essential macronutrient that can modulate primary root growth, primary root length was measured every three days on the vertical plates.

[00524] Preliminary results showed that hho5 mutant and Col0 plants respond equally to the lowest concentration of N (0.1 mM) (Fig. 56A). However, at higher N concentrations (1mM and 10mM), *hho5* plants have a defect in root growth compared to Col0 plants. For example, at 1 mM KNO_3 *hho5* primary root length is statistically different (based on ANOVA) to Col-0 roots (Fig. 56A). *hho5* roots were shorter than Col0 roots when N was supplied at 1 and 10mM. The same phenotype was observed when N was supplied as ammonium nitrate (KNO_3 and NH_4NO_3) (Fig. 56A and 57A). It was also determined that shoot dry weight is lower in the hho5 mutants, compared to wild-type (Fig. 56B and Fig. 57B).

15.2.3. The hho5 mutant shows an impairment in root growth and shoot biomass that is dependent on the N-concentration.

[00525] Since seeds are considered the ultimate storage organ for nitrogen metabolites, the total N content was quantified in seeds of plants grown in soil by the Kjeldahl method. It was found that *hho5* seeds had less total N content compared to wild-type plants (Fig. 58). This finding indicates that the hho5 mutants have a deficiency in N-

assimilation and N-storage in seeds, compared to wild-type plants (Col0). Significance of results are indicated by p values in the accompanying figures.

[00526] Given the role of HHO5 in nitrogen use efficiency, the ectopic expression of HHO5 or orthologs thereof by transgenic plants are going to have increased nitrogen use efficiency. Also, given the role of HHO5 in nitrogen use efficiency, HHO5 orthology analysis of 33 fully sequenced plant genomes was conducted and orthologs described in Table 39 were identified.

Table 39. HHO5 orthologous genes include 104 members from 33 plant species.

Species	Gene
Citrus clementina	Ciclev10028556m
Citrus sinensis	orange1.1g015403m
Linum usitatissimum	Lus10023857
Linum usitatissimum	Lus10020995
Linum usitatissimum	Lus10012056
Linum usitatissimum	Lus10027927
Populus trichocarpa	Potri.004G144800
Populus trichocarpa	Potri.009G106600
Ricinus communis	29780.m001324
Ricinus communis	29788.m000327
Manihot esculenta	cassava4.1_030151m
Manihot esculenta	cassava4.1_009052m
Cucumis sativus	Cucsa.220080
Cucumis sativus	Cucsa.110080
Glycine max	Glyma07g29490
Glycine max	Glyma20g01260
Phaseolus vulgaris	Phvul.003G012400
Glycine max	Glyma07g33130
Glycine max	Glyma02g15320
Phaseolus vulgaris	Phvul.003G293800

Medicago truncatula	Medtr4g086840
Malus domestica	MDP0000124687
Malus domestica	MDP0000265555
Prunus persica	ppa006812m
Fragaria vesca	mrna31899
Gossypium raimondii	Gorai.008G026300
Theobroma cacao	Thecc1EG006998t1
Gossypium raimondii	Gorai.012G150500
Gossypium raimondii	Gorai.013G040600
Carica papaya	evm.model.supercontig_62.51
Eucalyptus grandis	Eucgr.G01503
Vitis vinifera	GSVIVT01031804001
Solanum tuberosum	PGSC0003DMP400044726
Solanum lycopersicum	Solyc01g108300.2
Populus trichocarpa	Potri.007G039400
Populus trichocarpa	Potri.005G134600
Manihot esculenta	cassava4.1_010485m
Manihot esculenta	cassava4.1_009666m
Ricinus communis	29676.m001636
Brassica rapa	Bra010581
Brassica rapa	Bra017795
Arabidopsis thaliana	AT4G37180.2
Arabidopsis lyrata	490936
Capsella rubella	Carubv10004940m
Thellungiella halophila	Thhalv10025593m
Brassica rapa	Bra011720
Medicago truncatula	Medtr5g017980
Phaseolus vulgaris	Phvul.002G021400
Glycine max	Glyma01g39040
Glycine max	Glyma11g06230

Glycine max	Glyma05g09690
Glycine max	Glyma17g20520.2
Phaseolus vulgaris	Phvul.003G246900
Gossypium raimondii	Gorai.007G053100
Gossypium raimondii	Gorai.003G021300
Theobroma cacao	Thecc1EG000558t1
Gossypium raimondii	Gorai.008G073300
Eucalyptus grandis	Eucgr.H01993
Cucumis sativus	Cucsa.102260
Malus domestica	MDP0000200243
Prunus persica	ppa006879m
Fragaria vesca	mrna24094
Linum usitatissimum	Lus10019639
Linum usitatissimum	Lus10009334
Vitis vinifera	GSVIVT01003551001
Carica papaya	evm.model.supercontig_6.397
Solanum lycopersicum	Solyc02g090400.2
Solanum tuberosum	PGSC0003DMP400017819
Brassica rapa	Bra018794
Brassica rapa	Bra040662
Thellungiella halophila	Thhalv10011605m
Arabidopsis thaliana	AT1G49560
Arabidopsis lyrata	474091
Capsella rubella	Carubv10009677m
Setaria italica	Si030286m
Sorghum bicolor	Sb02g001600
Zea mays	GRMZM2G173882_T01
Oryza sativa	LOC_Os07g02800.3
Brachypodium disctachyon	Bradi1g07630
Setaria italica	Si036412m

Sorghum bicolor	Sb01g007130
Zea mays	GRMZM2G124540_T01
Zea mays	GRMZM2G171468_T01
Oryza sativa	LOC_Os03g55590
Zea mays	GRMZM2G100176_T02
Oryza sativa	LOC_Os12g39640
Zea mays	AC234520.1_FGT003
Setaria italica	Si022287m
Sorghum bicolor	Sb08g019720
Brachypodium disctachyon	Bradi4g03160
Brachypodium disctachyon	Bradi1g58830
Theobroma cacao	Thecc1EG019009t1
Gossypium raimondii	Gorai.001G206600
Manihot esculenta	cassava4.1_027101m
Ricinus communis	29790.m000831
Carica papaya	evm.model.supercontig_14.231
Carica papaya	evm.model.supercontig_14.230
Citrus sinensis	orange1.1g048452m
Citrus clementina	Ciclev10026557m
Eucalyptus grandis	Eucgr.I01178
Aquilegia coerulea	Aquilegia coerulea_010_00298
Physcomitrella patens	Pp1s166_107V6
Physcomitrella patens	Pp1s24_189V6
Physcomitrella patens	Pp1s83_100V6

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16. EQUIVALENTS

[00527] Although the invention is described in detail with reference to specific embodiments thereof, it will be understood that variations which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

[00528] All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference in their entireties.

WHAT IS CLAIMED IS:

1. A transgenic plant having a heterologous gene construct comprising a polynucleotide encoding HHO5 and/or WRKY28, wherein the transgenic plant exhibits increased nitrogen use efficiency (NUE).

2. A transgenic plant that ectopically expresses one or more transcription factor genes conserved in Arabidopsis and Maize, wherein said one or more transcription factor genes comprises a polynucleotide that encodes AT5G44190, AT2G20570, AT1G01060, AT2G46830, AT5G24800, AT2G22430, AT1G68840, AT1G53910, AT1G80840, AT3G04070, AT1G77450, AT1G01720, AT3G01560, AT2G38470, AT3G60030, and/or AT5G49450, and wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

3. A transgenic plant that ectopically expresses one or more transcription factor genes conserved in Arabidopsis and Maize, wherein said one or more transcription factor genes comprises a polynucleotide that encodes GRMZM2G026833, GRMZM2G087804, GRMZM2G409974, GRMZM2G026833, GRMZM2G087804, GRMZM2G474769, GRMZM2G145041, GRMZM2G181030, GRMZM2G014902, GRMZM2G170148, GRMZM2G103647, GRMZM2G098904, GRMZM2G122076, GRMZM2G041127, GRMZM2G018336, GRMZM2G110333, GRMZM2G148333, GRMZM2G120320, GRMZM2G176677, GRMZM2G031001, GRMZM2G123667, GRMZM2G054252, GRMZM2G167018, GRMZM2G127379, GRMZM2G180328, GRMZM2G159500, GRMZM2G104400, GRMZM2G025215, GRMZM2G012724, GRMZM2G054125, GRMZM2G169270, GRMZM2G081127, GRMZM2G133646, GRMZM2G101499, GRMZM2G093020, , GRMZM2G361611, GRMZM2G444748, and/or GRMZM2G092137, and wherein said transgenic plant exhibits increased nitrogen use efficiency (NUE).

4. The transgenic plant of any one of claims 1-3, wherein the plant is species of woody, ornamental, decorative, crop, cereal, fruit, or vegetable.

5. The transgenic plant of any one of claims 1-3, wherein said plant is a species of one of the following genuses: *Acorus, Aegilops, Allium, Amborella, Antirrhinum, Apium, Arabidopsis,*

Arachis, Beta, Betula, Brassica, Capsicum, Ceratopteris, Citrus, Cryptomeria, Cycas, Descurainia, Eschscholzia, Eucalyptus, Glycine, Gossypium, Hedyotis, Helianthus, Hordeum, Ipomoea, Lactuca, Linum, Liriodendron, Lotus, Lupinus, Lycopersicon, Medicago, Mesembryanthemum, Nicotiana, Nuphar, Pennisetum, Persea, Phaseolus, Physcomitrella, Picea, Pinus, Poncirus, Populus, Prunus, Robinia, Rosa, Saccharum, Schedonorus, Secale, Sesamum, Solanum, Sorghum, Stevia, Thellungiella, Theobroma, Triphysaria, Triticum, Vitis, Zea, or *Zinnia*.

6. A transgenic plant-derived commercial product, which is derived from a transgenic plant according to any one of claims 1-5.

7. The transgenic plant-derived commercial product of claim 6, wherein said transgenic plant is a tree, and said commercial product is pulp, paper, a paper product, or lumber.

8. The transgenic plant-derived commercial product of claim 6, wherein said transgenic plant is tobacco, and said commercial product is a cigarette, cigar, or chewing tobacco.

9. The transgenic plant-derived commercial product of claim 6, wherein said transgenic plant is a crop, and said commercial product is a fruit or vegetable.

10. The transgenic plant-derived commercial product of claim 6, wherein said transgenic plant is a grain, and said commercial product is bread, flour, cereal, oat meal, or rice.

11. The transgenic plant-derived commercial product of claim 6, wherein said commercial product is a biofuel or plant oil.

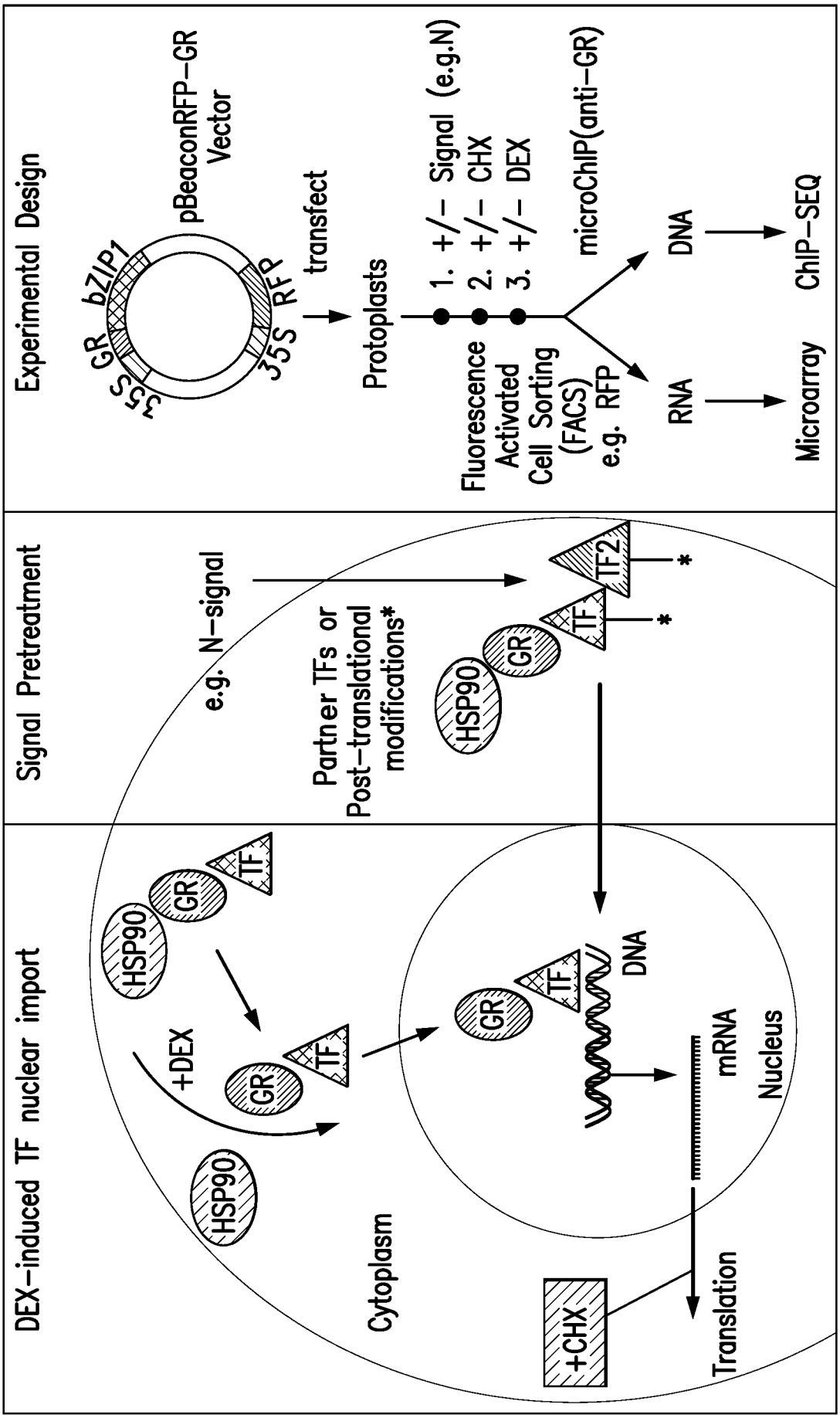


FIG. 1A

FIG. 1B

FIG. 1C

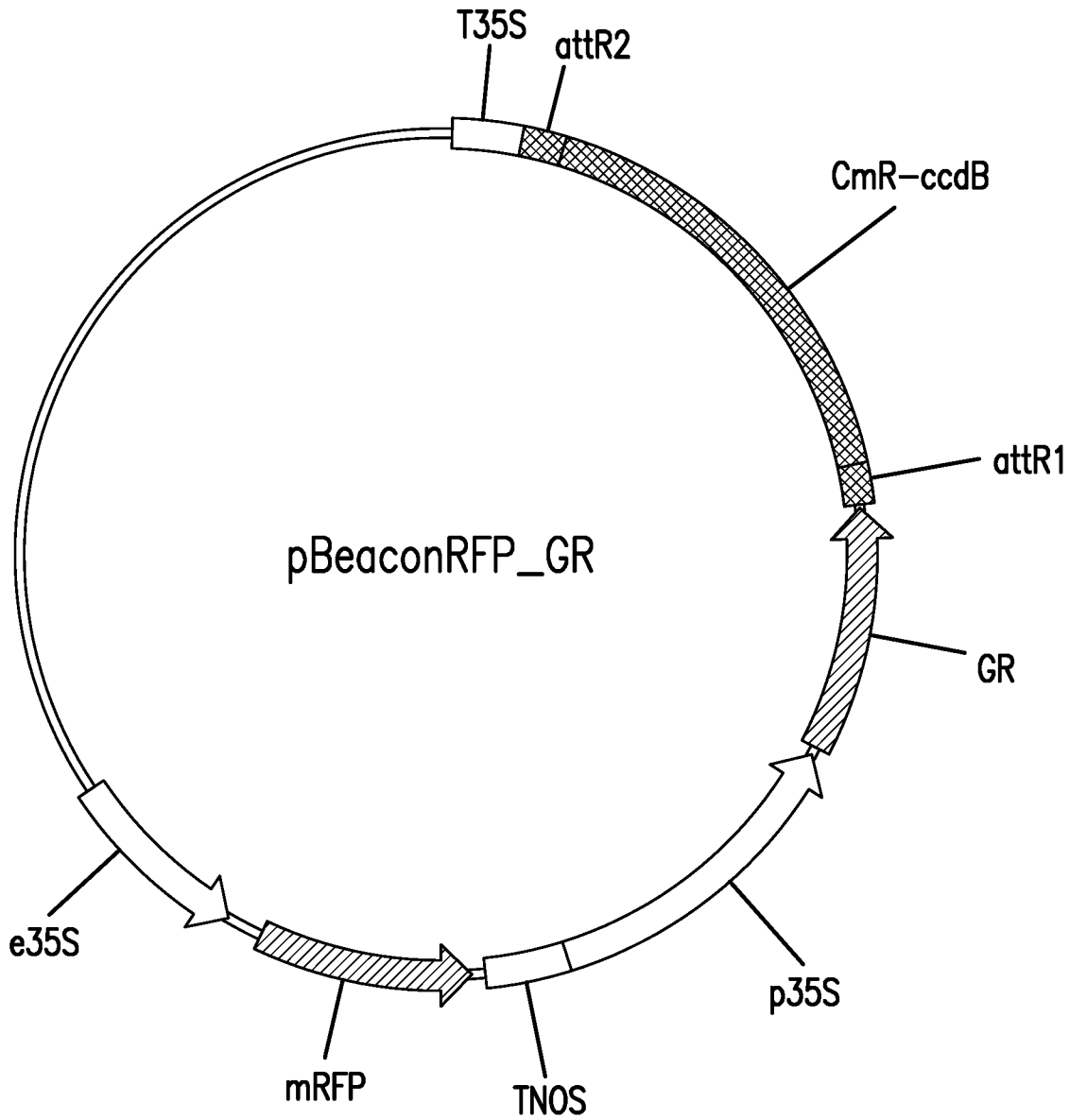

T35S
attR2
CmR–ccdB
attR1
pBeaconRFP_GR
GR
e35S
mRFP
TNOS
p35S

FIG. 2

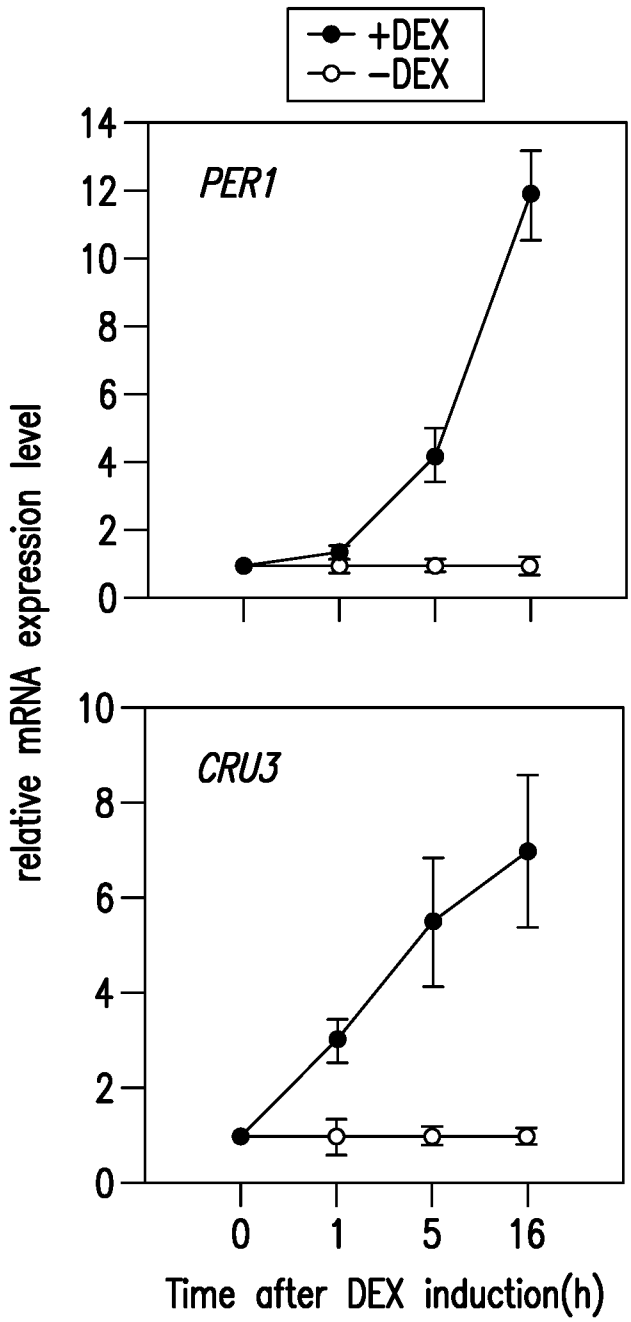

+DEX
−DEX
PER1
CRU3
relative mRNA expression level
0
2
4
6
8
10
12
14
0
1
5
16
Time after DEX induction(h)

FIG. 3A

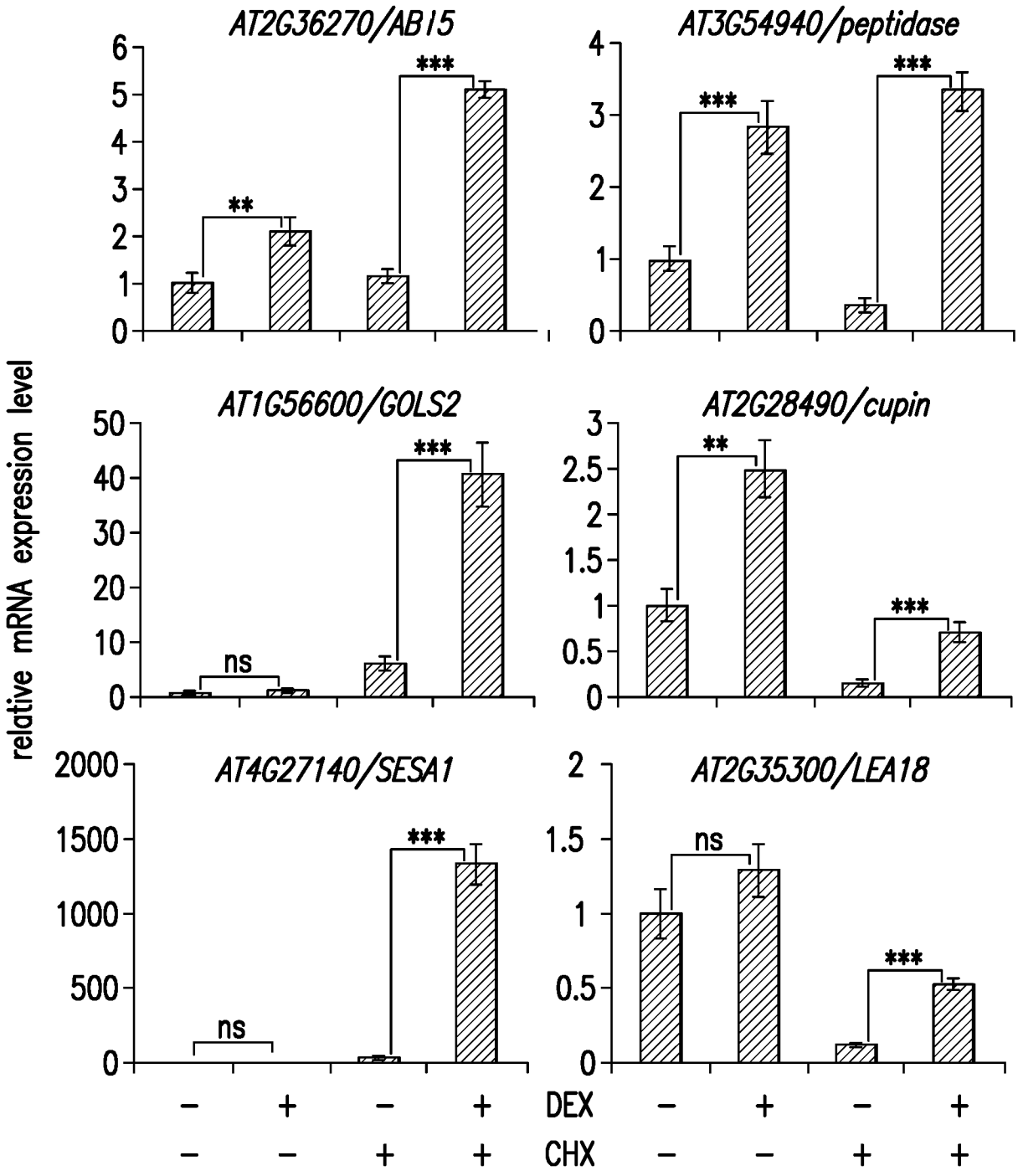

AT2G36270/AB15
AT3G54940/peptidase
AT1G56600/GOLS2
AT2G28490/cupin
AT4G27140/SESA1
AT2G35300/LEA18
relative mRNA expression level
ns
**
***
DEX
CHX

FIG. 3B

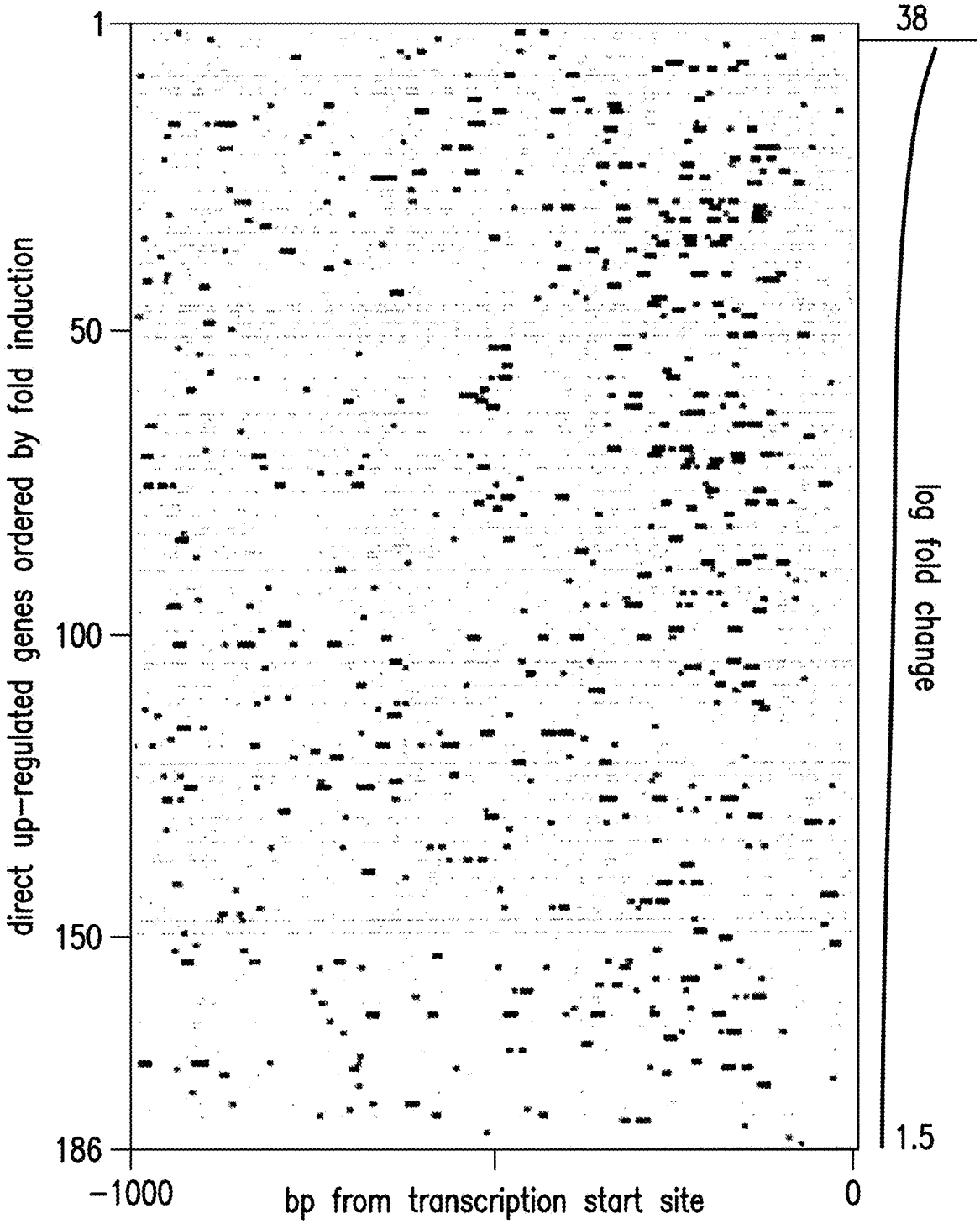

1
50
100
150
186
direct up-regulated genes ordered by fold induction
−1000
bp from transcription start site
0
38
1.5
log fold change

FIG. 4A

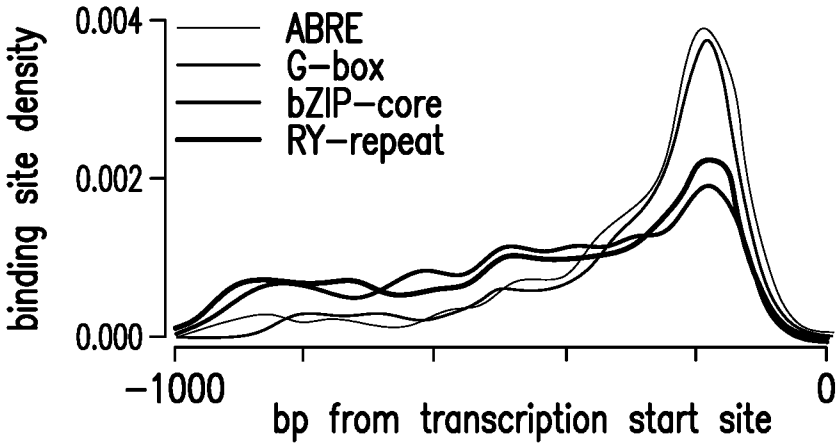


FIG. 4B

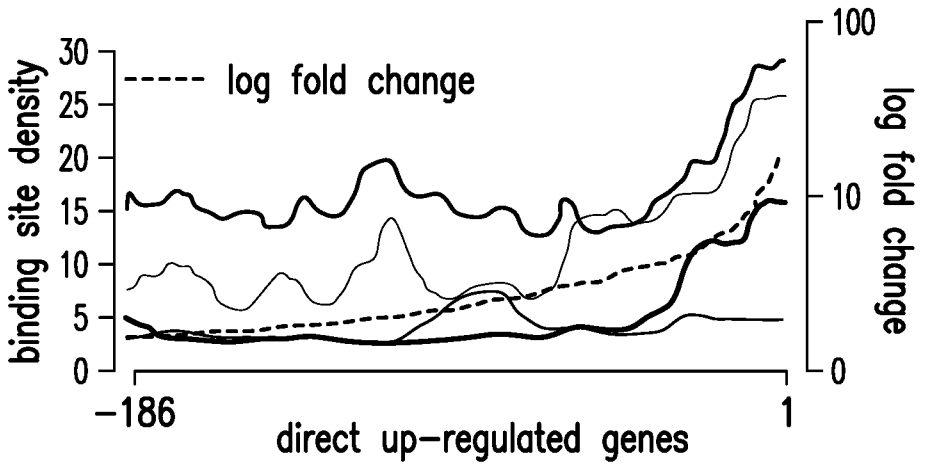


FIG. 4C

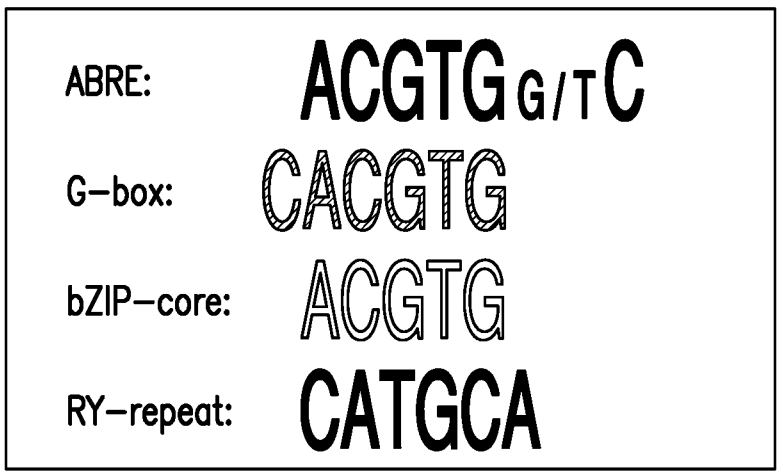


FIG. 4D

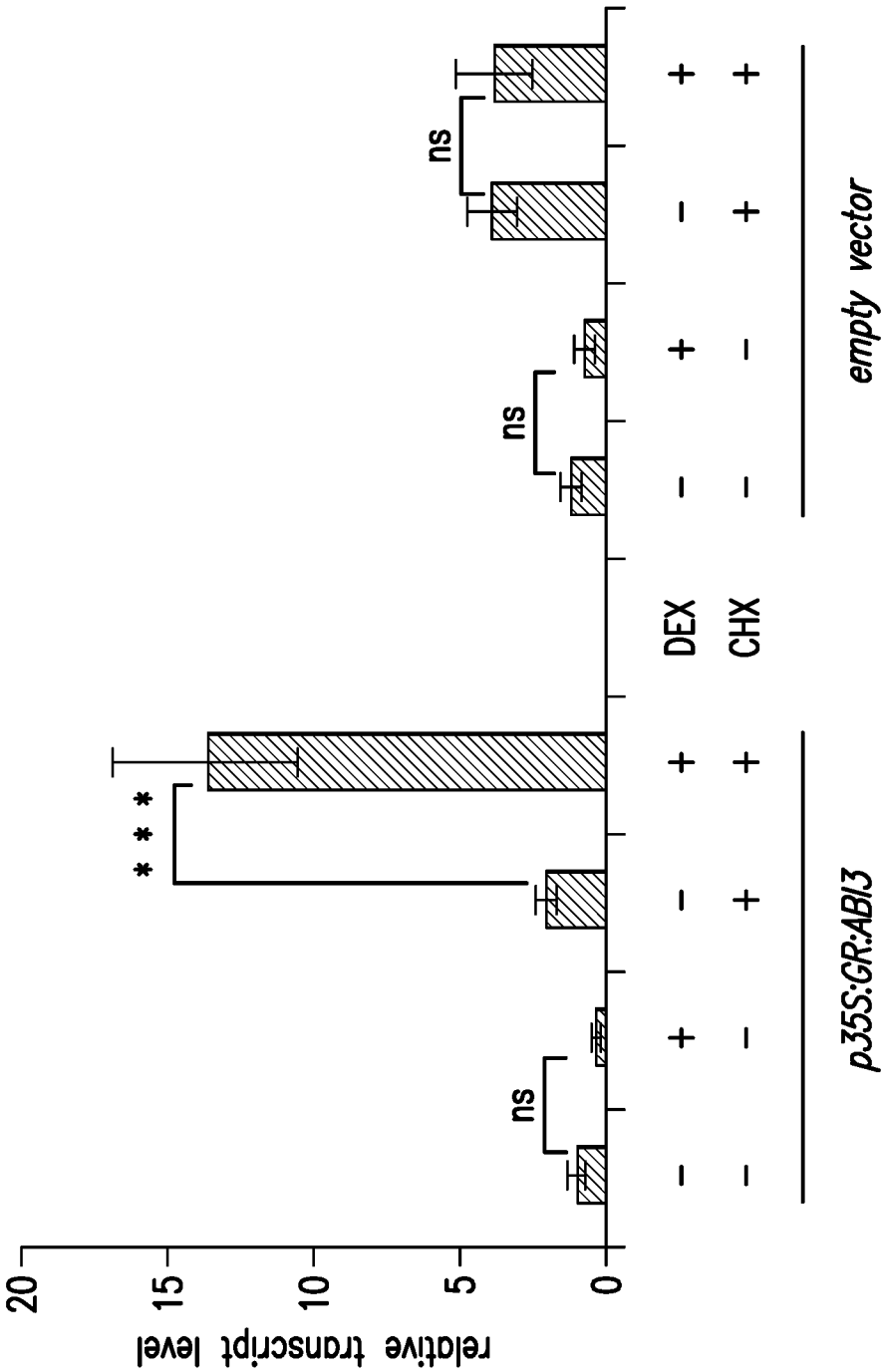

CRU3
relative transcript level
20
15
10
5
0
ns
***
ns
ns
DEX
CHX
p35S:GR:ABI3
empty vector

FIG. 5

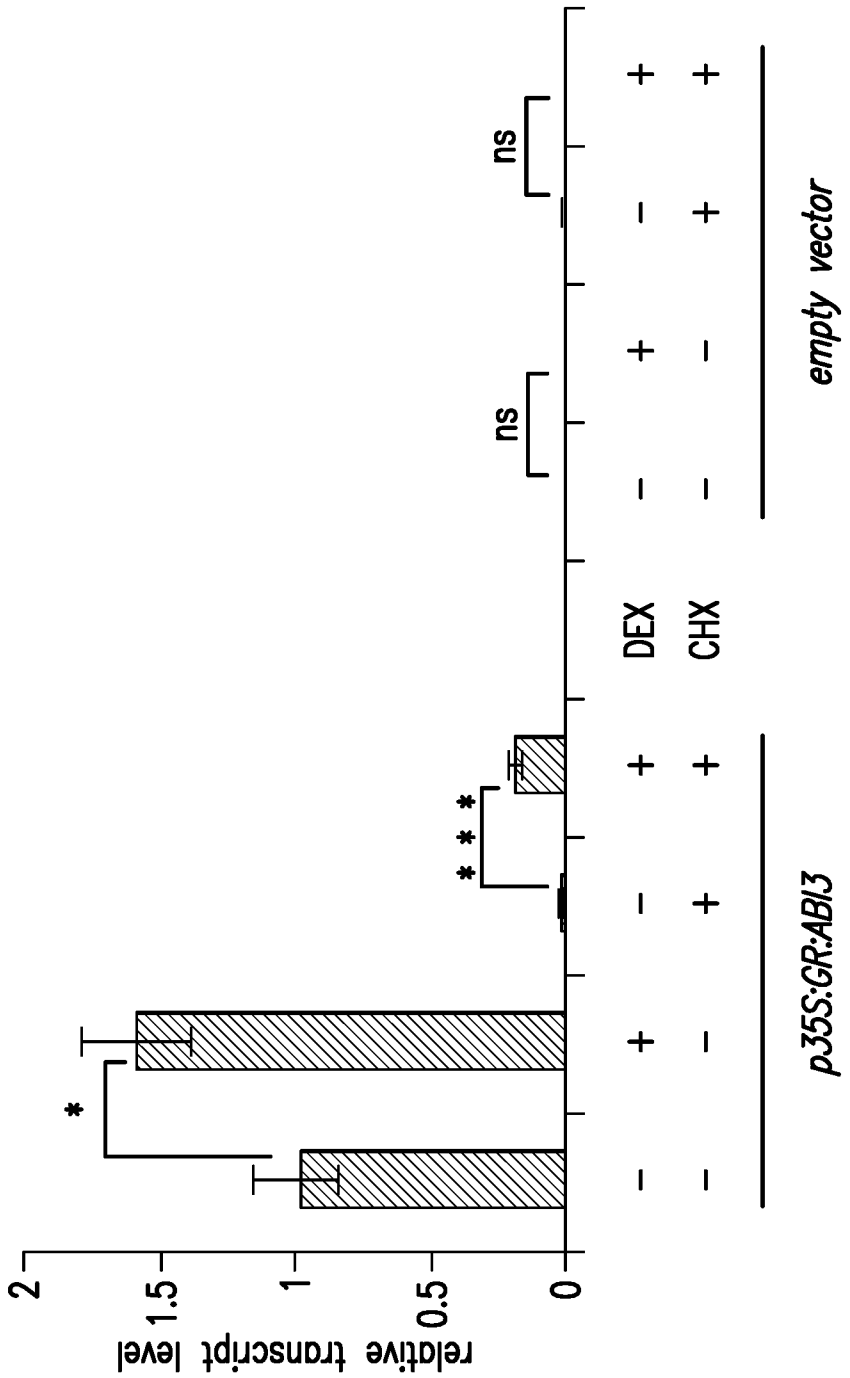

PER1
relative transcript level
2
1.5
1
0.5
0
*
***
ns
ns
DEX
CHX
p35S:GR:ABI3
empty vector

