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(54) Title: PLANTS HAVING ENHANCED YIELD-RELATED TRAITS AND A METHOD FOR MAKING THE SAME

(57) Abstract: The present invention concerns a method for enhancing yield-related traits in plants by modulating expression of a particular type of NAC transcription factor in plants. The particular type of NAC transcription factor is one having an amino acid sequence, which when used in the construction of a NAC phylogenetic tree, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 2, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with any other NAC group. The present invention also concerns plants having modulated expression of a nucleic acid encoding such a NAC transcription factor, which plants have enhanced yield-related relative to control plants. The present invention further concerns a method for enhancing yield-related traits in plants by modulating expression in a plant of a nucleic acid encoding an AP2-2 polypeptide. The present invention also concerns plants having modulated expression of a nucleic acid encoding an AP2-2 polypeptide, which plants have enhanced yield-related traits relative to control plants. The present invention further concerns a method for enhancing yield-related traits in plants by modulating expression in a plant of a nucleic acid encoding an APETELA2-70-like (AP2-70-like) polypeptide. The present invention also concerns plants having modulated expression of a nucleic acid encoding an AP2-70-like polypeptide, which plants have enhanced yield-related traits relative to control plants. The invention also provides hitherto unknown NAC, AP2-2 and AP2-70-like-encoding nucleic acids, and constructs comprising the same, useful in performing the methods of the invention. The invention also provides constructs useful in the methods of the invention.



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Plants having enhanced yield-related traits and a method for making the same

The present invention relates generally to the field of molecular biology and concerns a method for enhancing various economically important yield-related traits in plants. More specifically, the present invention concerns methods for enhancing yield-related traits in plants by modulating expression in a plant of a nucleic acid encoding a particular type of NAC transcription factor. The present invention also concerns plants having modulated expression of a nucleic acid encoding a NAC transcription factor, which plants have enhanced yield-related traits relative to control plants.

In addition, the present invention concerns a method for enhancing yield-related traits in plants by modulating expression in a plant of a nucleic acid encoding a *Apetala 2-2* (AP2-2) polypeptide. The present invention also concerns plants having modulated expression of a nucleic acid encoding an AP2-2 polypeptide, which plants have enhanced yield-related traits relative to control plants. The present invention also concerns a method for enhancing yield-related traits in plants by modulating expression in a plant of a nucleic acid encoding an *APETALA2-70-like* (AP2-70-like) polypeptide. The present invention also concerns plants having modulated expression of a nucleic acid encoding an AP2-70-like polypeptide, which plants have enhanced yield-related traits relative to control plants. The invention also provides hitherto unknown AP2-70-like-encoding nucleic acids, and constructs comprising the same, useful in performing the methods of the invention.

The invention also provides constructs useful in the methods of the invention.

The ever-increasing world population and the dwindling supply of arable land available for agriculture fuels research towards increasing the efficiency of agriculture. Conventional means for crop and horticultural improvements utilise selective breeding techniques to identify plants having desirable characteristics. However, such selective breeding techniques have several drawbacks, namely that these techniques are typically labour intensive and result in plants that often contain heterogeneous genetic components that may not always result in the desirable trait being passed on from parent plants. Advances in molecular biology have allowed mankind to modify the germplasm of animals and plants. Genetic engineering of plants entails the isolation and manipulation of genetic material (typically in the form of DNA or RNA) and the subsequent introduction of that genetic material into a plant. Such technology has the capacity to deliver crops or plants having various improved economic, agronomic and horticultural traits.

A trait of particular economic interest is increased yield. Yield is normally defined as the measurable produce of economic value from a crop. This may be defined in terms of quantity and/or quality. Yield is directly dependent on several factors, for example, the number and size of the organs, plant architecture (for example, the number of branches), seed production, leaf senescence and more. Root development, nutrient uptake, stress tolerance and early vigour may also be important factors in determining yield. Optimizing the abovementioned factors may therefore contribute to increasing crop yield.

Seed yield is a particularly important trait, since the seeds of many plants are important for human and animal nutrition. Crops such as, corn, rice, wheat, canola and soybean account for over half the total human caloric intake, whether through direct consumption of the seeds themselves or through consumption of meat products raised on processed seeds. They are also a source of sugars, oils and many kinds of metabolites used in industrial processes. Seeds contain an embryo (the source of new shoots and roots) and an endosperm (the source of nutrients for embryo growth during germination and during early growth of seedlings). The development of a seed involves many genes, and requires the transfer of metabolites from the roots, leaves and stems into the growing seed. The endosperm, in particular, assimilates the metabolic precursors of carbohydrates, oils and proteins and synthesizes them into storage macromolecules to fill out the grain.

A further trait of economic importance for many crops is early vigour. Improving early vigour is an important objective of modern rice breeding programs in both temperate and tropical rice cultivars. Long roots are important for proper soil anchorage in water-seeded rice. Where rice is sown directly into flooded fields, and where plants must emerge rapidly through water, longer shoots are associated with vigour. Where drill-seeding is practiced, longer mesocotyls and coleoptiles are important for good seedling emergence. Early vigour may also result from increased plant fitness due to, for example, the plants being better adapted to their environment (i.e. being more able to cope with various abiotic or biotic stress factors). Plants having early vigour also show better establishment of the crop (with the crop growing in a more uniform manner, i.e. with the majority of plants reaching the various stages of development at substantially the same time), and show better growth and often better yield.

A further important trait is improved abiotic stress tolerance. Abiotic stress is a primary cause of crop loss worldwide, reducing average yields for most major crop plants by more than 50% (Wang *et al.*, Planta (2003) 218: 1-14). Abiotic stresses may be caused by drought, salinity, extremes of temperature, chemical toxicity and oxidative stress. The ability to improve plant tolerance to abiotic stress would be of great economic advantage to farmers worldwide and would allow for the cultivation of crops during adverse conditions and in territories where cultivation of crops may not otherwise be possible.

The ability to engineer abiotic stress tolerance or early vigour into plants would be of great importance in agriculture, as would the ability to increase plant seed yield, whether through seed number, seed biomass, seed development, seed filling, or any other seed-related trait. Aside from the many applications in agriculture including in the production of ornamental plants, arboriculture, horticulture and forestry, increasing yield would also have many non-agricultural uses, such as in the production of algae for use in bioreactors (for the biotechnological production of substances such as pharmaceuticals, antibodies or vaccines or for the bioconversion of organic waste) and other such areas.

Transcription factors are usually defined as proteins that show sequence-specific DNA binding and that are capable of activating and/or repressing transcription. The *Arabidopsis* genome codes for at least 1533 transcriptional regulators, which account for ~5.9% of its estimated total number of genes. About 45% of these transcription factors are reported to be from families specific to plants (Riechmann *et al.*, 2000 (Science Vol. 290, 2105-2109)).

The present invention concerns the use of a particular type of NAC transcription factor for enhancing yield-related traits in plants.

NAC is an acronym derived from the names of the three genes first described as containing a NAC domain, namely *NAM* (*no apical meristem*), *ATAF1,2* and *CUC2* (*cup-shaped cotyledon*). NAC proteins appear to be widespread in plants, with the genome of *Arabidopsis thaliana* estimated to contain at least a hundred NAC-encoding genes, but without any examples having been found to date in other eukaryotes (Riechmann *et al.*, 2000).

The NAC protein family comprises a variety of plant proteins that are identifiable by the presence of a highly conserved N-terminal NAC domain, accompanied by diverse C-terminal domains. The DNA-binding ability of NAC proteins is generally localized to the NAC domain, with the C-terminal regions constituting transcriptional activation domains. Several NAC genes have been found to be hormone inducible. NAC domains have also been implicated in interactions with other proteins, such as viral proteins and RING finger proteins. NAC proteins have also been implicated in transcriptional control in a variety of plant processes, including in the development of the shoot apical meristem and floral organs, and in the formation of lateral roots. NAC proteins have also been implicated in responses to stress and viral infections, Ernst *et al.*, 2004 (EMBO Reports 5, 3, 297-303).

US patent 6,844,486 describes a member of the NAC family, *NAC1*, isolated from *Arabidopsis thaliana*. *NAC1* was reported to be involved in the regulation of cotyledon and lateral root development. Overexpression of the *nacl* gene was reported to give larger plants with larger roots and more lateral roots than wild-type plants.

Surprisingly, it has now been found that modulating expression in a plant of a nucleic acid encoding a particular type of NAC transcription factor gives plants having enhanced yield-related traits relative to control plants. The particular class of NAC transcription factor suitable for enhancing yield-related traits in plants is described in detail below.

The present invention provides a method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding a particular type of NAC transcription factor.

- 5 In addition, the present invention concerns the use of an Apetala type transcription factor, AP2-2, for enhancing yield-related traits in plants.

AP2 (APETALA2) and EREBPs (ethylene-responsive element binding proteins, or ERF, ethylene response factors) are the prototypic members of a family of transcription factors unique to plants, whose distinguishing characteristic is that they contain the so-called AP2 DNA-binding domain. AP2/EREBP genes form a large multigene family (the AP2/ERF superfamily), and they play a variety of roles throughout the plant life cycle: from being key regulators of several developmental processes, like floral organ identity determination or control of leaf epidermal cell identity, to forming part of the mechanisms used by plants to respond to various types of biotic and environmental stress. Within the AP2/ERF superfamily, 3 large families are discriminated: the AP2 family with two AP2/ERF domains, the ERF family with a single AP2/ERF domain and the RAV family comprising a B3-type DNA binding domain. Nakano et al. (Plant Physiology 140, 411-432, 2006) studied the *ERF* gene family in *Arabidopsis* and rice, and divided the *Arabidopsis* *ERF* gene family into 12 groups (designated Group I to X, and a Group VI-like and Group Xb-like), whereas in the case of rice 15 groups were discriminated. The *Arabidopsis* Group VII proteins are characterised by a conserved N-terminal motif, referred to as Conserved Motif VII-1 (CMVII-1). In rice, Group VII comprises more proteins than the *Arabidopsis* Group VII, and though many conserved motifs are in common between the rice and *Arabidopsis* Group VII, a separate rice Group VIIb was created for a sequence lacking this typical CMVII-1 motif. Functionally, members of Group VII are described to be involved in osmotic stress and disease responses (for example in WO 2003007699). Ectopic overexpression of tomato JERF3 in tobacco increased the salt tolerance of the transgenics (Wang et al., Plant Molecular Biology 58, 183-192, 2004), and pepper transcription factor CaPF1 overexpression resulted in increased osmotic tolerance in pine (Tang et al, Plant Cell Rep. 26, 115-124, 2007), but also increased pathogen resistance in *Arabidopsis* (Yi et al., Plant Physiol. 136, 2862-2874, 2004). A similar observation was made for barley HvRAF (Jung et al., Planta Epub 26 August 2006). Furthermore, a Group VII type ERF protein was used in a process for the production of Methionine (EP2005003297).