FIG. 6

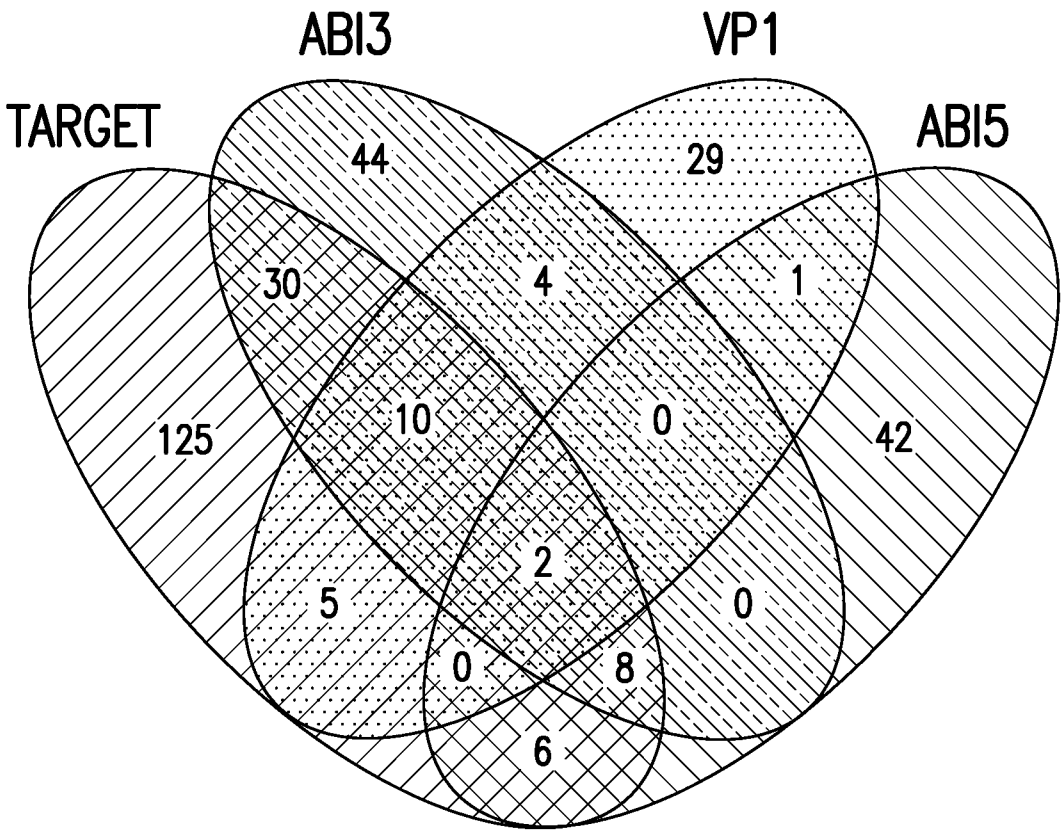
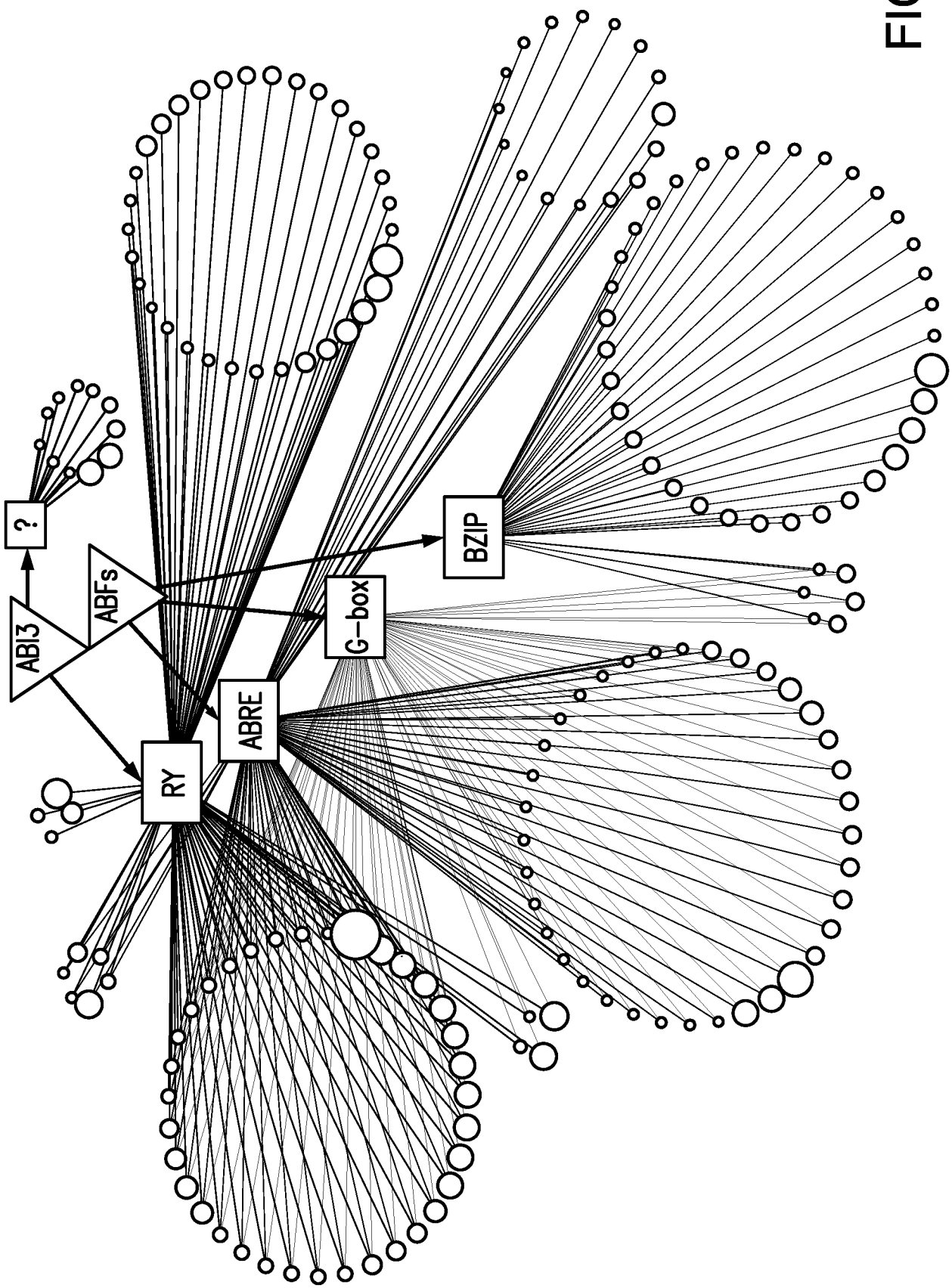


FIG. 7

FIG. 8



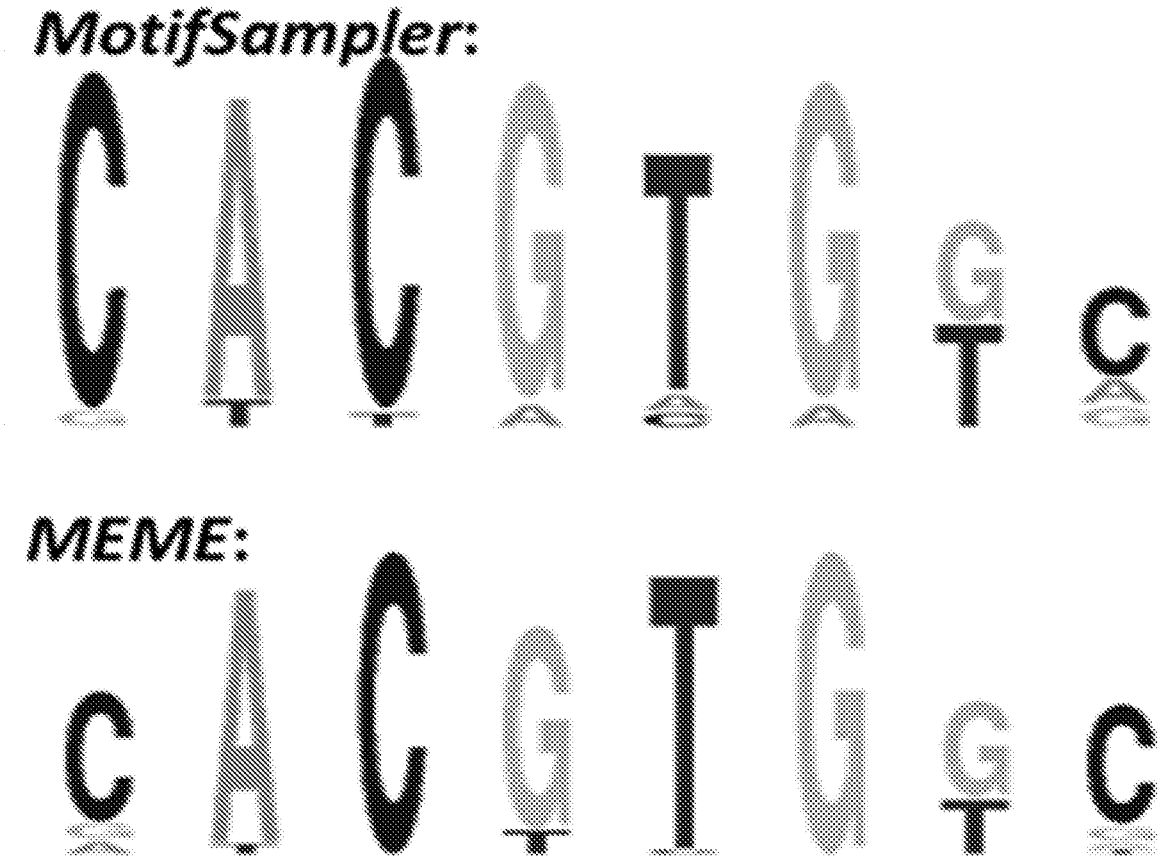


FIG. 9

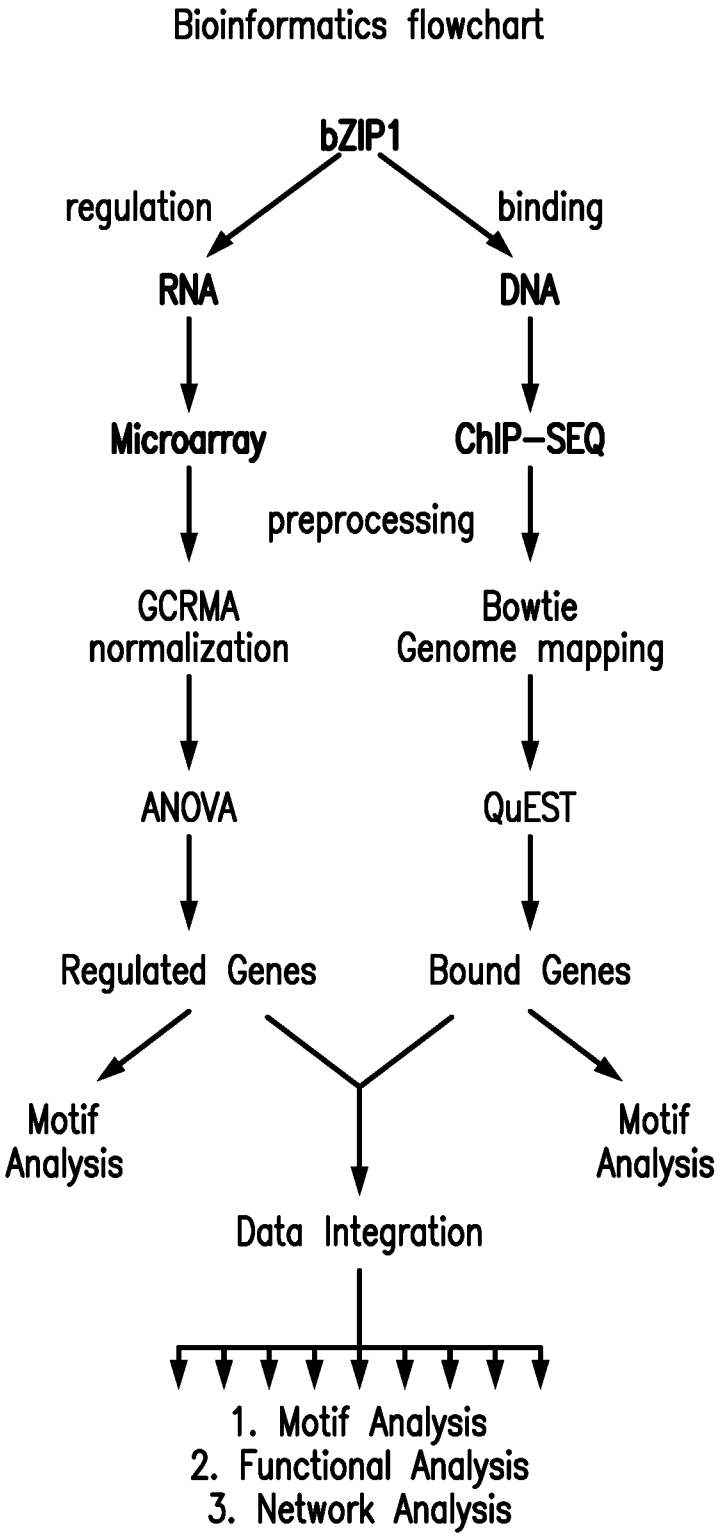

Bioinformatics flowchart
bZIP1
regulation
binding
RNA
DNA
Microarray
ChIP-SEQ
preprocessing
GCRMA normalization
Bowtie Genome mapping
ANOVA
QuEST
Regulated Genes
Bound Genes
Motif Analysis
Motif Analysis
Data Integration
1. Motif Analysis
2. Functional Analysis
3. Network Analysis

FIG. 10A

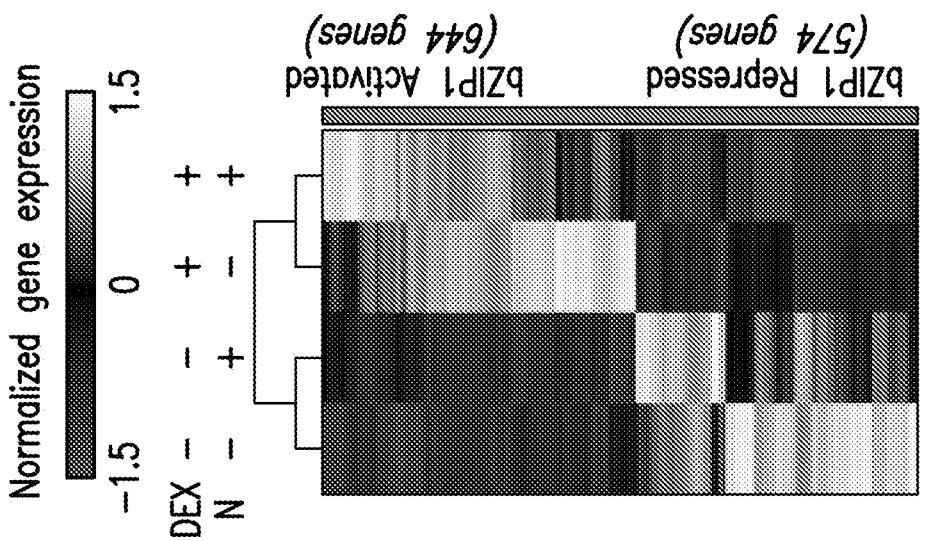


FIG. 10B

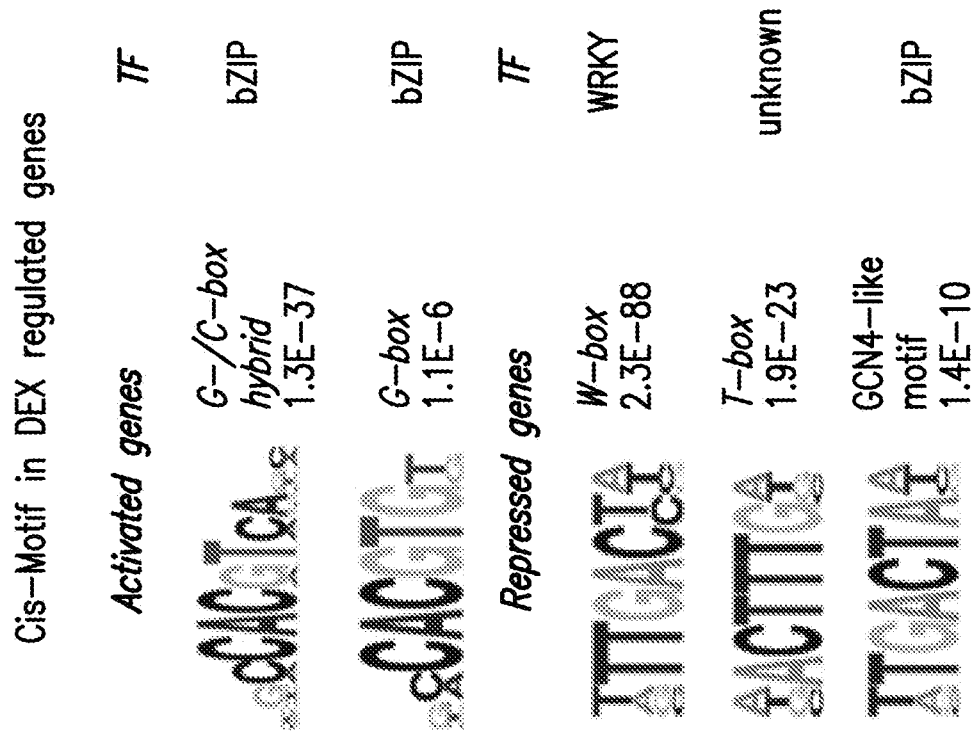


FIG. 10C

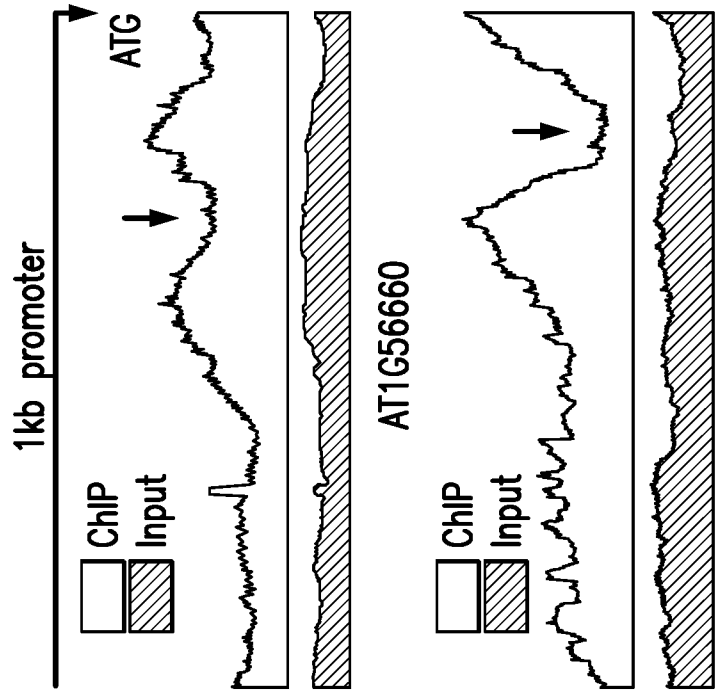


FIG. 10D

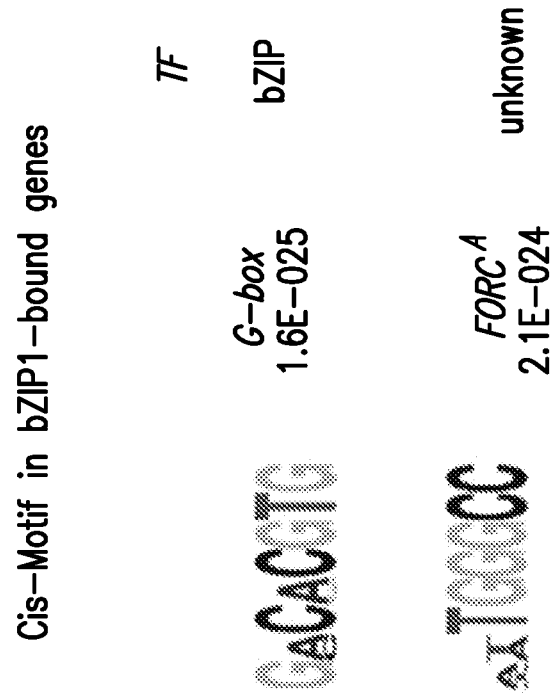


FIG. 10E

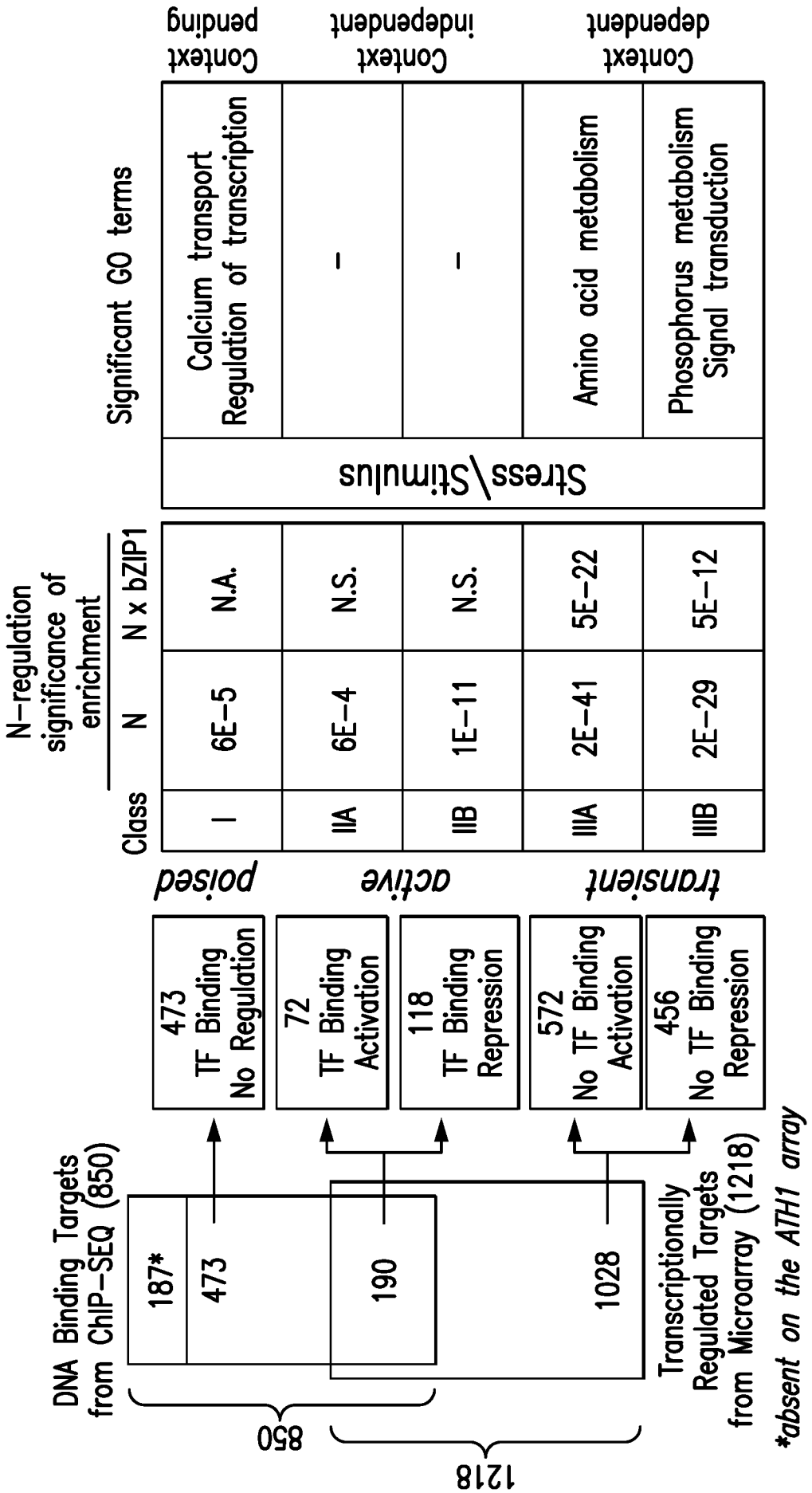

DNA Binding Targets from ChIP-SEQ (850)
187*
473
190
1028
850
1218
Transcriptionally Regulated Targets from Microarray (1218)
*absent on the ATH1 array
473 TF Binding No Regulation
72 TF Binding Activation
118 TF Binding Repression
572 No TF Binding Activation
456 No TF Binding Repression
poised
active
transient
N-regulation significance of enrichment
Class
N
N x bZIP1
I
6E-5
N.A.
IIA
6E-4
N.S.
IIB
1E-11
N.S.
IIIA
2E-41
5E-22
IIIB
2E-29
5E-12
Significant GO terms
Stress\Stimulus
Calcium transport
Regulation of transcription
-
-
Amino acid metabolism
Phosophorus metabolism
Signal transduction
Context pending
Context independent
Context dependent

FIG. 11A

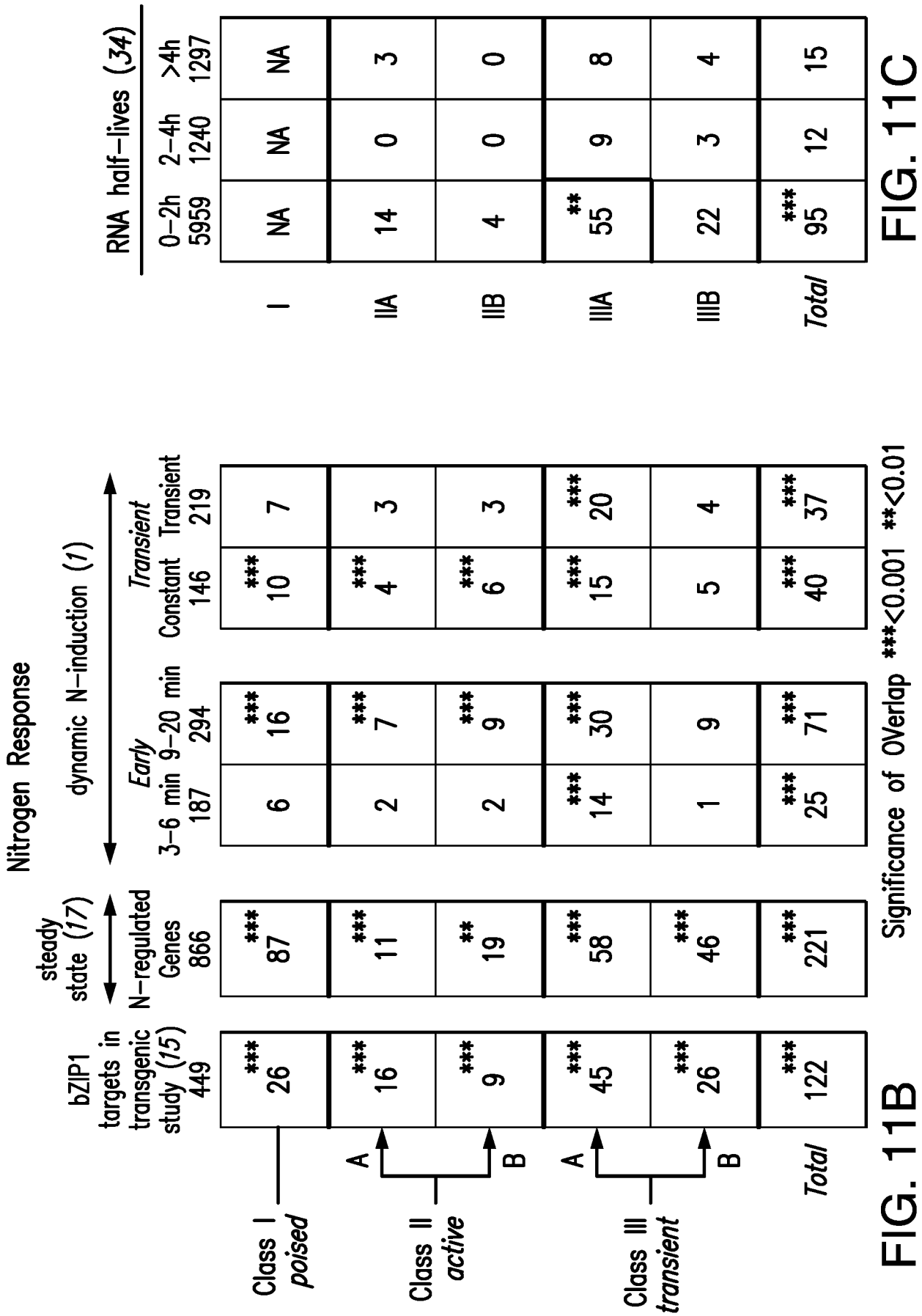


FIG. 11B

RNA half-lives (34)

	0–2h 5959	2–4h 1240	>4h 1297
I	NA	NA	NA
IIA	14	0	3
IIB	4	0	0
IIIA	** 55	9	8
IIIB	22	3	4
Total	*** 95	12	15

FIG. 11C

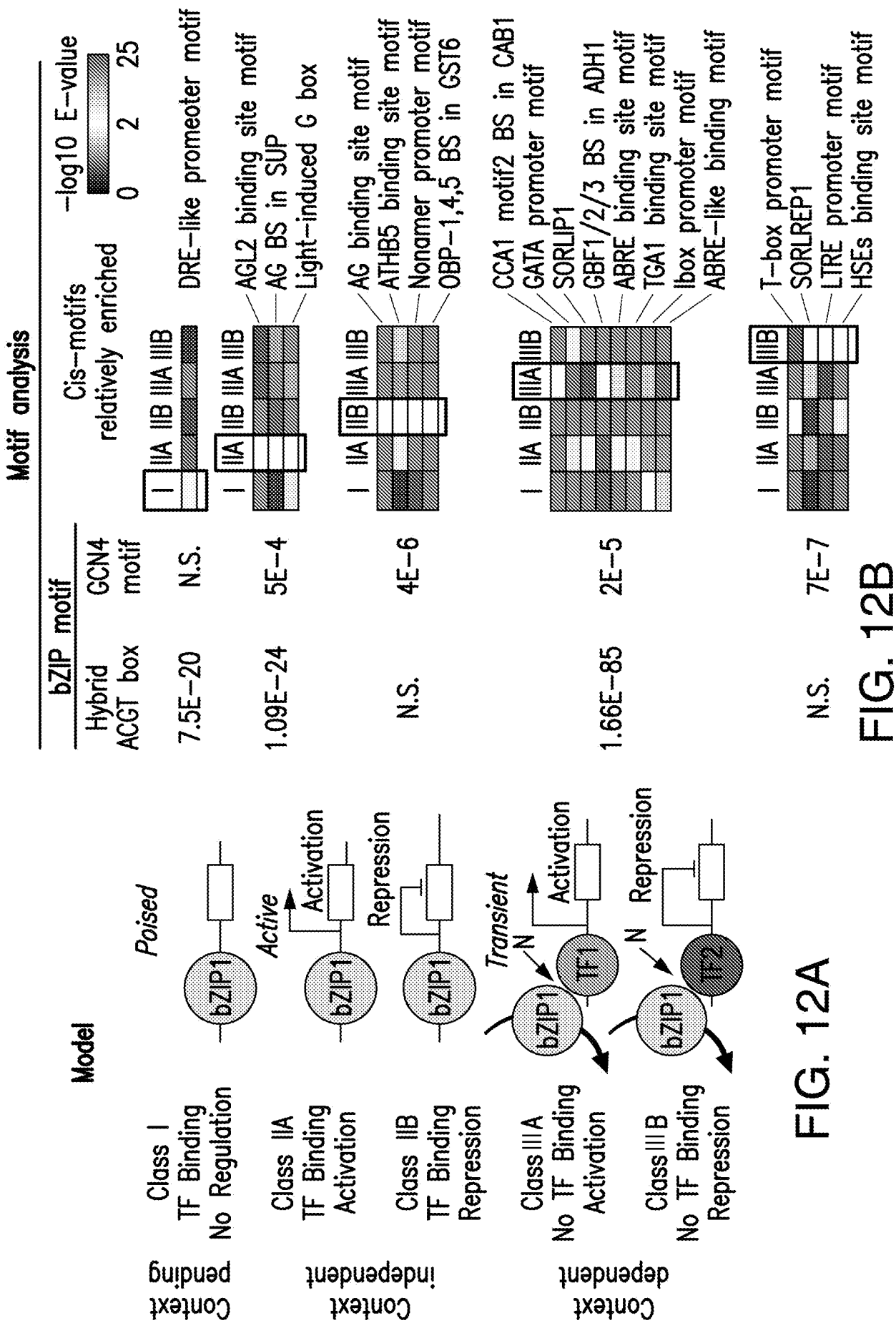


FIG. 12A

FIG. 12B

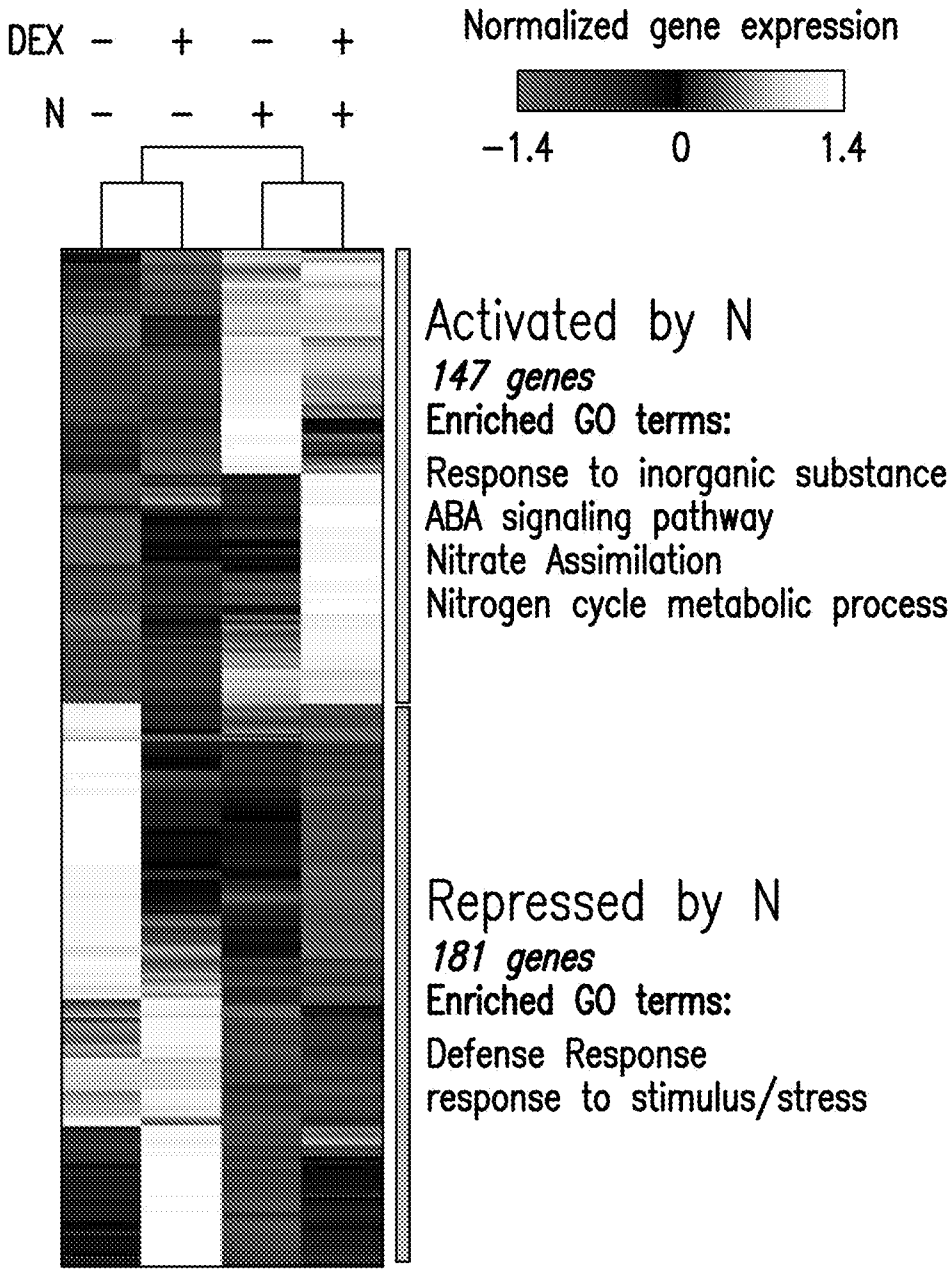

DEX − + − +
N − − + +
Normalized gene expression
−1.4 0 1.4
Activated by N
147 genes
Enriched GO terms:
Response to inorganic substance
ABA signaling pathway
Nitrate Assimilation
Nitrogen cycle metabolic process
Repressed by N
181 genes
Enriched GO terms:
Defense Response
response to stimulus/stress

FIG. 13

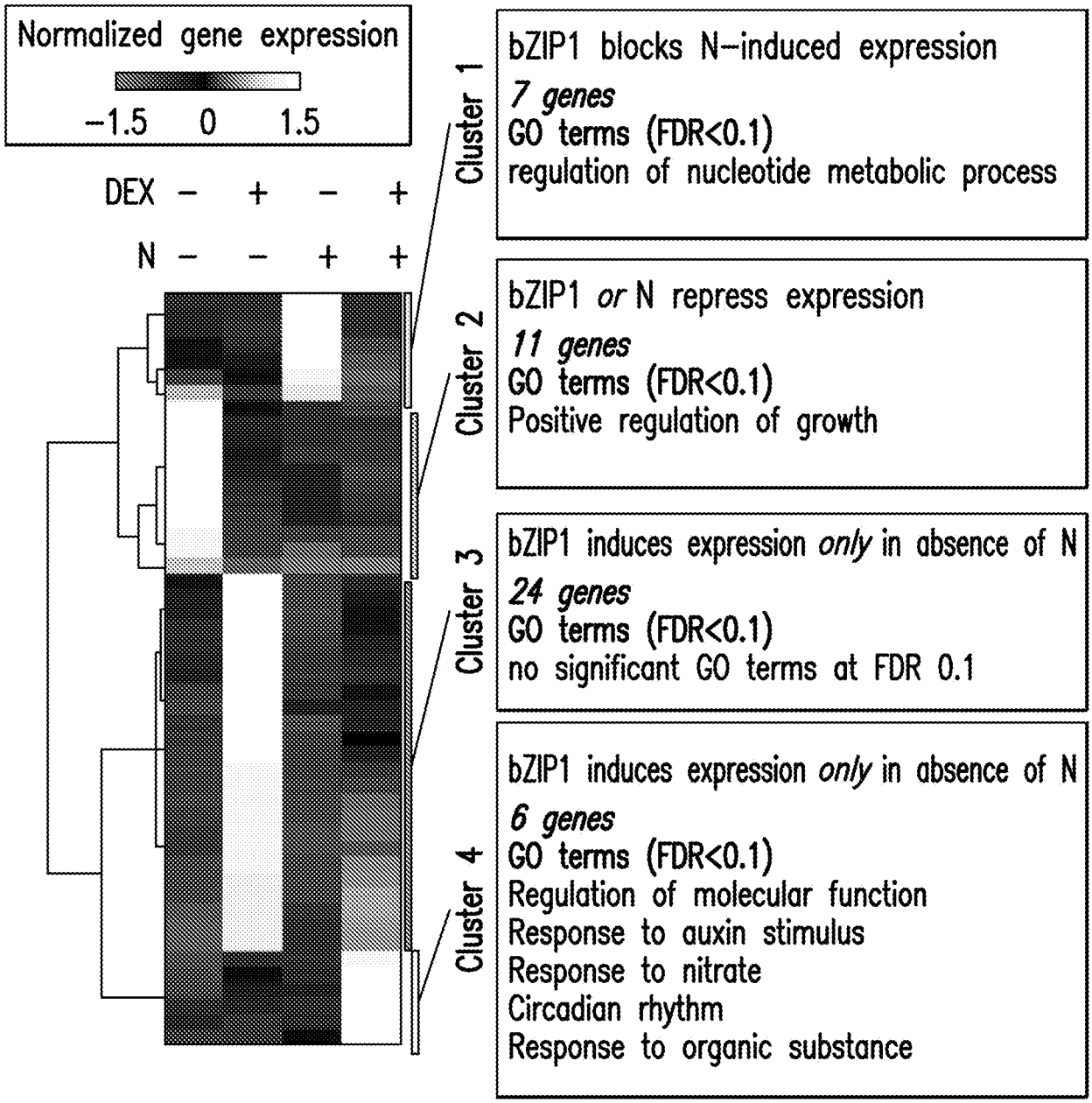

Normalized gene expression
−1.5 0 1.5
DEX − + − +
N − − + +
Cluster 1
bZIP1 blocks N−induced expression
7 genes
GO terms (FDR<0.1)
regulation of nucleotide metabolic process
Cluster 2
bZIP1 or N repress expression
11 genes
GO terms (FDR<0.1)
Positive regulation of growth
Cluster 3
bZIP1 induces expression only in absence of N
24 genes
GO terms (FDR<0.1)
no significant GO terms at FDR 0.1
Cluster 4
bZIP1 induces expression only in absence of N
6 genes
GO terms (FDR<0.1)
Regulation of molecular function
Response to auxin stimulus
Response to nitrate
Circadian rhythm
Response to organic substance

FIG. 14A

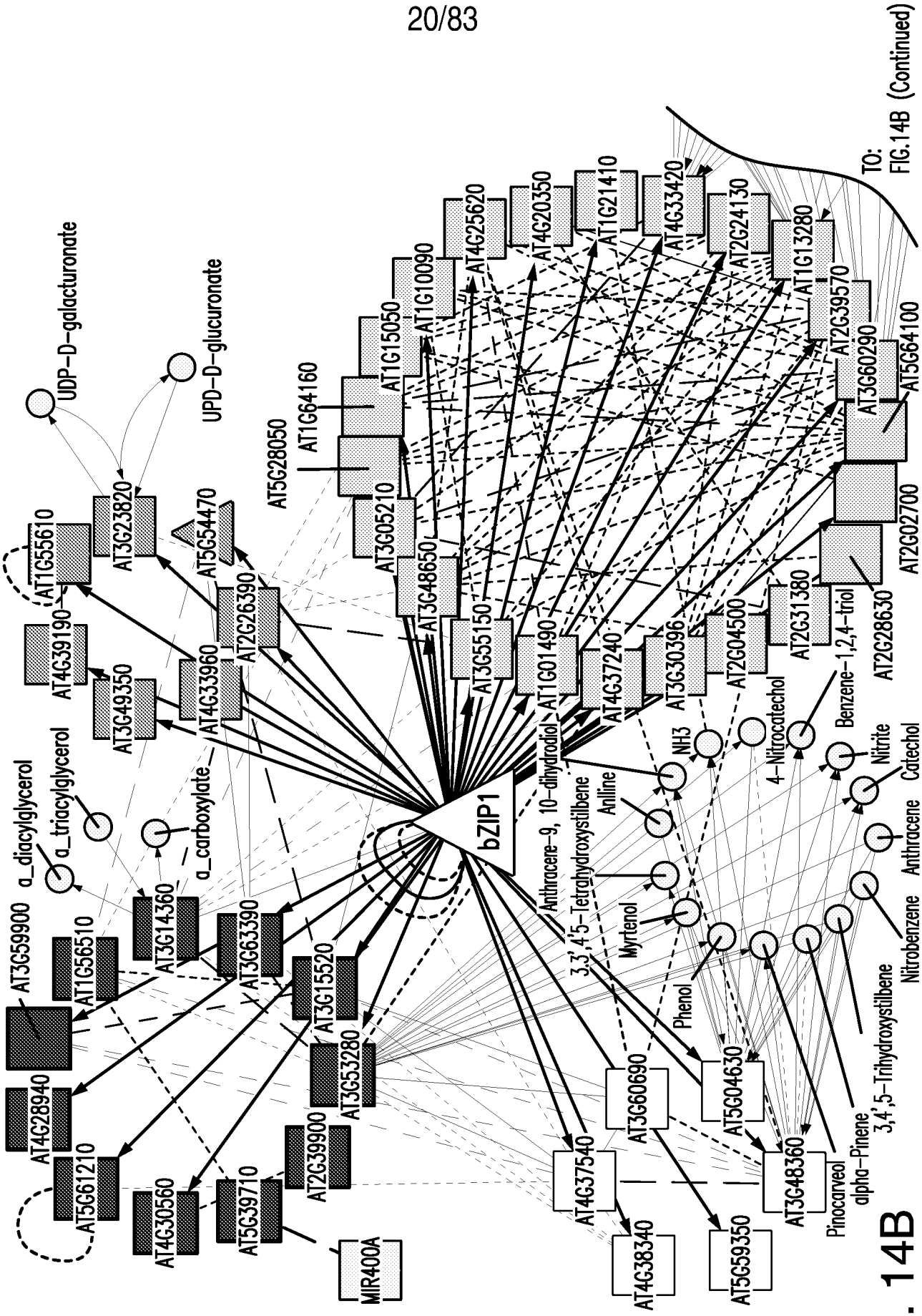

bZIP1
UDP-D-galacturonate
UPD-D-glucuronate
a_diacylglycerol
a_triacylglycerol
a_carboxylate
AT3G59900
AT1G56510
AT4G28940
AT5G61210
AT3G14360
AT4G30560
AT3G63390
AT5G39710
AT3G15520
AT3G53280
AT2G39900
MIR400A
AT1G55610
AT3G23820
AT4G39190
AT3G49350
AT4G33960
AT2G26390
AT5G54470
AT5G28050
AT1G64160
AT3G05210
AT3G48650
AT1G15050
AT1G10090
AT4G25620
AT4G20350
AT1G21410
AT4G33420
AT2G24130
AT1G13280
AT2G39570
AT3G60290
AT5G64100
AT2G02700
AT2G28630
AT3G55150
AT1G01490
AT4G37240
AT3G30396
AT2G04500
AT2G31380
Anthracene-9, 10-dihydrodiol
3,3',4',5-Tetrahydroxystilbene
Myrtenol
Phenol
Aniline
NH3
4-Nitrocatechol
Benzene-1,2,4-triol
Nitrite
Catechol
Anthracene
Nitrobenzene
3,4',5-Trihydroxystilbene
alpha-Pinene
Pinocarveol
AT4G37540
AT3G60690
AT5G04630
AT3G48360
AT4G38340
AT5G59350
TO:
FIG.14B (Continued)

FIG. 14B

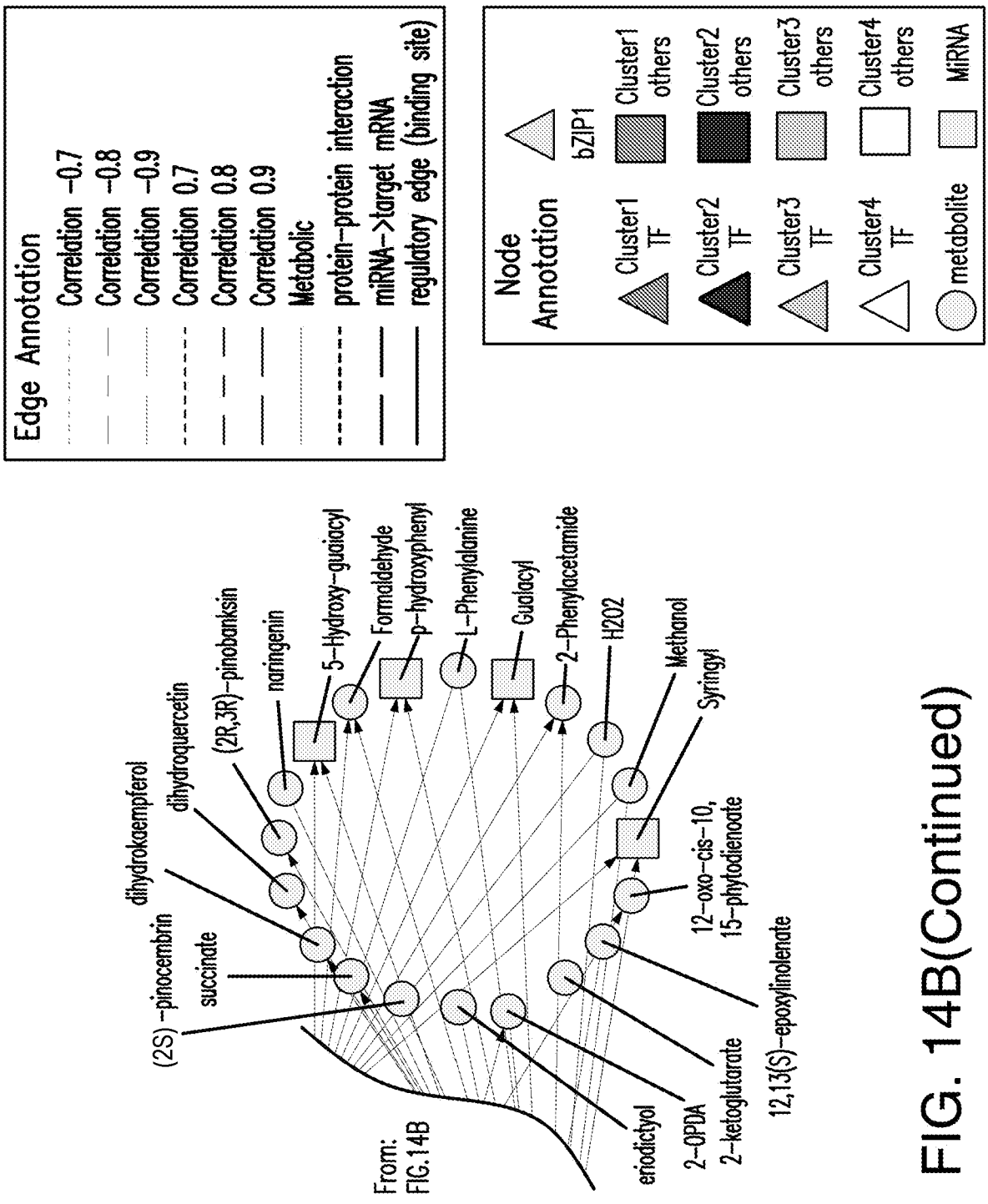


FIG. 14B(Continued)

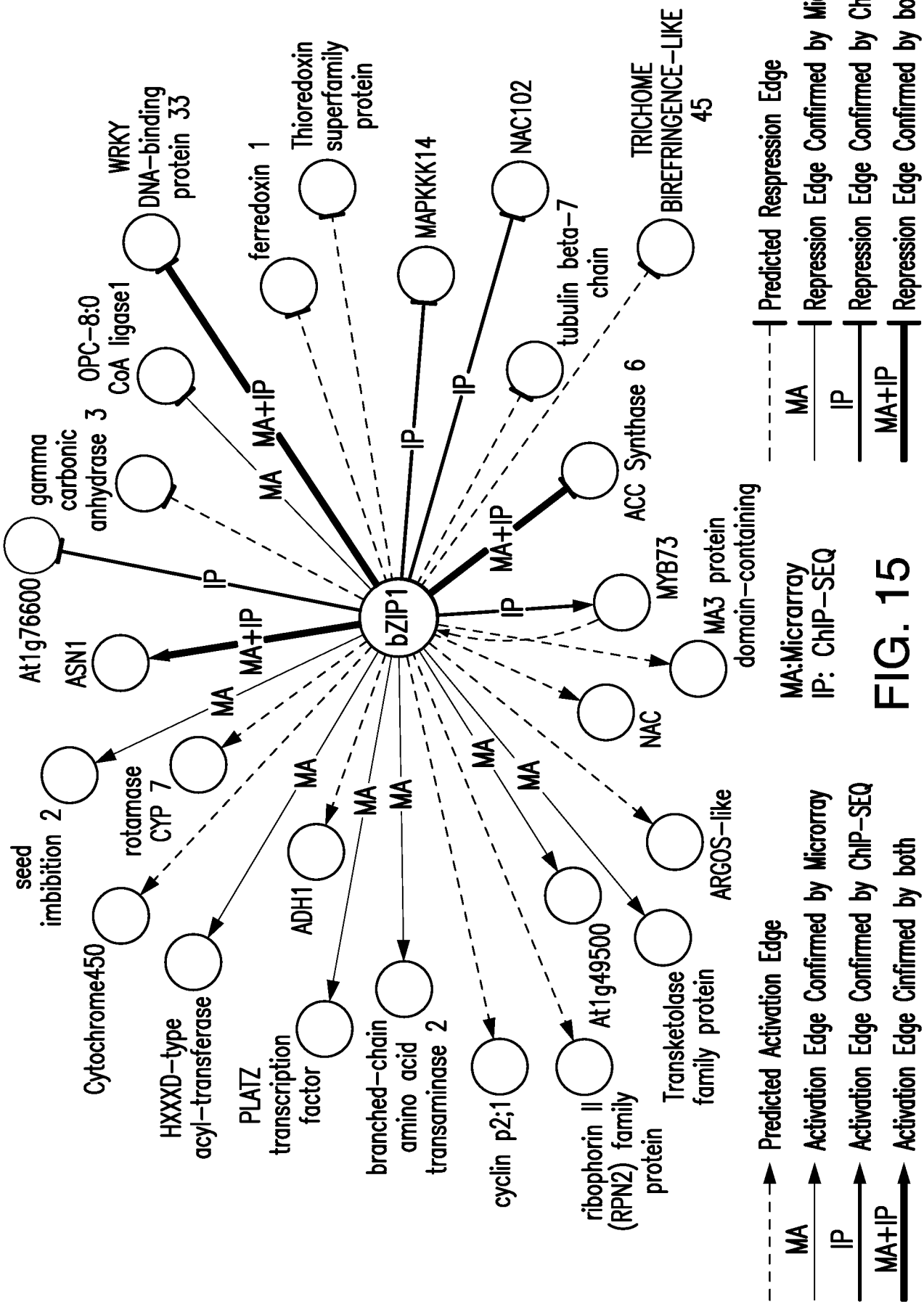

bZIP1
At1g76600
gamma carbonic anhydrase 3
ASN1
OPC-8:0 CoA ligase1
WRKY DNA-binding protein 33
ferredoxin 1
Thioredoxin superfamily protein
MAPKKK14
NAC102
tubulin beta-7 chain
ACC Synthase 6
TRICHOME BIREFRINGENCE-LIKE 45
MYB73
MA3 protein domain-containing
NAC
ARGOS-like
Transketolase family protein
ribophorin II (RPN2) family protein
At1g49500
cyclin p2;1
branched-chain amino acid transaminase 2
PLATZ transcription factor
ADH1
HXXXD-type acyl-transferase
Cytochrome450
rotamase CYP 7
seed imbibition 2
MA
IP
MA+IP
MA:Micrarray
IP: ChIP-SEQ
Predicted Activation Edge
Activation Edge Confirmed by Microrray
Activation Edge Confirmed by ChIP-SEQ
Activation Edge Cinfirmed by both
Predicted Respression Edge
Repression Edge Confirmed by Microrray
Repression Edge Confirmed by ChIP-SEQ
Repression Edge Confirmed by both

FIG. 15

		−CHX	
		DEX−down (457)	DEX−up (334)
Class I	Binding No Regulation (473)	16	21***
Class II A	Binding Activation (72)	0	33***
Class II B	Binding Repression (118)	6	1
Class III A	No Binding Activation (572)	7	155***
Class III B	No Binding Repression (456)	53***	4
	Total	82***	214***

Significance of Overlap pvalue ***<0.001 **< 0.01

FIG. 16A

Response to C/L (Krouk, 2009)

		ROOT				SHOOT				
		Sugar Starvation		Dark		Sugar Starvation		Dark		
		up (544)	down (259)	up (571)	down (387)		up (68)	down (33)	up (1054)	down (1830)
Class I	Binding No Regulation (473)	18**	9	23***	7	I	2	1	50***	30
Class II A	Binding Activation (72)	16***	0	16***	0	IIA	2**	0	28***	2
Class II B	Binding Repression (118)	2	2	2	3	IIB	1	0	8	10
Class III A	No Binding Activation (572)	132***	5	133***	9	IIIA	7**	1	187***	22
Class III B	No Binding Repression (456)	15	2	16	5	IIIB	1	2	41***	30
	Total	183***	18	190***	24	Total	13***	4	314***	94

Significance of Overlap pvalue ***<0.001 **< 0.01

FIG. 16B

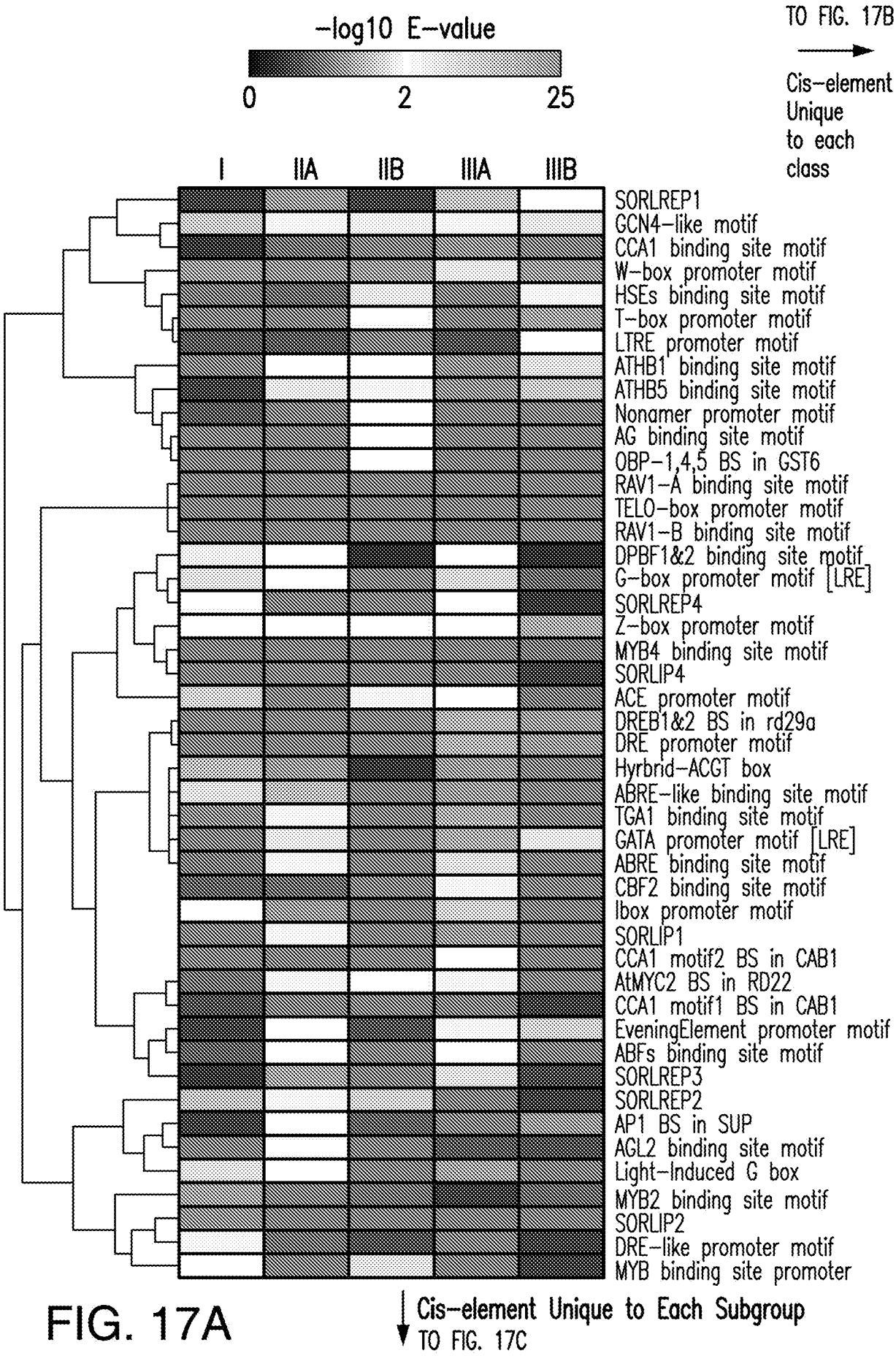

−log10 E−value
0
2
25
TO FIG. 17B
Cis−element Unique to each class
I
IIA
IIB
IIIA
IIIB
SORLREP1
GCN4−like motif
CCA1 binding site motif
W−box promoter motif
HSEs binding site motif
T−box promoter motif
LTRE promoter motif
ATHB1 binding site motif
ATHB5 binding site motif
Nonamer promoter motif
AG binding site motif
OBP−1,4,5 BS in GST6
RAV1−A binding site motif
TELO−box promoter motif
RAV1−B binding site motif
DPBF1&2 binding site motif
G−box promoter motif [LRE]
SORLREP4
Z−box promoter motif
MYB4 binding site motif
SORLIP4
ACE promoter motif
DREB1&2 BS in rd29a
DRE promoter motif
Hyrbrid−ACGT box
ABRE−like binding site motif
TGA1 binding site motif
GATA promoter motif [LRE]
ABRE binding site motif
CBF2 binding site motif
Ibox promoter motif
SORLIP1
CCA1 motif2 BS in CAB1
AtMYC2 BS in RD22
CCA1 motif1 BS in CAB1
EveningElement promoter motif
ABFs binding site motif
SORLREP3
SORLREP2
AP1 BS in SUP
AGL2 binding site motif
Light−Induced G box
MYB2 binding site motif
SORLIP2
DRE−like promoter motif
MYB binding site promoter
Cis−element Unique to Each Subgroup
TO FIG. 17C

FIG. 17A

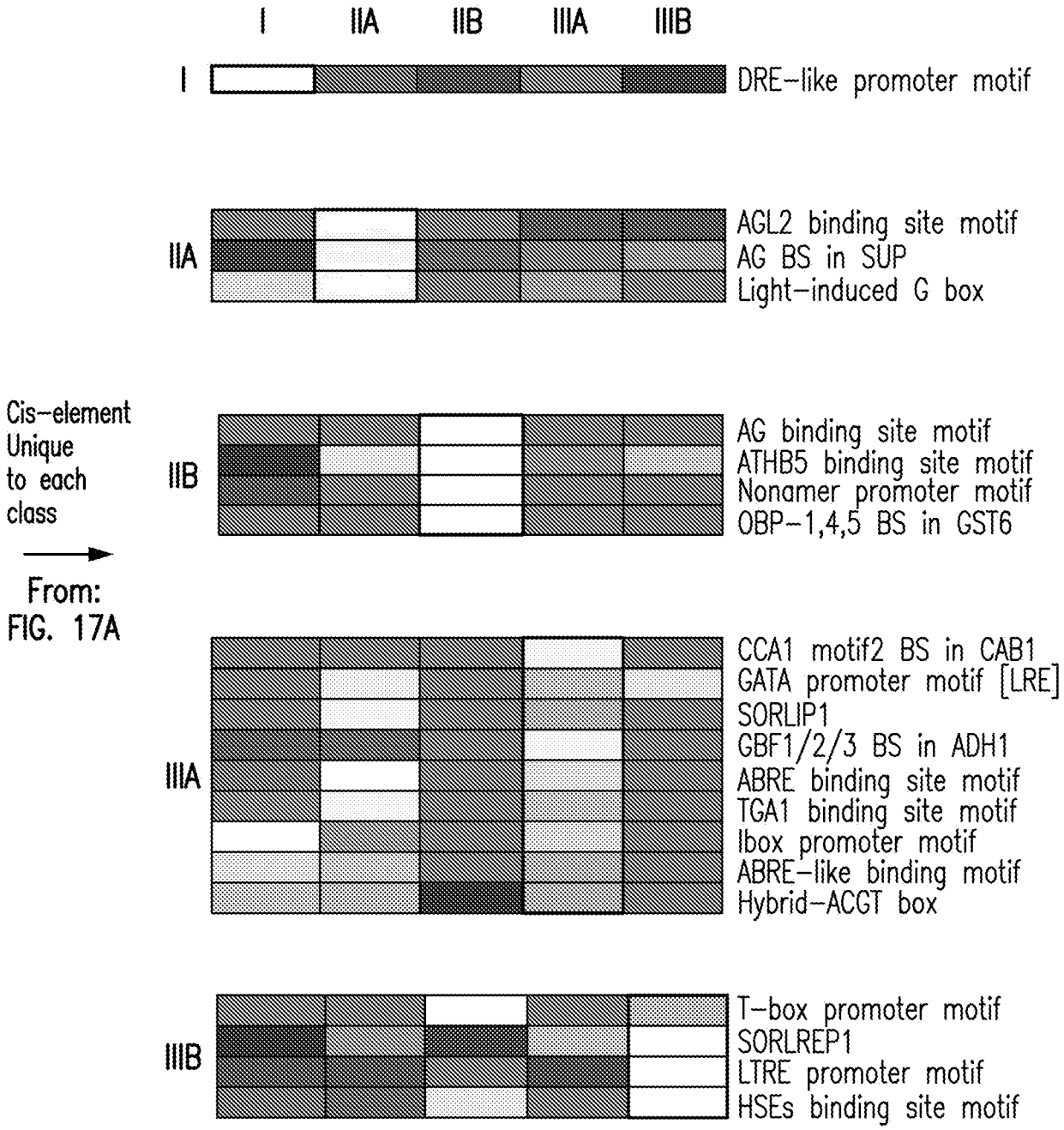

I
IIA
IIB
IIIA
IIIB
I
DRE-like promoter motif
IIA
AGL2 binding site motif
AG BS in SUP
Light-induced G box
Cis-element Unique to each class
IIB
AG binding site motif
ATHB5 binding site motif
Nonamer promoter motif
OBP-1,4,5 BS in GST6
From: FIG. 17A
IIIA
CCA1 motif2 BS in CAB1
GATA promoter motif [LRE]
SORLIP1
GBF1/2/3 BS in ADH1
ABRE binding site motif
TGA1 binding site motif
Ibox promoter motif
ABRE-like binding motif
Hybrid-ACGT box
IIIB
T-box promoter motif
SORLREP1
LTRE promoter motif
HSEs binding site motif

FIG. 17B

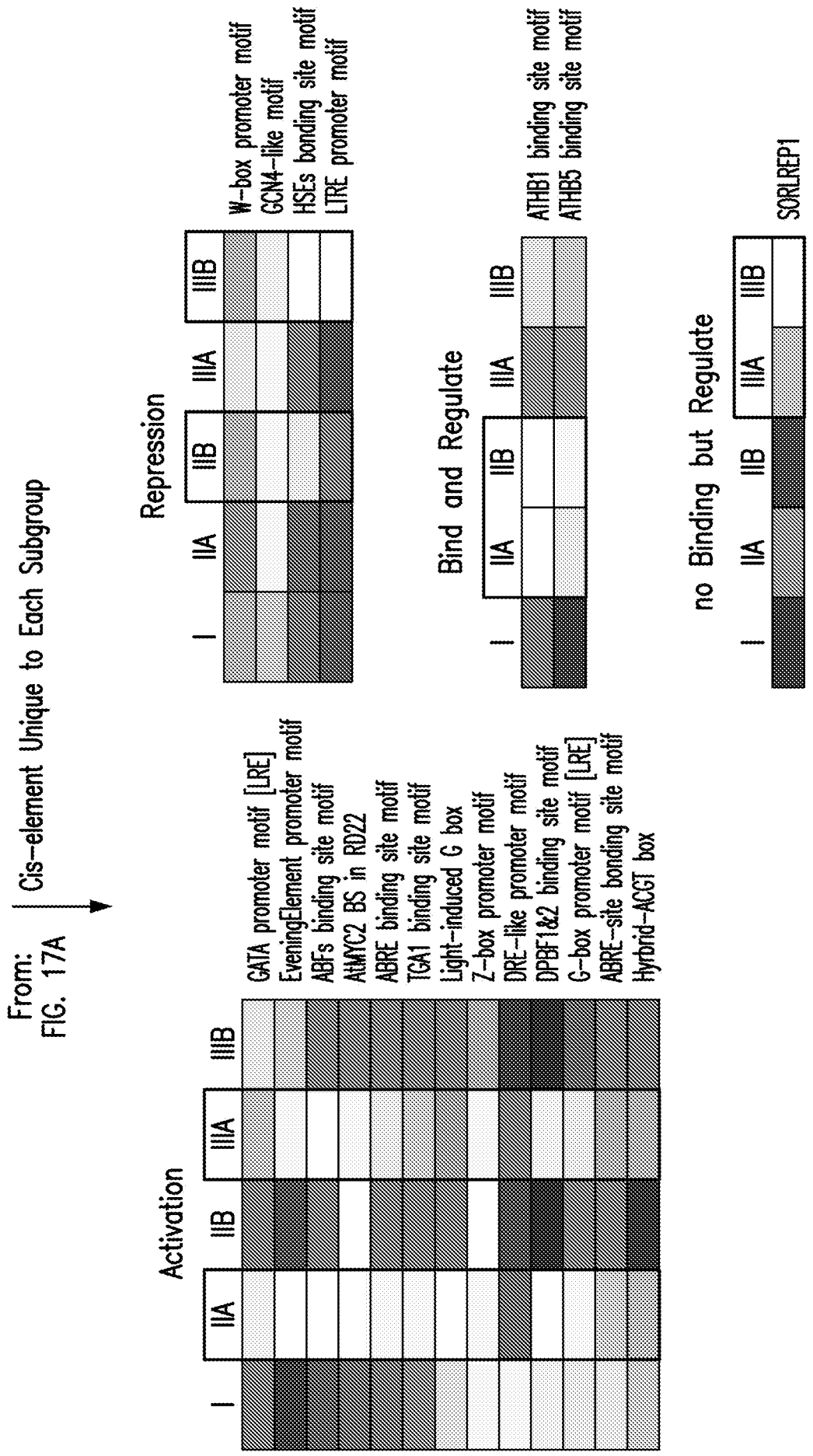

From: FIG. 17A
Cis-element Unique to Each Subgroup
Activation
I
IIA
IIB
IIIA
IIIB
GATA promoter motif [LRE]
EveningElement promoter motif
ABFs binding site motif
AtMYC2 BS in RD22
ABRE binding site motif
TGA1 binding site motif
Light-induced G box
Z-box promoter motif
DRE-like promoter motif
DPBF1&2 binding site motif
G-box promoter motif [LRE]
ABRE-site bonding site motif
Hybrid-ACGT box
Repression
W-box promoter motif
GCN4-like motif
HSEs bonding site motif
LTRE promoter motif
Bind and Regulate
ATHB1 binding site motif
ATHB5 binding site motif
no Binding but Regulate
SORLREP1

FIG. 17C

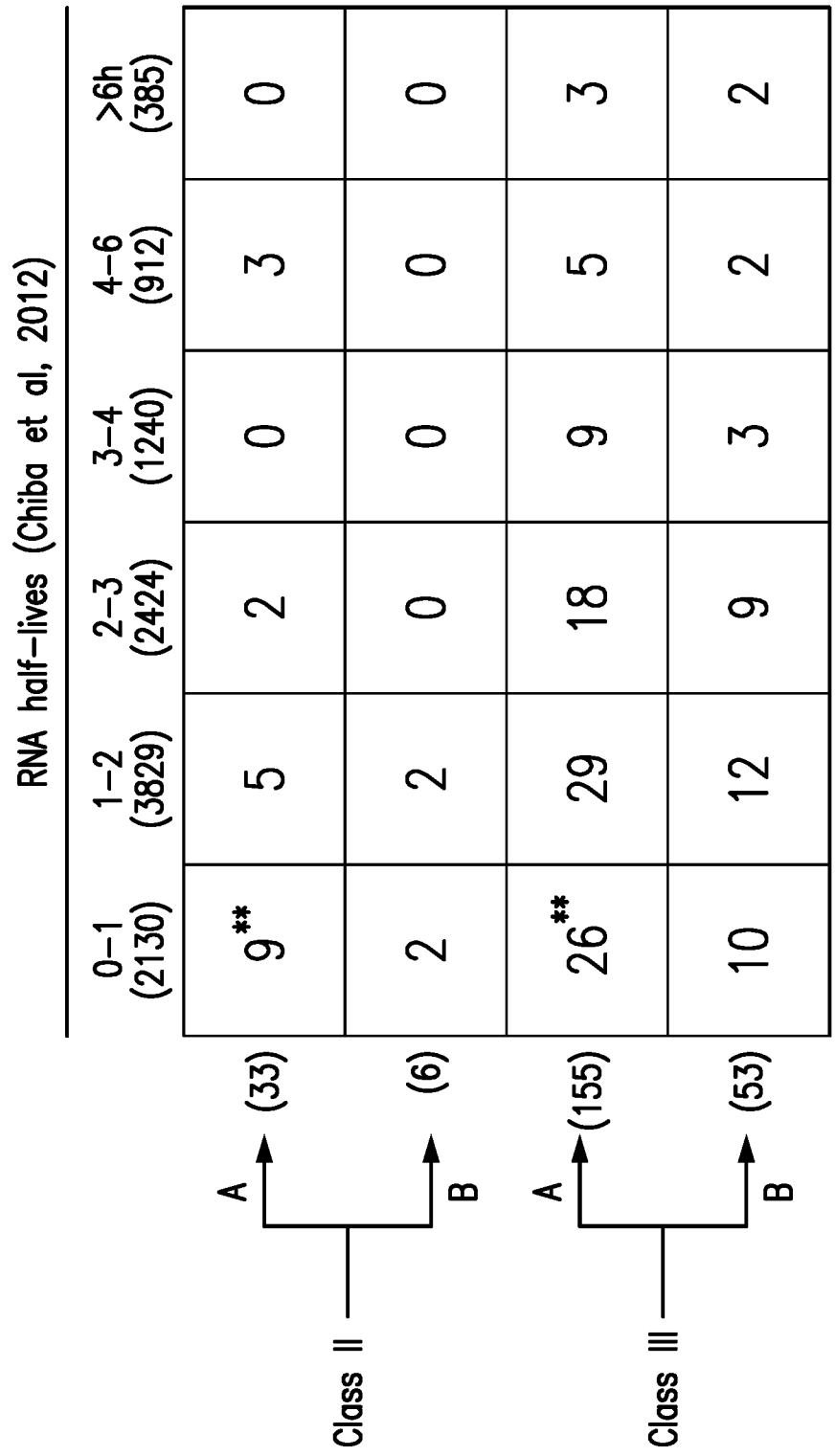

RNA half-lives (Chiba et al, 2012)
0–1 (2130)
1–2 (3829)
2–3 (2424)
3–4 (1240)
4–6 (912)
>6h (385)
Class II
A (33)
9**
5
2
0
3
0
B (6)
2
2
0
0
0
0
Class III
A (155)
26**
29
18
9
5
3
B (53)
10
12
9
3
2
2
Signigicance of Overlap ***<0.001 **<0.01

FIG. 18

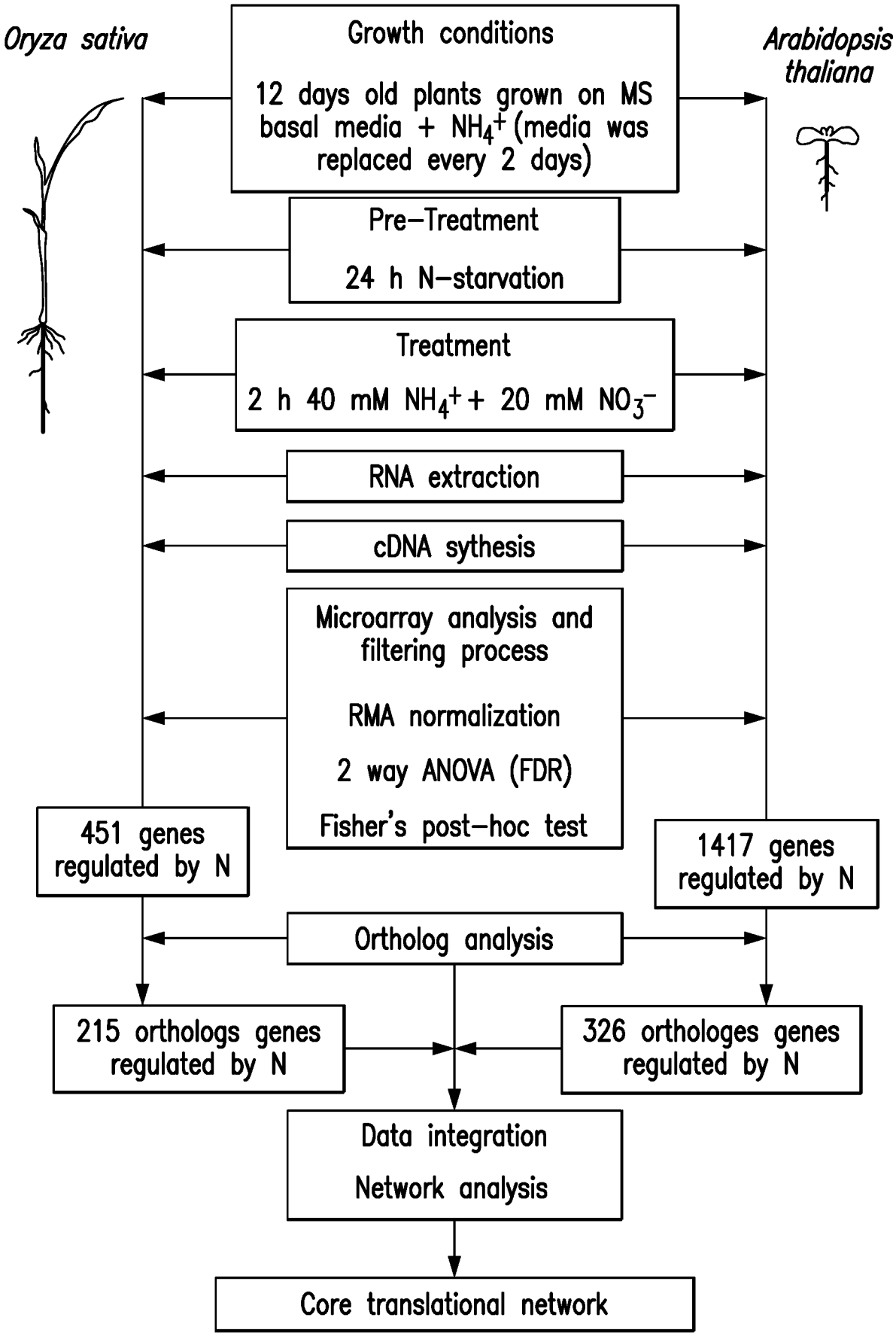

Oryza sativa
Growth conditions
12 days old plants grown on MS basal media + NH_4^+ (media was replaced every 2 days)
Arabidopsis thaliana
Pre–Treatment
24 h N–starvation
Treatment
2 h 40 mM NH_4^+ + 20 mM NO_3^-
RNA extraction
cDNA sythesis
Microarray analysis and filtering process
RMA normalization
2 way ANOVA (FDR)
Fisher's post–hoc test
451 genes regulated by N
1417 genes regulated by N
Ortholog analysis
215 orthologs genes regulated by N
326 orthologes genes regulated by N
Data integration
Network analysis
Core translational network

FIG. 19

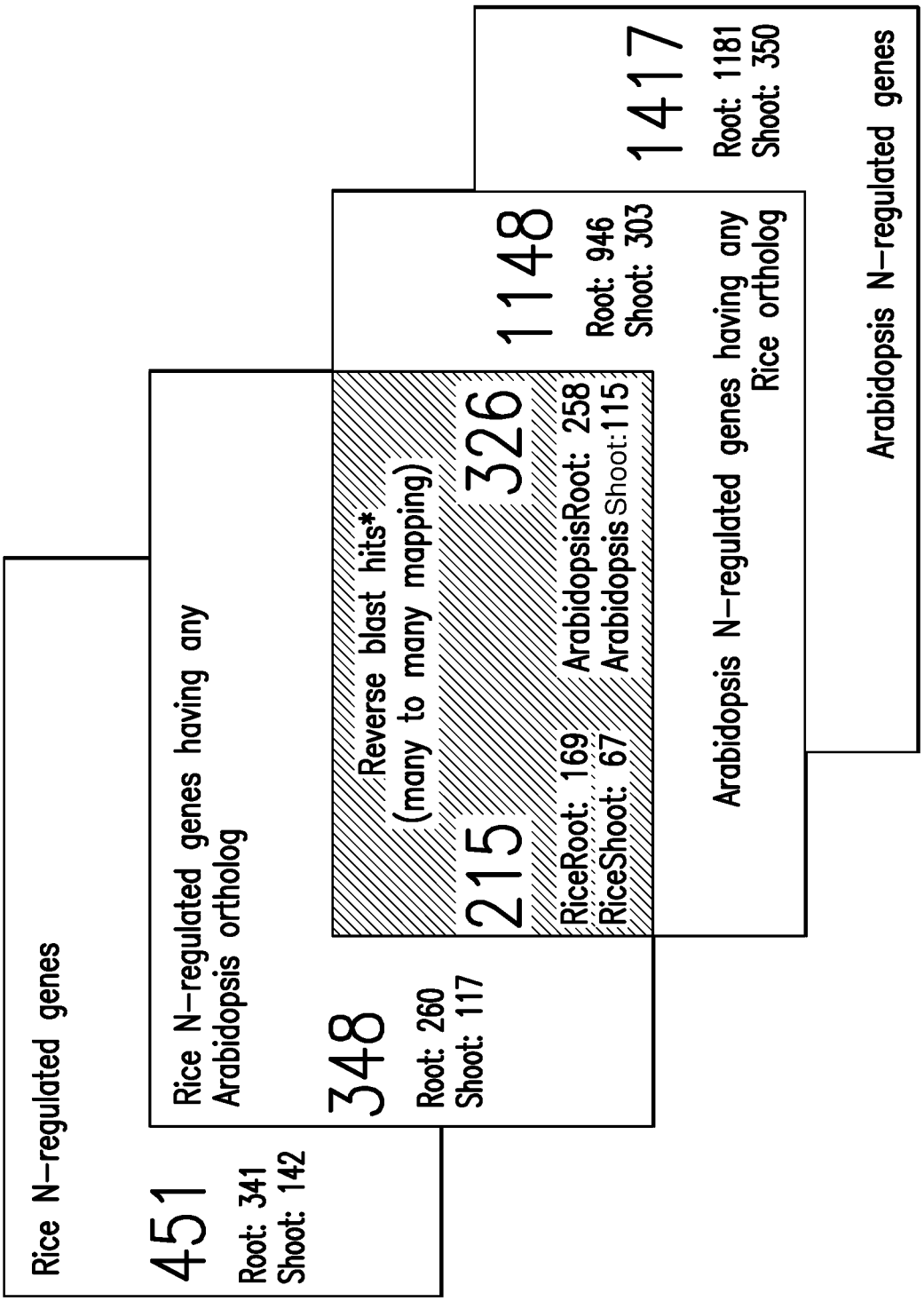

Rice N-regulated genes
451
Root: 341
Shoot: 142
Rice N-regulated genes having any Arabidopsis ortholog
348
Root: 260
Shoot: 117
Reverse blast hits*
(many to many mapping)
215
326
RiceRoot: 169
RiceShoot: 67
ArabidopsisRoot: 258
ArabidopsisShoot:115
Arabidopsis N-regulated genes having any Rice ortholog
1148
Root: 946
Shoot: 303
Arabidopsis N-regulated genes
1417
Root: 1181
Shoot: 350