Surprisingly, it has now been found that modulating expression in a plant of a nucleic acid encoding a Group VII ERF protein (hereafter named AP2-2 polypeptide) gives plants having enhanced yield-related traits relative to control plants. These enhanced yield-related traits were not the result of increased stress resistance.

The ERF (Ethylene Response Factor) family is a large gene family of transcription factors and is part of the AP2/ERF superfamily, which also contains the AP2 and RAV families. The AP2/ERF superfamily is

defined by the AP2/ERF domain, which consists of about 60 to 70 amino acids and is involved in DNA binding. These three families have been defined as follows. The AP2 family of proteins contain two repeated AP2/ERF domains, the ERF family of proteins contain a single AP2/ERF domain, and the RAV family proteins contain a B3 domain, which is a DNA-binding domain conserved in other plant-specific transcription factors, including VP1/ABI3, in addition to the single AP2/ERF domain. The ERF family is sometimes further divided into two major subfamilies, the ERF subfamily and the CBF/DREB subfamily. 147 genes have been identified in the AP2/ERF superfamily in the Arabidopsis genome, including 122 genes in the ERF family. The AP2 domain was first identified as a repeated motif within the Arabidopsis (*Arabidopsis thaliana*) AP2 protein, which is involved in flower development. Nakano *et al.*, 2006 (Plant Physiol. Vol. 140, pp.411-432).

Nakano *et al.*, 2006 further report that genes in the AP2 family have been shown to participate in the regulation of developmental processes, e.g. flower development, spikelet meristem determinacy, leaf epidermal cell identity, and embryo development. Several proteins in the ERF family have been identified and implicated in many diverse functions in cellular processes, such as hormonal signal transduction, response to biotic and abiotic stresses, and regulation of metabolism, and in developmental processes in various plant species.

Surprisingly, it has now been found that modulating expression in a plant of a nucleic acid encoding an AP2-70-like polypeptide gives plants having enhanced yield-related traits relative to control plants.

AP2-70-like polypeptides described herein as being useful in enhancing yield-related traits in plants are classified in Group Ib (A-6) according to the classification system of Nakano *et al.*, 2006. Nakano reports that DBF1 from maize (*Zea mays*) – a member of Group Ib - has been shown to activate the drought-responsive element 2 (DRE2)-dependent transcription of ABA-responsive *rab17* in transiently transformed maize callus. In another Group Ib member, *Medicago truncatula* WXP1, overexpression of the same was reported to activate wax production in transgenic alfalfa (*Medicago sativa*).

Definitions

Polypeptide(s)/Protein(s)

The terms "polypeptide" and "protein" are used interchangeably herein and refer to amino acids in a polymeric form of any length, linked together by peptide bonds.

Polynucleotide(s)/Nucleic acid(s)/Nucleic acid sequence(s)/nucleotide sequence(s)

The terms "polynucleotide(s)", "nucleic acid sequence(s)", "nucleotide sequence(s)", "nucleic acid(s)", "nucleic acid molecule" are used interchangeably herein and refer to nucleotides, either ribonucleotides or deoxyribonucleotides or a combination of both, in a polymeric unbranched form of any length.

Control plant(s)

The choice of suitable control plants is a routine part of an experimental setup and may include corresponding wild type plants or corresponding plants without the gene of interest. The control plant is typically of the same plant species or even of the same variety as the plant to be assessed. The control plant may also be a nullizygote of the plant to be assessed. Nullizygotes are individuals missing the transgene by segregation. A "control plant" as used herein refers not only to whole plants, but also to plant parts, including seeds and seed parts.

Homologue(s)

"Homologues" of a protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived.

A deletion refers to removal of one or more amino acids from a protein.

An insertion refers to one or more amino acid residues being introduced into a predetermined site in a protein. Insertions may comprise N-terminal and/or C-terminal fusions as well as intra-sequence insertions of single or multiple amino acids. Generally, insertions within the amino acid sequence will be smaller than N- or C-terminal fusions, of the order of about 1 to 10 residues. Examples of N- or C-terminal fusion proteins or peptides include the binding domain or activation domain of a transcriptional activator as used in the yeast two-hybrid system, phage coat proteins, (histidine)-6-tag, glutathione S-transferase-tag, protein A, maltose-binding protein, dihydrofolate reductase, Tag-100 epitope, c-myc epitope, FLAG[®]-epitope, lacZ, CMP (calmodulin-binding peptide), HA epitope, protein C epitope and VSV epitope.

A substitution refers to replacement of amino acids of the protein with other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α -helical structures or β -sheet structures). Amino acid substitutions are typically of single residues, but may be clustered depending upon functional constraints placed upon the polypeptide; insertions will usually be of the order of about 1 to 10 amino acid residues. The amino acid substitutions are preferably conservative amino acid substitutions. Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company (Eds) and Table 1 below).

Table 1: Examples of conserved amino acid substitutions

Residue	Conservative Substitutions	Residue	Conservative Substitutions
Ala	Ser	Leu	Ile; Val

Arg	Lys	Lys	Arg; Gln
Asn	Gln; His	Met	Leu; Ile
Asp	Glu	Phe	Met; Leu; Tyr
Gln	Asn	Ser	Thr; Gly
Cys	Ser	Thr	Ser; Val
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp; Phe
His	Asn; Gln	Val	Ile; Leu
Ile	Leu, Val		

Amino acid substitutions, deletions and/or insertions may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by recombinant DNA manipulation. Methods for the manipulation of DNA sequences to produce substitution, insertion or deletion variants of a protein are well known in the art. For example, techniques for making substitution mutations at predetermined sites in DNA are well known to those skilled in the art and include M13 mutagenesis, T7-Gen in vitro mutagenesis (USB, Cleveland, OH), QuickChange Site Directed mutagenesis (Stratagene, San Diego, CA), PCR-mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

Derivatives

"Derivatives" include peptides, oligopeptides, polypeptides which may, compared to the amino acid sequence of the naturally-occurring form of the protein, such as the protein of interest, comprise substitutions of amino acids with non-naturally occurring amino acid residues, or additions of non-naturally occurring amino acid residues. "Derivatives" of a protein also encompass peptides, oligopeptides, polypeptides which comprise naturally occurring altered (glycosylated, acylated, prenylated, phosphorylated, myristoylated, sulphated etc.) or non-naturally altered amino acid residues compared to the amino acid sequence of a naturally-occurring form of the polypeptide. A derivative may also comprise one or more non-amino acid substituents or additions compared to the amino acid sequence from which it is derived, for example a reporter molecule or other ligand, covalently or non-covalently bound to the amino acid sequence, such as a reporter molecule which is bound to facilitate its detection, and non-naturally occurring amino acid residues relative to the amino acid sequence of a naturally-occurring protein. Furthermore, "derivatives" also include fusions of the naturally-occurring form of the protein with tagging peptides such as FLAG, HIS6 or thioredoxin (for a review of tagging peptides, see Terpe, Appl. Microbiol. Biotechnol. 60, 523-533, 2003).

Orthologue(s)/Parologue(s)

Orthologues and paralogues encompass evolutionary concepts used to describe the ancestral relationships of genes. Paralogues are genes within the same species that have originated through

duplication of an ancestral gene; orthologues are genes from different organisms that have originated through speciation, and are also derived from a common ancestral gene.

Domain

- 5 The term "domain" refers to a set of amino acids conserved at specific positions along an alignment of sequences of evolutionarily related proteins. While amino acids at other positions can vary between homologues, amino acids that are highly conserved at specific positions indicate amino acids that are likely essential in the structure, stability or function of a protein. Identified by their high degree of conservation in aligned sequences of a family of protein homologues, they can be used as identifiers to
10 determine if any polypeptide in question belongs to a previously identified polypeptide family.

Motif/Consensus sequence/Signature

- The term "motif" or "consensus sequence" or "signature" refers to a short conserved region in the sequence of evolutionarily related proteins. Motifs are frequently highly conserved parts of domains, but
15 may also include only part of the domain, or be located outside of conserved domain (if all of the amino acids of the motif fall outside of a defined domain).

Hybridisation

- The term "hybridisation" as defined herein is a process wherein substantially homologous
20 complementary nucleotide sequences anneal to each other. The hybridisation process can occur entirely in solution, i.e. both complementary nucleic acids are in solution. The hybridisation process can also occur with one of the complementary nucleic acids immobilised to a matrix such as magnetic beads, Sepharose beads or any other resin. The hybridisation process can furthermore occur with one of the complementary nucleic acids immobilised to a solid support such as a nitro-cellulose or nylon
25 membrane or immobilised by e.g. photolithography to, for example, a siliceous glass support (the latter known as nucleic acid arrays or microarrays or as nucleic acid chips). In order to allow hybridisation to occur, the nucleic acid molecules are generally thermally or chemically denatured to melt a double strand into two single strands and/or to remove hairpins or other secondary structures from single stranded nucleic acids.

- 30 The term "stringency" refers to the conditions under which a hybridisation takes place. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration, ionic strength and hybridisation buffer composition. Generally, low stringency conditions are selected to be about 30°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.
35 Medium stringency conditions are when the temperature is 20°C below T_m , and high stringency conditions are when the temperature is 10°C below T_m . High stringency hybridisation conditions are typically used for isolating hybridising sequences that have high sequence similarity to the target nucleic acid sequence. However, nucleic acids may deviate in sequence and still encode a substantially

identical polypeptide, due to the degeneracy of the genetic code. Therefore medium stringency hybridisation conditions may sometimes be needed to identify such nucleic acid molecules.