FIG. 20

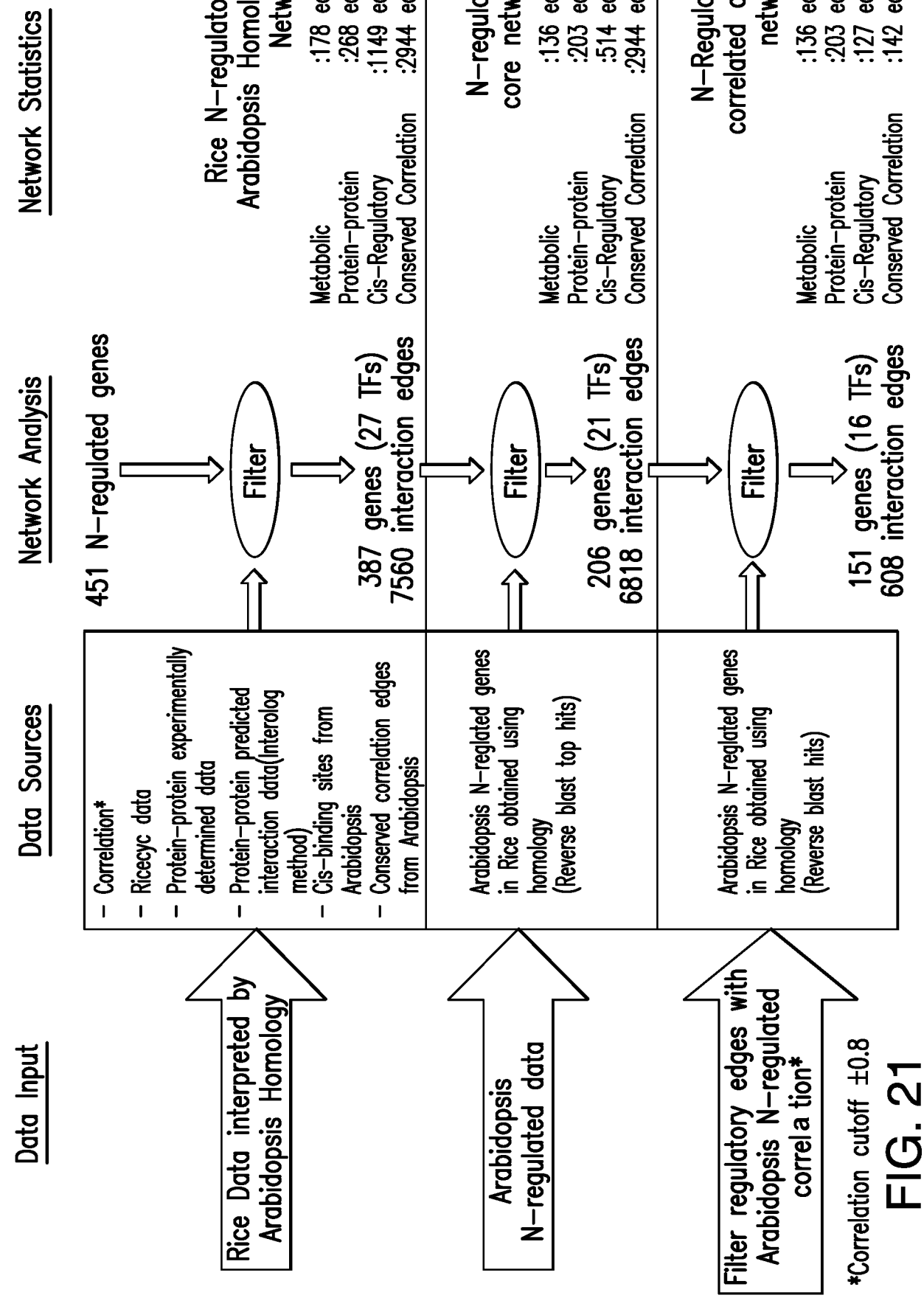

Data Input
Data Sources
Network Analysis
Network Statistics
Rice Data interpreted by Arabidopsis Homology
- Correlation*
- Ricecyc data
- Protein–protein experimentally determined data
- Protein–protein predicted interaction data(Interolog method)
- Cis–binding sites from Arabidopsis
- Conserved correlation edges from Arabidopsis
451 N–regulated genes
Filter
387 genes (27 TFs)
7560 interaction edges
Rice N–regulatory+ Arabidopsis Homology Network
Metabolic :178 edges
Protein–protein :268 edges
Cis–Regulatory :1149 edges
Conserved Correlation :2944 edges
Arabidopsis N–regulated data
Arabidopsis N–reglated genes in Rice obtained using homology (Reverse blast top hits)
Filter
206 genes (21 TFs)
6818 interaction edges
N–regulated core network
Metabolic :136 edges
Protein–protein :203 edges
Cis–Regulatory :514 edges
Conserved Correlation :2944 edges
Filter regulatory edges with Arabidopsis N–regulated correla tion*
Arabidopsis N–reglated genes in Rice obtained using homology (Reverse blast hits)
Filter
151 genes (16 TFs)
608 interaction edges
N–Regulated correlated core network
Metabolic :136 edges
Protein–protein :203 edges
Cis–Regulatory :127 edges
Conserved Correlation :142 edges
*Correlation cutoff ±0.8

FIG. 21

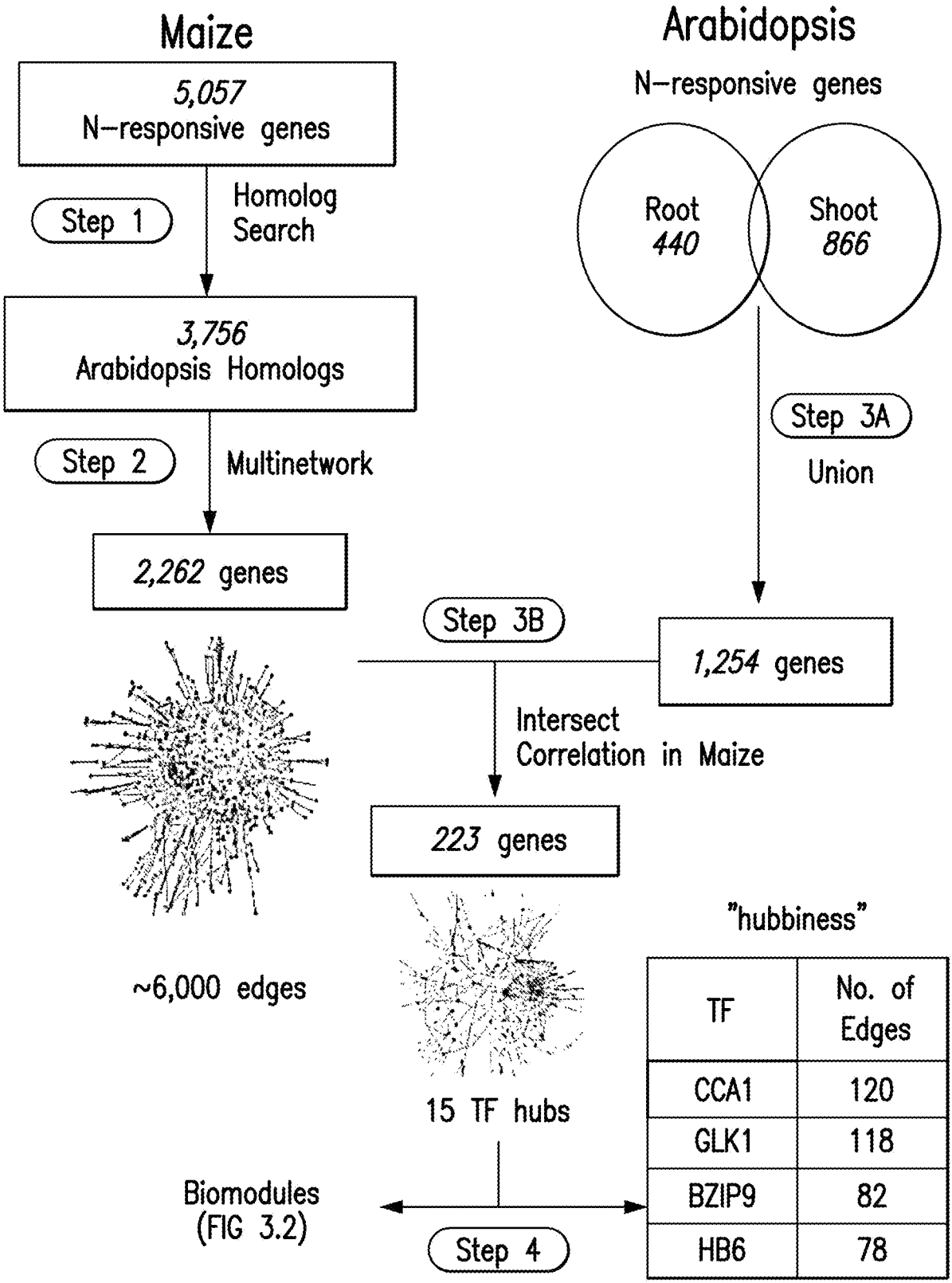

Maize
5,057
N-responsive genes
Step 1
Homolog Search
3,756
Arabidopsis Homologs
Step 2
Multinetwork
2,262 genes
~6,000 edges
Arabidopsis
N-responsive genes
Root
440
Shoot
866
Step 3A
Union
Step 3B
1,254 genes
Intersect
Correlation in Maize
223 genes
15 TF hubs
Biomodules
(FIG 3.2)
Step 4
"hubbiness"
TF
No. of Edges
CCA1
120
GLK1
118
BZIP9
82
HB6
78

FIG. 22

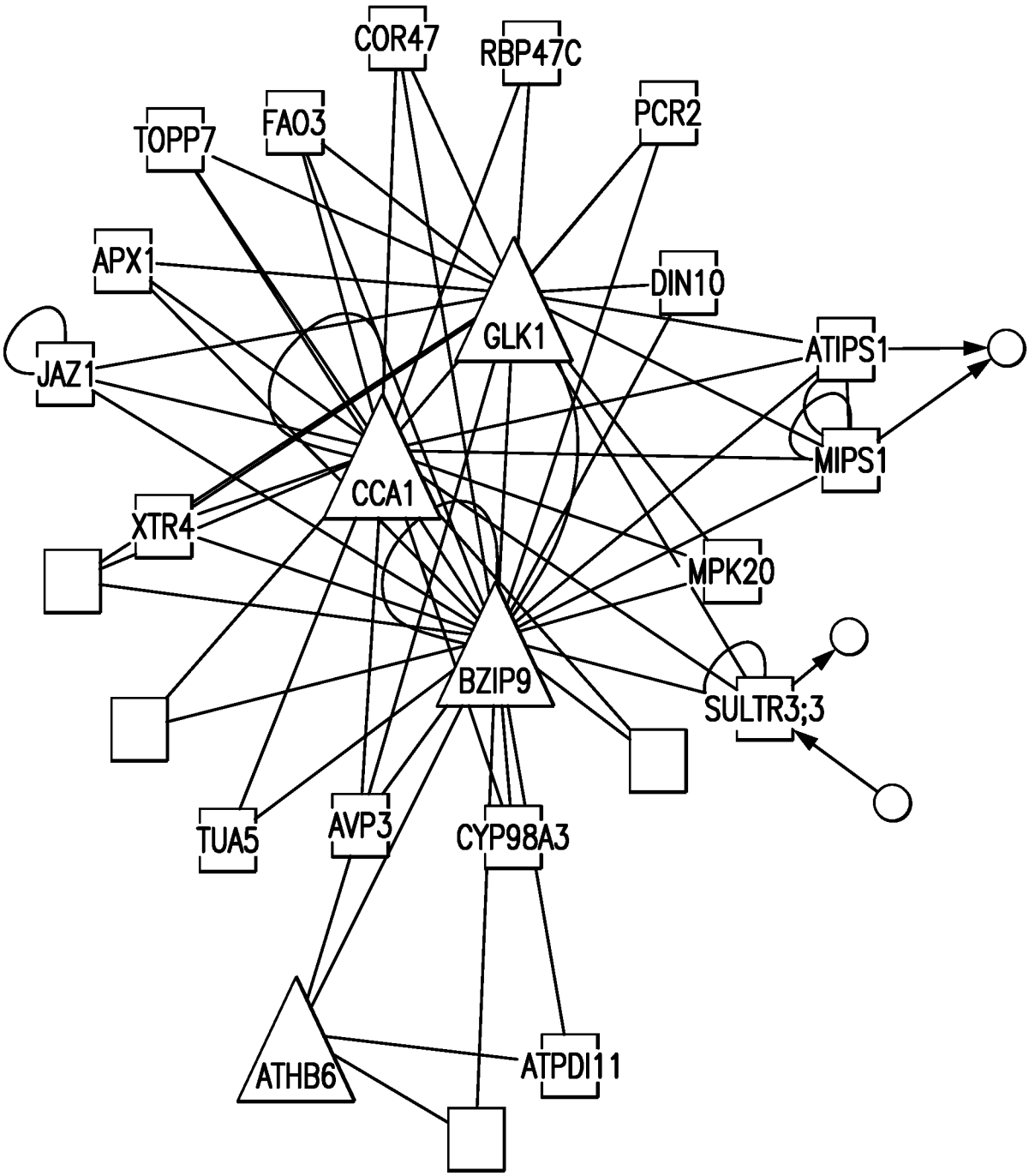

COR47
RBP47C
PCR2
FAO3
TOPP7
APX1
DIN10
GLK1
ATIPS1
JAZ1
MIPS1
CCA1
XTR4
MPK20
BZIP9
SULTR3;3
TUA5
AVP3
CYP98A3
ATHB6
ATPDI11

FIG. 23

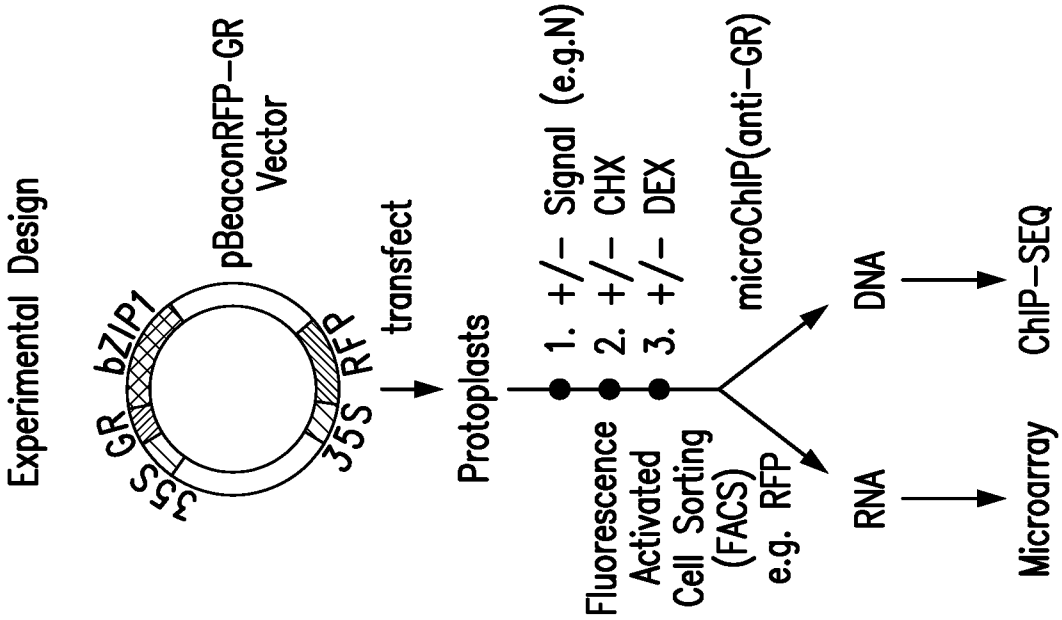


FIG. 24C

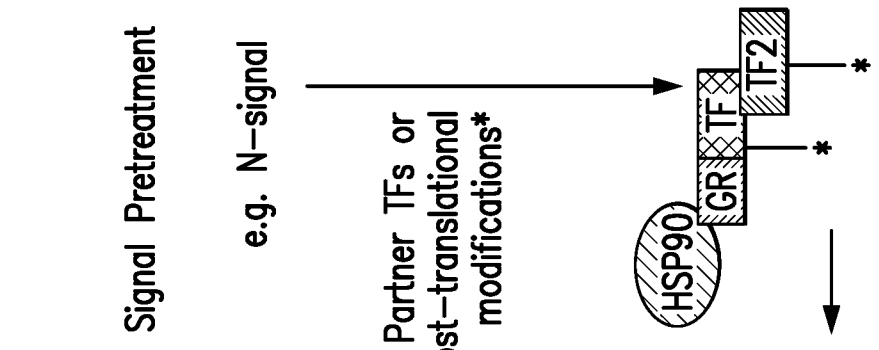


FIG. 24B

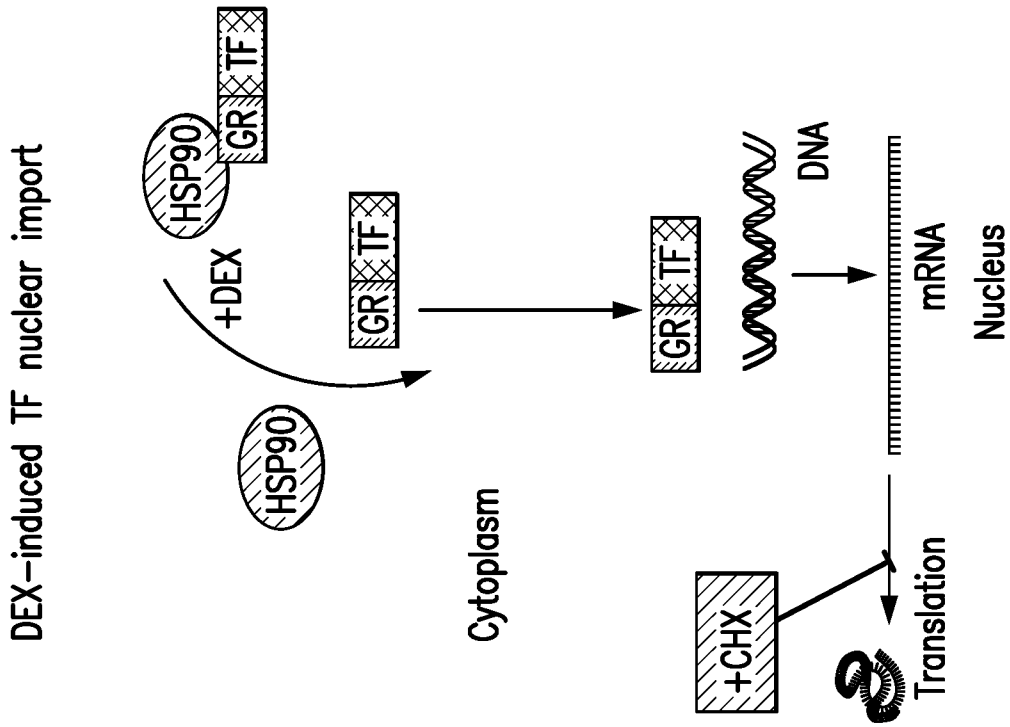


FIG. 24A

D. Bioinformatics flowchart

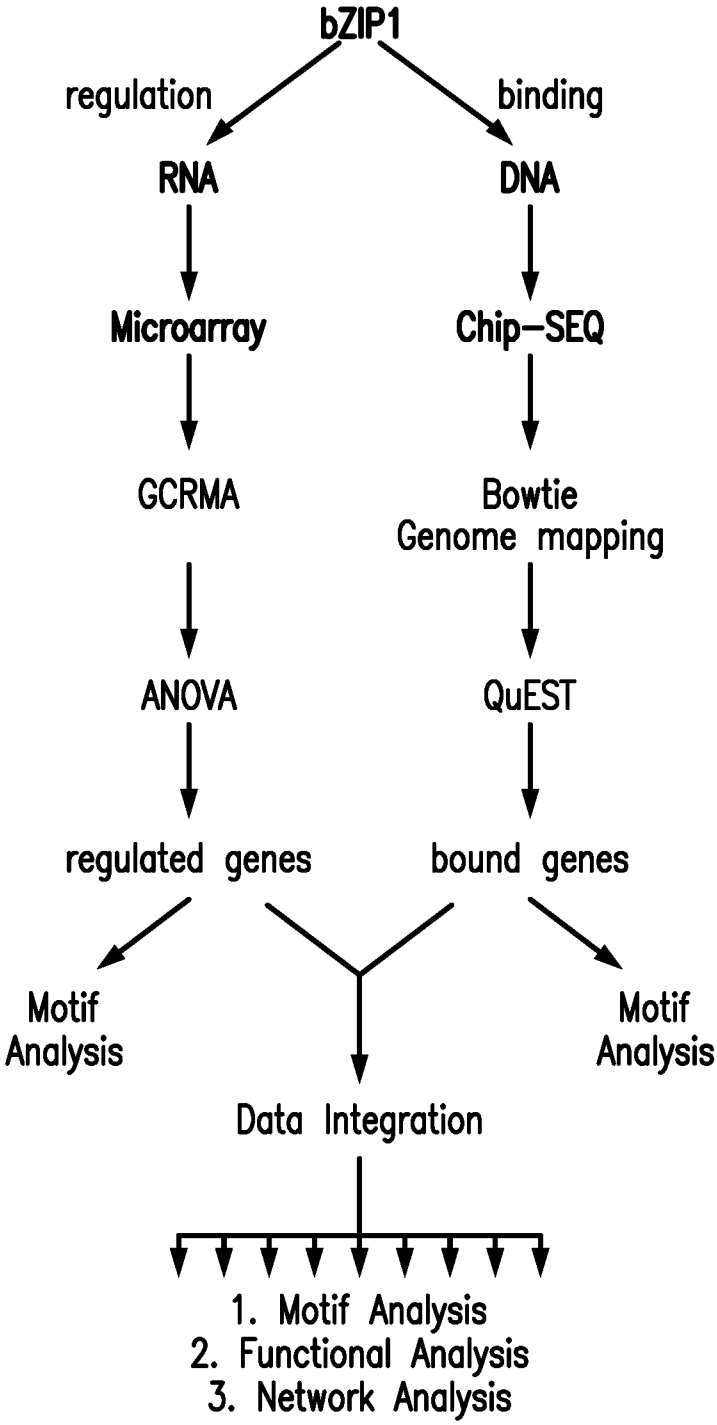


FIG. 24D

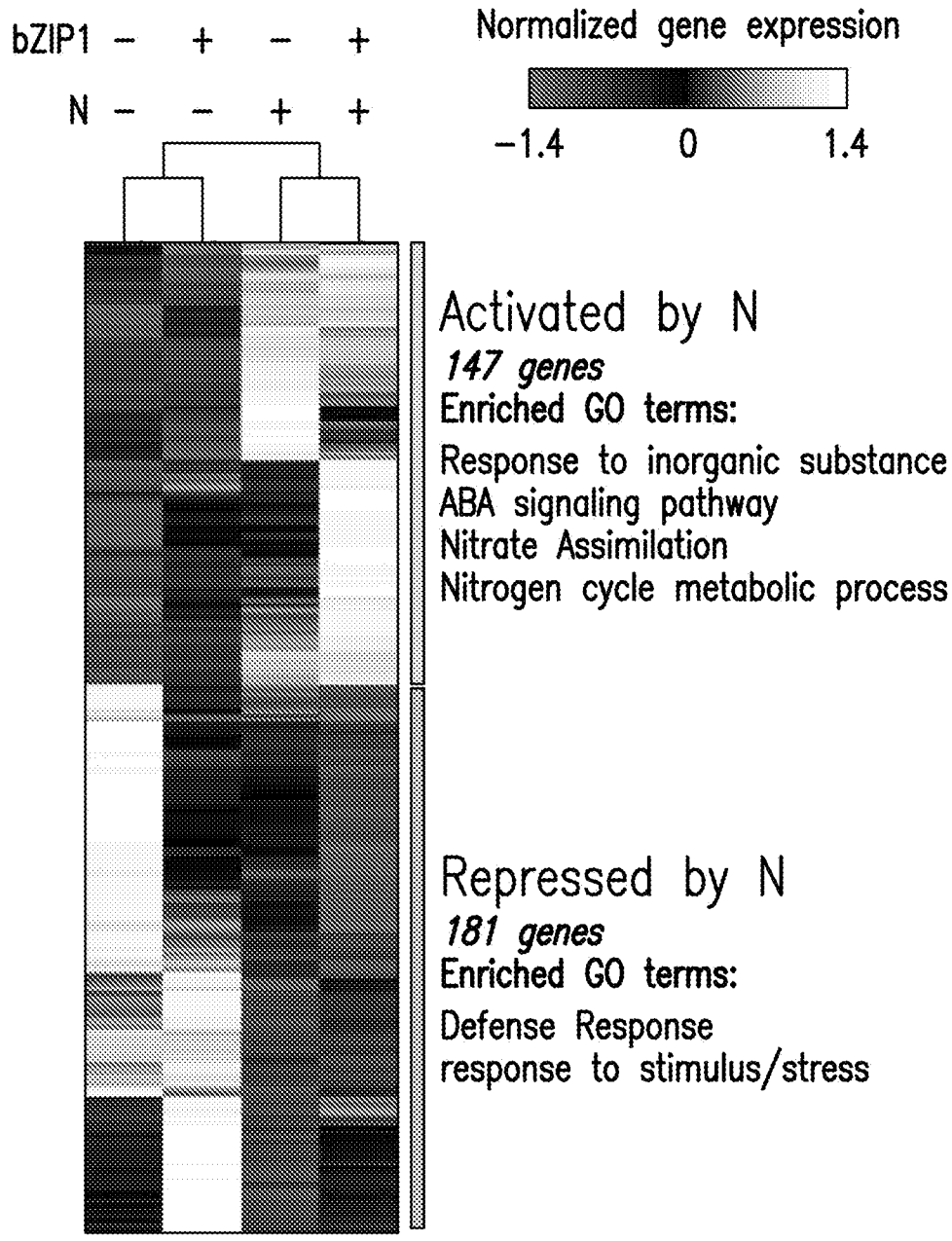

bZIP1 − + − +
N − − + +
Normalized gene expression
−1.4 0 1.4
Activated by N
147 genes
Enriched GO terms:
Response to inorganic substance
ABA signaling pathway
Nitrate Assimilation
Nitrogen cycle metabolic process
Repressed by N
181 genes
Enriched GO terms:
Defense Response
response to stimulus/stress

FIG. 25

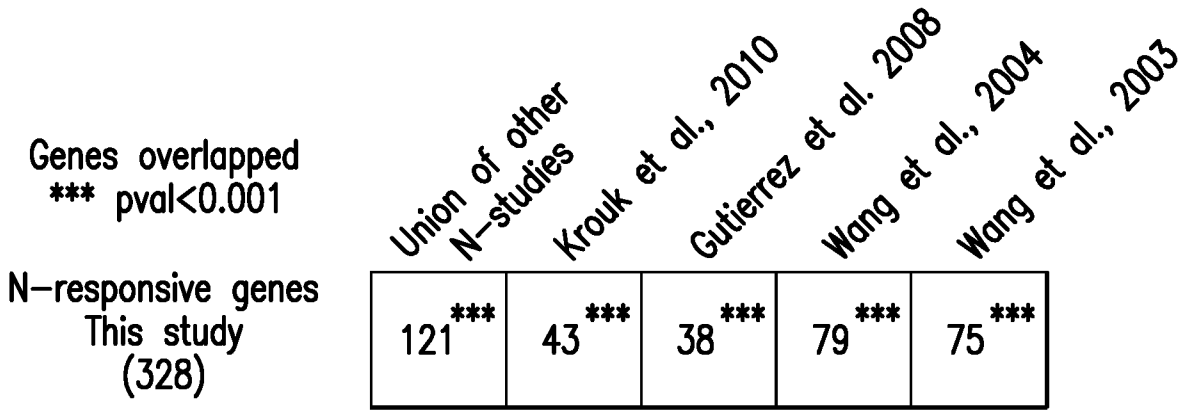

Genes overlapped
*** pval<0.001
Union of other N-studies
Krouk et al., 2010
Gutierrez et al. 2008
Wang et al., 2004
Wang et al., 2003
N-responsive genes This study (328)
121***
43***
38***
79***
75***

FIG. 26

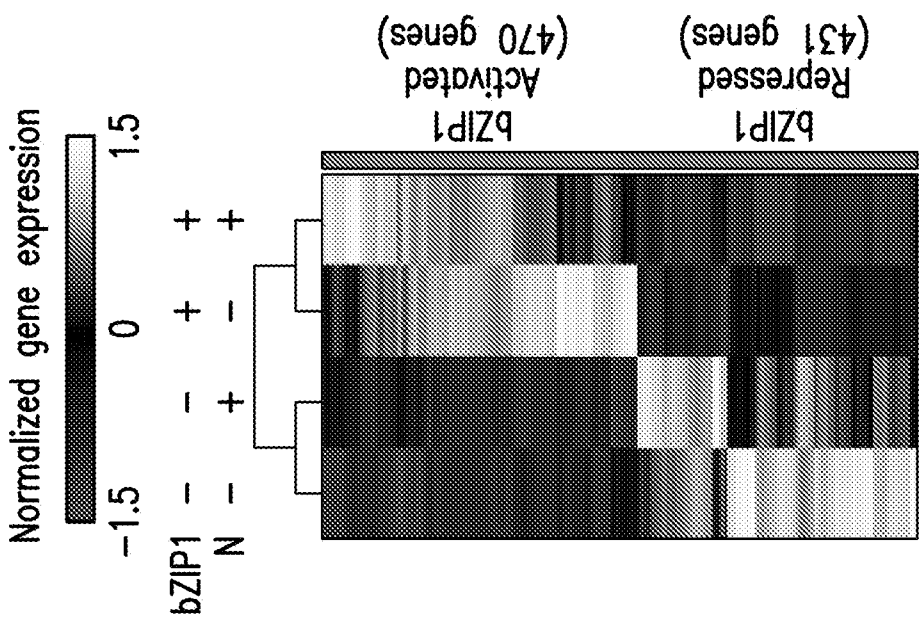


FIG. 27A

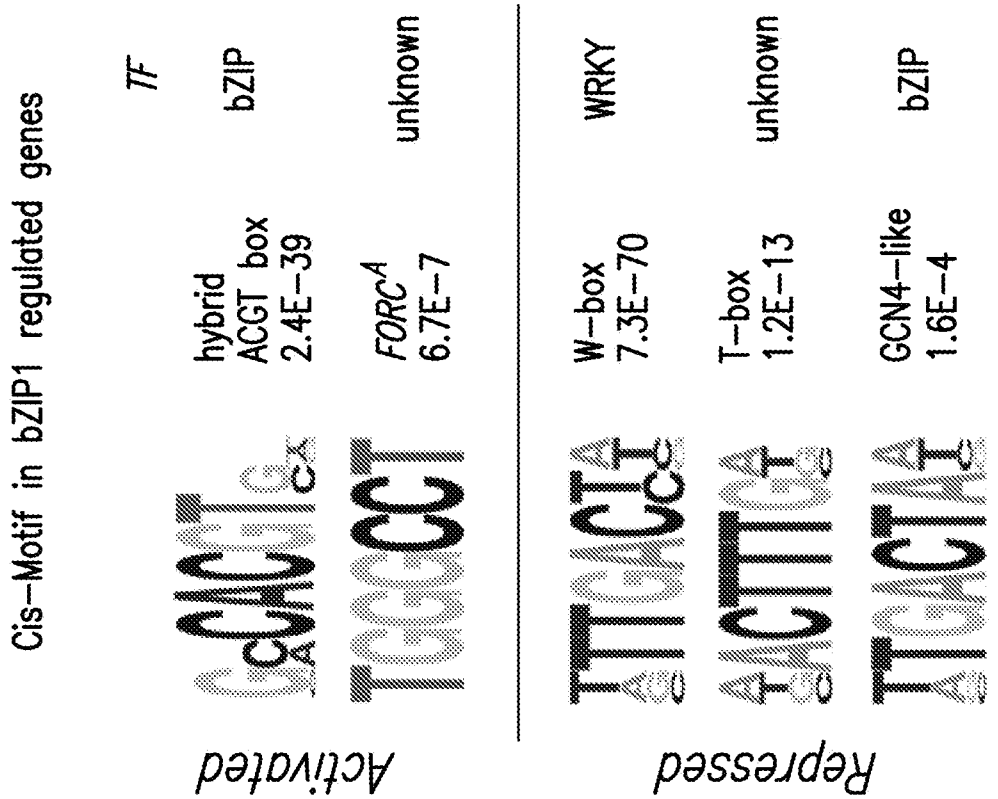


FIG. 27B

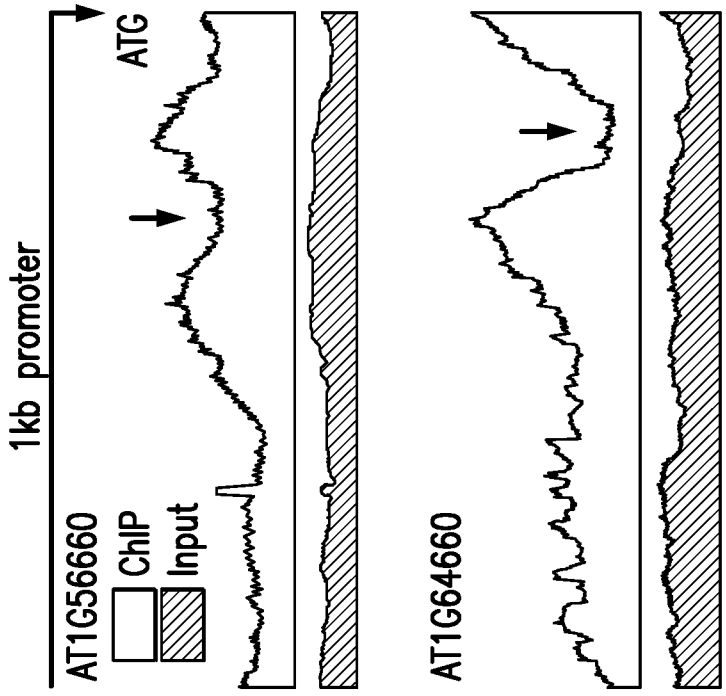


FIG. 27C

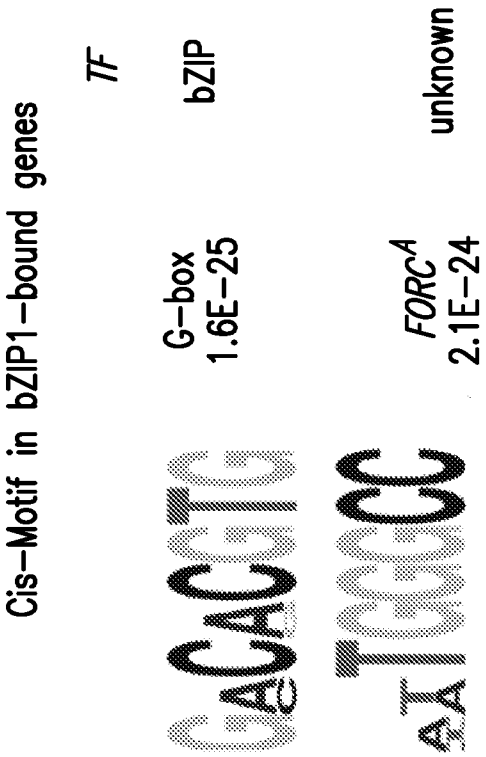


FIG. 27D

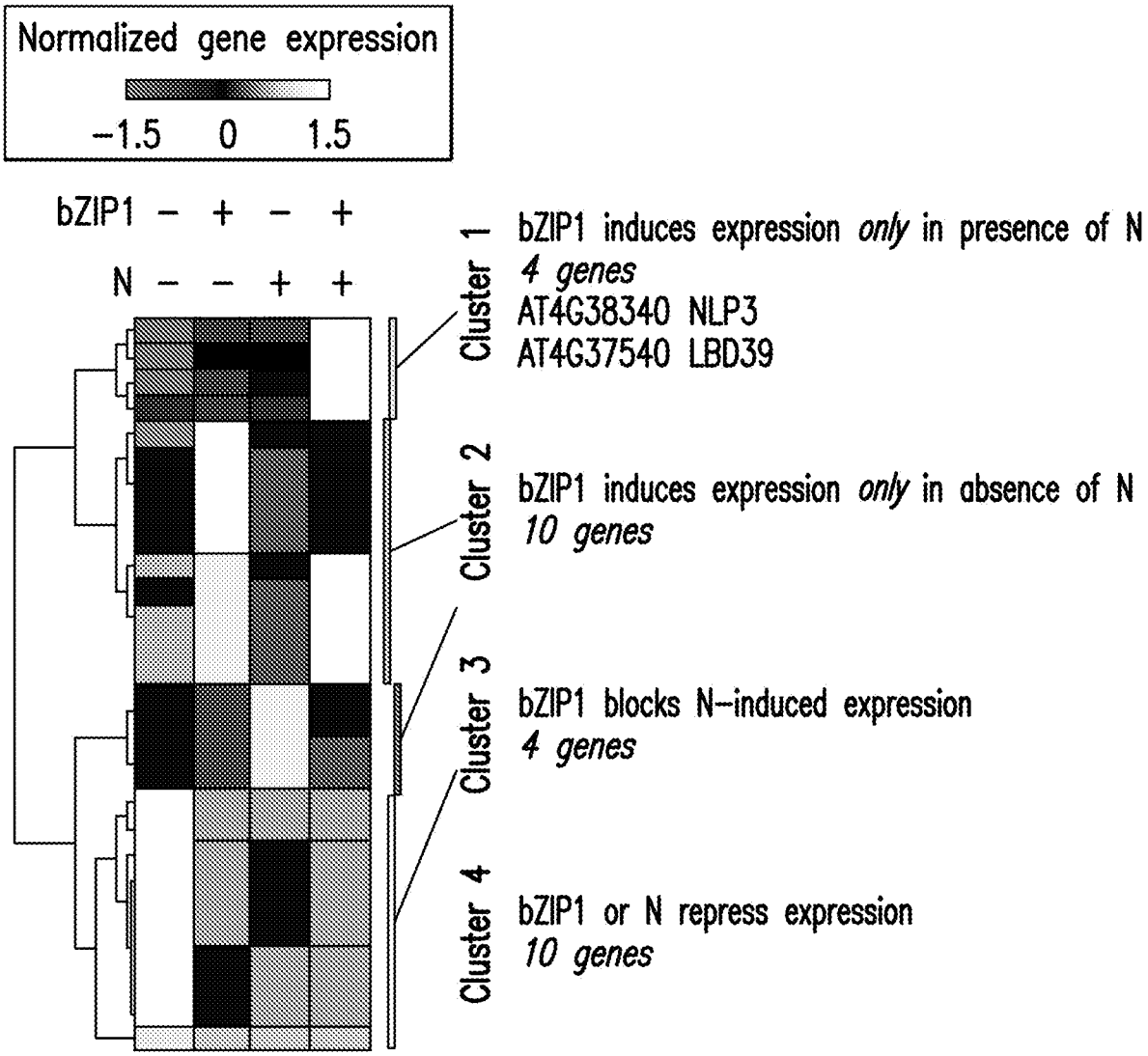

Normalized gene expression
−1.5 0 1.5
bZIP1 − + − +
N − − + +
Cluster 1
bZIP1 induces expression *only* in presence of N
4 genes
AT4G38340 NLP3
AT4G37540 LBD39
Cluster 2
bZIP1 induces expression *only* in absence of N
10 genes
Cluster 3
bZIP1 blocks N−induced expression
4 genes
Cluster 4
bZIP1 or N repress expression
10 genes

FIG. 28

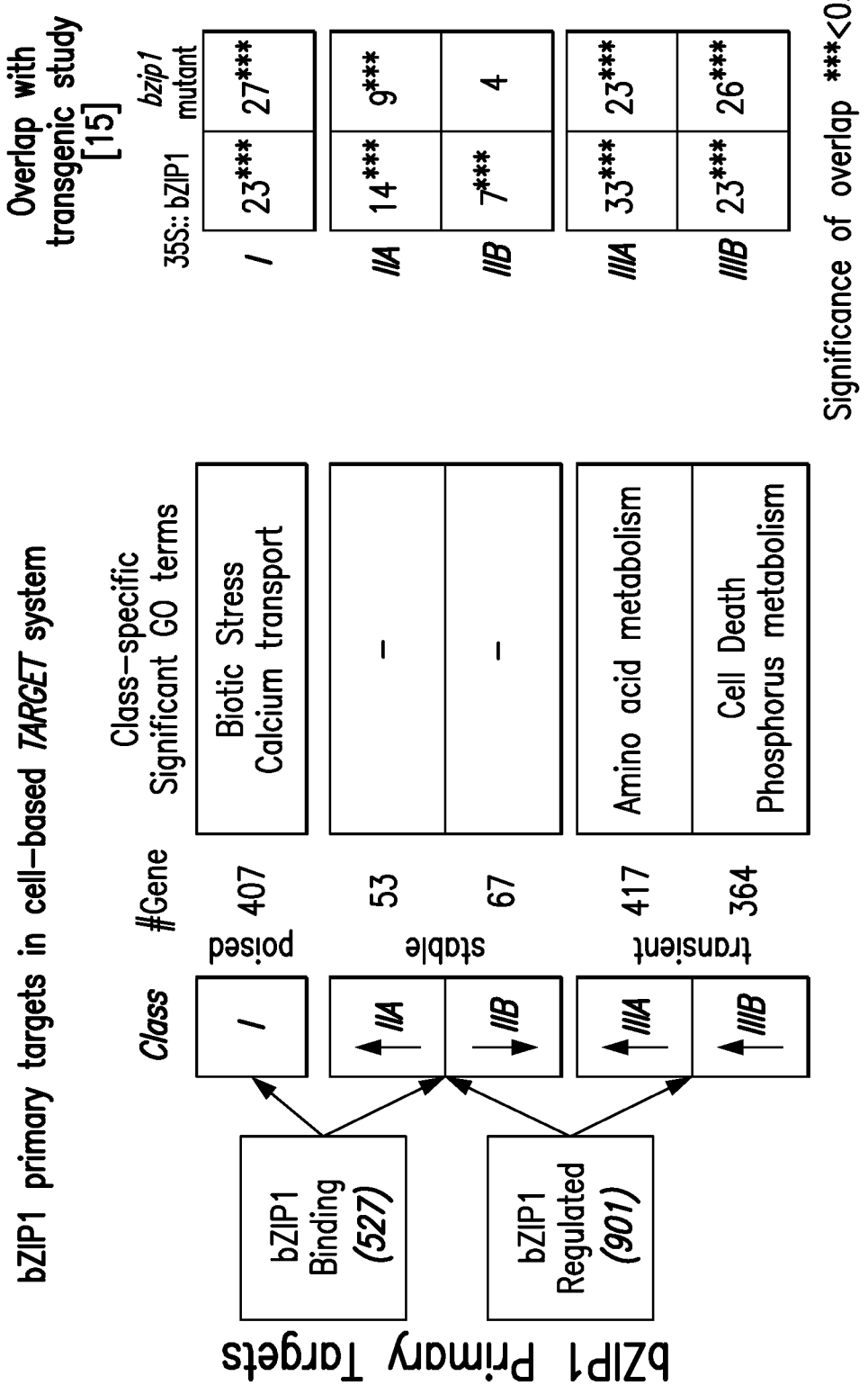


FIG. 29A

FIG. 29B

Overlap with N-responsive genes

	TARGET		*in planta*			
			Early			Union
	N	NXbZIP1	3-6 min [1]	20 min [24]	Transient [1]	[1,17, 24,25]
I	6	NA	6	17	7	140***
IIA	1	0	1	6**	2	26***
IIB	1	0	2	7**	2	33***
IIIA	27***	14***	9***	37***	15***	146***
IIIB	2	14***	0	18**	4	93***

Significance of overlap ***<0.001 **<0.01

FIG. 29C

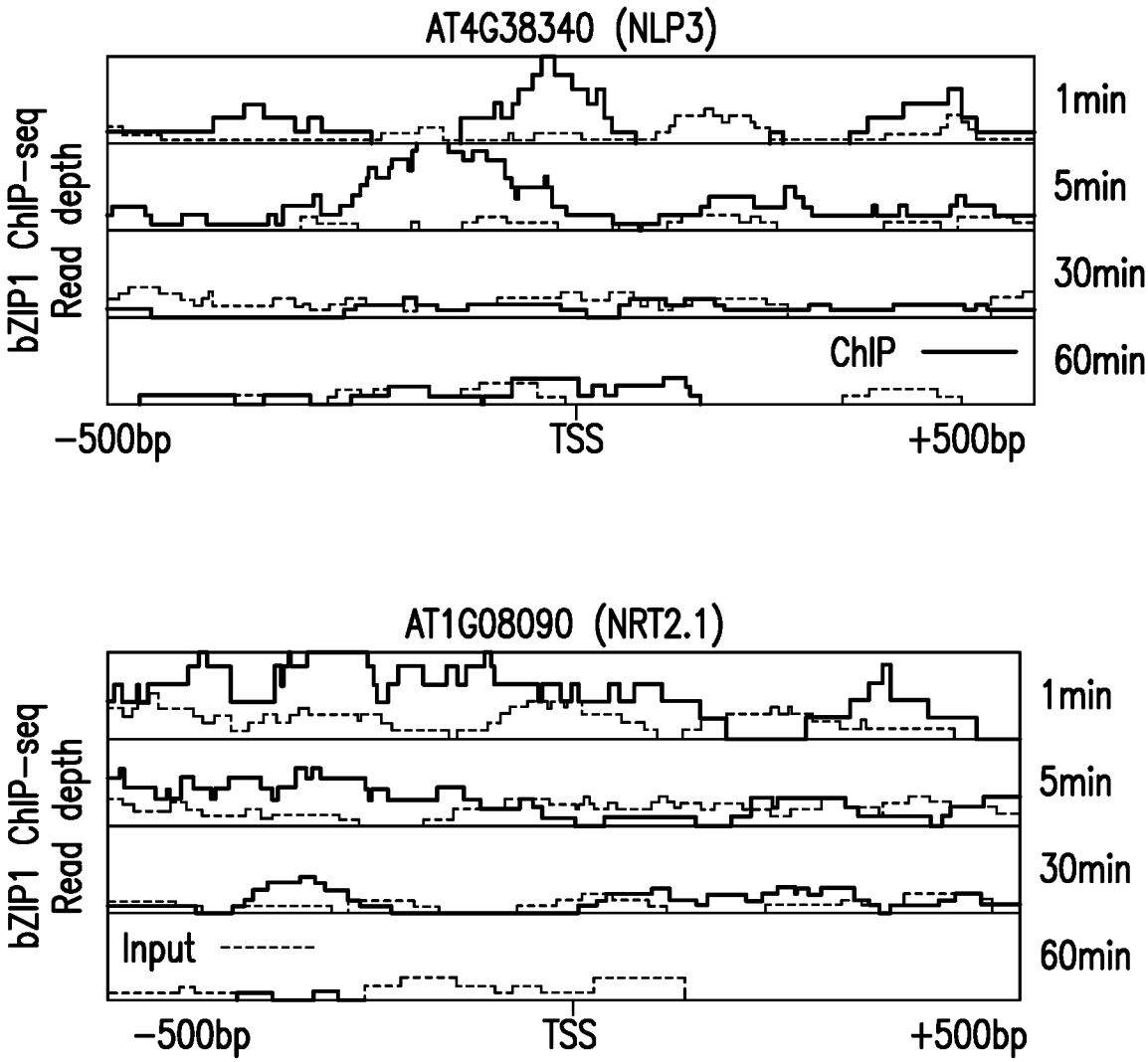

AT4G38340 (NLP3)
bZIP1 ChIP-seq Read depth
1min
5min
30min
60min
ChIP
−500bp
TSS
+500bp
AT1G08090 (NRT2.1)
bZIP1 ChIP-seq Read depth
1min
5min
30min
60min
Input
−500bp
TSS
+500bp

FIG. 29D

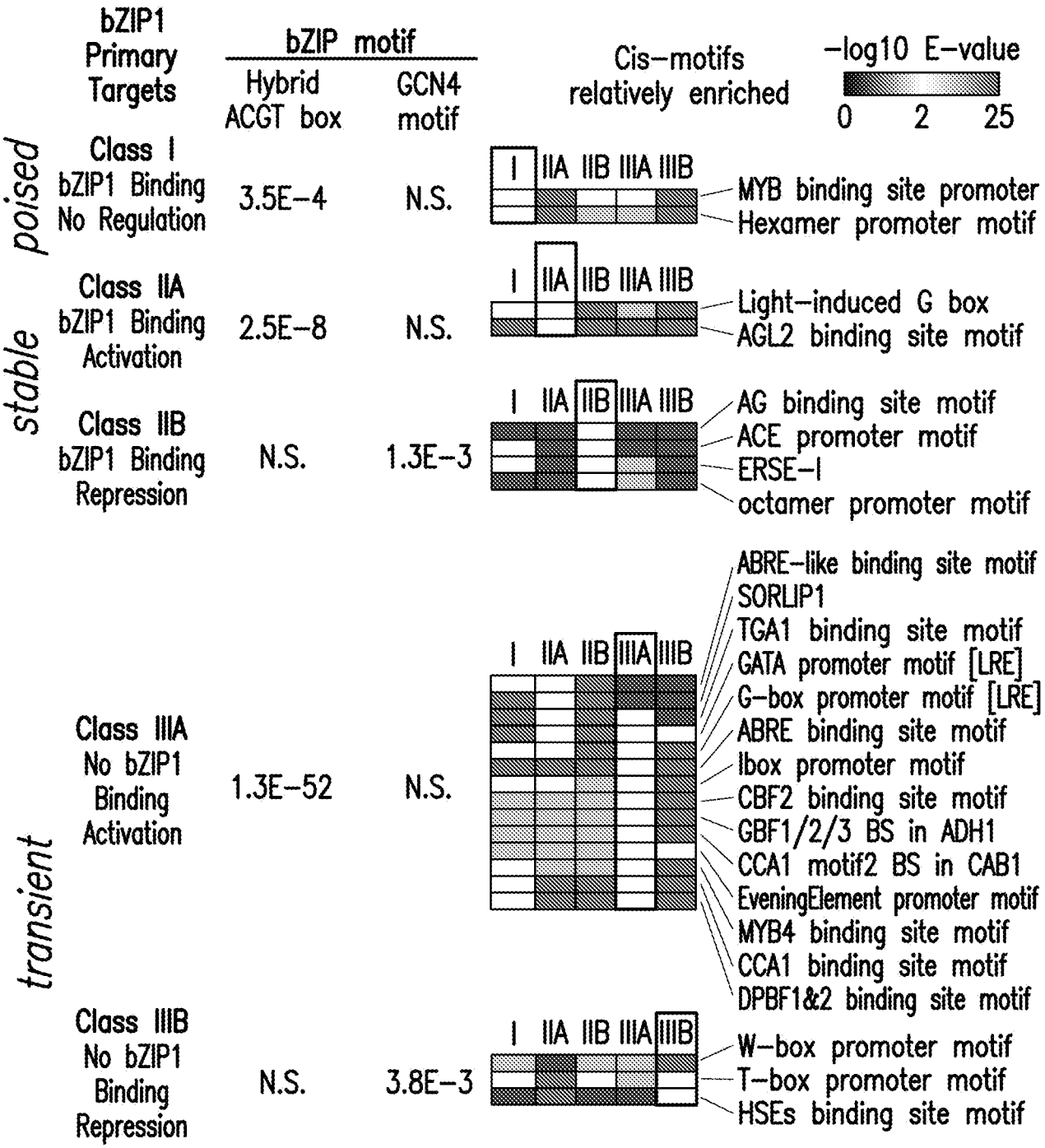

bZIP1 Primary Targets
bZIP motif
Hybrid ACGT box
GCN4 motif
Cis-motifs relatively enriched
-log10 E-value
0 2 25
poised
stable
transient
Class I
bZIP1 Binding
No Regulation
3.5E-4
N.S.
I IIA IIB IIIA IIIB
MYB binding site promoter
Hexamer promoter motif
Class IIA
bZIP1 Binding
Activation
2.5E-8
N.S.
Light-induced G box
AGL2 binding site motif
Class IIB
bZIP1 Binding
Repression
N.S.
1.3E-3
AG binding site motif
ACE promoter motif
ERSE-I
octamer promoter motif
Class IIIA
No bZIP1
Binding
Activation
1.3E-52
N.S.
ABRE-like binding site motif
SORLIP1
TGA1 binding site motif
GATA promoter motif [LRE]
G-box promoter motif [LRE]
ABRE binding site motif
Ibox promoter motif
CBF2 binding site motif
GBF1/2/3 BS in ADH1
CCA1 motif2 BS in CAB1
EveningElement promoter motif
MYB4 binding site motif
CCA1 binding site motif
DPBF1&2 binding site motif
Class IIIB
No bZIP1
Binding
Repression
N.S.
3.8E-3
W-box promoter motif
T-box promoter motif
HSEs binding site motif

FIG. 30

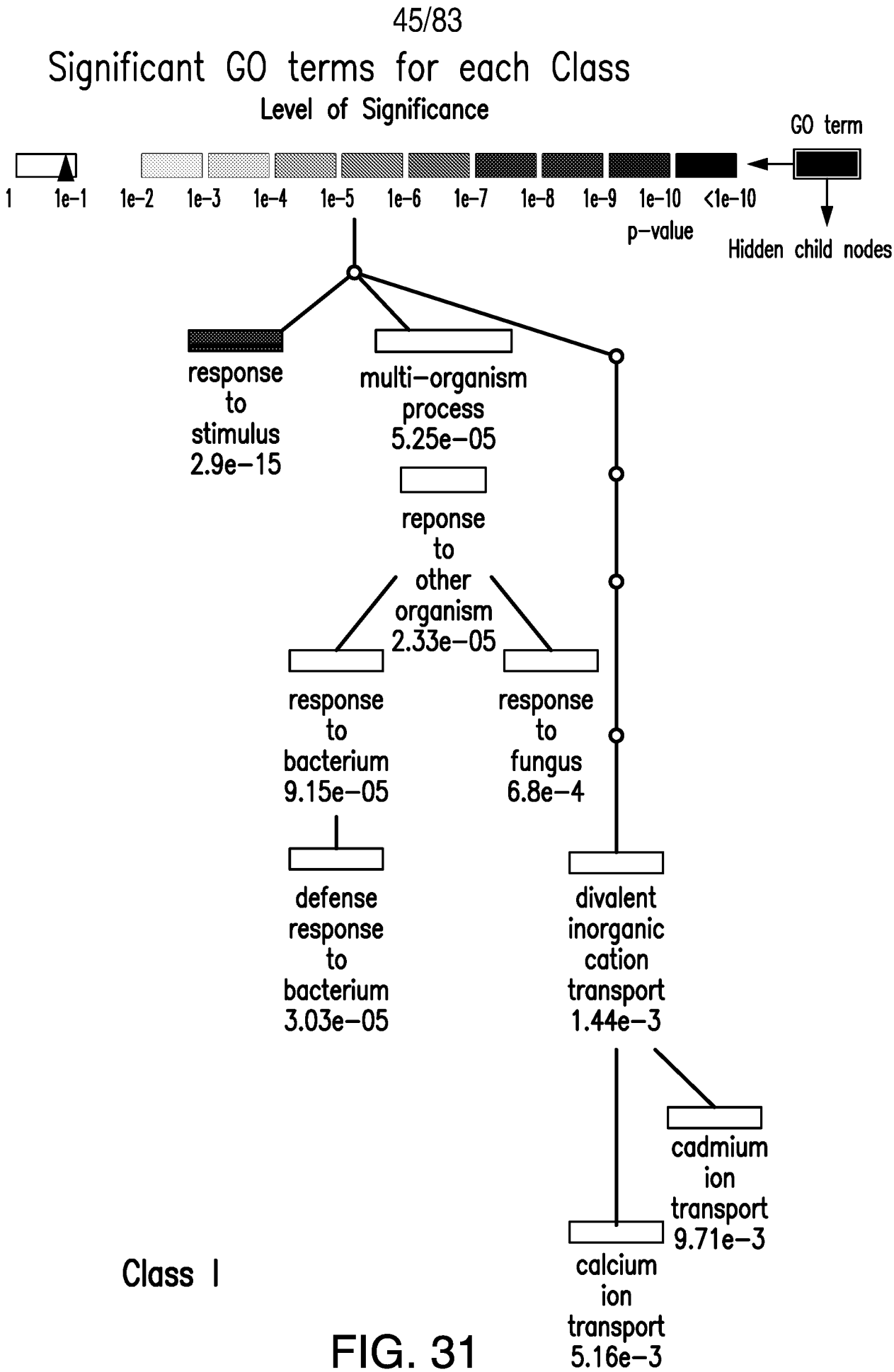

Significant GO terms for each Class
Level of Significance
GO term
1
1e-1
1e-2
1e-3
1e-4
1e-5
1e-6
1e-7
1e-8
1e-9
1e-10
<1e-10
p-value
Hidden child nodes
response to stimulus 2.9e-15
multi-organism process 5.25e-05
reponse to other organism 2.33e-05
response to bacterium 9.15e-05
response to fungus 6.8e-4
defense response to bacterium 3.03e-05
divalent inorganic cation transport 1.44e-3
cadmium ion transport 9.71e-3
calcium ion transport 5.16e-3
Class I

FIG. 31

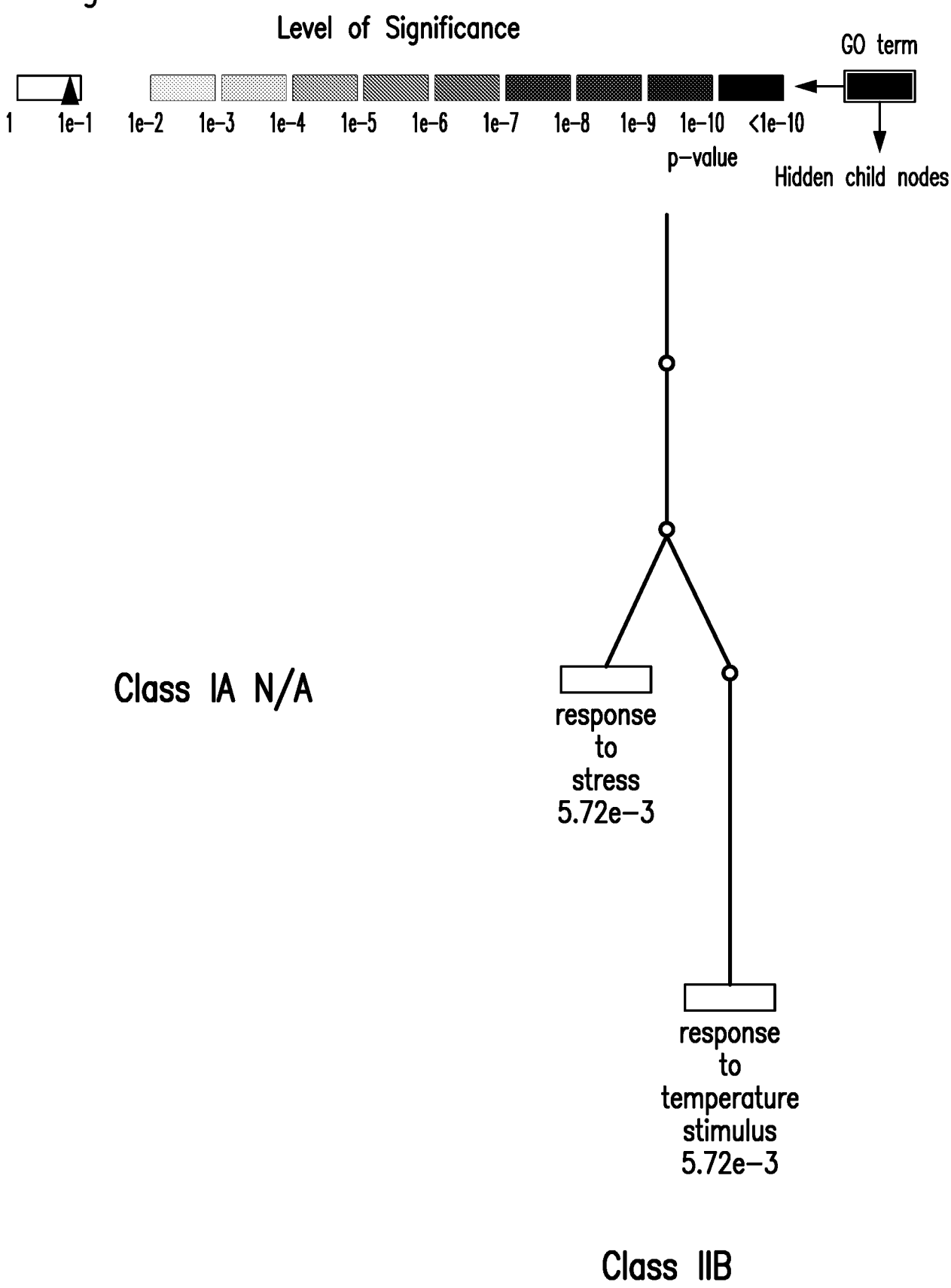


FIG. 31(Continued)

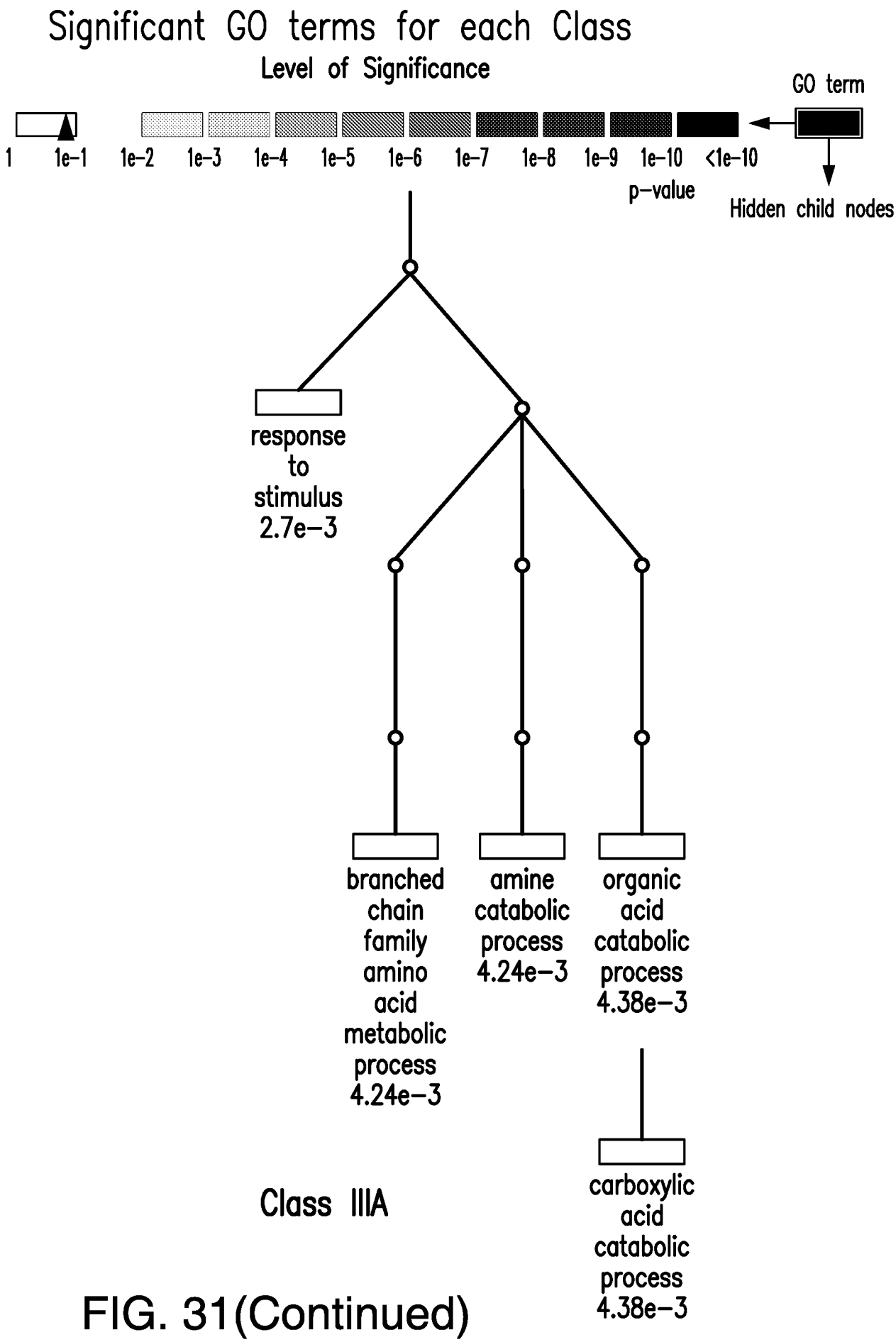
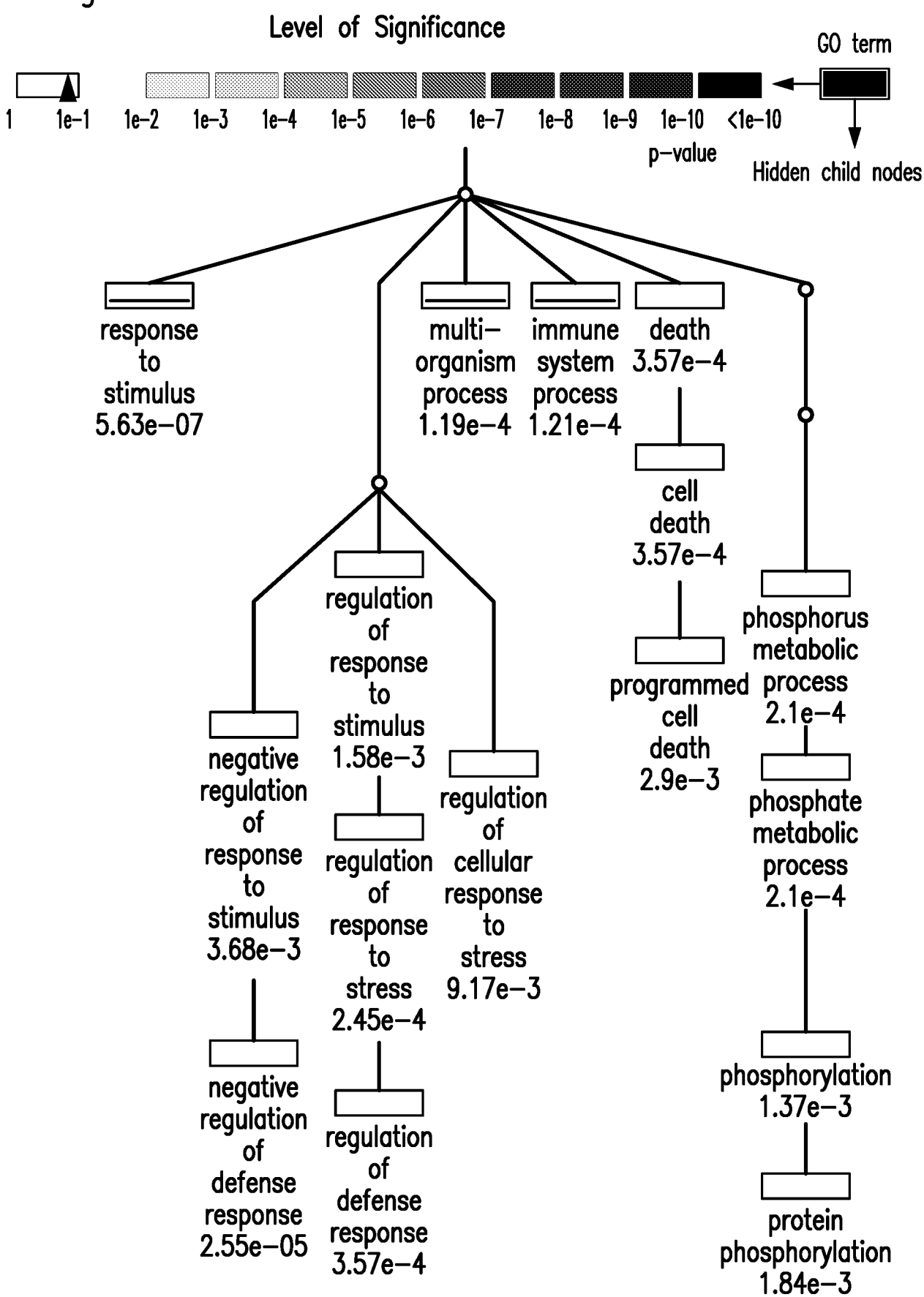


FIG. 31(Continued)



Class IIIB

FIG. 31(Continued)

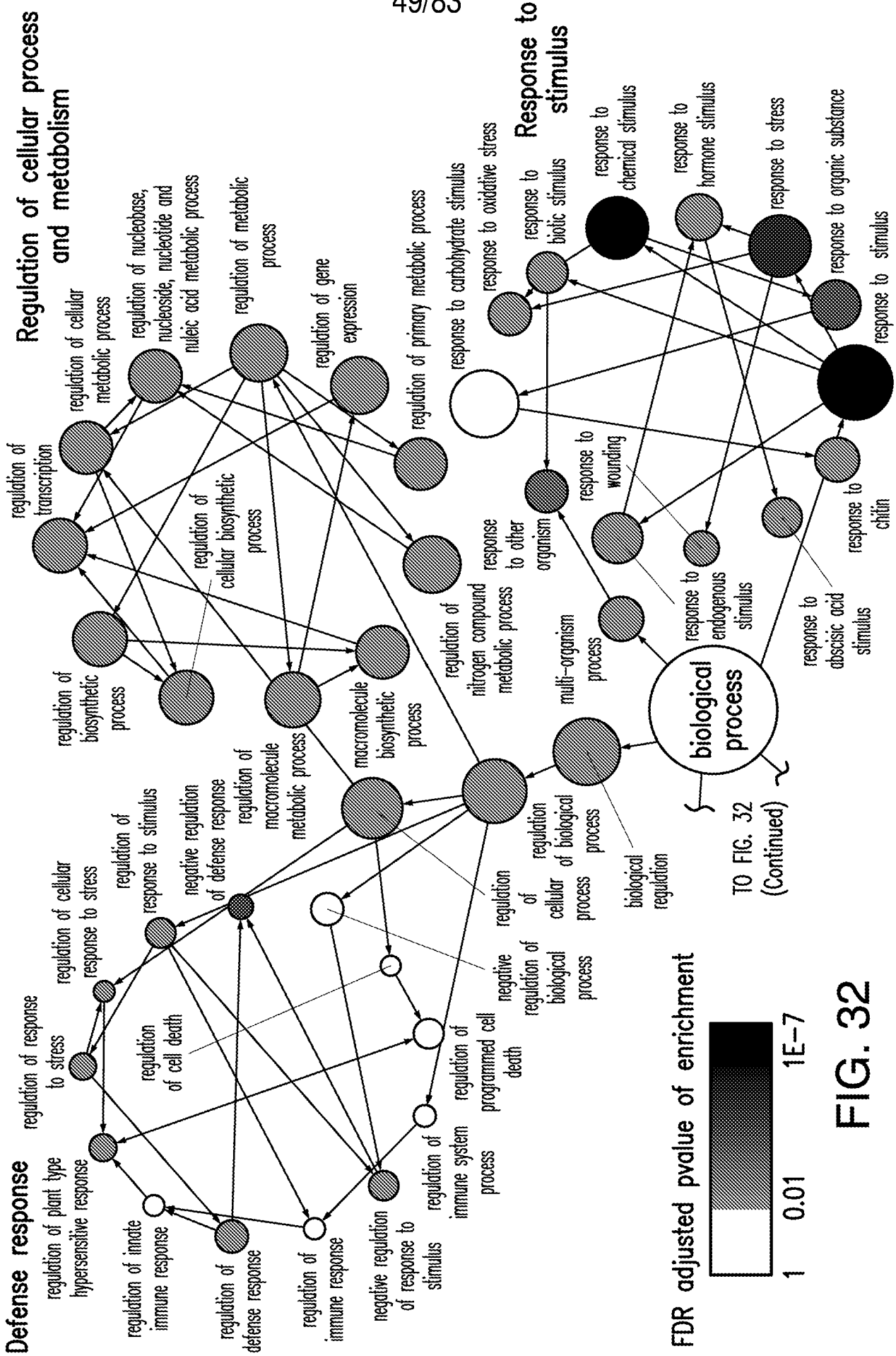

Defense response
regulation of response to stress
regulation of plant type hypersensitive response
regulation of innate immune response
regulation of defense response
regulation of immune response
negative regulation of response to stimulus
regulation of immune system process
regulation of programmed cell death
regulation of cell death
regulation of cellular response to stress
regulation of response to stimulus
negative regulation of defense response
negative regulation of biological process
regulation of biological process
regulation of macromolecule metabolic process
macromolecule biosynthetic process
regulation of biosynthetic process
regulation of cellular biosynthetic process
regulation of transcription
regulation of cellular metabolic process
regulation of nucleobase, nucleoside, nucleotide and nuleic acid metabolic process
regulation of metabolic process
regulation of gene expression
regulation of primary metabolic process
regulation of nitrogen compound metabolic process
Regulation of cellular process and metabolism
biological process
multi-organism process
biological regulation
response to other organism
response to wounding
response to endogenous stimulus
response to abscisic acid stimulus
response to chitin
response to carbohydrate stimulus
response to oxidative stress
response to biotic stimulus
response to chemical stimulus
response to hormone stimulus
response to stress
response to organic substance
response to stimulus
Response to stimulus
TO FIG. 32 (Continued)
FDR adjusted pvalue of enrichment
1
0.01
1E-7

FIG. 32

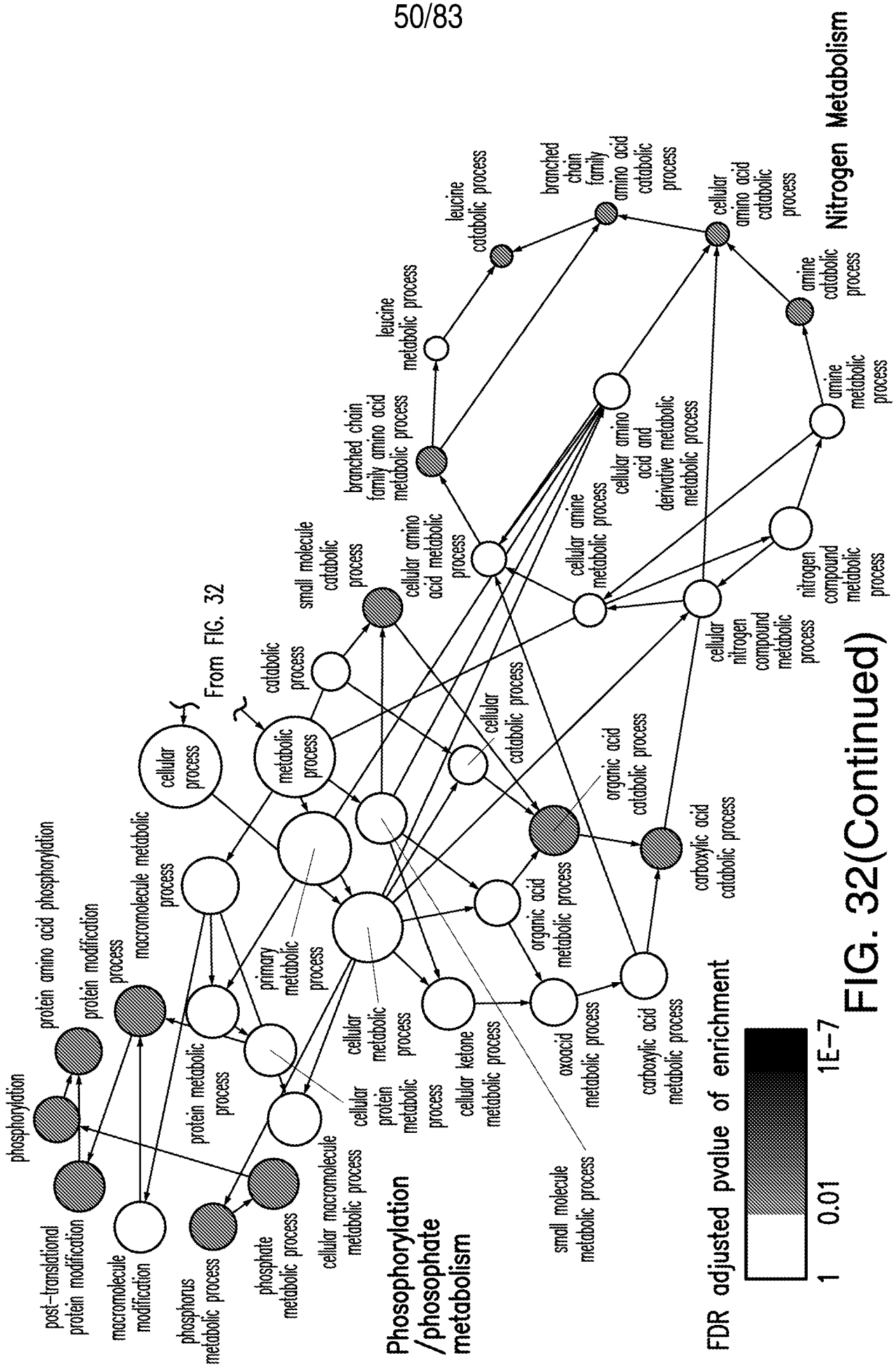


FIG. 32(Continued)

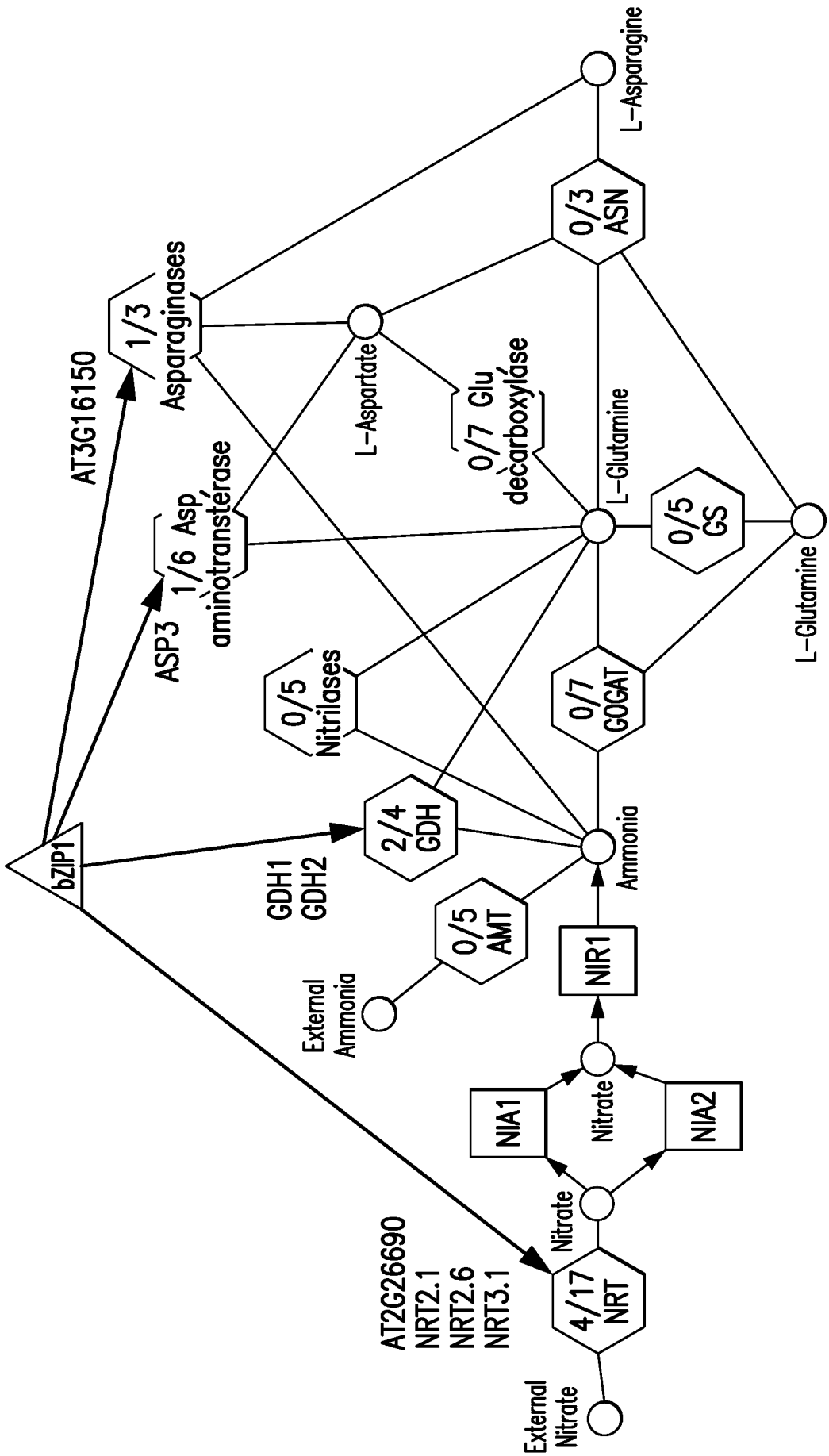

AT3G16150
1/3
Asparaginases
ASP3
1/6 Asp,
aminotransférase
L-Aspartate
0/7 Glu
décarboxylase
L-Asparagine
0/3
ASN
L-Glutamine
0/5
GS
L-Glutamine
0/5
Nitrilases
0/7
GOGAT
bZIP1
GDH1
GDH2
2/4
GDH
Ammonia
0/5
AMT
External
Ammonia
NIR1
NIA1
Nitrate
NIA2
Nitrate
AT2G26690
NRT2.1
NRT2.6
NRT3.1
4/17
NRT
External
Nitrate