The T_m is the temperature under defined ionic strength and pH, at which 50% of the target sequence hybridises to a perfectly matched probe. The T_m is dependent upon the solution conditions and the base composition and length of the probe. For example, longer sequences hybridise specifically at higher temperatures. The maximum rate of hybridisation is obtained from about 16°C up to 32°C below T_m . The presence of monovalent cations in the hybridisation solution reduce the electrostatic repulsion between the two nucleic acid strands thereby promoting hybrid formation; this effect is visible for sodium concentrations of up to 0.4M (for higher concentrations, this effect may be ignored). Formamide reduces the melting temperature of DNA-DNA and DNA-RNA duplexes with 0.6 to 0.7°C for each percent formamide, and addition of 50% formamide allows hybridisation to be performed at 30 to 45°C, though the rate of hybridisation will be lowered. Base pair mismatches reduce the hybridisation rate and the thermal stability of the duplexes. On average and for large probes, the T_m decreases about 1°C per % base mismatch. The T_m may be calculated using the following equations, depending on the types of hybrids:

1) DNA-DNA hybrids (Meinkoth and Wahl, Anal. Biochem., 138: 267-284, 1984):

$$T_m = 81.5^\circ\text{C} + 16.6 \times \log_{10}[\text{Na}^+]^a + 0.41 \times \%[\text{G/C}^b] - 500 \times [\text{L}^c]^{-1} - 0.61 \times \% \text{ formamide}$$

2) DNA-RNA or RNA-RNA hybrids:

$$T_m = 79.8 + 18.5 (\log_{10}[\text{Na}^+]^a) + 0.58 (\% \text{G/C}^b) + 11.8 (\% \text{G/C}^b)^2 - 820/\text{L}^c$$

3) oligo-DNA or oligo-RNA^d hybrids:

$$\text{For } <20 \text{ nucleotides: } T_m = 2 (I_n)$$

$$\text{For } 20\text{--}35 \text{ nucleotides: } T_m = 22 + 1.46 (I_n)$$

^a or for other monovalent cation, but only accurate in the 0.01–0.4 M range.

^b only accurate for %GC in the 30% to 75% range.

^c L = length of duplex in base pairs.

^d oligo, oligonucleotide; I_n = effective length of primer = $2 \times (\text{no. of G/C}) + (\text{no. of A/T})$.

Non-specific binding may be controlled using any one of a number of known techniques such as, for example, blocking the membrane with protein containing solutions, additions of heterologous RNA, DNA, and SDS to the hybridisation buffer, and treatment with Rnase. For non-homologous probes, a series of hybridizations may be performed by varying one of (i) progressively lowering the annealing temperature (for example from 68°C to 42°C) or (ii) progressively lowering the formamide concentration (for example from 50% to 0%). The skilled artisan is aware of various parameters which may be altered during hybridisation and which will either maintain or change the stringency conditions.

Besides the hybridisation conditions, specificity of hybridisation typically also depends on the function of post-hybridisation washes. To remove background resulting from non-specific hybridisation, samples

are washed with dilute salt solutions. Critical factors of such washes include the ionic strength and temperature of the final wash solution: the lower the salt concentration and the higher the wash temperature, the higher the stringency of the wash. Wash conditions are typically performed at or below hybridisation stringency. A positive hybridisation gives a signal that is at least twice of that of the background. Generally, suitable stringent conditions for nucleic acid hybridisation assays or gene amplification detection procedures are as set forth above. More or less stringent conditions may also be selected. The skilled artisan is aware of various parameters which may be altered during washing and which will either maintain or change the stringency conditions.

For example, typical high stringency hybridisation conditions for DNA hybrids longer than 50 nucleotides encompass hybridisation at 65°C in 1x SSC or at 42°C in 1x SSC and 50% formamide, followed by washing at 65°C in 0.3x SSC. Examples of medium stringency hybridisation conditions for DNA hybrids longer than 50 nucleotides encompass hybridisation at 50°C in 4x SSC or at 40°C in 6x SSC and 50% formamide, followed by washing at 50°C in 2x SSC. The length of the hybrid is the anticipated length for the hybridising nucleic acid. When nucleic acids of known sequence are hybridised, the hybrid length may be determined by aligning the sequences and identifying the conserved regions described herein. 1xSSC is 0.15M NaCl and 15mM sodium citrate; the hybridisation solution and wash solutions may additionally include 5x Denhardt's reagent, 0.5-1.0% SDS, 100 µg/ml denatured, fragmented salmon sperm DNA, 0.5% sodium pyrophosphate.

For the purposes of defining the level of stringency, reference can be made to Sambrook et al. (2001) Molecular Cloning: a laboratory manual, 3rd Edition, Cold Spring Harbor Laboratory Press, CSH, New York or to Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989 and yearly updates).

Splice variant

The term "splice variant" as used herein encompasses variants of a nucleic acid sequence in which selected introns and/or exons have been excised, replaced, displaced or added, or in which introns have been shortened or lengthened. Such variants will be ones in which the biological activity of the protein is substantially retained; this may be achieved by selectively retaining functional segments of the protein.

Such splice variants may be found in nature or may be manmade. Methods for predicting and isolating such splice variants are well known in the art (see for example Foissac and Schiex (2005) BMC Bioinformatics 6: 25).

Allelic variant

Alleles or allelic variants are alternative forms of a given gene, located at the same chromosomal position. Allelic variants encompass Single Nucleotide Polymorphisms (SNPs), as well as Small Insertion/Deletion Polymorphisms (INDELs). The size of INDELs is usually less than 100 bp. SNPs and INDELs form the largest set of sequence variants in naturally occurring polymorphic strains of most organisms.

Gene shuffling/Directed evolution

Gene shuffling or directed evolution consists of iterations of DNA shuffling followed by appropriate screening and/or selection to generate variants of nucleic acids or portions thereof encoding proteins having a modified biological activity (Castle et al., (2004) Science 304(5674): 1151-4; US patents 5,811,238 and 6,395,547).

Regulatory element/Control sequence/Promoter

The terms "regulatory element", "control sequence" and "promoter" are all used interchangeably herein and are to be taken in a broad context to refer to regulatory nucleic acid sequences capable of effecting expression of the sequences to which they are ligated. The term "promoter" typically refers to a nucleic acid control sequence located upstream from the transcriptional start of a gene and which is involved in recognising and binding of RNA polymerase and other proteins, thereby directing transcription of an operably linked nucleic acid. Encompassed by the aforementioned terms are transcriptional regulatory sequences derived from a classical eukaryotic genomic gene (including the TATA box which is required for accurate transcription initiation, with or without a CCAAT box sequence) and additional regulatory elements (i.e. upstream activating sequences, enhancers and silencers) which alter gene expression in response to developmental and/or external stimuli, or in a tissue-specific manner. Also included within the term is a transcriptional regulatory sequence of a classical prokaryotic gene, in which case it may include a -35 box sequence and/or -10 box transcriptional regulatory sequences. The term "regulatory element" also encompasses a synthetic fusion molecule or derivative that confers, activates or enhances expression of a nucleic acid molecule in a cell, tissue or organ.

A "plant promoter" comprises regulatory elements, which mediate the expression of a coding sequence segment in plant cells. Accordingly, a plant promoter need not be of plant origin, but may originate from viruses or micro-organisms, for example from viruses which attack plant cells. The "plant promoter" can also originate from a plant cell, e.g. from the plant which is transformed with the nucleic acid sequence to be expressed in the inventive process and described herein. This also applies to other "plant" regulatory signals, such as "plant" terminators. The promoters upstream of the nucleotide sequences useful in the methods of the present invention can be modified by one or more nucleotide substitution(s), insertion(s) and/or deletion(s) without interfering with the functionality or activity of either the promoters, the open reading frame (ORF) or the 3'-regulatory region such as terminators or other 3' regulatory regions which are located away from the ORF. It is furthermore possible that the activity of the promoters is increased by modification of their sequence, or that they are replaced completely by more active promoters, even promoters from heterologous organisms. For expression in plants, the nucleic acid molecule must, as described above, be linked operably to or comprise a suitable promoter which expresses the gene at the right point in time and with the required spatial expression pattern.

For the identification of functionally equivalent promoters, the promoter strength and/or expression pattern of a candidate promoter may be analysed for example by operably linking the promoter to a reporter gene and assaying the expression level and pattern of the reporter gene in various tissues of the plant. Suitable well-known reporter genes include for example beta-glucuronidase or beta-galactosidase. The promoter activity is assayed by measuring the enzymatic activity of the beta-glucuronidase or beta-galactosidase. The promoter strength and/or expression pattern may then be compared to that of a reference promoter (such as the one used in the methods of the present invention). Alternatively, promoter strength may be assayed by quantifying mRNA levels or by comparing mRNA levels of the nucleic acid used in the methods of the present invention, with mRNA levels of housekeeping genes such as 18S rRNA, using methods known in the art, such as Northern blotting with densitometric analysis of autoradiograms, quantitative real-time PCR or RT-PCR (Heid et al., 1996 Genome Methods 6: 986-994). Generally by "weak promoter" is intended a promoter that drives expression of a coding sequence at a low level. By "low level" is intended at levels of about 1/10,000 transcripts to about 1/100,000 transcripts, to about 1/500,000 transcripts per cell. Conversely, a "strong promoter" drives expression of a coding sequence at high level, or at about 1/10 transcripts to about 1/100 transcripts to about 1/1000 transcripts per cell.

Operably linked

The term "operably linked" as used herein refers to a functional linkage between the promoter sequence and the gene of interest, such that the promoter sequence is able to initiate transcription of the gene of interest.

Constitutive promoter

A "constitutive promoter" refers to a promoter that is transcriptionally active during most, but not necessarily all, phases of growth and development and under most environmental conditions, in at least one cell, tissue or organ. Table 2a below gives examples of constitutive promoters.

Table 2a: Examples of constitutive promoters

Gene Source	Reference
Actin	McElroy et al, Plant Cell, 2: 163-171, 1990
HMGP	WO 2004/070039
CAMV 35S	Odell et al, Nature, 313: 810-812, 1985
CaMV 19S	Nilsson et al., Physiol. Plant. 100:456-462, 1997
GOS2	de Pater et al, Plant J Nov;2(6):837-44, 1992, WO 2004/065596
Ubiquitin	Christensen et al, Plant Mol. Biol. 18: 675-689, 1992
Rice cyclophilin	Buchholz et al, Plant Mol Biol. 25(5): 837-43, 1994
Maize H3 histone	Lepetit et al, Mol. Gen. Genet. 231:276-285, 1992
Alfalfa H3 histone	Wu et al. Plant Mol. Biol. 11:641-649, 1988
Actin 2	An et al, Plant J. 10(1); 107-121, 1996

34S FMV	Sanger et al., Plant. Mol. Biol., 14, 1990: 433-443
Rubisco small subunit	US 4,962,028
OCS	Leisner (1988) Proc Natl Acad Sci USA 85(5): 2553
SAD1	Jain et al., Crop Science, 39 (6), 1999: 1696
SAD2	Jain et al., Crop Science, 39 (6), 1999: 1696
nos	Shaw et al. (1984) Nucleic Acids Res. 12(20):7831-7846
V-ATPase	WO 01/14572
Super promoter	WO 95/14098
G-box proteins	WO 94/12015

Ubiquitous promoter

A ubiquitous promoter is active in substantially all tissues or cells of an organism.