FIG. 33

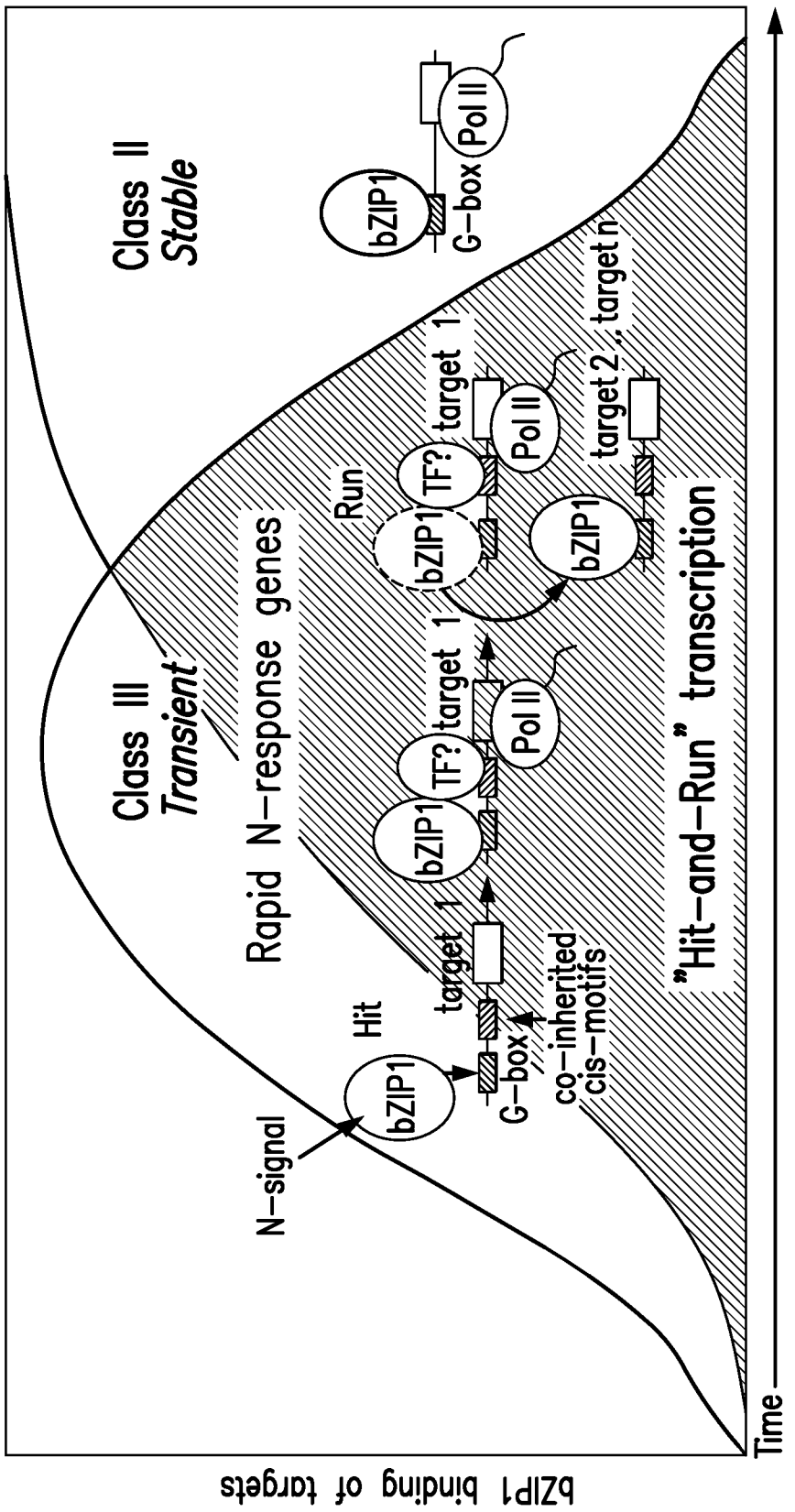

bZIP1 binding of targets
Time
Class II
Stable
Class III
Transient
Rapid N-response genes
"Hit-and-Run" transcription
N-signal
Hit
bZIP1
G-box
target 1
co-inherited
cis-motifs
TF?
Pol II
Run
target 2
target n

FIG. 34

FIG. 35A

4sU RNA tagging captured active transcription bZIP1 primary targets

bZIP1−regulated new RNA synthesis at 5h after bZIP1 nuclear import	I	IIA	IIB	IIIA	IIIB
bZIP1 induced	31	11**	0	121***	21
bZIP1 repressed	12	0	3	21	42***

FIG. 35B

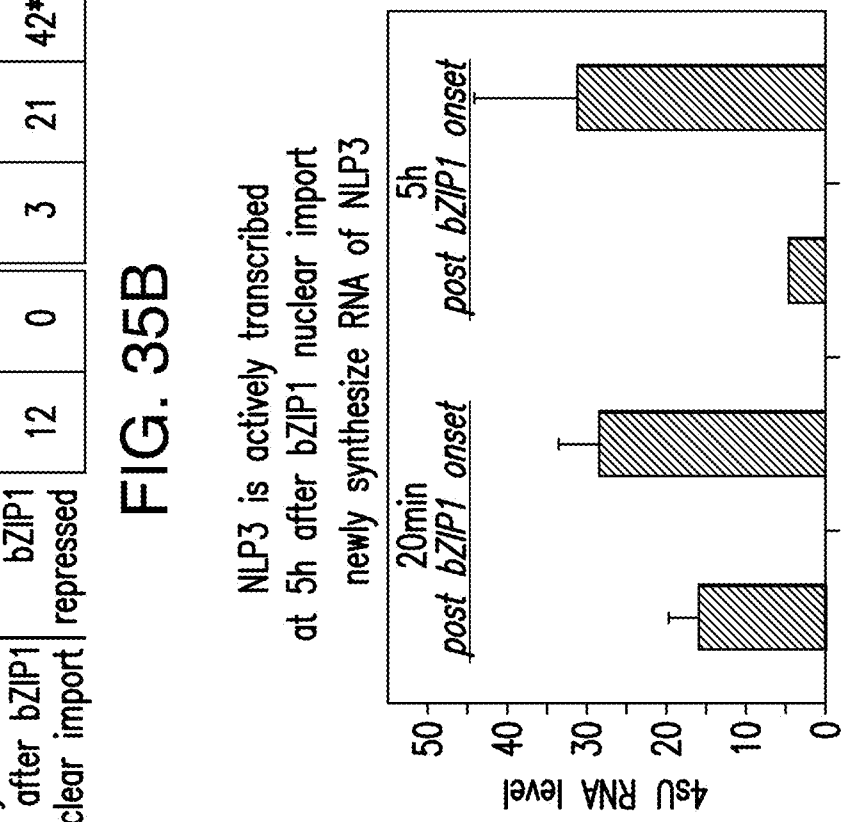


FIG. 35D

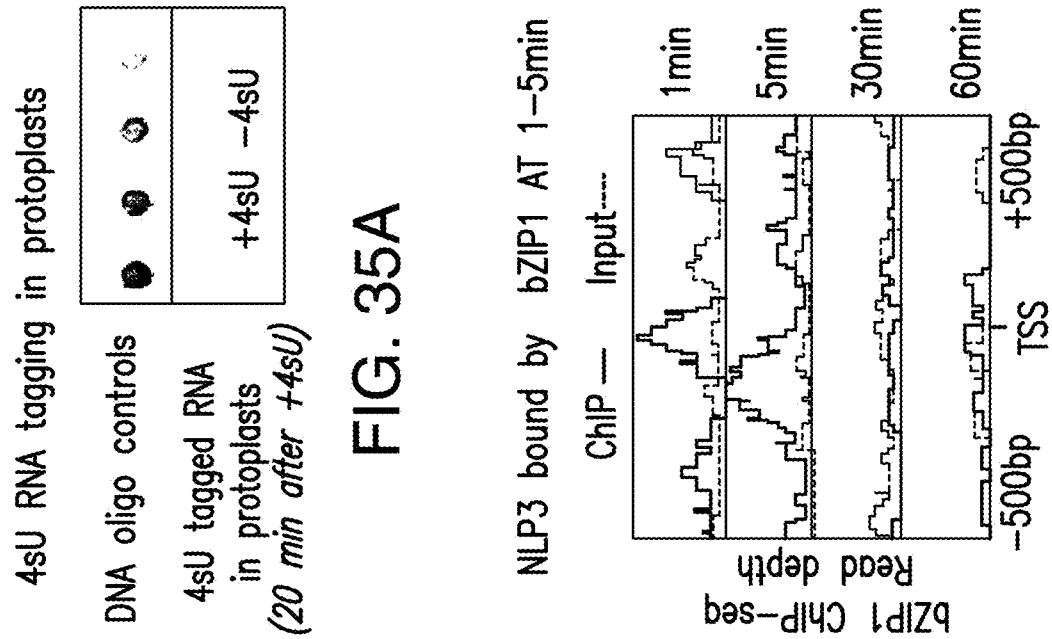


FIG. 35C

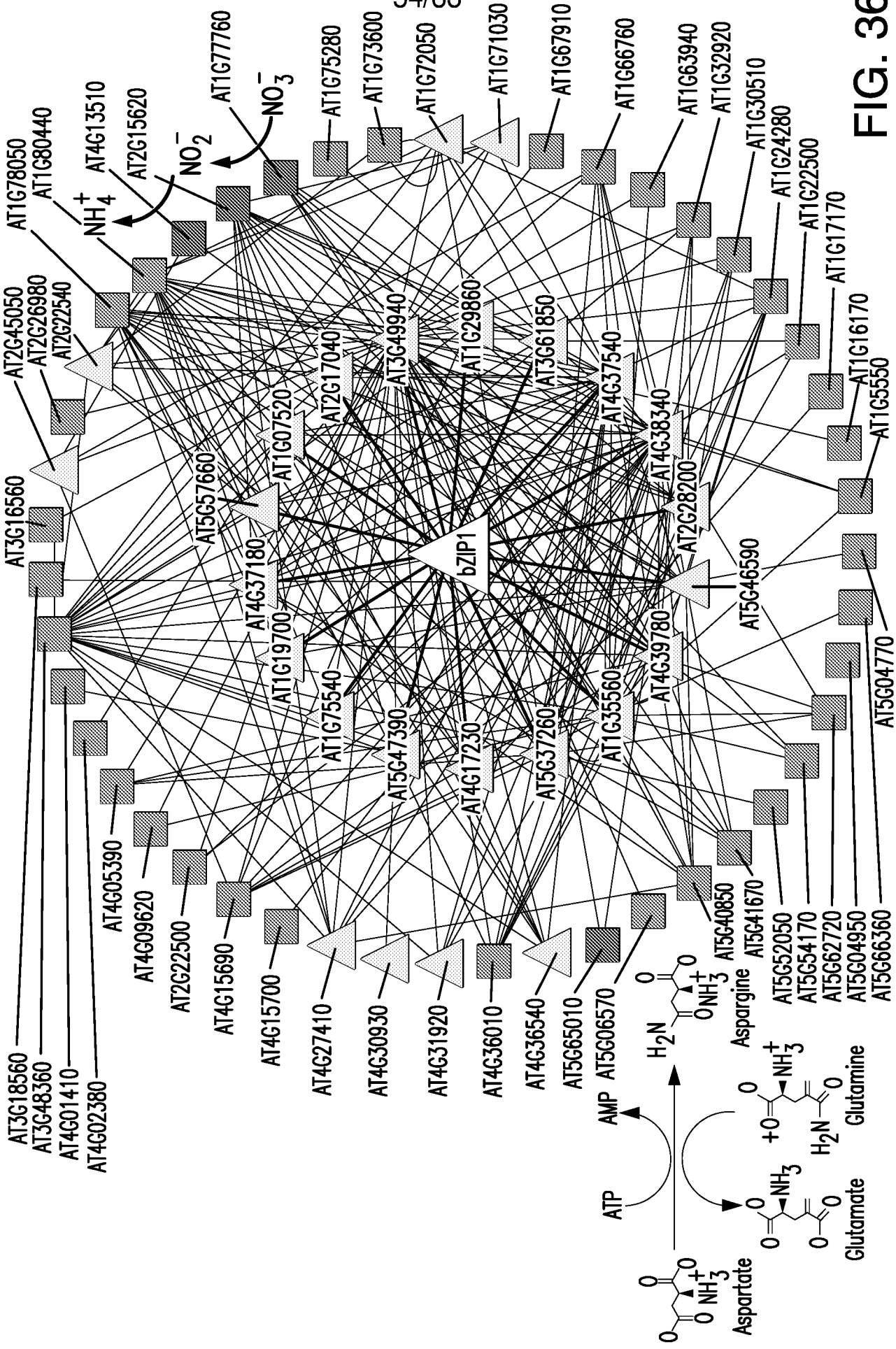

AT3G18560
AT3G48360
AT4G01410
AT4G02380
AT3G16560
AT2G45050
AT2G26980
AT2G22540
AT1G78050
AT1G80440
NH_4^+
AT4G13510
AT2G15620
NO_2^-
AT1G77760
NO_3^-
AT1G75280
AT1G73600
AT1G72050
AT1G71030
AT1G67910
AT1G66760
AT1G63940
AT1G32920
AT1G30510
AT1G24280
AT1G22500
AT1G17170
AT1G16170
AT1G15550
AT4G05390
AT4G09620
AT2G22500
AT4G15690
AT4G15700
AT4G27410
AT4G30930
AT4G31920
AT4G36010
AT4G36540
AT5G65010
AT5G06570
AT5G40850
AT5G41670
AT5G52050
AT5G54170
AT5G62720
AT5G04950
AT5G66360
AT5G04770
AT5G46590
AT2G28200
AT4G38340
AT4G37540
AT3G61850
AT1G29860
AT3G49940
AT2G17040
AT1G07520
AT5G57660
AT4G37180
AT1G19700
AT1G75540
AT5G47390
AT4G17230
AT5G37260
AT1G35560
AT4G39780
bZIP1
AMP
ATP
Aspartate
Asparagine
Glutamate
Glutamine

FIG. 36

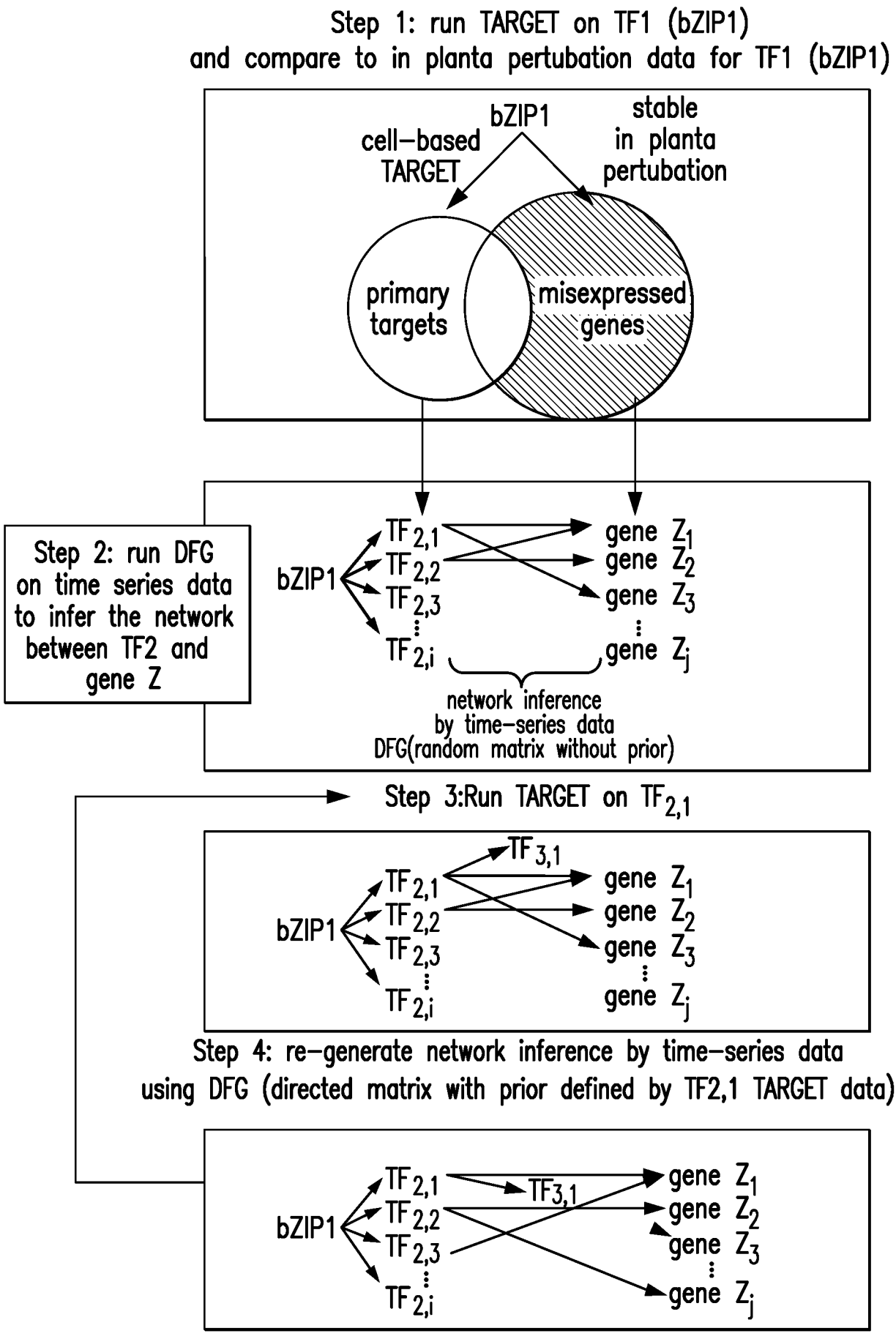

Step 1: run TARGET on TF1 (bZIP1)
and compare to in planta pertubation data for TF1 (bZIP1)
bZIP1
cell-based TARGET
stable in planta pertubation
primary targets
misexpressed genes
Step 2: run DFG on time series data to infer the network between TF2 and gene Z
bZIP1
TF 2,1
TF 2,2
TF 2,3
TF 2,i
gene Z1
gene Z2
gene Z3
gene Zj
network inference by time-series data DFG(random matrix without prior)
Step 3:Run TARGET on TF 2,1
TF 3,1
Step 4: re-generate network inference by time-series data using DFG (directed matrix with prior defined by TF2,1 TARGET data)

FIG. 37

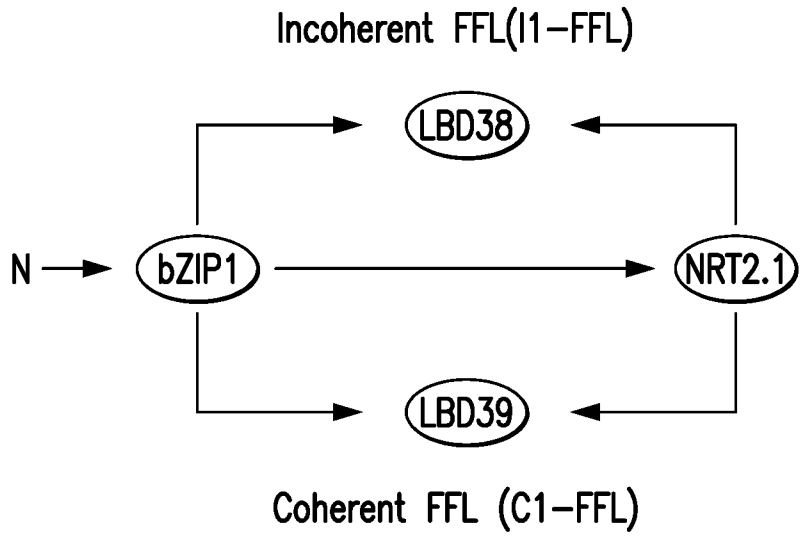


FIG. 38A

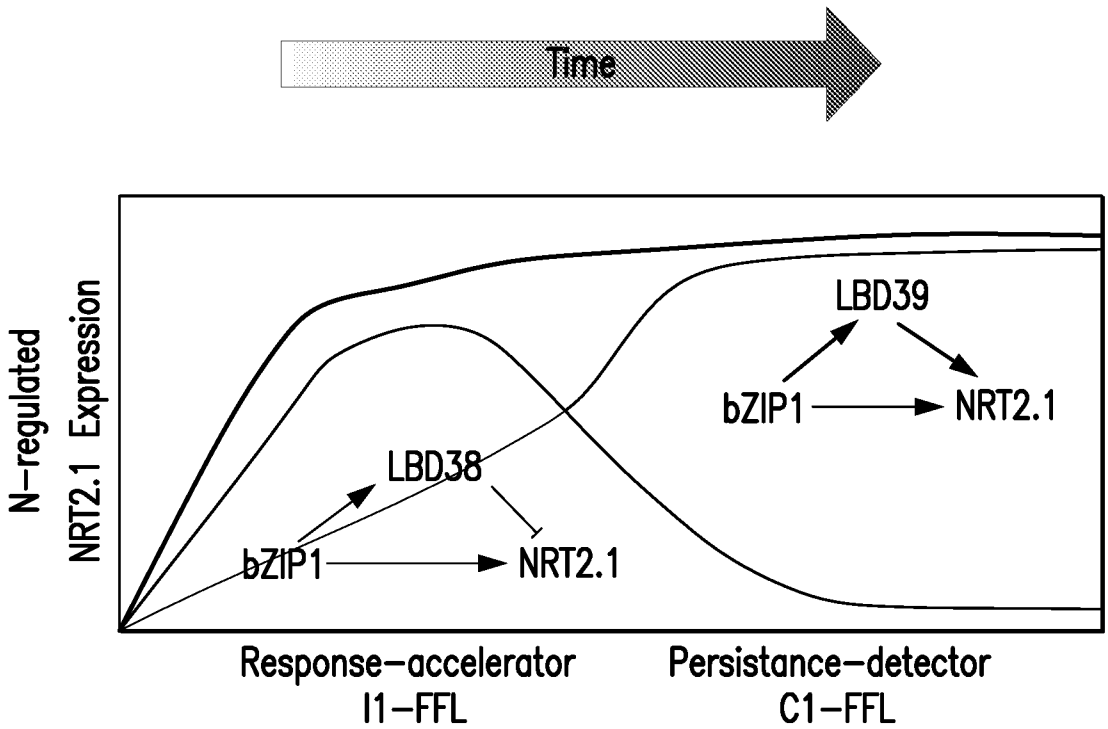


FIG. 38B

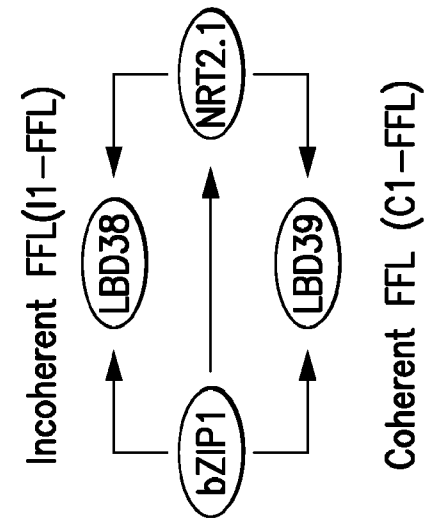


FIG. 39B

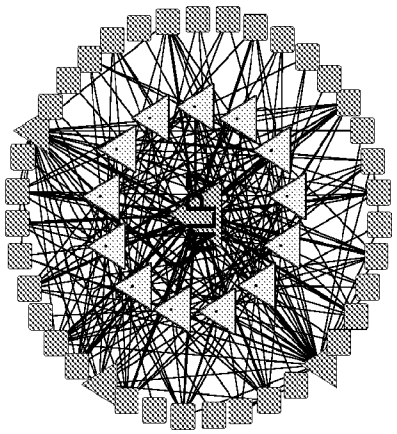


FIG. 39C

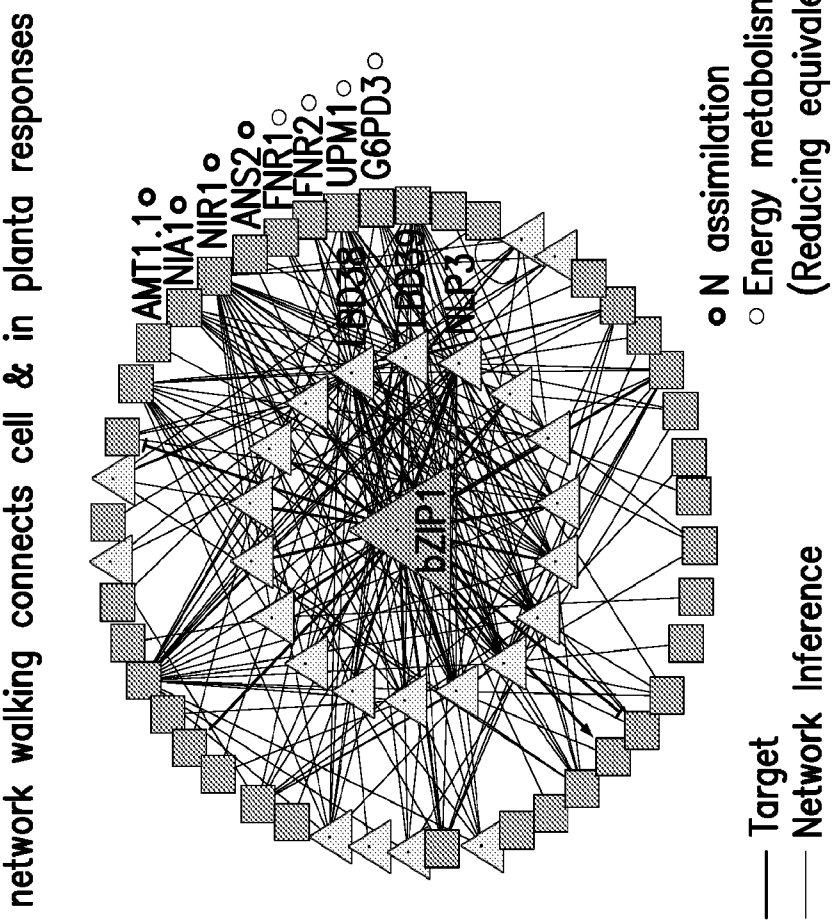


FIG. 39A

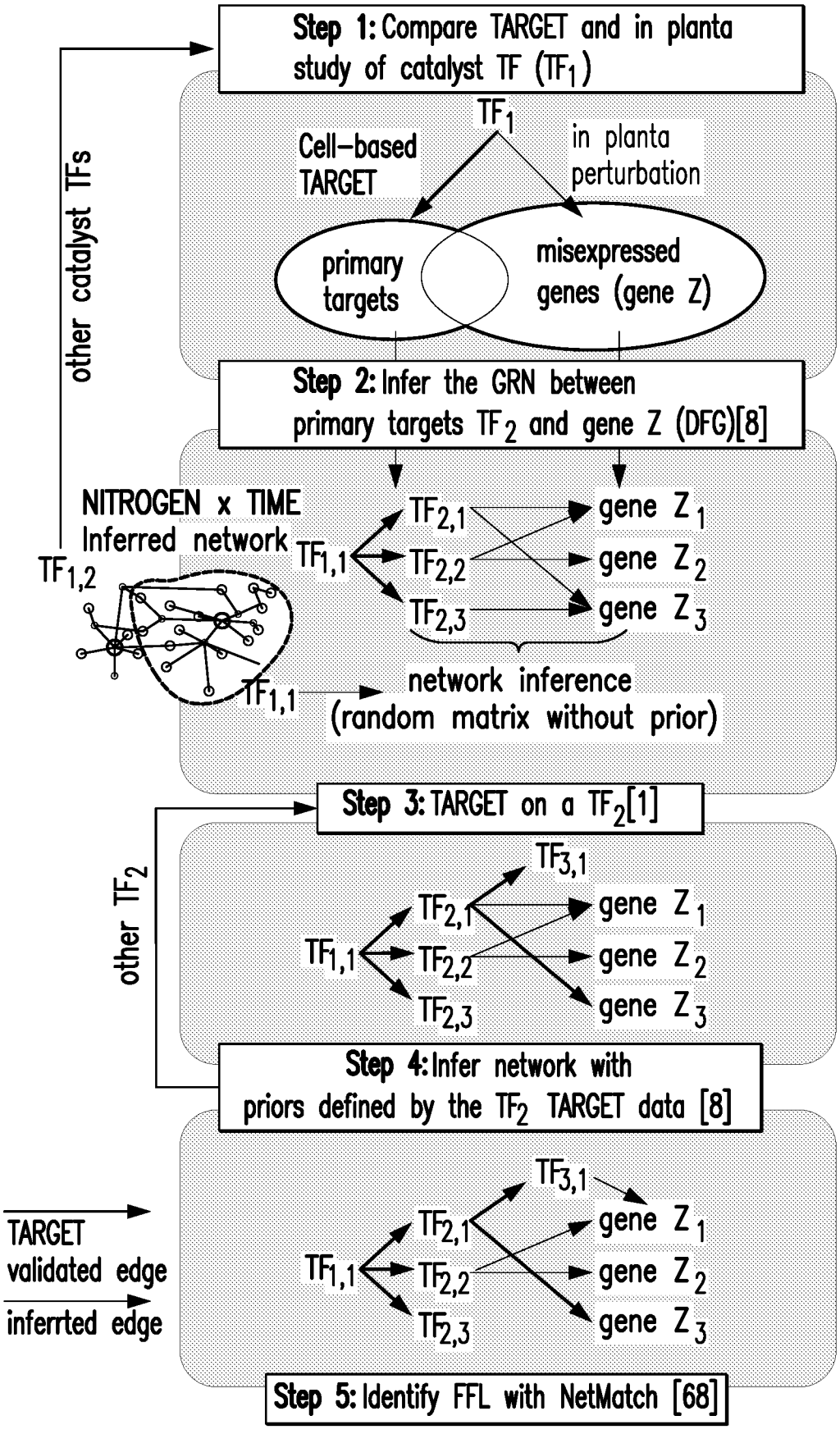

Step 1: Compare TARGET and in planta study of catalyst TF (TF_1)
TF_1
Cell–based TARGET
in planta perturbation
primary targets
misexpressed genes (gene Z)
other catalyst TFs
Step 2: Infer the GRN between primary targets TF_2 and gene Z (DFG)[8]
NITROGEN x TIME
Inferred network
$TF_{1,2}$
$TF_{1,1}$
$TF_{2,1}$
$TF_{2,2}$
$TF_{2,3}$
gene Z_1
gene Z_2
gene Z_3
$TF_{1,1}$
network inference
(random matrix without prior)
Step 3: TARGET on a TF_2[1]
other TF_2
$TF_{3,1}$
$TF_{2,1}$
$TF_{1,1}$
$TF_{2,2}$
$TF_{2,3}$
gene Z_1
gene Z_2
gene Z_3
Step 4: Infer network with priors defined by the TF_2 TARGET data [8]
$TF_{3,1}$
$TF_{2,1}$
$TF_{1,1}$
$TF_{2,2}$
$TF_{2,3}$
gene Z_1
gene Z_2
gene Z_3
TARGET validated edge
inferrted edge
Step 5: Identify FFL with NetMatch [68]

FIG. 40

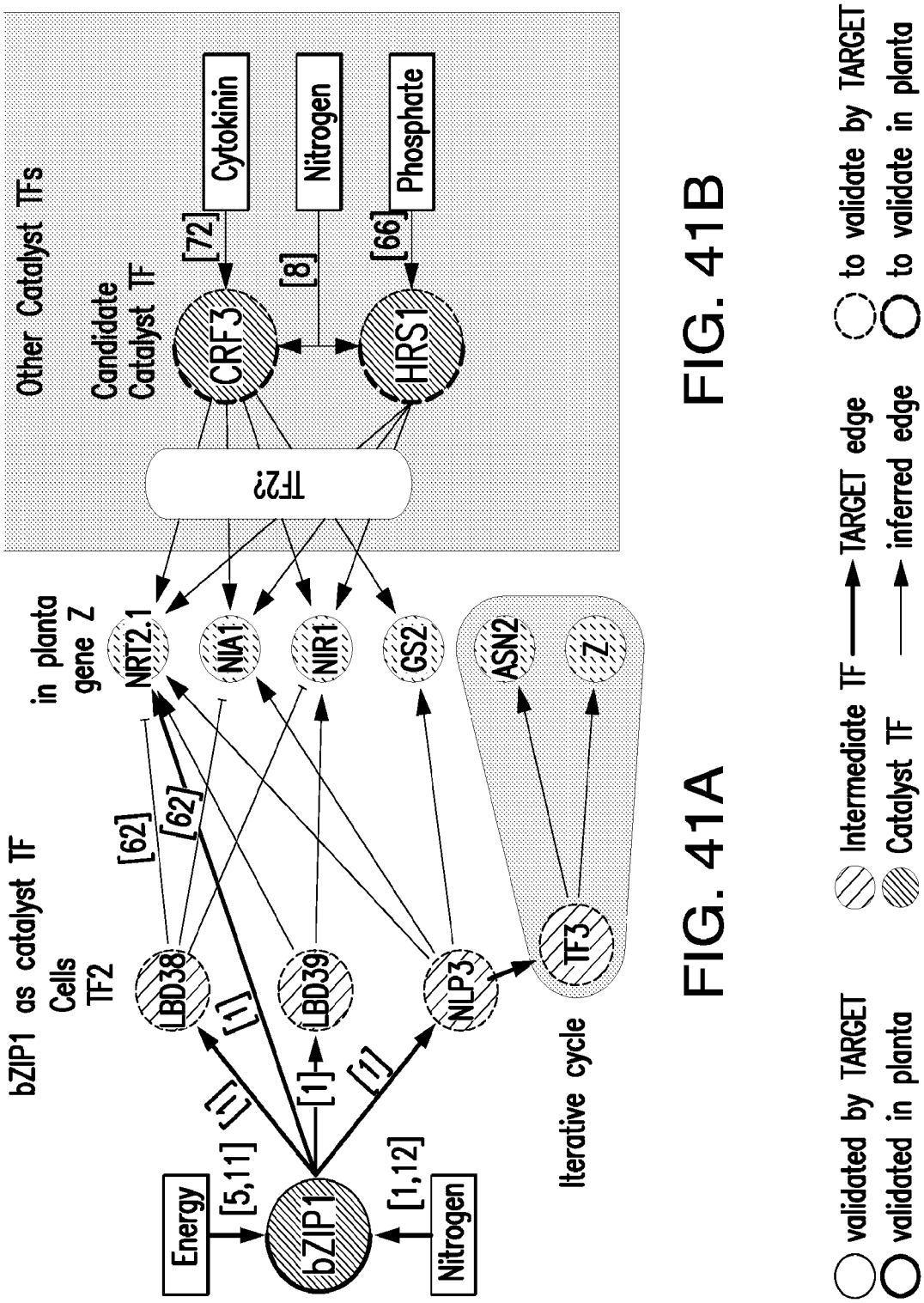


FIG. 41A

FIG. 41B

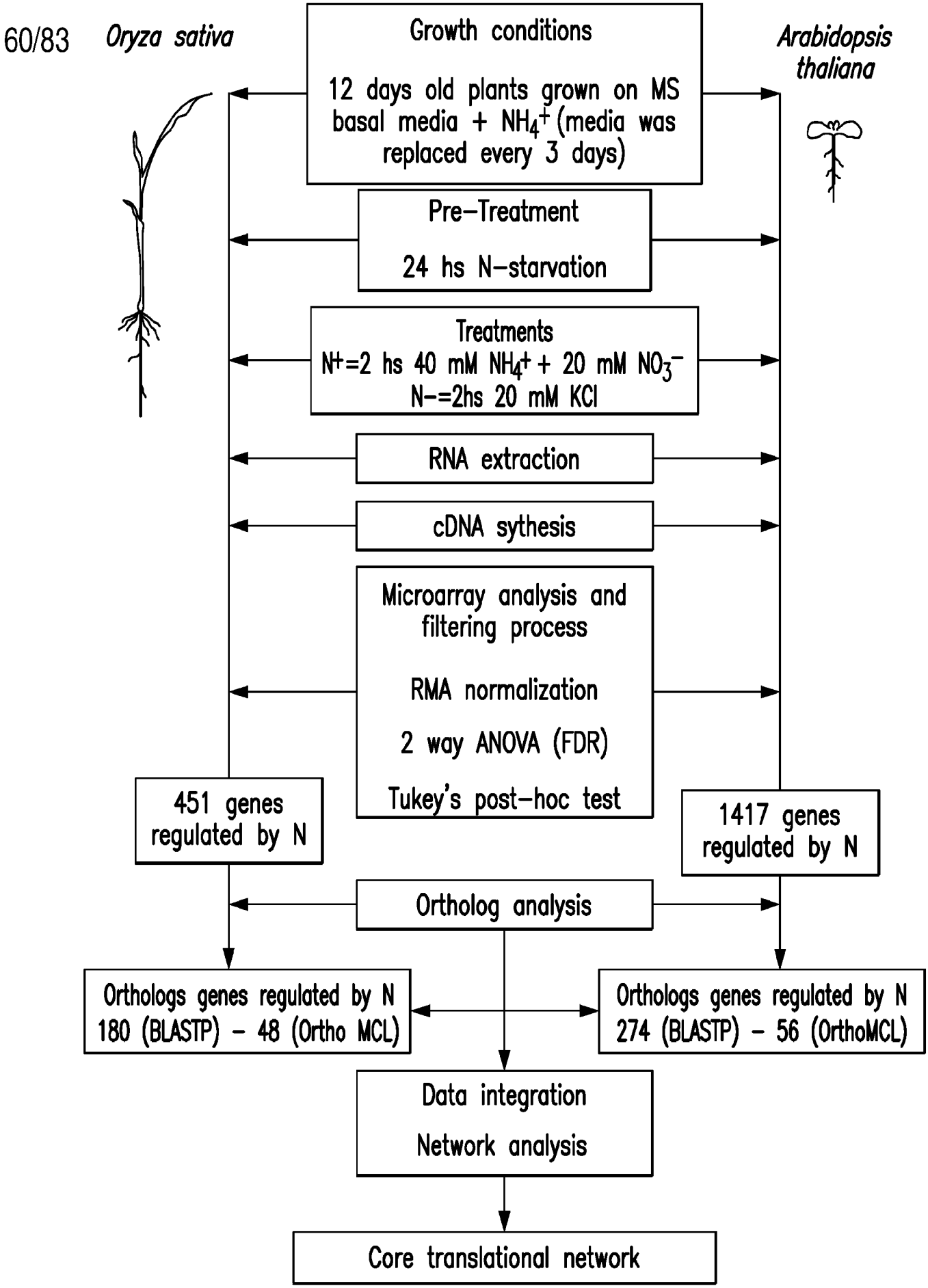

Oryza sativa
Growth conditions
12 days old plants grown on MS basal media + NH_4^+ (media was replaced every 3 days)
Arabidopsis thaliana
Pre-Treatment
24 hs N-starvation
Treatments
N+=2 hs 40 mM NH_4^+ + 20 mM NO_3^-
N-=2hs 20 mM KCl
RNA extraction
cDNA sythesis
Microarray analysis and filtering process
RMA normalization
2 way ANOVA (FDR)
Tukey's post-hoc test
451 genes regulated by N
1417 genes regulated by N
Ortholog analysis
Orthologs genes regulated by N 180 (BLASTP) - 48 (Ortho MCL)
Orthologs genes regulated by N 274 (BLASTP) - 56 (OrthoMCL)
Data integration
Network analysis
Core translational network

FIG. 42

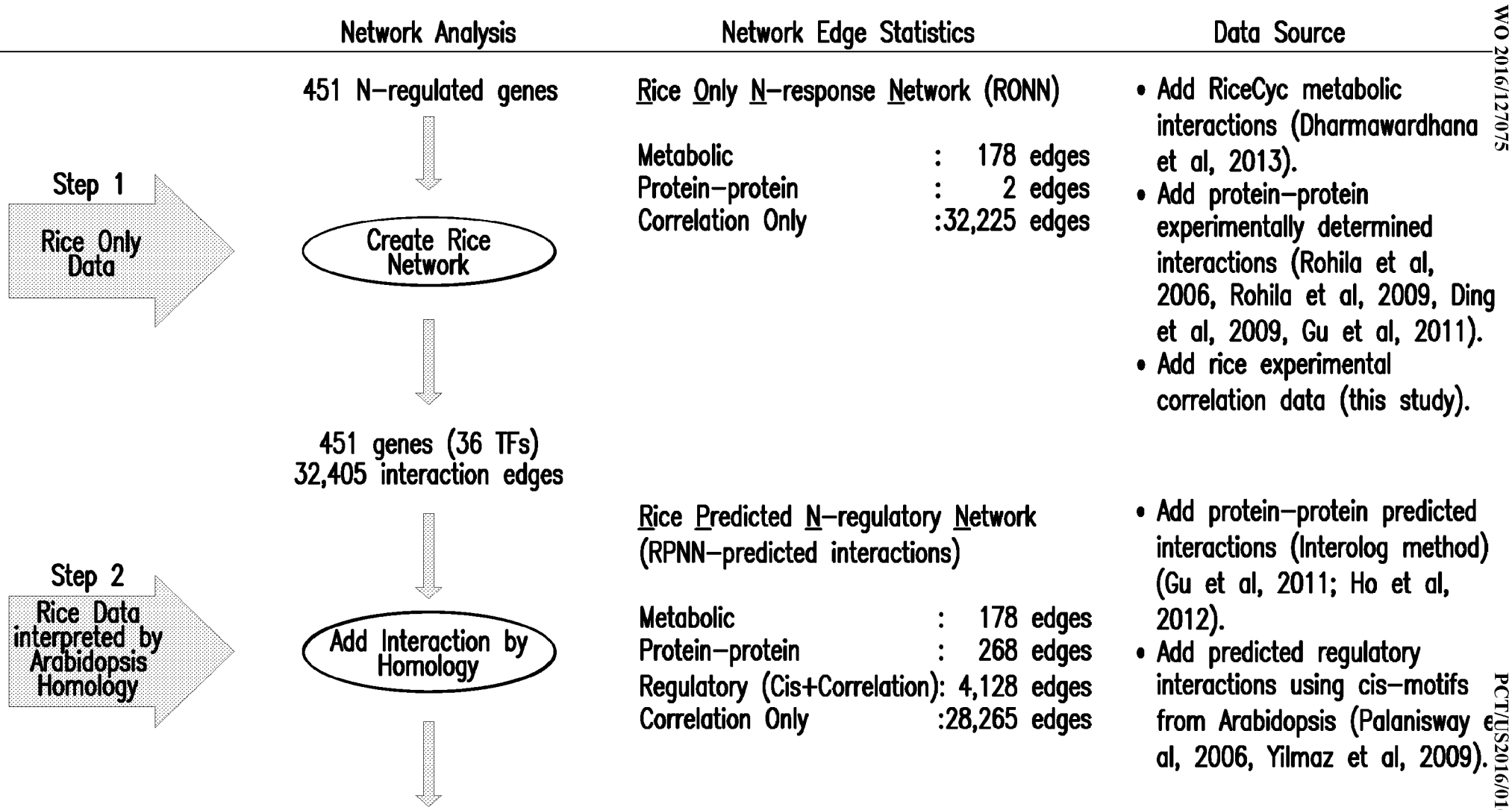


FIG. 43

SUBSTITUTE SHEET (RULE 26)

FIG. 43(Continued)

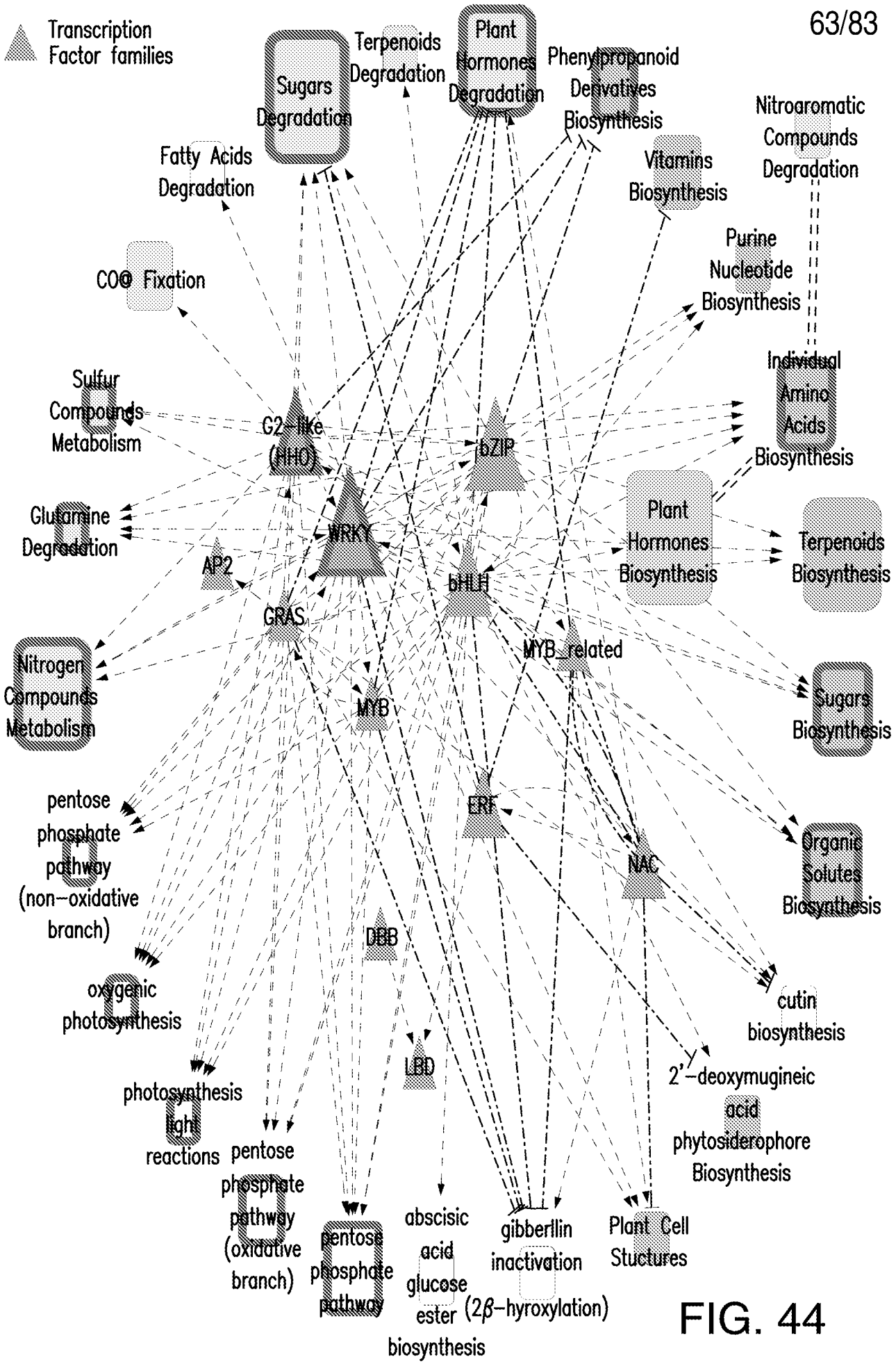

Transcription Factor families
Sugars Degradation
Terpenoids Degradation
Plant Hormones Degradation
Phenylpropanoid Derivatives Biosynthesis
Nitroaromatic Compounds Degradation
Fatty Acids Degradation
Vitamins Biosynthesis
CO@ Fixation
Purine Nucleotide Biosynthesis
Individual Amino Acids Biosynthesis
Sulfur Compounds Metabolism
G2-like (HHO)
bZIP
Glutamine Degradation
WRKY
Plant Hormones Biosynthesis
Terpenoids Biosynthesis
AP2
bHLH
GRAS
MYB_related
Nitrogen Compounds Metabolism
MYB
Sugars Biosynthesis
pentose phosphate pathway (non-oxidative branch)
ERF
Organic Solutes Biosynthesis
NAC
DBB
oxygenic photosynthesis
cutin biosynthesis
LBD
2'-deoxymugineic acid phytosiderophore Biosynthesis
photosynthesis light reactions
pentose phosphate pathway (oxidative branch)
pentose phosphate pathway
abscisic acid glucose ester biosynthesis
gibberllin inactivation (2β-hyroxylation)
Plant Cell Stuctures

FIG. 44

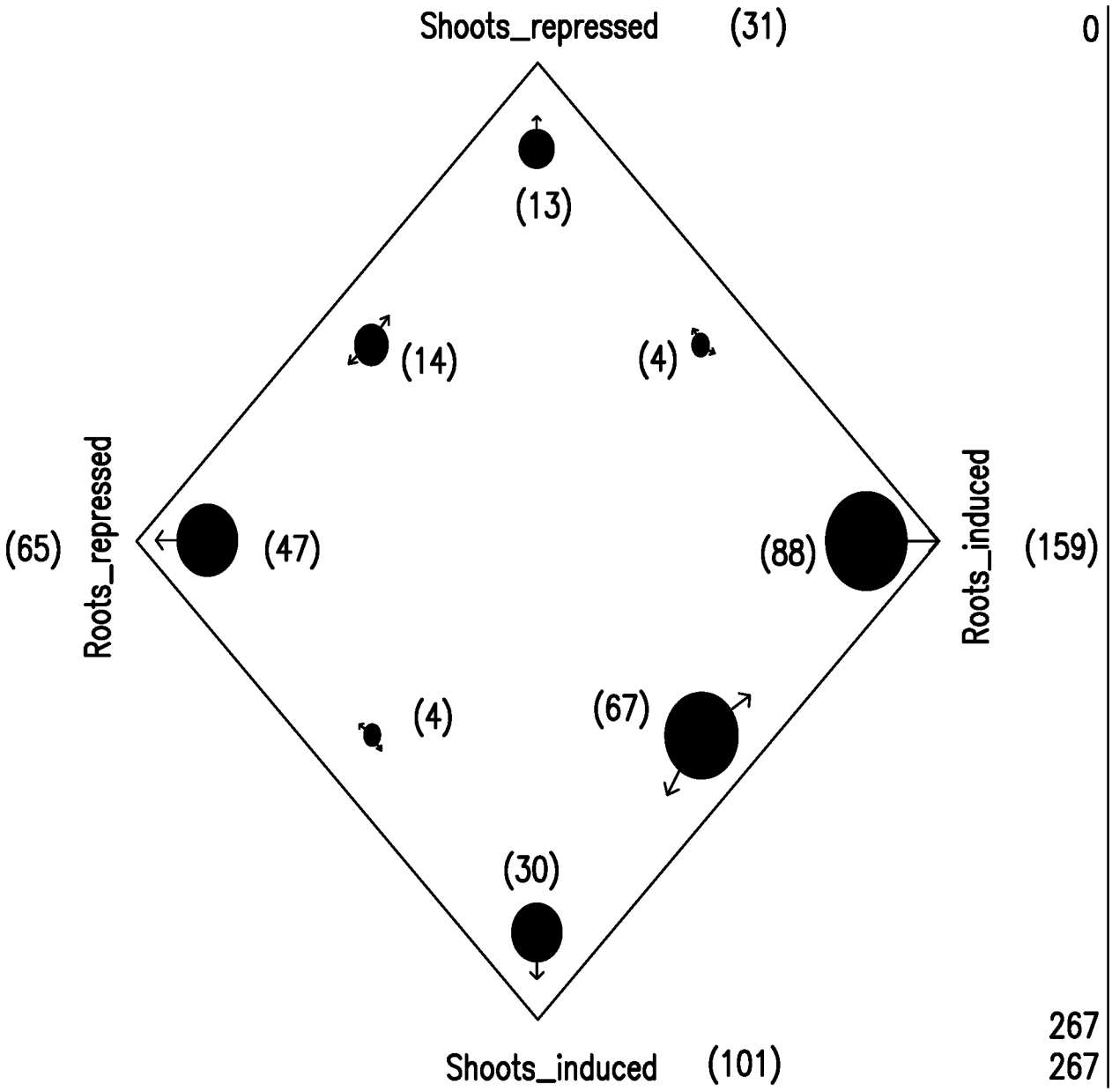

Shoots_repressed
(31)
0
(13)
(14)
(4)
(65)
Roots_repressed
(47)
(88)
Roots_induced
(159)
(4)
(67)
(30)
Shoots_induced
(101)
267
267

FIG. 45

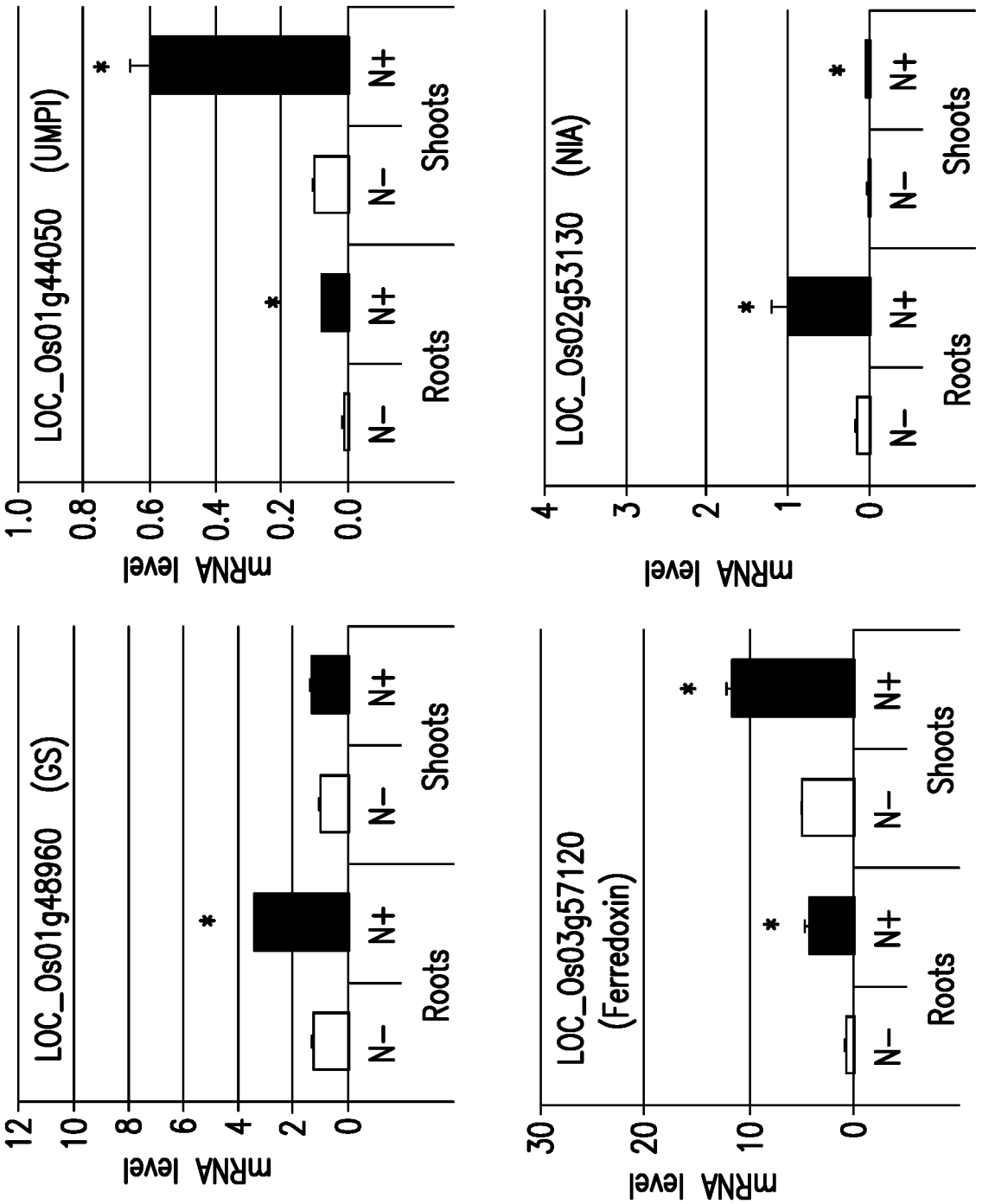

LOC_Os01g44050 (UMPI)
LOC_Os02g53130 (NIA)
LOC_Os01g48960 (GS)
LOC_Os03g57120 (Ferredoxin)
mRNA level
N–
N+
Roots
Shoots
*

FIG. 46

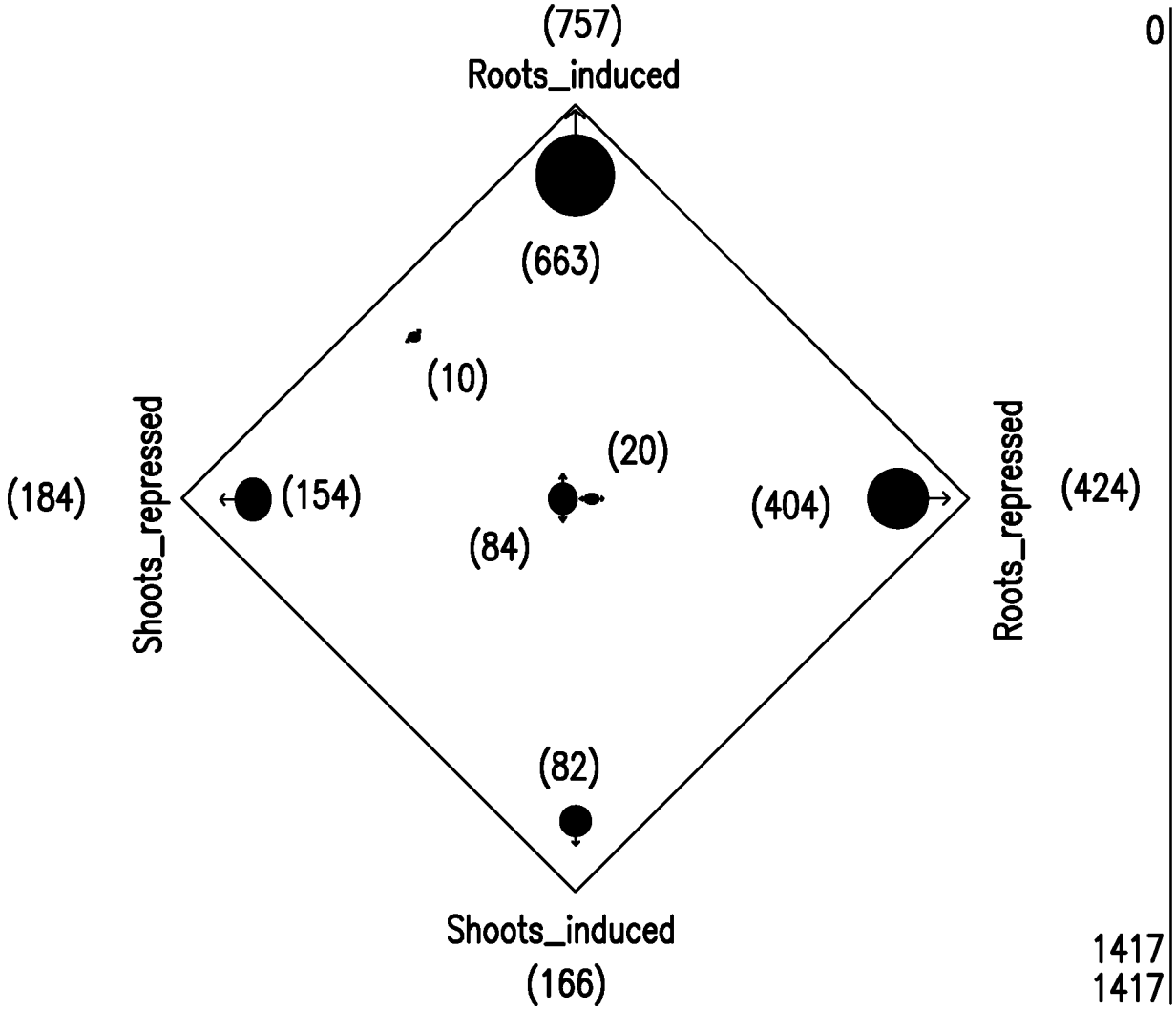

(757)
Roots_induced
(663)
(10)
(20)
(84)
(184)
Shoots_repressed
(154)
(404)
Roots_repressed
(424)
(82)
Shoots_induced
(166)
0
1417
1417

FIG. 47

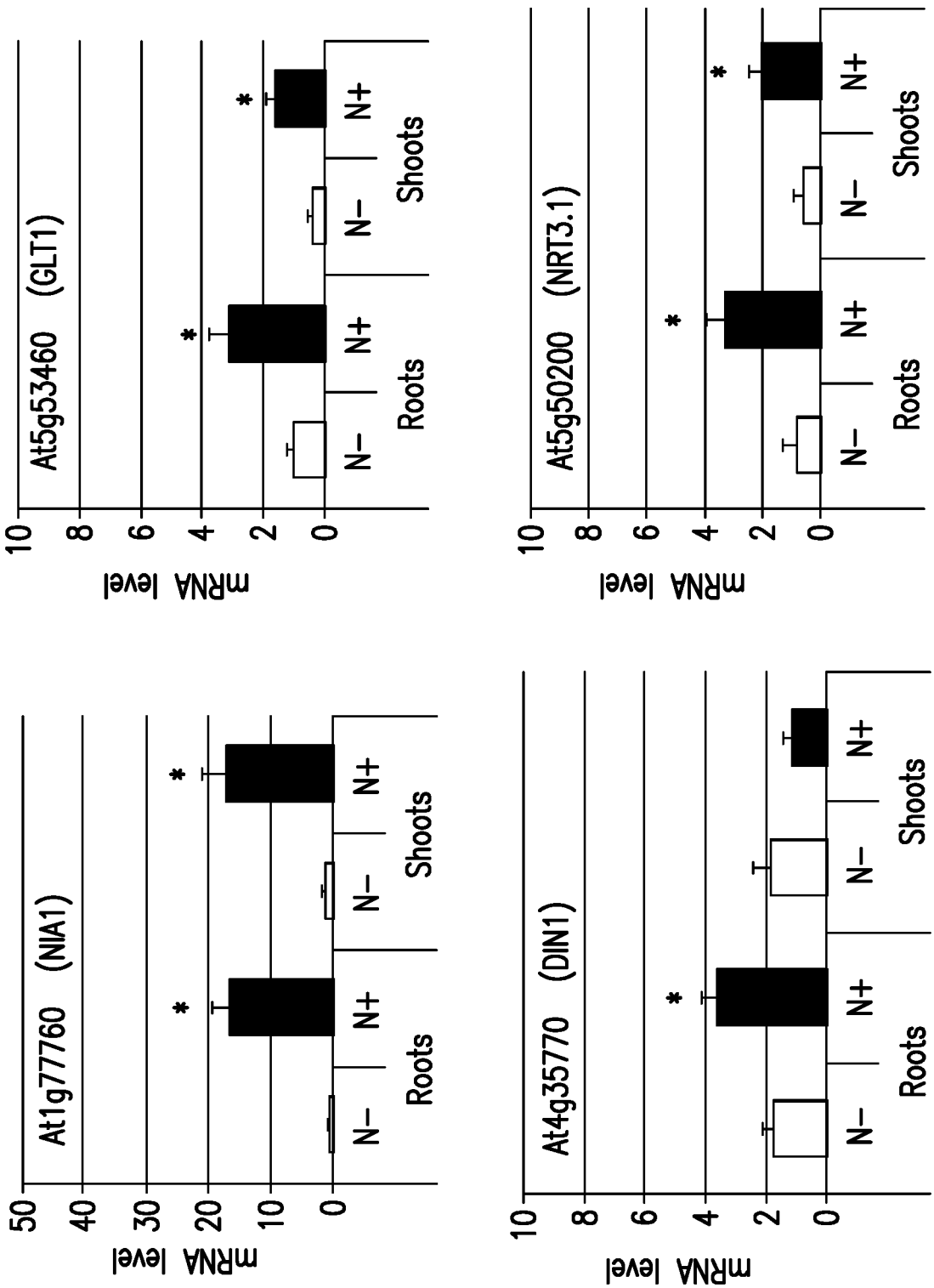

At5g53460 (GLT1)
At5g50200 (NRT3.1)
At1g77760 (NIA1)
At4g35770 (DIN1)
mRNA level
Roots
Shoots
N−
N+
*

FIG. 48

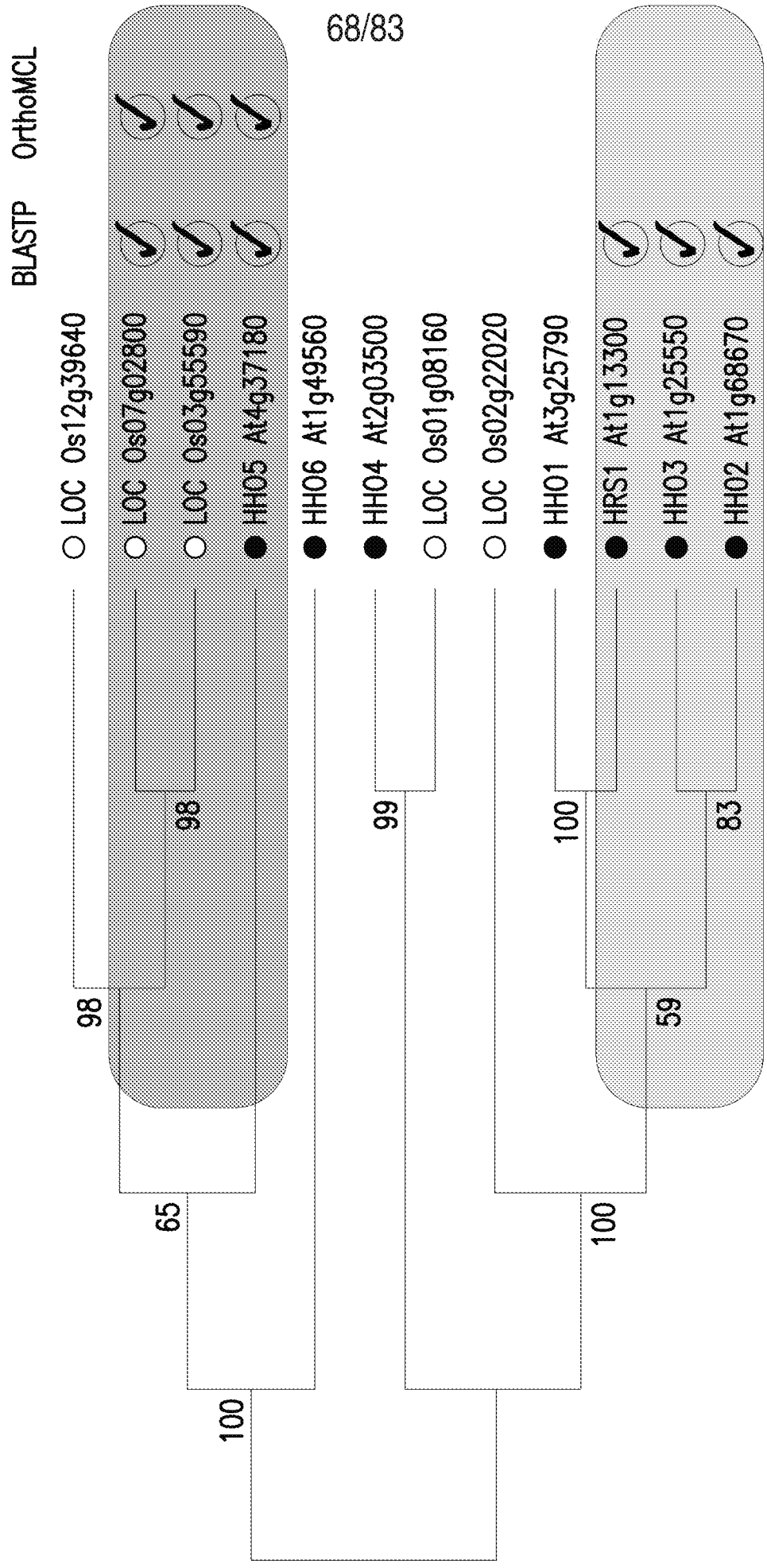

BLASTP
OrthoMCL
LOC Os12g39640
LOC Os07g02800
LOC Os03g55590
HHO5 At4g37180
HHO6 At1g49560
HHO4 At2g03500
LOC Os01g08160
LOC Os02g22020
HHO1 At3g25790
HRS1 At1g13300
HHO3 At1g25550
HHO2 At1g68670
68/83
98
98
99
100
83
59
65
100
100

FIG. 49

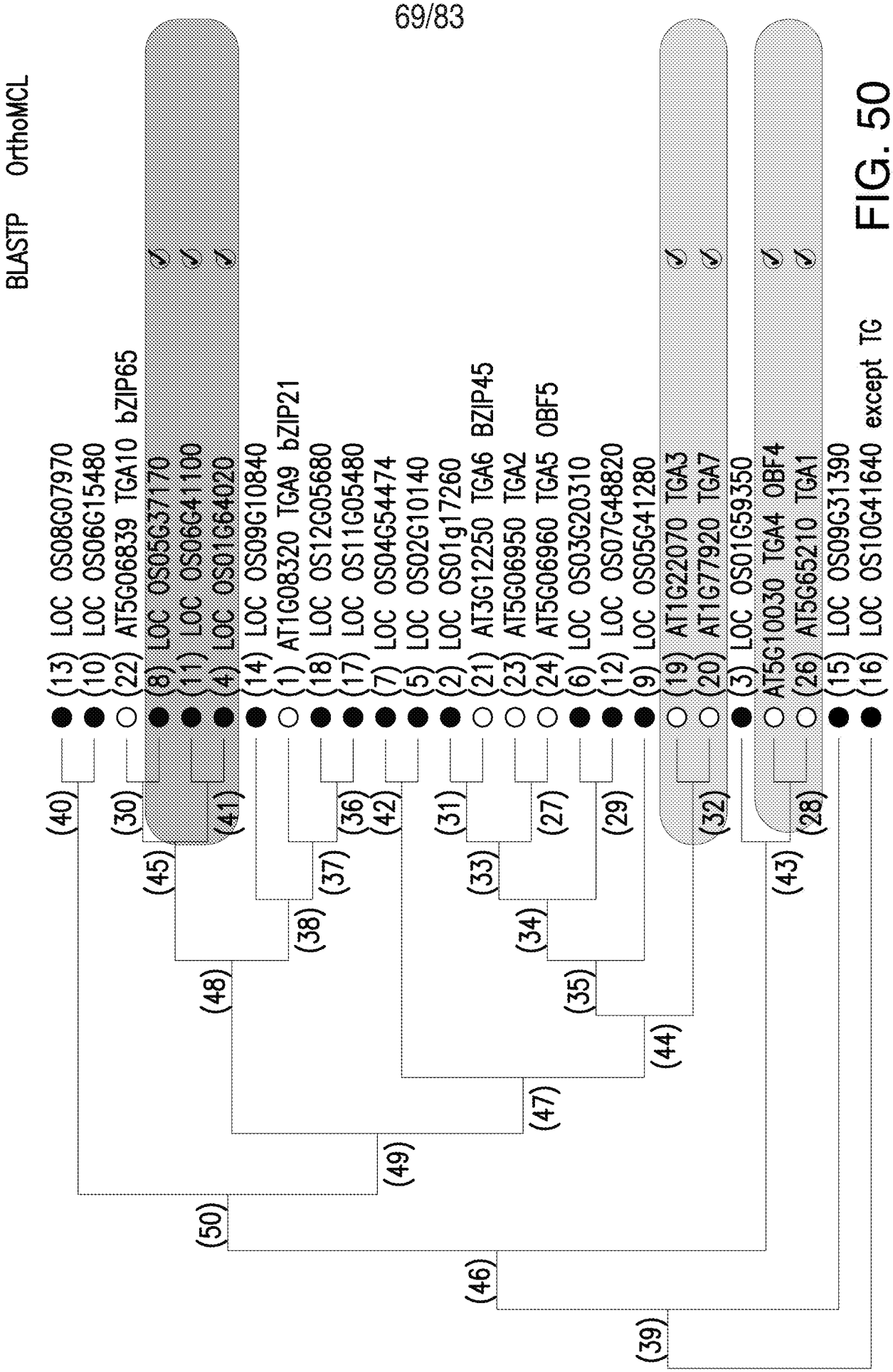

BLASTP OrthoMCL
(13) LOC OS08G07970
(10) LOC OS06G15480
(22) AT5G06839 TGA10 bZIP65
(8) LOC OS05G37170
(11) LOC OS06G41100
(4) LOC OS01G64020
(14) LOC OS09G10840
(1) AT1G08320 TGA9 bZIP21
(18) LOC OS12G05680
(17) LOC OS11G05480
(7) LOC OS04G54474
(5) LOC OS02G10140
(2) LOC OS01g17260
(21) AT3G12250 TGA6 BZIP45
(23) AT5G06950 TGA2
(24) AT5G06960 TGA5 OBF5
(6) LOC OS03G20310
(12) LOC OS07G48820
(9) LOC OS05G41280
(19) AT1G22070 TGA3
(20) AT1G77920 TGA7
(3) LOC OS01G59350
AT5G10030 TGA4 OBF4
(26) AT5G65210 TGA1
(15) LOC OS09G31390
(16) LOC OS10G41640 except TG
(40)
(30)
(41)
(45)
(38)
(37)
(36)
(42)
(31)
(33)
(27)
(34)
(29)
(48)
(35)
(44)
(32)
(47)
(43)
(28)
(49)
(50)
(46)
(39)

FIG. 50

SUBSTITUTE SHEET (RULE 26)

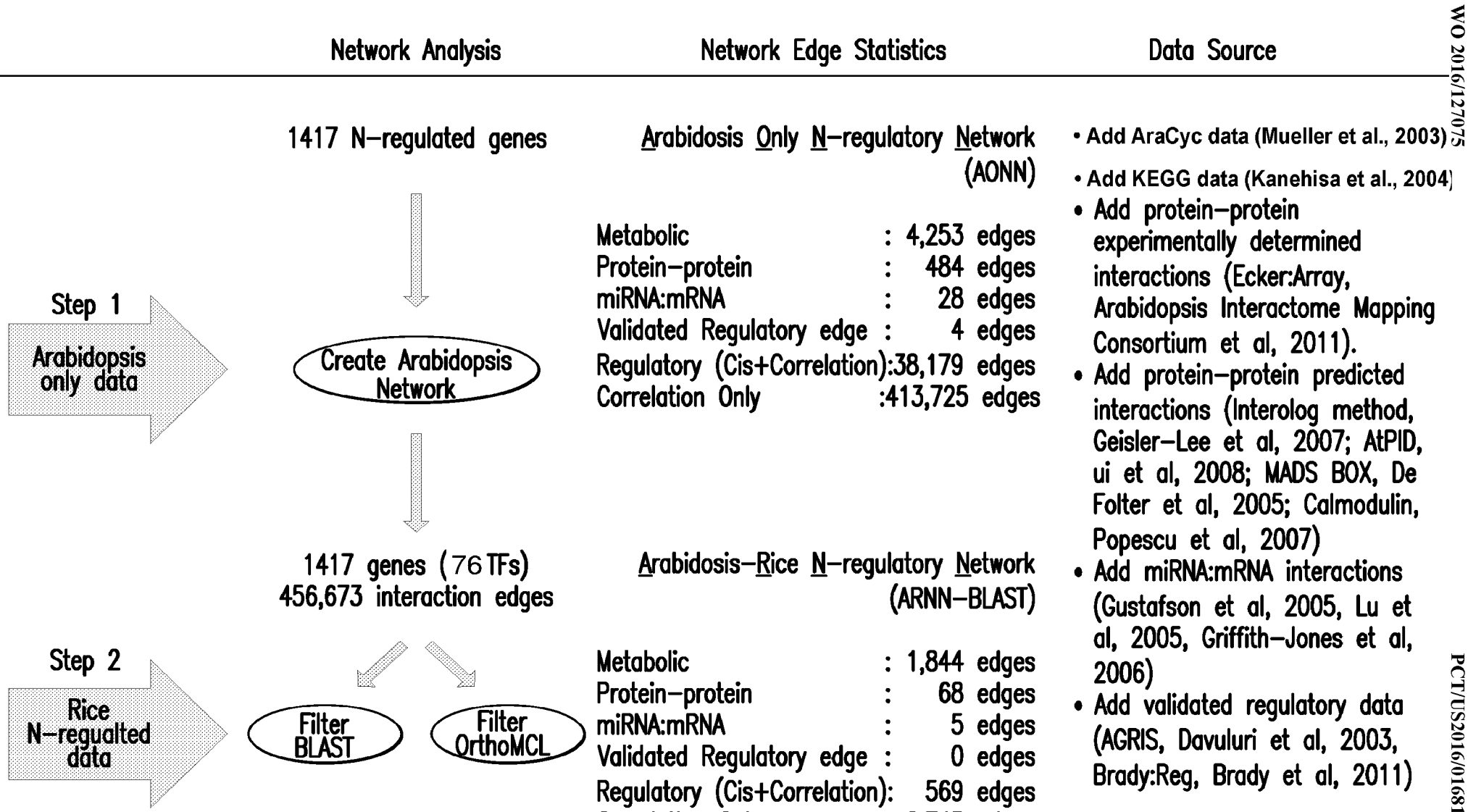


FIG. 51

FIG. 51(Continued)

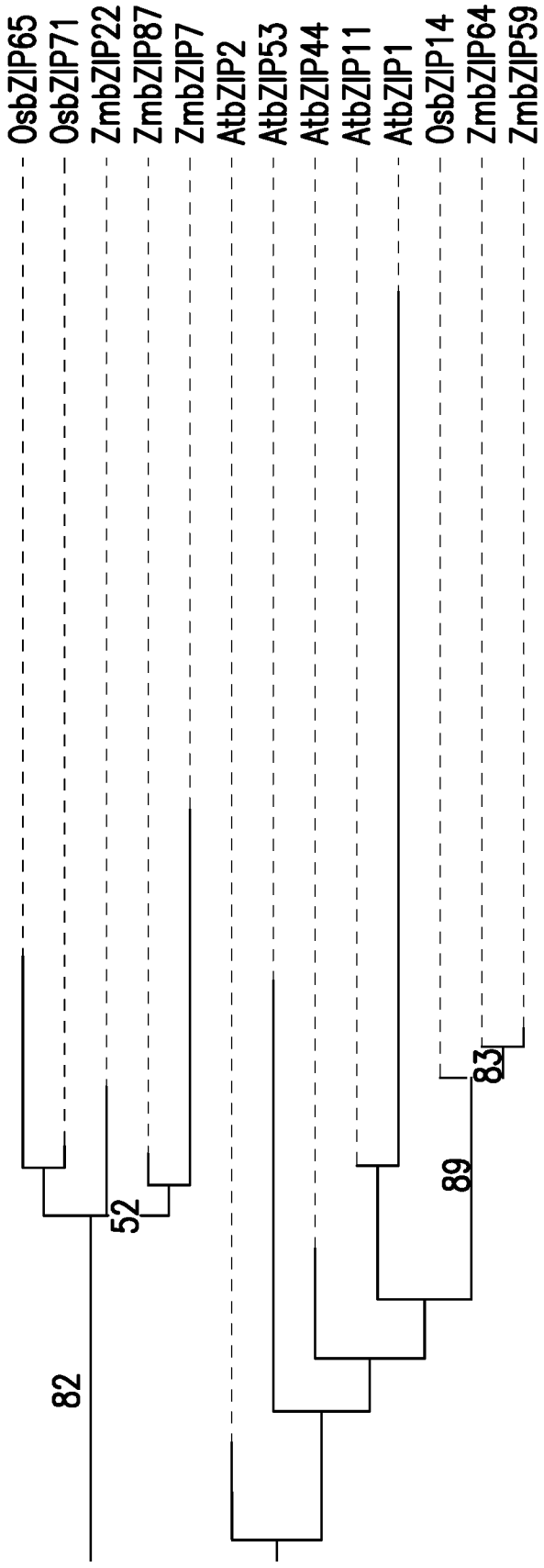

OsbZIP65
OsbZIP71
ZmbZIP22
ZmbZIP87
ZmbZIP7
AtbZIP2
AtbZIP53
AtbZIP44
AtbZIP11
AtbZIP1
OsbZIP14
ZmbZIP64
ZmbZIP59
82
52
89
83

FIG. 52

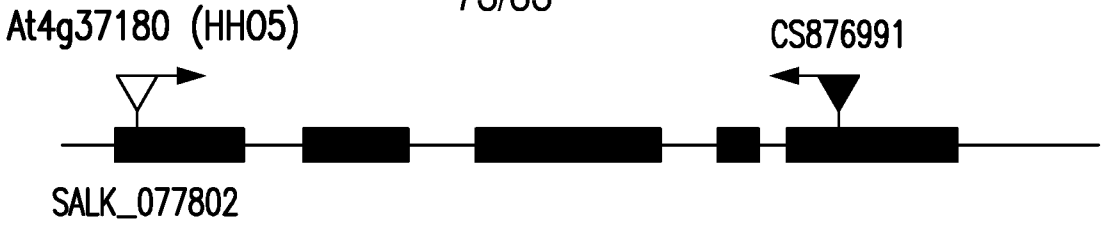


FIG. 53

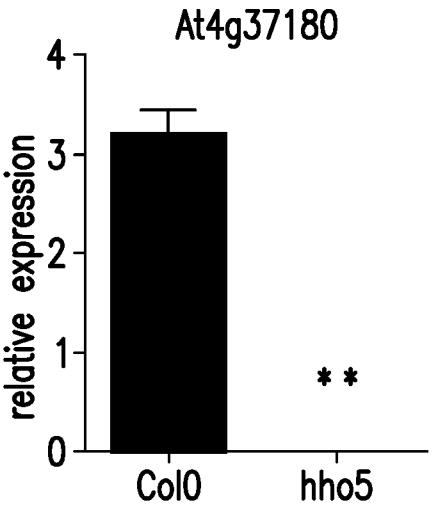


FIG. 54A

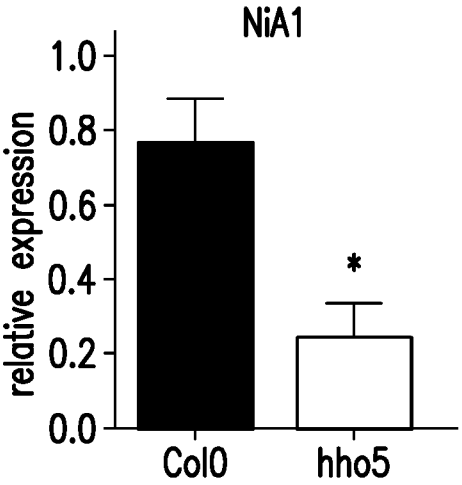


FIG. 54B

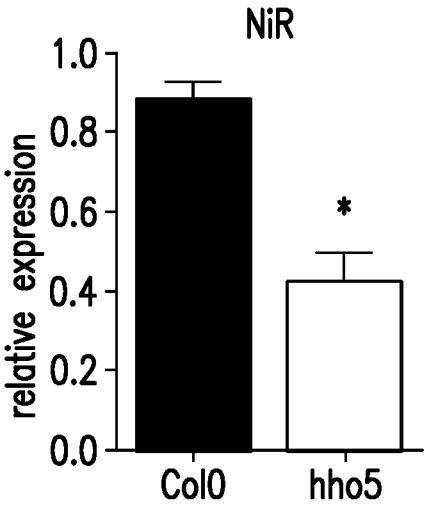


FIG. 54C

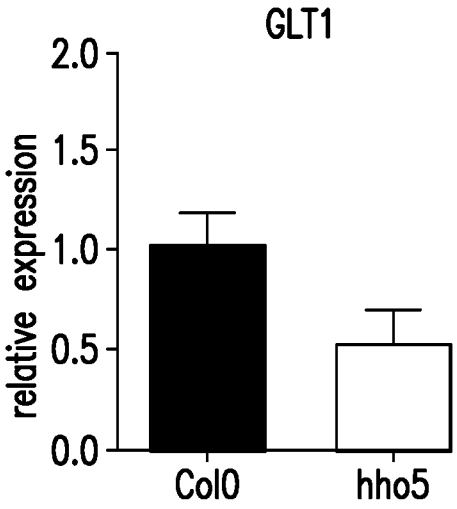


FIG. 54D

Expression levels of tested genes were normalized to expression levels of the clathrin genes (** $p<0.001$, * $p<0.05$).