5 Developmentally-regulated promoter

A developmentally-regulated promoter is active during certain developmental stages or in parts of the plant that undergo developmental changes.

Inducible promoter

- 10 An inducible promoter has induced or increased transcription initiation in response to a chemical (for a review see Gatz 1997, Annu. Rev. Plant Physiol. Plant Mol. Biol., 48:89-108), environmental or physical stimulus, or may be "stress-inducible", i.e. activated when a plant is exposed to various stress conditions, or a "pathogen-inducible" i.e. activated when a plant is exposed to exposure to various pathogens.

- 15 Organ-specific/Tissue-specific promoter
- An organ-specific or tissue-specific promoter is one that is capable of preferentially initiating transcription in certain organs or tissues, such as the leaves, roots, seed tissue etc. For example, a "root-specific promoter" is a promoter that is transcriptionally active predominantly in plant roots, substantially to the exclusion of any other parts of a plant, whilst still allowing for any leaky expression in these other plant parts. Promoters able to initiate transcription in certain cells only are referred to herein as "cell-specific".
- 20

Examples of root-specific promoters are listed in Table 2b below:

25 **Table 2b:** Examples of root-specific promoters

Gene Source	Reference
RCc3	Plant Mol Biol. 1995 Jan;27(2):237-48
Arabidopsis phosphate transporter PHT1	Kovama et al., 2005
Medicago phosphate transporter	Xiao et al., 2006
Arabidopsis Pyk10	Nitz et al. (2001) Plant Sci 161(2): 337-346

A seed-specific promoter is transcriptionally active predominantly in seed tissue, but not necessarily exclusively in seed tissue (in cases of leaky expression). The seed-specific promoter may be active during seed development and/or during germination.

5 A green tissue-specific promoter as defined herein is a promoter that is transcriptionally active predominantly in green tissue, substantially to the exclusion of any other parts of a plant, whilst still allowing for any leaky expression in these other plant parts.

10 Examples of green tissue-specific promoters which may be used to perform the methods of the invention are shown in Table 2c below.

Table 2c: Examples of green tissue-specific promoters

Gene	Expression	Reference
Maize Orthophosphate dikinase	Leaf specific	Fukavama et al., 2001
Maize Phosphoenolpyruvate carboxylase	Leaf specific	Kausch et al., 2001
Rice Phosphoenolpyruvate carboxylase	Leaf specific	Liu et al., 2003
Rice small subunit Rubisco	Leaf specific	Nomura et al., 2000
rice beta expansin EXBP9	Shoot specific	WO 2004/070039
Pigeonpea small subunit Rubisco	Leaf specific	Panguluri et al., 2005
Pea RBCS3A	Leaf specific	

15 Another example of a tissue-specific promoter is a meristem-specific promoter, which is transcriptionally active predominantly in meristematic tissue, substantially to the exclusion of any other parts of a plant, whilst still allowing for any leaky expression in these other plant parts.

Terminator

20 The term "terminator" encompasses a control sequence which is a DNA sequence at the end of a transcriptional unit which signals 3' processing and polyadenylation of a primary transcript and termination of transcription. The terminator can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The terminator to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less
25 preferably from any other eukaryotic gene.

Modulation

The term "modulation" means in relation to expression or gene expression, a process in which the expression level is changed by said gene expression in comparison to the control plant, preferably the
30 expression level is increased. The original, unmodulated expression may be of any kind of expression of a structural RNA (rRNA, tRNA) or mRNA with subsequent translation. The term "modulating the activity"

shall mean any change of the expression of the inventive nucleic acid sequences or encoded proteins, which leads to increased yield and/or increased growth of the plants.

Expression

The term "expression" or "gene expression" means the transcription of a specific gene or specific genes or specific genetic construct. The term "expression" or "gene expression" in particular means the transcription of a gene or genes or genetic construct into structural RNA (rRNA, tRNA) or mRNA with or without subsequent translation of the latter into a protein. The process includes transcription of DNA and processing of the resulting mRNA product.

Increased expression/overexpression

The term "increased expression" or "overexpression" as used herein means any form of expression that is additional to the original wild-type expression level.

Methods for increasing expression of genes or gene products are well documented in the art and include, for example, overexpression driven by appropriate promoters, the use of transcription enhancers or translation enhancers. Isolated nucleic acids which serve as promoter or enhancer elements may be introduced in an appropriate position (typically upstream) of a non-heterologous form of a polynucleotide so as to upregulate expression of a nucleic acid encoding the polypeptide of interest. For example, endogenous promoters may be altered in vivo by mutation, deletion, and/or substitution (see, Kmiec, US 5,565,350; Zarling et al., WO9322443), or isolated promoters may be introduced into a plant cell in the proper orientation and distance from a gene of the present invention so as to control the expression of the gene.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added may be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence may also be added to the 5' untranslated region (UTR) or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold (Buchman and Berg (1988) Mol. Cell Biol. 8: 4395-4405; Callis et al. (1987) Genes Dev 1:1183-1200). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of the maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. For general information see: The Maize Handbook, Chapter 116, Freeling and Walbot, Eds., Springer, N.Y. (1994).

Optionally, one or more terminator sequences may be used in the construct introduced into a plant. Additional regulatory elements may include transcriptional as well as translational enhancers. Other control sequences (besides promoter, enhancer, silencer, intron sequences, 3'UTR and/or 5'UTR regions) may be protein and/or RNA stabilizing elements. Such sequences would be known or may readily be obtained by a person skilled in the art.

The genetic constructs of the invention may further include an origin of replication sequence that is required for maintenance and/or replication in a specific cell type. One example is when a genetic construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule). Preferred origins of replication include, but are not limited to, the f1-ori and colE1.

Endogenous gene

Reference herein to an "endogenous" gene not only refers to the gene in question as found in a plant in its natural form (i.e., without there being any human intervention), but also refers to that same gene (or a substantially homologous nucleic acid/gene) in an isolated form subsequently (re)introduced into a plant (a transgene). For example, a transgenic plant containing such a transgene may encounter a substantial reduction of the transgene expression and/or substantial reduction of expression of the endogenous gene. The isolated gene may be isolated from an organism or may be manmade, for example by chemical synthesis.

Decreased expression

Reference herein to "decreased expression" or "reduction or substantial elimination" of expression is taken to mean a decrease in endogenous gene expression and/or polypeptide levels and/or polypeptide activity relative to control plants. The reduction or substantial elimination is in increasing order of preference at least 10%, 20%, 30%, 40% or 50%, 60%, 70%, 80%, 85%, 90%, or 95%, 96%, 97%, 98%, 99% or more reduced compared to that of control plants. Reduction or substantial elimination of expression may be achieved using routine tools and techniques known in the art.

Selectable marker (gene)/Reporter gene

"Selectable marker", "selectable marker gene" or "reporter gene" includes any gene that confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells that are transfected or transformed with a nucleic acid construct of the invention. These marker genes enable the identification of a successful transfer of the nucleic acid molecules via a series of different principles. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance, that introduce a new metabolic trait or that allow visual selection. Examples of selectable marker genes include genes conferring resistance to antibiotics (such as nptII that phosphorylates neomycin and kanamycin, or hpt, phosphorylating hygromycin, or genes conferring resistance to, for example, bleomycin, streptomycin, tetracyclin, chloramphenicol, ampicillin, gentamycin, geneticin (G418),

spectinomycin or blasticidin), to herbicides (for example bar which provides resistance to Basta®; *aroA* or *gox* providing resistance against glyphosate, or the genes conferring resistance to, for example, imidazolinone, phosphinothricin or sulfonyleurea), or genes that provide a metabolic trait (such as *manA* that allows plants to use mannose as sole carbon source or xylose isomerase for the utilisation of xylose, or antinutritive markers such as the resistance to 2-deoxyglucose). Expression of visual marker genes results in the formation of colour (for example β -glucuronidase, GUS or β -galactosidase with its coloured substrates, for example X-Gal), luminescence (such as the luciferin/luciferase system) or fluorescence (Green Fluorescent Protein, GFP, and derivatives thereof). This list represents only a small number of possible markers. The skilled worker is familiar with such markers. Different markers are preferred, depending on the organism and the selection method.

It is known that upon stable or transient integration of nucleic acids into plant cells, only a minority of the cells takes up the foreign DNA and, if desired, integrates it into its genome, depending on the expression vector used and the transfection technique used. To identify and select these integrants, a gene coding for a selectable marker (such as the ones described above) is usually introduced into the host cells together with the gene of interest. These markers can for example be used in mutants in which these genes are not functional by, for example, deletion by conventional methods. Furthermore, nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector that comprises the sequence encoding the polypeptides of the invention or used in the methods of the invention, or else in a separate vector. Cells which have been stably transfected with the introduced nucleic acid can be identified for example by selection (for example, cells which have integrated the selectable marker survive whereas the other cells die).

Since the marker genes, particularly genes for resistance to antibiotics and herbicides, are no longer required or are undesired in the transgenic host cell once the nucleic acids have been introduced successfully, the process according to the invention for introducing the nucleic acids advantageously employs techniques which enable the removal or excision of these marker genes. One such a method is what is known as co-transformation. The co-transformation method employs two vectors simultaneously for the transformation, one vector bearing the nucleic acid according to the invention and a second bearing the marker gene(s). A large proportion of transformants receives or, in the case of plants, comprises (up to 40% or more of the transformants), both vectors. In case of transformation with *Agrobacteria*, the transformants usually receive only a part of the vector, i.e. the sequence flanked by the T-DNA, which usually represents the expression cassette. The marker genes can subsequently be removed from the transformed plant by performing crosses. In another method, marker genes integrated into a transposon are used for the transformation together with desired nucleic acid (known as the *Ac/Ds* technology). The transformants can be crossed with a transposase source or the transformants are transformed with a nucleic acid construct conferring expression of a transposase, transiently or stable. In some cases (approx. 10%), the transposon jumps out of the genome of the host cell once transformation has taken place successfully and is lost. In a further number of cases, the

transposon jumps to a different location. In these cases the marker gene must be eliminated by performing crosses. In microbiology, techniques were developed which make possible, or facilitate, the detection of such events. A further advantageous method relies on what is known as recombination systems; whose advantage is that elimination by crossing can be dispensed with. The best-known system of this type is what is known as the Cre/lox system. Cre1 is a recombinase that removes the sequences located between the loxP sequences. If the marker gene is integrated between the loxP sequences, it is removed once transformation has taken place successfully, by expression of the recombinase. Further recombination systems are the HIN/HIX, FLP/FRT and REP/STB system (Tribble et al., J. Biol. Chem., 275, 2000: 22255-22267; Velmurugan et al., J. Cell Biol., 149, 2000: 553-566). A site-specific integration into the plant genome of the nucleic acid sequences according to the invention is possible. Naturally, these methods can also be applied to microorganisms such as yeast, fungi or bacteria.