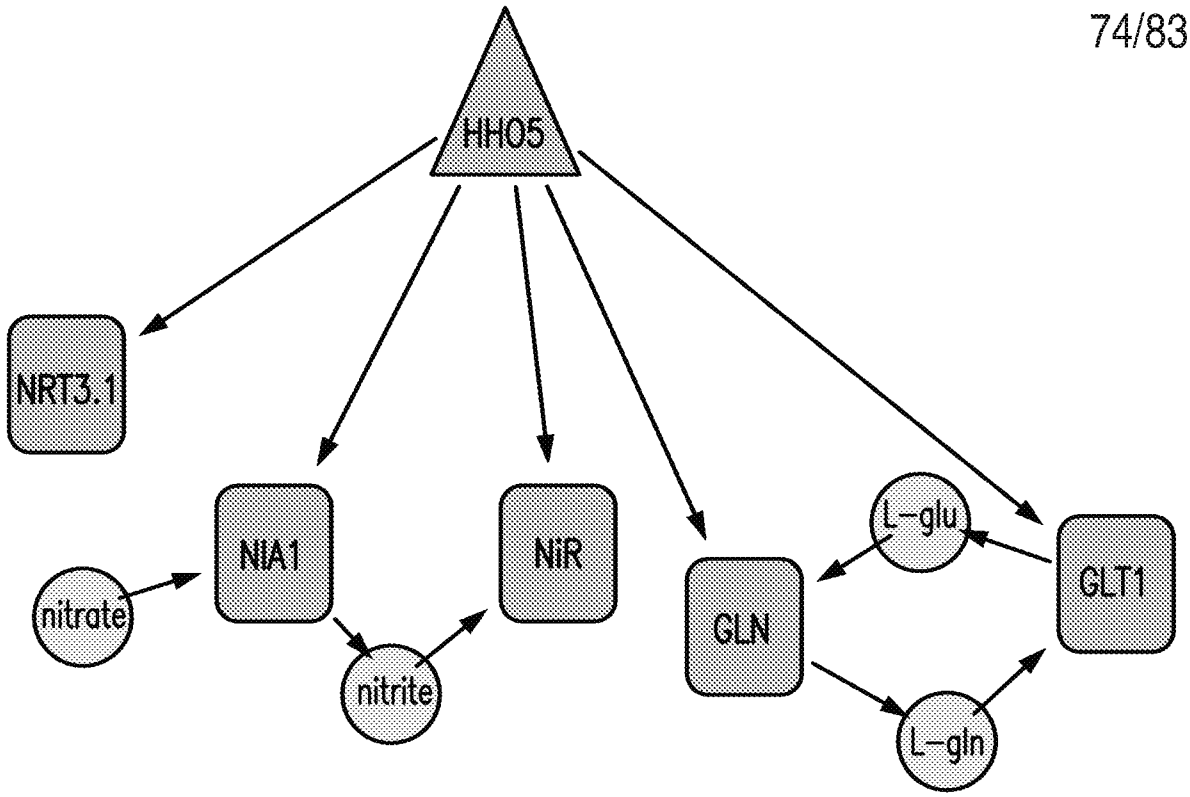


FIG. 54E

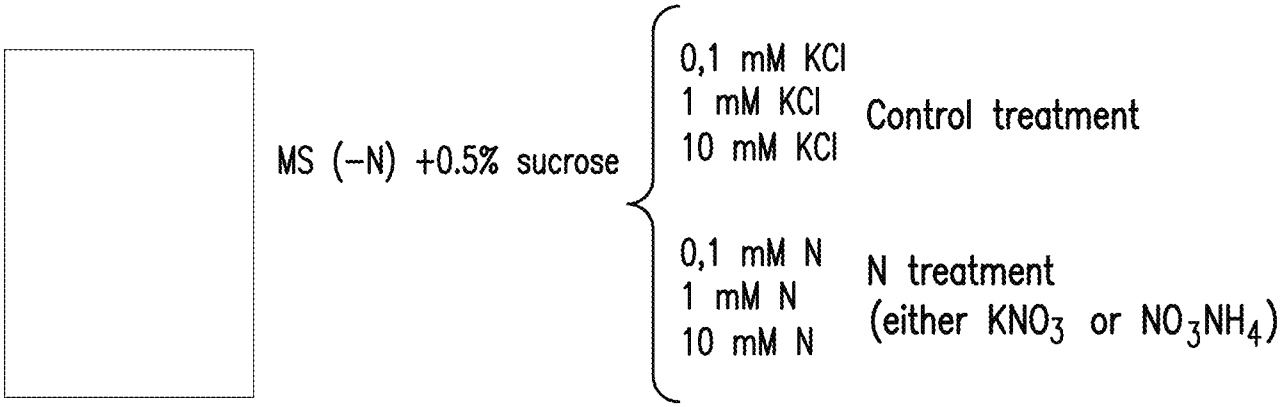
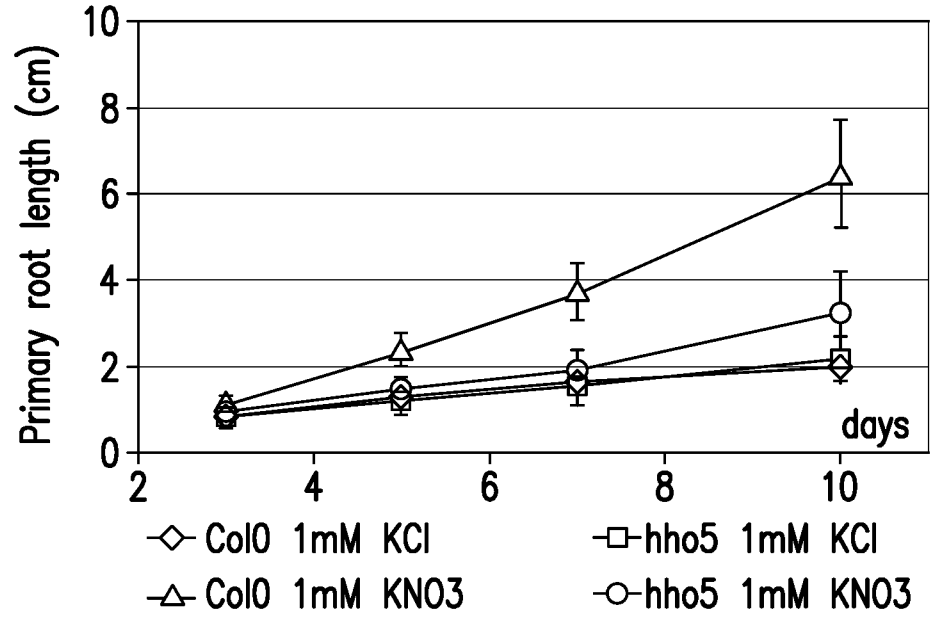
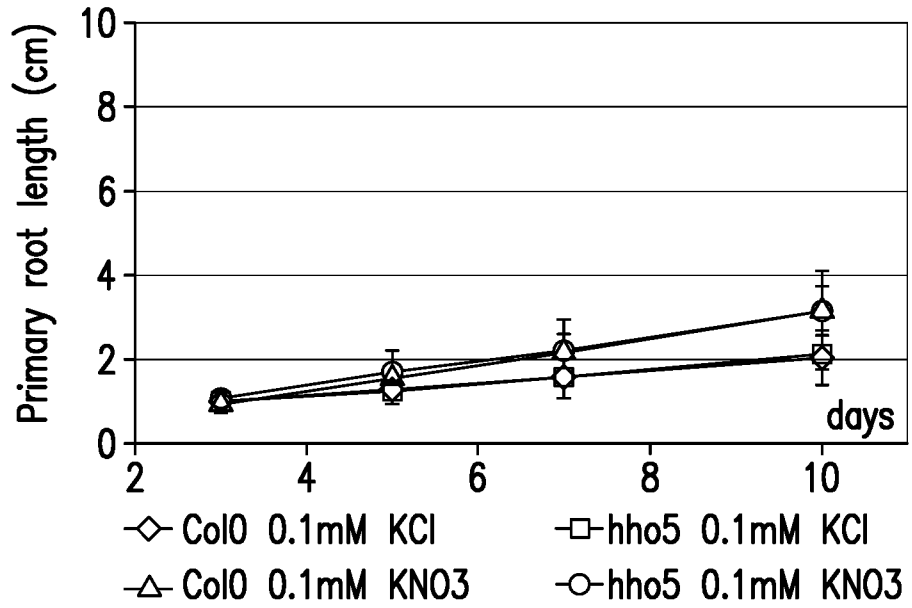


FIG. 55


Primary root length (cm)
10
8
6
4
2
0
2
4
6
8
10
days
Col0 1mM KCl
hho5 1mM KCl
Col0 1mM KNO3
hho5 1mM KNO3


Primary root length (cm)
10
8
6
4
2
0
2
4
6
8
10
days
Col0 0.1mM KCl
hho5 0.1mM KCl
Col0 0.1mM KNO3
hho5 0.1mM KNO3

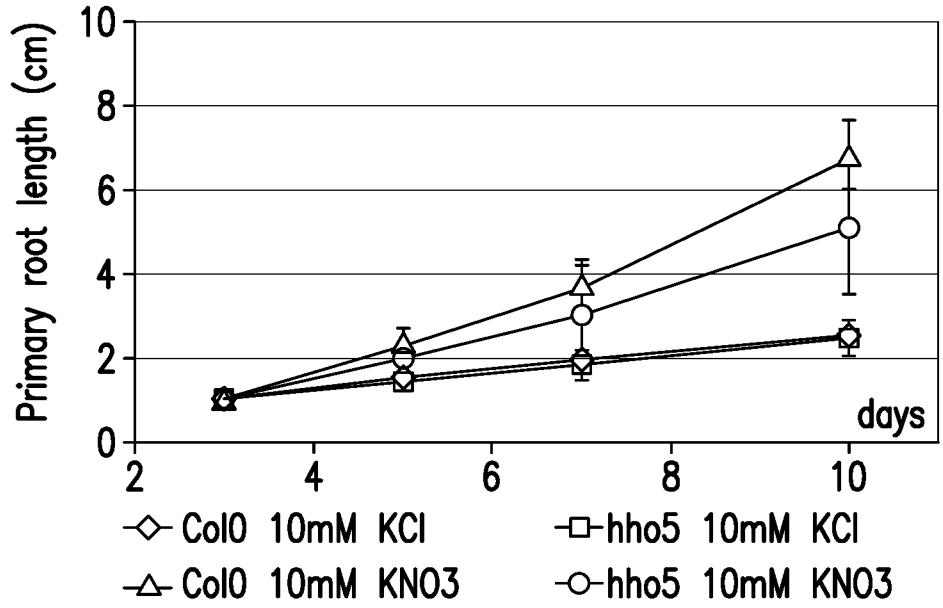

Primary root length (cm)
10
8
6
4
2
0
2
4
6
8
10
days
Col0 10mM KCl
hho5 10mM KCl
Col0 10mM KNO3
hho5 10mM KNO3

FIG. 56A

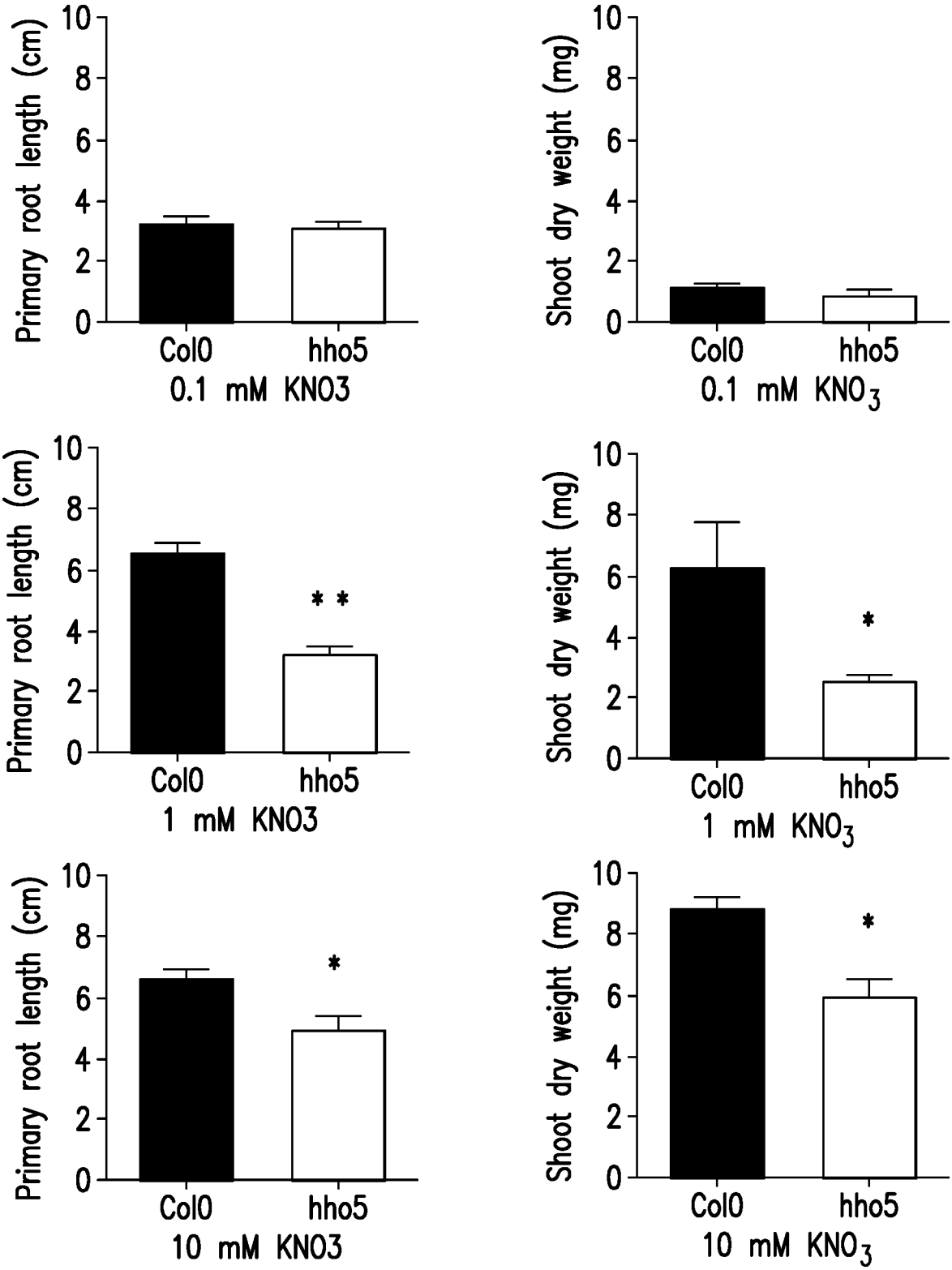

Primary root length (cm)
Shoot dry weight (mg)
Col0
hho5
0.1 mM KNO3
0.1 mM KNO3
1 mM KNO3
1 mM KNO3
10 mM KNO3
10 mM KNO3
* p<0.05, ** p<0.01

FIG. 56B

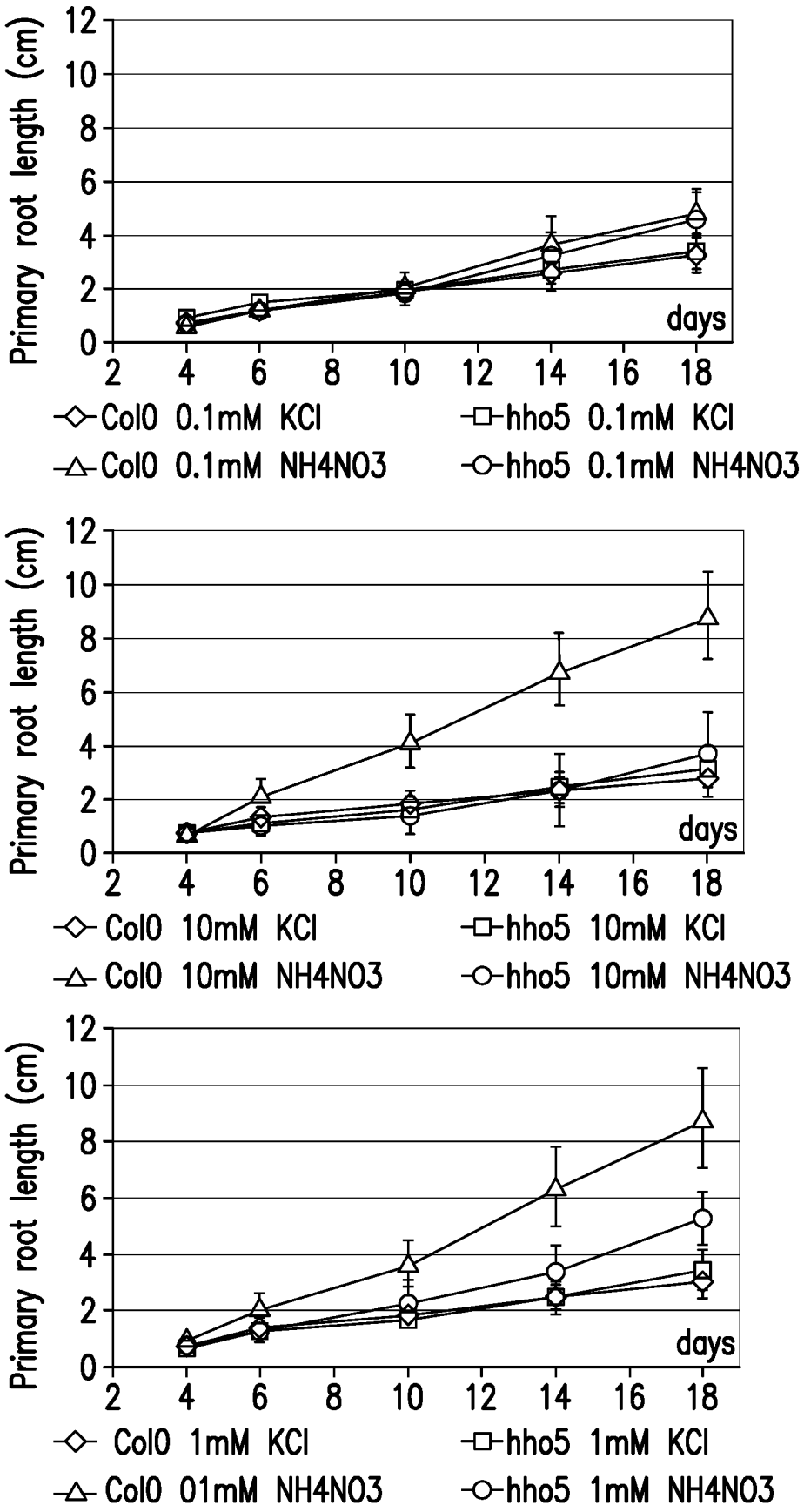
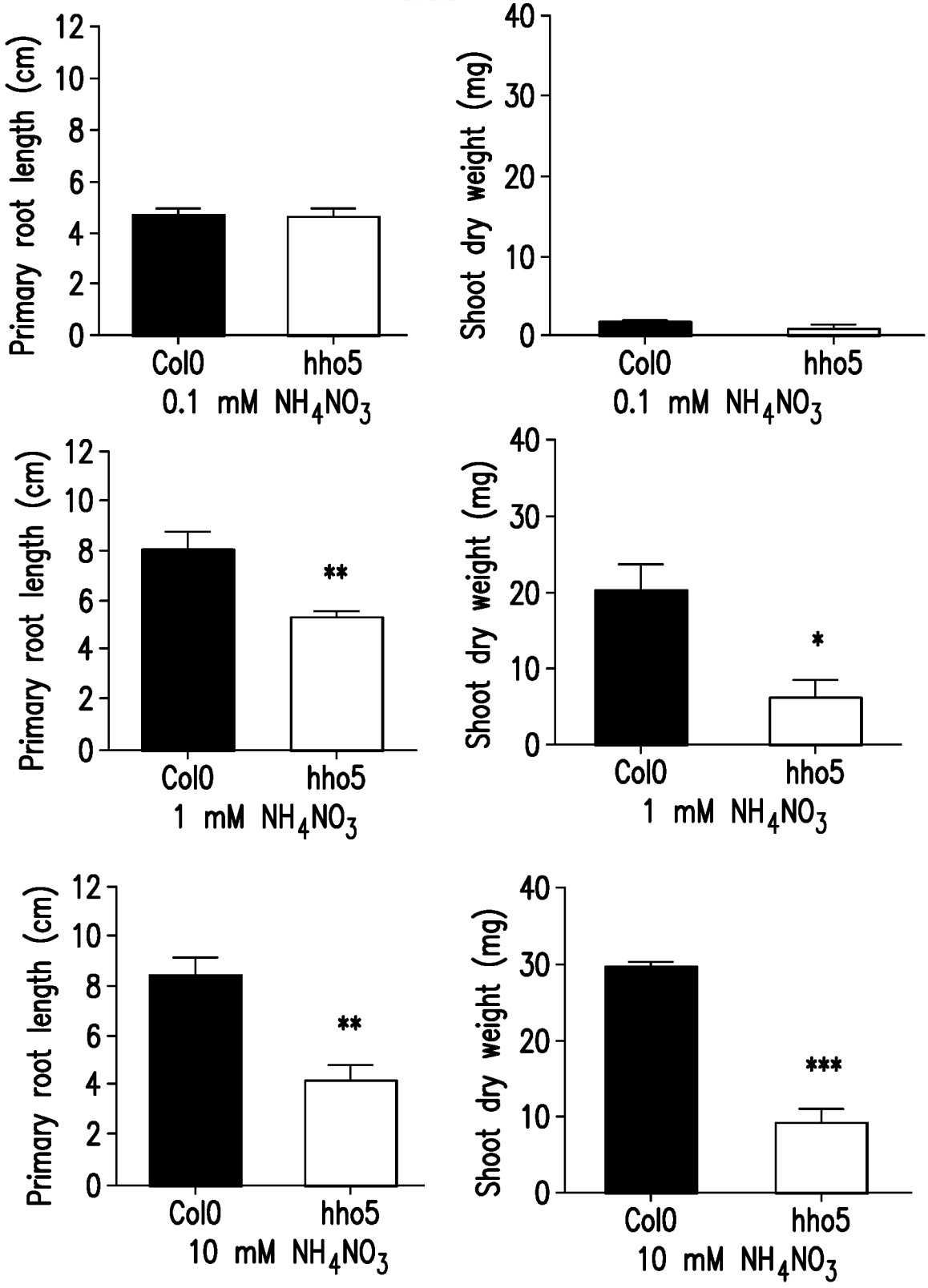

Primary root length (cm)
12
10
8
6
4
2
0
2 4 6 8 10 12 14 16 18
days
Col0 0.1mM KCl
hho5 0.1mM KCl
Col0 0.1mM NH4NO3
hho5 0.1mM NH4NO3
Primary root length (cm)
12
10
8
6
4
2
0
2 4 6 8 10 12 14 16 18
days
Col0 10mM KCl
hho5 10mM KCl
Col0 10mM NH4NO3
hho5 10mM NH4NO3
Primary root length (cm)
12
10
8
6
4
2
0
2 4 6 8 10 12 14 16 18
days
Col0 1mM KCl
hho5 1mM KCl
Col0 01mM NH4NO3
hho5 1mM NH4NO3

FIG. 57A



* p<0.05, ** p<0.01, *** p<0.0001

FIG. 57B

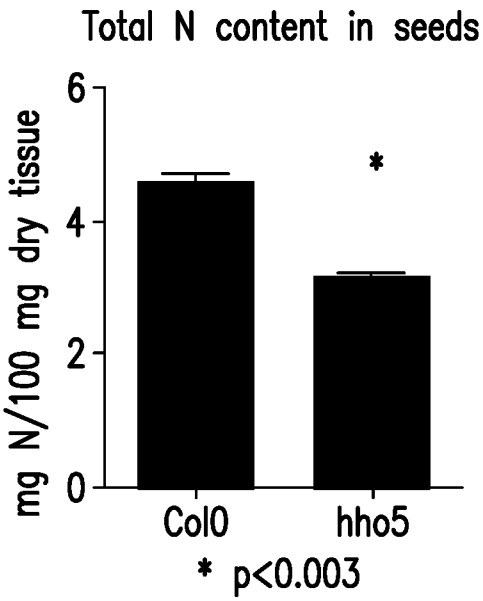

Total N content in seeds
mg N/100 mg dry tissue
6
4
2
0
*
Col0
hho5
* p<0.003

FIG. 58

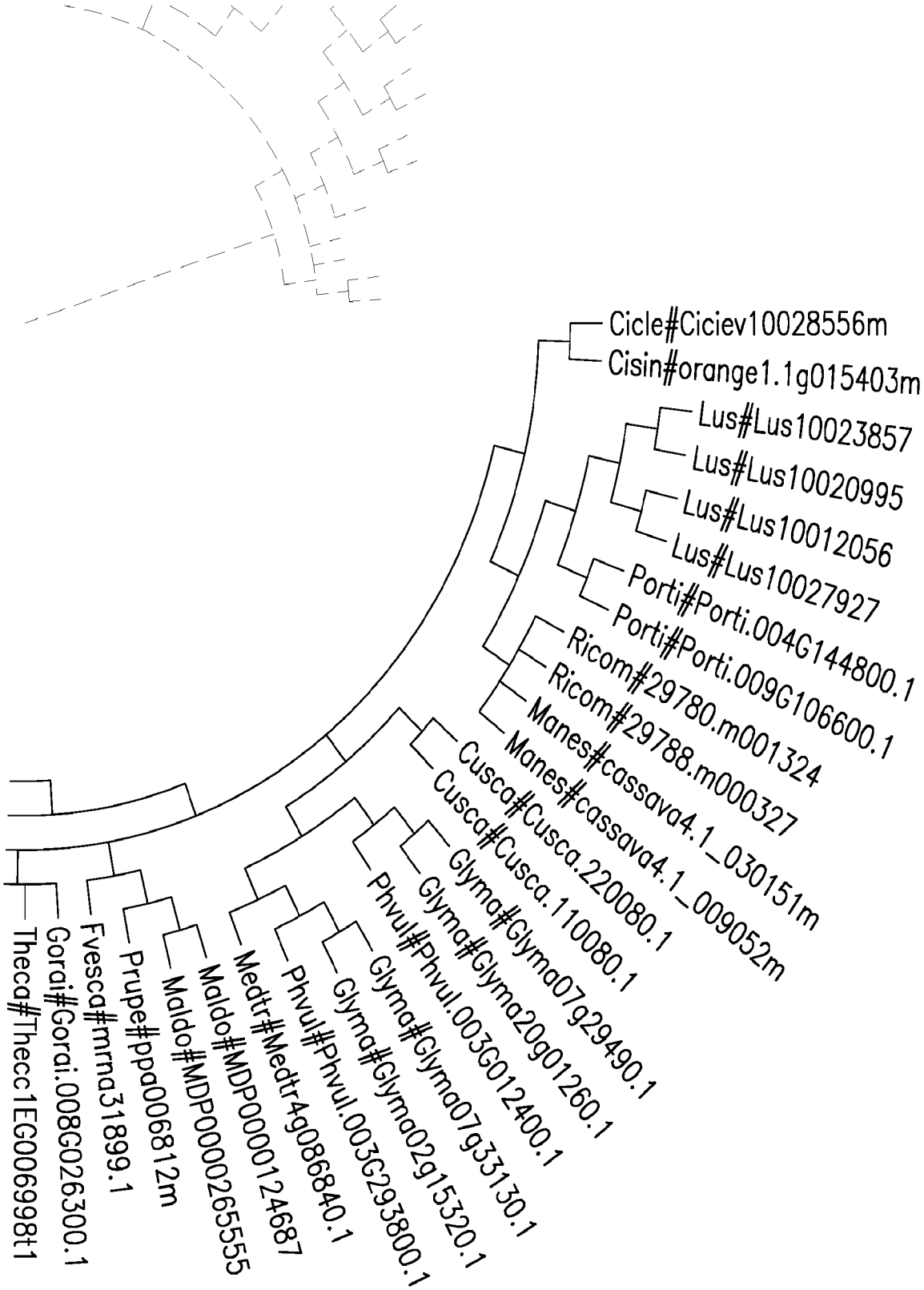

Cicle#Ciciev10028556m
Cisin#orange1.1g015403m
Lus#Lus10023857
Lus#Lus10020995
Lus#Lus10012056
Lus#Lus10027927
Porti#Porti.004G144800.1
Porti#Porti.009G106600.1
Ricom#29780.m001324
Ricom#29788.m000327
Manes#cassava4.1_030151m
Manes#cassava4.1_009052m
Cusca#Cusca.220080.1
Cusca#Cusca.110080.1
Glyma#Glyma07g29490.1
Glyma#Glyma20g01260.1
Phvul#Phvul.003G012400.1
Glyma#Glyma07g33130.1
Glyma#Glyma02g15320.1
Glyma#Glyma03g33800.1
Phvul#Phvul.003G293800.1
Medtr#Medtr4g086840.1
Maldo#MDP0000124687
Maldo#MDP0000265555
Prupe#ppa006812m
Fvesca#mrna31899.1
Gorai#Gorai.008G026300.1
Theca#Thecc1EG006998t1

FIG. 59

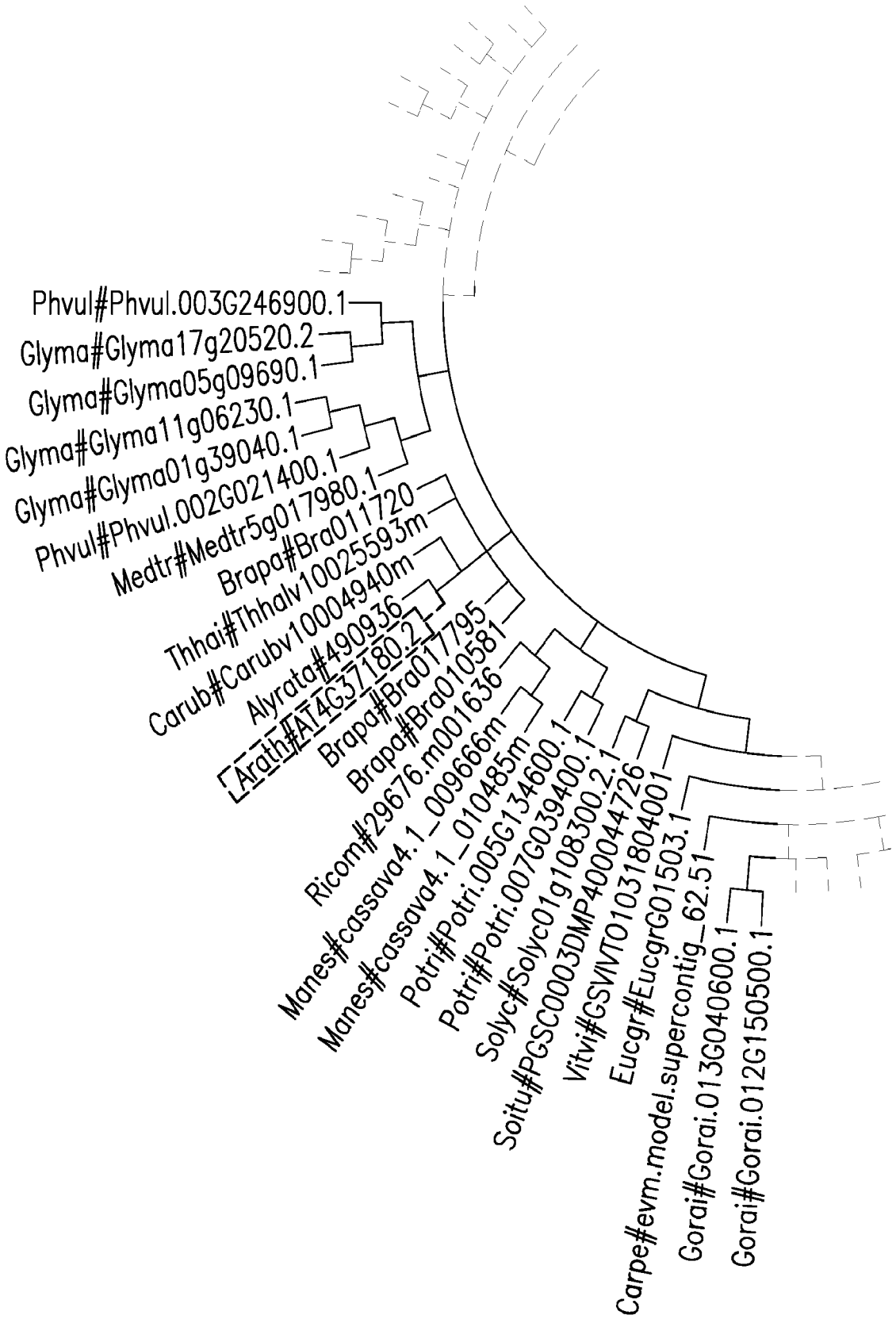


FIG. 59 (Continued)

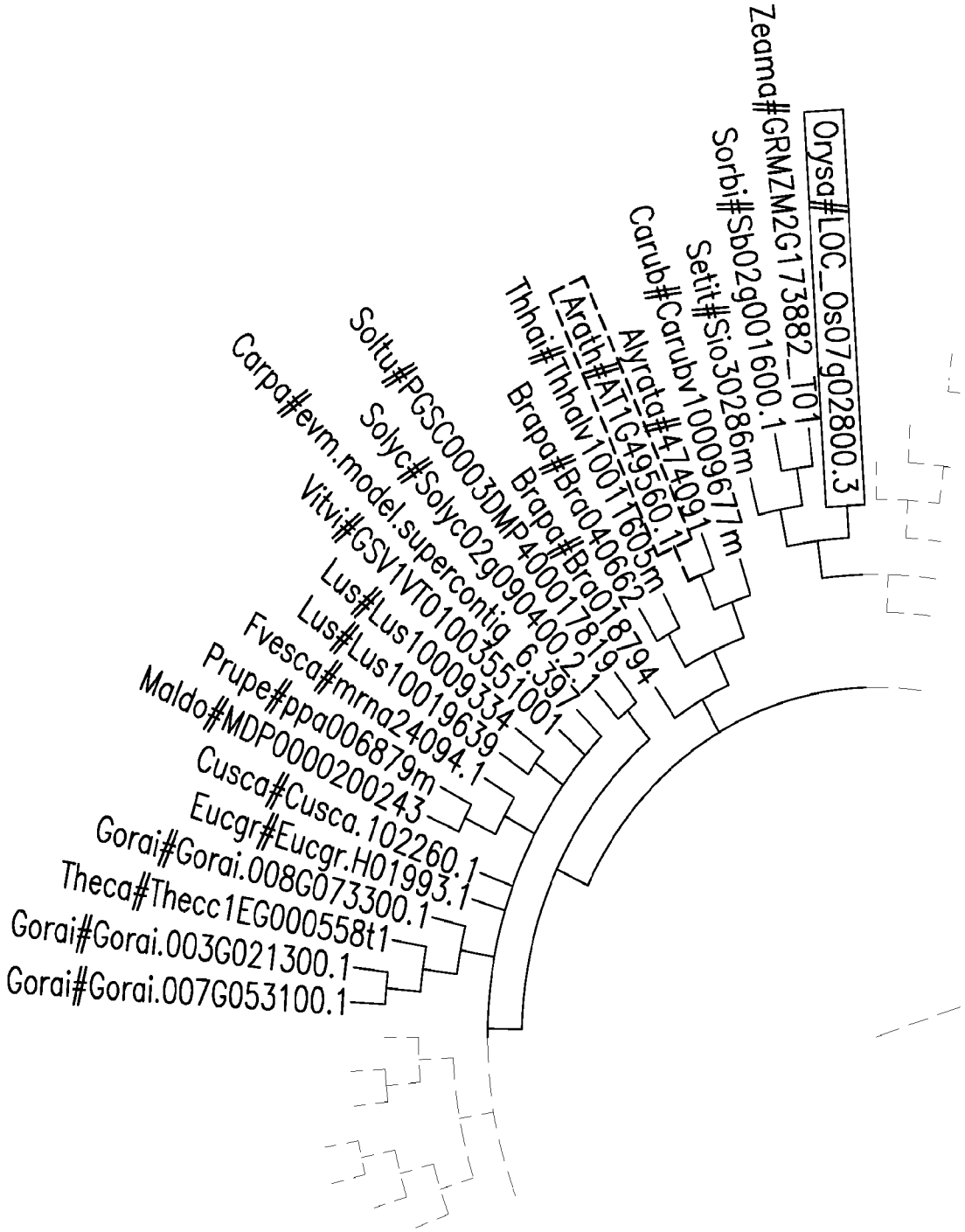


FIG. 59 (Continued)

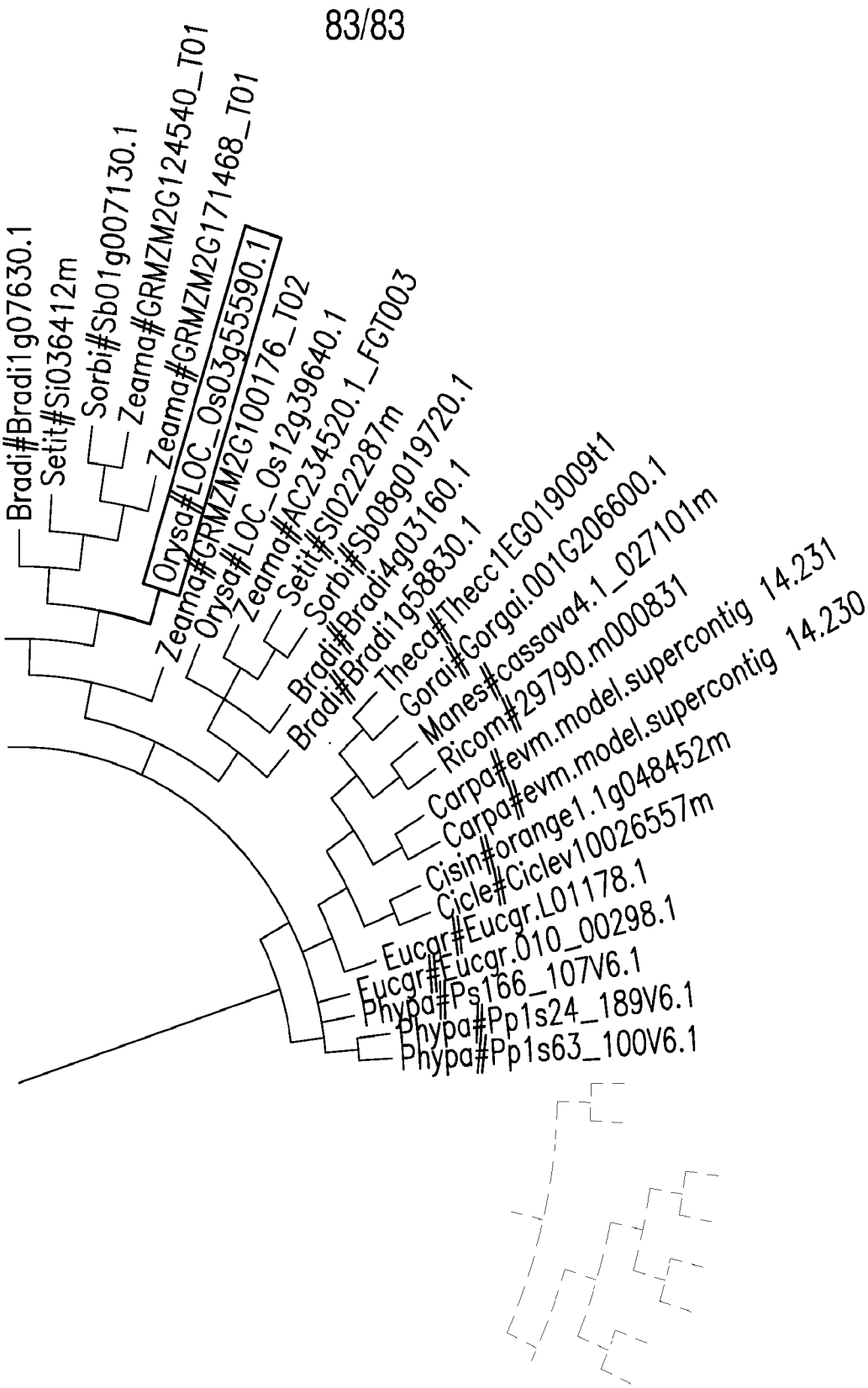


FIG. 59 (Continued)