Transgenic/Transgene/Recombinant

For the purposes of the invention, "transgenic", "transgene" or "recombinant" means with regard to, for example, a nucleic acid sequence, an expression cassette, gene construct or a vector comprising the nucleic acid sequence or an organism transformed with the nucleic acid sequences, expression cassettes or vectors according to the invention, all those constructions brought about by recombinant methods in which either

- (a) the nucleic acid sequences encoding proteins useful in the methods of the invention, or
- (b) genetic control sequence(s) which is operably linked with the nucleic acid sequence according to the invention, for example a promoter, or
- (c) a) and b)

are not located in their natural genetic environment or have been modified by recombinant methods, it being possible for the modification to take the form of, for example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. The natural genetic environment is understood as meaning the natural genomic or chromosomal locus in the original plant or the presence in a genomic library. In the case of a genomic library, the natural genetic environment of the nucleic acid sequence is preferably retained, at least in part. The environment flanks the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, especially preferably at least 1000 bp, most preferably at least 5000 bp. A naturally occurring expression cassette – for example the naturally occurring combination of the natural promoter of the nucleic acid sequences with the corresponding nucleic acid sequence encoding a polypeptide useful in the methods of the present invention, as defined above – becomes a transgenic expression cassette when this expression cassette is modified by non-natural, synthetic ("artificial") methods such as, for example, mutagenic treatment. Suitable methods are described, for example, in US 5,565,350 or WO 00/15815.

A transgenic plant for the purposes of the invention is thus understood as meaning, as above, that the nucleic acids used in the method of the invention are not at their natural locus in the genome of said

plant, it being possible for the nucleic acids to be expressed homologously or heterologously. However, as mentioned, transgenic also means that, while the nucleic acids according to the invention or used in the inventive method are at their natural position in the genome of a plant, the sequence has been modified with regard to the natural sequence, and/or that the regulatory sequences of the natural sequences have been modified. Transgenic is preferably understood as meaning the expression of the nucleic acids according to the invention at an unnatural locus in the genome, i.e. homologous or, preferably, heterologous expression of the nucleic acids takes place. Preferred transgenic plants are mentioned herein.

Transformation

The term "introduction" or "transformation" as referred to herein encompasses the transfer of an exogenous polynucleotide into a host cell, irrespective of the method used for transfer. Plant tissue capable of subsequent clonal propagation, whether by organogenesis or embryogenesis, may be transformed with a genetic construct of the present invention and a whole plant regenerated there from.

The particular tissue chosen will vary depending on the clonal propagation systems available for, and best suited to, the particular species being transformed. Exemplary tissue targets include leaf disks, pollen, embryos, cotyledons, hypocotyls, megagametophytes, callus tissue, existing meristematic tissue (e.g., apical meristem, axillary buds, and root meristems), and induced meristem tissue (e.g., cotyledon meristem and hypocotyl meristem). The polynucleotide may be transiently or stably introduced into a host cell and may be maintained non-integrated, for example, as a plasmid. Alternatively, it may be integrated into the host genome. The resulting transformed plant cell may then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

The transfer of foreign genes into the genome of a plant is called transformation. Transformation of plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the gene of interest into a suitable ancestor cell. The methods described for the transformation and regeneration of plants from plant tissues or plant cells may be utilized for transient or for stable transformation. Transformation methods include the use of liposomes, electroporation, chemicals that increase free DNA uptake, injection of the DNA directly into the plant, particle gun bombardment, transformation using viruses or pollen and microprojection. Methods may be selected from the calcium/polyethylene glycol method for protoplasts (Krens, F.A. et al., (1982) Nature 296, 72-74; Negrutiu I et al. (1987) Plant Mol Biol 8: 363-373); electroporation of protoplasts (Shillito R.D. et al. (1985) Bio/Technol 3, 1099-1102); microinjection into plant material (Crossway A et al., (1986) Mol. Gen Genet 202: 179-185); DNA or RNA-coated particle bombardment (Klein TM et al., (1987) Nature 327: 70) infection with (non-integrative) viruses and the like. Transgenic plants, including transgenic crop plants, are preferably produced via *Agrobacterium*-mediated transformation. An advantageous transformation method is the transformation *in planta*. To this end, it is possible, for example, to allow the agrobacteria to act on plant seeds or to inoculate the plant meristem with agrobacteria. It has proved particularly expedient in accordance with the invention to allow a

suspension of transformed agrobacteria to act on the intact plant or at least on the flower primordia. The plant is subsequently grown on until the seeds of the treated plant are obtained (Clough and Bent, Plant J. (1998) 16, 735–743). Methods for *Agrobacterium*-mediated transformation of rice include well known methods for rice transformation, such as those described in any of the following: European patent application EP 1198985 A1, Aldemita and Hodges (Planta 199: 612-617, 1996); Chan et al. (Plant Mol Biol 22 (3): 491-506, 1993), Hiei et al. (Plant J 6 (2): 271-282, 1994), which disclosures are incorporated by reference herein as if fully set forth. In the case of corn transformation, the preferred method is as described in either Ishida et al. (Nat. Biotechnol 14(6): 745-50, 1996) or Frame et al. (Plant Physiol 129(1): 13-22, 2002), which disclosures are incorporated by reference herein as if fully set forth. Said methods are further described by way of example in B. Jené et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press (1993) 128-143 and in Potrykus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205-225). The nucleic acids or the construct to be expressed is preferably cloned into a vector, which is suitable for transforming *Agrobacterium tumefaciens*, for example pBin19 (Bevan et al., Nucl. Acids Res. 12 (1984) 8711). *Agrobacteria* transformed by such a vector can then be used in known manner for the transformation of plants, such as plants used as a model, like *Arabidopsis* (*Arabidopsis thaliana* is within the scope of the present invention not considered as a crop plant), or crop plants such as, by way of example, tobacco plants, for example by immersing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media. The transformation of plants by means of *Agrobacterium tumefaciens* is described, for example, by Höfgen and Willmitzer in Nucl. Acid Res. (1988) 16, 9877 or is known inter alia from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press, 1993, pp. 15-38.

In addition to the transformation of somatic cells, which then have to be regenerated into intact plants, it is also possible to transform the cells of plant meristems and in particular those cells which develop into gametes. In this case, the transformed gametes follow the natural plant development, giving rise to transgenic plants. Thus, for example, seeds of *Arabidopsis* are treated with agrobacteria and seeds are obtained from the developing plants of which a certain proportion is transformed and thus transgenic [Feldman, KA and Marks MD (1987). Mol Gen Genet 208:274-289; Feldmann K (1992). In: C Koncz, N-H Chua and J Shell, eds, Methods in Arabidopsis Research. Word Scientific, Singapore, pp. 274-289]. Alternative methods are based on the repeated removal of the inflorescences and incubation of the excision site in the center of the rosette with transformed agrobacteria, whereby transformed seeds can likewise be obtained at a later point in time (Chang (1994). Plant J. 5: 551-558; Katavic (1994). Mol Gen Genet, 245: 363-370). However, an especially effective method is the vacuum infiltration method with its modifications such as the "floral dip" method. In the case of vacuum infiltration of *Arabidopsis*, intact plants under reduced pressure are treated with an agrobacterial suspension [Bechthold, N (1993). C R Acad Sci Paris Life Sci, 316: 1194-1199], while in the case of the "floral dip" method the developing floral tissue is incubated briefly with a surfactant-treated agrobacterial suspension [Clough, SJ and Bent AF

(1998) The Plant J. 16, 735-743]. A certain proportion of transgenic seeds are harvested in both cases, and these seeds can be distinguished from non-transgenic seeds by growing under the above-described selective conditions. In addition the stable transformation of plastids is of advantages because plastids are inherited maternally is most crops reducing or eliminating the risk of transgene flow through pollen.

5 The transformation of the chloroplast genome is generally achieved by a process which has been schematically displayed in Klaus et al., 2004 [Nature Biotechnology 22 (2), 225-229]. Briefly the sequences to be transformed are cloned together with a selectable marker gene between flanking sequences homologous to the chloroplast genome. These homologous flanking sequences direct site specific integration into the plastome. Plastidal transformation has been described for many different
10 plant species and an overview is given in Bock (2001) Transgenic plastids in basic research and plant biotechnology. J Mol Biol. 2001 Sep 21; 312 (3):425-38 or Maliga, P (2003) Progress towards commercialization of plastid transformation technology. Trends Biotechnol. 21, 20-28. Further biotechnological progress has recently been reported in form of marker free plastid transformants, which can be produced by a transient co-integrated marker gene (Klaus et al., 2004, Nature Biotechnology
15 22(2), 225-229).

T-DNA activation tagging

T-DNA activation tagging (Hayashi et al. Science (1992) 1350-1353), involves insertion of T-DNA, usually containing a promoter (may also be a translation enhancer or an intron), in the genomic region of
20 the gene of interest or 10 kb up- or downstream of the coding region of a gene in a configuration such that the promoter directs expression of the targeted gene. Typically, regulation of expression of the targeted gene by its natural promoter is disrupted and the gene falls under the control of the newly introduced promoter. The promoter is typically embedded in a T-DNA. This T-DNA is randomly inserted into the plant genome, for example, through *Agrobacterium* infection and leads to modified expression of
25 genes near the inserted T-DNA. The resulting transgenic plants show dominant phenotypes due to modified expression of genes close to the introduced promoter.

TILLING

The term "TILLING" is an abbreviation of "Targeted Induced Local Lesions In Genomes" and refers to a
30 mutagenesis technology useful to generate and/or identify nucleic acids encoding proteins with modified expression and/or activity. TILLING also allows selection of plants carrying such mutant variants. These mutant variants may exhibit modified expression, either in strength or in location or in timing (if the mutations affect the promoter for example). These mutant variants may exhibit higher activity than that exhibited by the gene in its natural form. TILLING combines high-density mutagenesis with high-
35 throughput screening methods. The steps typically followed in TILLING are: (a) EMS mutagenesis (Redei GP and Koncz C (1992) In Methods in Arabidopsis Research, Koncz C, Chua NH, Schell J, eds. Singapore, World Scientific Publishing Co, pp. 16-82; Feldmann et al., (1994) In Meyerowitz EM, Somerville CR, eds, Arabidopsis. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp 137-172; Lightner J and Caspar T (1998) In J Martinez-Zapater, J Salinas, eds, Methods on Molecular

Biology, Vol. 82. Humana Press, Totowa, NJ, pp 91-104); (b) DNA preparation and pooling of individuals; (c) PCR amplification of a region of interest; (d) denaturation and annealing to allow formation of heteroduplexes; (e) DHPLC, where the presence of a heteroduplex in a pool is detected as an extra peak in the chromatogram; (f) identification of the mutant individual; and (g) sequencing of the mutant PCR product. Methods for TILLING are well known in the art (McCallum et al., (2000) Nat Biotechnol 18: 455-457; reviewed by Stemple (2004) Nat Rev Genet 5(2): 145-50).

Homologous recombination

Homologous recombination allows introduction in a genome of a selected nucleic acid at a defined selected position. Homologous recombination is a standard technology used routinely in biological sciences for lower organisms such as yeast or the moss *Physcomitrella*. Methods for performing homologous recombination in plants have been described not only for model plants (Offringa et al. (1990) EMBO J 9(10): 3077-84) but also for crop plants, for example rice (Terada et al. (2002) Nat Biotech 20(10): 1030-4; Iida and Terada (2004) Curr Opin Biotech 15(2): 132-8).

Yield

The term "yield" in general means a measurable produce of economic value, typically related to a specified crop, to an area, and to a period of time. Individual plant parts directly contribute to yield based on their number, size and/or weight, or the actual yield is the yield per acre for a crop and year, which is determined by dividing total production (includes both harvested and appraised production) by planted acres. The term "yield" of a plant may relate to vegetative biomass (root and/or shoot biomass), to reproductive organs, and/or to propagules (such as seeds) of that plant.

Taking corn as an example, a yield increase may be manifested as one or more of the following: increase in the number of plants established per hectare or acre, an increase in the number of ears per plant, an increase in the number of rows, number of kernels per row, kernel weight, thousand kernel weight, ear length/diameter, increase in the seed filling rate (which is the number of filled seeds divided by the total number of seeds and multiplied by 100), among others. Taking rice as an example, a yield increase may manifest itself as an increase in one or more of the following: number of plants per hectare or acre, number of panicles per plant, number of spikelets per panicle, number of flowers (florets) per panicle (which is expressed as a ratio of the number of filled seeds over the number of primary panicles), increase in the seed filling rate (which is the number of filled seeds divided by the total number of seeds and multiplied by 100), increase in thousand kernel weight, among others.

Early vigour

"Early vigour" refers to active healthy well-balanced growth especially during early stages of plant growth, and may result from increased plant fitness due to, for example, the plants being better adapted to their environment (i.e. optimizing the use of energy resources and partitioning between shoot and root). Plants having early vigour also show increased seedling survival and a better establishment of the

crop, which often results in highly uniform fields (with the crop growing in uniform manner, i.e. with the majority of plants reaching the various stages of development at substantially the same time), and often better and higher yield. Therefore, early vigour may be determined by measuring various factors, such as thousand kernel weight, percentage germination, percentage emergence, seedling growth, seedling height, root length, root and shoot biomass and many more.

Increase/Improve/Enhance

The terms "increase", "improve" or "enhance" are interchangeable and shall mean in the sense of the application at least a 3%, 4%, 5%, 6%, 7%, 8%, 9% or 10%, preferably at least 15% or 20%, more preferably 25%, 30%, 35% or 40% more yield and/or growth in comparison to control plants as defined herein.

Greenness Index

The "greenness index" as used herein is calculated from digital images of plants. For each pixel belonging to the plant object on the image, the ratio of the green value versus the red value (in the RGB model for encoding color) is calculated. The greenness index is expressed as the percentage of pixels for which the green-to-red ratio exceeds a given threshold. Under normal growth conditions, under salt stress growth conditions, and under reduced nutrient availability growth conditions, the greenness index of plants is measured in the last imaging before flowering. In contrast, under drought stress growth conditions, the greenness index of plants is measured in the first imaging after drought.

Seed yield

Increased seed yield may manifest itself as one or more of the following: a) an increase in seed biomass (total seed weight) which may be on an individual seed basis and/or per plant and/or per hectare or acre; b) increased number of flowers per plant; c) increased number of (filled) seeds; d) increased seed filling rate (which is expressed as the ratio between the number of filled seeds divided by the total number of seeds; e) increased harvest index, which is expressed as a ratio of the yield of harvestable parts, such as seeds, divided by the total biomass; and f) increased thousand kernel weight (TKW), which is extrapolated from the number of filled seeds counted and their total weight. An increased TKW may result from an increased seed size and/or seed weight, and may also result from an increase in embryo and/or endosperm size.

An increase in seed yield may also be manifested as an increase in seed size and/or seed volume. Furthermore, an increase in seed yield may also manifest itself as an increase in seed area and/or seed length and/or seed width and/or seed perimeter. Increased yield may also result in modified architecture, or may occur because of modified architecture.

Increased growth rate

Since the transgenic plants according to the present invention have increased yield, it is likely that these plants exhibit an increased growth rate (during at least part of their life cycle), relative to the growth rate of corresponding wild type plants at a corresponding stage in their life cycle. Besides the increased yield capacity, an increased efficiency of nutrient uptake may also contribute to the increase in yield. It is observed that the plants according to the present invention show a higher efficiency in nutrient uptake. Increased efficiency of nutrient uptake allows better growth of the plant, whether the plant is under stress or non-stress conditions.

The increased growth rate may be specific to one or more parts of a plant (including seeds), or may be throughout substantially the whole plant. A plant having an increased growth rate may even exhibit early flowering. The increase in growth rate may take place at one or more stages in the life cycle of a plant or during substantially the whole plant life cycle. Increased growth rate during the early stages in the life cycle of a plant may reflect enhanced vigour (increased seedling vigor at emergence). The increase in growth rate may alter the harvest cycle of a plant allowing plants to be sown later and/or harvested sooner than would otherwise be possible. If the growth rate is sufficiently increased, it may allow for the further sowing of seeds of the same plant species (for example sowing and harvesting of rice plants followed by sowing and harvesting of further rice plants all within one conventional growing period). Similarly, if the growth rate is sufficiently increased, it may allow for the further sowing of seeds of different plants species (for example the sowing and harvesting of rice plants followed by, for example, the sowing and optional harvesting of soy bean, potato or any other suitable plant). Harvesting additional times from the same rootstock in the case of some crop plants may also be possible. Altering the harvest cycle of a plant may lead to an increase in annual biomass production per acre (due to an increase in the number of times (say in a year) that any particular plant may be grown and harvested). An increase in growth rate may also allow for the cultivation of transgenic plants in a wider geographical area than their wild-type counterparts, since the territorial limitations for growing a crop are often determined by adverse environmental conditions either at the time of planting (early season) or at the time of harvesting (late season). Such adverse conditions may be avoided if the harvest cycle is shortened. The growth rate may be determined by deriving various parameters from growth curves, such parameters may be: T-Mid (the time taken for plants to reach 50% of their maximal size) and T-90 (time taken for plants to reach 90% of their maximal size), amongst others.

An increase in yield and/or growth rate occurs whether the plant is under non-stress conditions or whether the plant is exposed to various stresses compared to control plants. Plants typically respond to exposure to stress by growing more slowly. In conditions of severe stress, the plant may even stop growing altogether. Mild stress on the other hand is defined herein as being any stress to which a plant is exposed which does not result in the plant ceasing to grow altogether without the capacity to resume growth. Mild stress in the sense of the invention leads to a reduction in the growth of the stressed plants of less than 40%, 35% or 30%, preferably less than 25%, 20% or 15%, more preferably less than 14%,

13%, 12%, 11% or 10% or less in comparison to the control plant under non-stress conditions. Due to advances in agricultural practices (irrigation, fertilization, pesticide treatments) severe stresses are not often encountered in cultivated crop plants. As a consequence, the compromised growth induced by mild stress is often an undesirable feature for agriculture. Mild stresses are the everyday biotic and/or abiotic (environmental) stresses to which a plant is exposed. Abiotic stresses may be due to drought or excess water, anaerobic stress, salt stress, chemical toxicity, oxidative stress and hot, cold or freezing temperatures. The abiotic stress may be an osmotic stress caused by a water stress (particularly due to drought), salt stress, oxidative stress or an ionic stress. Biotic stresses are typically those stresses caused by pathogens, such as bacteria, viruses, fungi and insects.

In particular, the methods of the present invention may be performed under non-stress conditions to give plants having increased yield relative to control plants. As reported in Wang et al. (Planta (2003) 218: 1-14), abiotic stress leads to a series of morphological, physiological, biochemical and molecular changes that adversely affect plant growth and productivity. Drought, salinity, extreme temperatures and oxidative stress are known to be interconnected and may induce growth and cellular damage through similar mechanisms. Rabbani et al. (Plant Physiol (2003) 133: 1755-1767) describes a particularly high degree of "cross talk" between drought stress and high-salinity stress. For example, drought and/or salinisation are manifested primarily as osmotic stress, resulting in the disruption of homeostasis and ion distribution in the cell. Oxidative stress, which frequently accompanies high or low temperature, salinity or drought stress may cause denaturing of functional and structural proteins. As a consequence, these diverse environmental stresses often activate similar cell signaling pathways and cellular responses, such as the production of stress proteins, up-regulation of anti-oxidants, accumulation of compatible solutes and growth arrest. The term "non-stress" conditions as used herein are those environmental conditions that allow optimal growth of plants. Persons skilled in the art are aware of normal soil conditions and climatic conditions for a given location.

Plant

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, leaves, roots (including tubers), flowers, and tissues and organs, wherein each of the aforementioned comprise the gene/nucleic acid of interest. The term "plant" also encompasses plant cells, suspension cultures, callus tissue, embryos, meristematic regions, gametophytes, sporophytes, pollen and microspores, again wherein each of the aforementioned comprises the gene/nucleic acid of interest.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs selected from the list comprising *Acacia* spp., *Acer* spp., *Actinidia* spp., *Aesculus* spp., *Agathis australis*, *Albizia amara*, *Alsophila tricolor*, *Andropogon* spp., *Arachis* spp, *Areca catechu*, *Astelia fragrans*, *Astragalus cicer*, *Abelmoschus* spp.,

- Agave sisalana*, *Agropyron* spp., *Agrostis stolonifera*, *Allium* spp., *Amaranthus* spp., *Ammophila arenaria*, *Ananas comosus*, *Annona* spp., *Apium graveolens*, *Artocarpus* spp., *Asparagus officinalis*, *Avena* spp. (e.g. *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida*), *Averrhoa carambola*, *Baikiaea plurijuga*, *Betula* spp., *Bruguiera gymnorrhiza*, *Burkea africana*, *Butea frondosa*, *Bambusa* sp., *Benincasa hispida*, *Bertholletia excelsea*, *Beta vulgaris*, *Brassica* spp. (e.g. *Brassica napus*, *Brassica rapa* ssp. [canola, oilseed rape, turnip rape]), *Cadaba farinosa*, *Calliandra* spp., *Camellia sinensis*, *Canna indica*, *Capsicum* spp., *Cassia* spp., *Centroema pubescens*, *Chaenomeles* spp., *Cinnamomum cassia*, *Coffea arabica*, *Colophospermum mopane*, *Coronillia varia*, *Cotoneaster serotina*, *Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata*, *Cydonia oblonga*,
 5 *Cryptomeria japonica*, *Cymbopogon* spp., *Cynthea dealbata*, *Cydonia oblonga*, *Cadaba farinosa*, *Camellia sinensis*, *Cannabis sativa*, *Capsicum* spp., *Carex elata*, *Carica papaya*, *Carissa macrocarpa*, *Carya* spp., *Carthamus tinctorius*, *Castanea* spp., *Ceiba pentandra*, *Cichorium endivia*, *Cinnamomum* spp., *Citrullus lanatus*, *Citrus* spp., *Cocos* spp., *Coffea* spp., *Colocasia esculenta*, *Cola* spp., *Corchorus* sp., *Coriandrum sativum*, *Corylus* spp., *Crataegus* spp., *Crocus sativus*, *Cucurbita* spp., *Cynara* spp.,
 10 *Dalbergia monetaria*, *Davallia divaricata*, *Desmodium* spp., *Dicksonia squarosa*, *Diheteropogon amplexans*, *Dioclea* spp., *Dolichos* spp., *Dorycnium rectum*, *Daucus carota*, *Dimocarpus longan*, *Dioscorea* spp., *Diospyros* spp., *Echinochloa pyramidalis*, *Ehretia* spp., *Eleusine coracana*, *Eragrostis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperi*, *Eulalia villosa*, *Elaeis* (e.g. *Elaeis guineensis*, *Elaeis oleifera*), *Erianthus* sp., *Eriobotrya japonica*, *Eugenia uniflora*, *Fagopyrum* spp., *Feijoa sellowiana*, *Fragaria* spp., *Flemingia* spp., *Freycinetia banksii*, *Fagus* spp., *Festuca arundinacea*, *Ficus carica*, *Fortunella* spp., *Fragaria* spp., *Geranium thunbergii*, *Ginkgo biloba*, *Glycine* spp. (e.g. *Glycine max*, *Soja hispida* or *Soja max*), *Glycine javanica*, *Gliricidia* spp., *Gossypium hirsutum*, *Grevillea* spp., *Guibourtia coleosperma*, *Gossypium hirsutum*, *Helianthus* spp. (e.g. *Helianthus annuus*), *Hemerocallis fulva*, *Hedysarum* spp., *Hemarthria altissima*, *Heteropogon contortus*, *Hibiscus* spp., *Hordeum* spp. (e.g. *Hordeum vulgare*), *Hyparrhenia rufa*, *Hypericum erectum*, *Hyperthelia dissoluta*, *Indigo incarnata*, *Iris* spp., *Ipomoea batatas*, *Juglans* spp., *Leptarrhena pyrolifolia*, *Lespedeza* spp., *Lettuca* spp., *Leucaena leucocephala*, *Loudetia simplex*, *Lotonus bainesii*, *Lotus* spp., *Lactuca sativa*, *Lathyrus* spp., *Lens culinaris*, *Linum usitatissimum*, *Litchi chinensis*, *Luffa acutangula*, *Lupinus* spp., *Luzula sylvatica*, *Lycopersicon* spp. (e.g. *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*),
 25 *Macrotyloma* spp., *Macrotyloma axillare*, *Malus* spp., *Malus* spp., *Malpighia emarginata*, *Mammea americana*, *Mangifera indica*, *Manihot* spp., *Manihot esculenta*, *Medicago sativa*, *Metasequoia glyptostroboides*, *Manilkara zapota*, *Medicago sativa*, *Melilotus* spp., *Mentha* spp., *Miscanthus sinensis*, *Momordica* spp., *Morus nigra*, *Musa* spp., *Musa sapientum*, *Nicotianum* spp., *Onobrychis* spp., *Ornithopus* spp., *Peltophorum africanum*, *Pennisetum* spp., *Olea* spp., *Opuntia* spp., *Oryza* spp. (e.g. *Oryza sativa*, *Oryza latifolia*), *Panicum miliaceum*, *Panicum virgatum*, *Passiflora edulis*, *Pastinaca sativa*, *Pennisetum* sp., *Persea* spp., *Persea gratissima*, *Petunia* spp., *Phaseolus* spp., *Phoenix canariensis*, *Phormium cookianum*, *Photinia* spp., *Picea glauca*, *Pinus* spp., *Pisum sativum*, *Podocarpus totara*, *Pogonarthria fleckii*, *Pogonarthria squarrosa*, *Petroselinum crispum*, *Phalaris arundinacea*, *Phaseolus* spp., *Phleum pratense*, *Phoenix* spp., *Phragmites australis*, *Physalis* spp., *Pinus* spp.,

Pistacia vera, *Pisum* spp., *Poa* spp., *Populus* spp., *Prosopis* spp., *Prosopis cineraria*, *Prunus* spp., *Psidium* spp., *Punica granatum*, *Pyrus communis*, *Pseudotsuga menziesii*, *Pterolobium stellatum*, *Pyrus communis*, *Quercus* spp., *Rhaphiolepis umbellata*, *Rhopalostylis sapida*, *Rhus natalensis*, *Ribes grossularia*, *Ribes* spp., *Robinia pseudoacacia*, *Rosa* spp., *Raphanus sativus*, *Rheum rhabarbarum*,
 5 *Ricinus communis*, *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum*, *Sciadopitys verticillata*, *Sequoia sempervirens*, *Sequoiadendron giganteum*, *Saccharum* spp., *Sambucus* spp., *Secale cereale*, *Sesamum* spp., *Sinapis* sp., *Solanum* spp. (e.g. *Solanum tuberosum*, *Solanum integrifolium* or *Solanum lycopersicum*), *Sorghum bicolor*, *Spinacia* spp., *Sporobolus fimbriatus*, *Stiburus alopecuroides*, *Stylosanthos humilis*, *Syzygium* spp., *Tadehagi* spp., *Taxodium distichum*, *Themeda triandra*, *Trifolium*
 10 spp., *Triticum* spp. (e.g. *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernum*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare*), *Tagetes* spp., *Tamarindus indica*, *Theobroma cacao*, *Triticosecale rimpai*, *Tsuga heterophylla*, *Tropaeolum minus*, *Tropaeolum majus*, *Vaccinium* spp., *Vicia* spp., *Vitis vinifera*, *Vigna* spp., *Viola odorata*, *Vitis* spp., *Watsonia pyramidata*, *Zantedeschia aethiopica*, *Zea mays*, *Zizania palustris*, *Ziziphus* spp., amaranth, artichoke, asparagus, broccoli,
 15 Brussels sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, strawberry, sugar beet, sugarcane, sunflower, tomato, squash, tea and algae, amongst others.

Alignment of sequences

20 Methods for the alignment of sequences for comparison are well known in the art, such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch ((1970) J Mol Biol 48: 443-453) to find the global (over the whole the sequence) alignment of two sequences that maximizes the number of matches and minimizes the number of gaps. The BLAST algorithm (Altschul *et al.* (1990) J Mol Biol 215: 403-10) calculates percent sequence identity and
 25 performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information (NCBI). Homologues may readily be identified using, for example, the ClustalW multiple sequence alignment algorithm (version 1.83), with the default pairwise alignment parameters, and a scoring method in percentage. Global percentages of similarity and identity may also be determined using one of the
 30 methods available in the MatGAT software package (Campanella *et al.*, BMC Bioinformatics. 2003 Jul 10; 4:29. MatGAT: an application that generates similarity/identity matrices using protein or DNA sequences). Minor manual editing may be performed to optimise alignment between conserved motifs, as would be apparent to a person skilled in the art. Furthermore, instead of using full-length sequences for the identification of homologues, specific domains may also be used. The sequence identity values,
 35 which are indicated below in Example 3 as a percentage were determined over the entire nucleic acid or amino acid sequence, and/or over selected domains or conserved motif(s), using the programs mentioned above using the default parameters.

Reciprocal blast search

Reciprocal blast search typically involves a first BLAST involving BLASTing a query sequence (for example using any of the sequences listed in Table 1, Table 2, Table 14 of Example 9 or Table 18 of Example 18) against any sequence database, such as the publicly available NCBI database. BLASTN or TBLASTX (using standard default values) are generally used when starting from a nucleotide sequence, and BLASTP or TBLASTN (using standard default values) when starting from a protein sequence. The BLAST results may optionally be filtered. The full-length sequences of either the filtered results or non-filtered results are then BLASTed back (second BLAST) against sequences from the organism from which the query sequence is derived (where the query sequence is any of SEQ ID NO: 1 or SEQ ID NO: 2, or SEQ ID NO: 50 to SEQ ID NO: 59, or SEQ ID NO: 131 or SEQ ID NO: 132 or SEQ ID NO: 257 or SEQ ID NO: 258, the second BLAST would therefore be against *Oryza sativa* sequences). The results of the first and second BLASTs are then compared. A paralogue is identified if a high-ranking hit from the first blast is from the same species as from which the query sequence is derived, a BLAST back then ideally results in the query sequence as highest hit; an orthologue is identified if a high-ranking hit in the first BLAST is not from the same species as from which the query sequence is derived, and preferably results upon BLAST back in the query sequence being among the highest hits.

High-ranking hits are those having a low E-value. The lower the E-value, the more significant the score (or in other words the lower the chance that the hit was found by chance). Computation of the E-value is well known in the art. In addition to E-values, comparisons are also scored by percentage identity. Percentage identity refers to the number of identical nucleotides (or amino acids) between the two compared nucleic acid (or polypeptide) sequences over a particular length. In the case of large families, ClustalW may be used, followed by a neighbour joining tree, to help visualize clustering of related genes and to identify orthologues and paralogues.

Amplification

A variety of nucleic acid amplification-based methods for genetic and physical mapping may be carried out using the nucleic acids. Examples include allele-specific amplification (Kazazian (1989) J. Lab. Clin. Med 11:95-96), polymorphism of PCR-amplified fragments (CAPS; Sheffield *et al.* (1993) Genomics 16:325-332), allele-specific ligation (Landegren *et al.* (1988) Science 241:1077-1080), nucleotide extension reactions (Sokolov (1990) Nucleic Acid Res. 18:3671), Radiation Hybrid Mapping (Walter *et al.* (1997) Nat. Genet. 7:22-28) and Happy Mapping (Dear and Cook (1989) Nucleic Acid Res. 17:6795-6807). For these methods, the sequence of a nucleic acid is used to design and produce primer pairs for use in the amplification reaction or in primer extension reactions. The design of such primers is well known to those skilled in the art. In methods employing PCR-based genetic mapping, it may be necessary to identify DNA sequence differences between the parents of the mapping cross in the region corresponding to the instant nucleic acid sequence. This, however, is generally not necessary for mapping methods.

Detailed description of the invention

The present invention provides a method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding a NAC transcription factor. A preferred method for modulating (preferably, increasing) expression of a nucleic acid encoding a NAC transcription factor is by introducing and expressing in a plant a nucleic acid encoding a particular class of NAC transcription factor as further defined below.

In addition, the present invention provides a method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding an AP2-2 polypeptide. The present invention further provides a method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding an AP2-70-like polypeptide.

With regard to a NAC transcription factor, the nucleic acid to be introduced into a plant (and therefore useful in performing the methods of the invention) is any nucleic acid encoding the type of NAC transcription factor which will now be described. A "NAC transcription factor" as defined herein refers to any amino acid sequence which when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising an amino acid sequence represented by any one of SEQ ID NO: 2, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59, rather than with any other NAC group.

A person skilled in the art could readily determine whether any amino acid sequence in question falls within the definition of a "NAC transcription factor" using known techniques and software for the making of such a phylogenetic tree, such as a GCG, EBI or CLUSTAL package, using default parameters. The phylogenetic tree of Fig. 1 is taken from Ooka *et al.*, 2003 (DNA Research 10, 239-247, 2003). The method for constructing such a phylogenetic tree is described in Ooka *et al.*, 2003. In the phylogenetic tree of Fig. 1, SEQ ID NO: 2 is found in the group third up from the bottom, labelled "OsNAC7" and SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 and SEQ ID NO: 59 are found in the area starting from (and including) the group labelled on the right hand side of the page as "ONAC022" and ending with (and including) the group labelled on the right hand side of the page as "OsNAC3". Any sequence clustering within these areas, which comprises the sequences of SEQ ID NO: 2 on the one hand and SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 and SEQ ID NO: 59 on the other hand, would be considered to fall within the aforementioned definition of a NAC transcription factor, and would be considered suitable for use in the methods of the invention.

Additionally or alternatively, a "NAC transcription factor" as defined herein is one comprising any one or more of the Motifs described below.

Motif I: KIDLDIQELED, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif I.

5 Motif I is preferably K/P/R/G I/S/M D/A/E/Q L/I/V D I/V/F I Q/V/R/K E/D L/I/V D.

Motif II: CKYGXGHGGDEQTEW, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif II, where 'X' is taken to be any amino acid or a gap.

10 Motif II is preferably C K/R Y/L/I G XXX G/Y/N D/E E Q/R T/N/S EW, where 'X' is any amino acid or a gap.

Motif III: GWVVCRAFQKP, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif III.

Motif III is preferably GWVVCRA/V F X¹ K X², where 'X¹' and 'X²' may be any amino acid, preferably X¹ is Q/R/K, preferably X² is P/R/K.

20 Motifs I to III are found in the NACs represented by SEQ ID NO: 2, and are also typically found in NACs clustering (in a phylogenetic tree of NACs) with the group of NACs comprising SEQ ID NO: 2-rather than with any other NAC group.

Motif IV: PVPIIA, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif IV.

Motif IV is preferably A/P/S/N V/L/I/A P/S/D/V/Q V/I I A/T/G.

Motif V: NGSRPN, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif V.

Motif V is preferably N G/S S/Q/A/V RP N/S.

Motif VI: CRLYNKK, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif VI.

Motif VI is preferably C/Y R/K L/I Y/H/F N/K K K/N/C/S/T

Motifs III to VI are typically found in NACs of SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55 SEQ ID NO: 57 and SEQ ID NO: 59 and in NACs clustering (in a phylogenetic tree) with the NACs represented by the aforementioned SEQ ID NOs rather than with any other NAC group.

- 5 **Motif VII:** NEWKMQ, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif VII.

Motif VII is preferably N E/Q/T WEK M/V Q/R/K

- 10 **Motif VIII:** WGETRTPSE, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence Motif VIII.

Motif VIII is preferably WGE T/A RTPES E/D

- 15 **Motif IX:** VPKKESMDDA, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif IX.

Motif IX is preferably V/L PK K/E E S/R/A/V M/V/A/Q/R D/E D/E/L A/G/D

- 20 **Motif X:** SYDDIQGMYS, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif X.

Motif X is preferably S L/Y DD L/I Q G/S L/M/P G/Y S/N.

- 25 Motifs VII, VIII, IX and X are typically found in NACs of SEQ ID NO: 51 and in NACs clustering (in a phylogenetic tree) with the NAC of SEQ ID NO: 51 rather than with any other NAC group.

Motif XI: DSMPLRHADSSCSE, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif XI.

30

Motif XI is preferably DS M/V/I P R/K L/I/A H T/A/S D/E SS C/G SE.

- 35 Motif XI is typically found in NACs of SEQ ID NO: 53 and SEQ ID NO: 55 and in NACs clustering (in a phylogenetic tree) with the NACs represented by the aforementioned SEQ ID NOs rather than with any other NAC group.

Each of motifs I to XI may comprise one or more conservative amino acid substitution at any position.

Examples of NAC transcription factors as defined herein, i.e. any amino acid sequence which when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs represented by any one of SEQ ID NO: 2, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 and SEQ ID NO: 59 rather than with any other NAC group, are as given in

5 Tables 3 and 4 below.

Table 3: Examples of NAC transcription factors that cluster (in a phylogenetic tree) with the NAC represented by SEQ ID NO: 2 rather than with any other NAC group

Nucleic Acid	Amino Acid	NCBI Accession Number	Other name (if any)	Source
SEQ ID NO: 1	SEQ ID NO: 2	XM_479673.1	NAM2 (also called CDS4054 in the alignment of Fig. 2)	<i>Oryza sativa</i>
SEQ ID NO: 3	SEQ ID NO: 4	AK106313		<i>Oryza sativa</i>
SEQ ID NO: 5	SEQ ID NO: 6	NM_187584.1		<i>Oryza sativa</i>
SEQ ID NO: 7	SEQ ID NO: 8	XM_467007.1		<i>Oryza sativa</i>
SEQ ID NO: 9	SEQ ID NO: 10	XM_473322.1		<i>Oryza sativa</i>
SEQ ID NO: 11	SEQ ID NO: 12	ABE89364		<i>Medicago truncatula</i>
SEQ ID NO: 13	SEQ ID NO: 14	NM_101098.2	ANAC007/EMB2749	<i>Arabidopsis thaliana</i>
SEQ ID NO: 15	SEQ ID NO: 16	NM_104947.1	ANAC026	<i>Arabidopsis thaliana</i>
SEQ ID NO: 17	SEQ ID NO: 18	XM_476289.1		<i>Oryza sativa</i>
SEQ ID NO: 19	SEQ ID NO: 20	NM_127362.1	ANAC037	<i>Arabidopsis thaliana</i>
SEQ ID NO: 21	SEQ ID NO: 22	NM_119783.2	ANAC076	<i>Arabidopsis thaliana</i>
SEQ ID NO: 23	SEQ ID NO: 24	NM_187584.1		<i>Oryza sativa</i>
SEQ ID NO: 25	SEQ ID NO: 26	NM_125632.1	ANAC101	<i>Arabidopsis thaliana</i>
SEQ ID NO: 27	SEQ ID NO: 28	NM_126028.1	ANAC105	<i>Arabidopsis thaliana</i>
SEQ ID NO: 29	SEQ ID NO: 30	AK071064.1		<i>Oryza sativa</i>
SEQ ID NO: 31	SEQ ID NO: 32	NM_105851.1	ANAC030	<i>Arabidopsis thaliana</i>
SEQ ID NO: 33	SEQ ID NO: 34	NM_197511.1		<i>Oryza sativa</i>
SEQ ID NO: 35	SEQ ID NO: 36	AB217775.1		<i>Zinnia elegans</i>

SEQ ID NO: 37	SEQ ID NO: 38	AJ833965.1		<i>Zea mays</i>
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Table 4: Examples of NAC transcription factors that cluster (in a phylogenetic tree) with the NAC represented by any one of SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55 SEQ ID NO: 57 and SEQ ID NO: 59 rather than with any other NAC group

SEQ ID NO: 50	SEQ ID NO: 51	XM_470088.1	NAC1 (also known as CDS4035 in the alignment of Fig. 2)	<i>Oryza sativa</i>
SEQ ID NO: 52	SEQ ID NO: 53	AB028185.1 BAA89800.1	NAC4 (known as OsNAC6 in alignment of Fig. 2)	<i>Oryza sativa</i>
SEQ ID NO: 54	SEQ ID NO: 55	AB028184.1 BAA89799.1	NAC6 (known as OsNAC5 in alignment of Fig. 2)	<i>Oryza sativa</i>
SEQ ID NO: 56	SEQ ID NO: 57	AK107330.1	NAC7 (known as ONAC24 in alignment of Fig. 2)	<i>Oryza sativa</i>
SEQ ID NO: 58	SEQ ID NO: 59	AK069257.1	NAC3 (known as CDS4034 in alignment of Fig. 2)	<i>Oryza sativa</i>
SEQ ID NO: 60	SEQ ID NO: 61	AY625683.1 AAU08786.1	NAC2-like TaNAC2	<i>Triticum aestivum</i>
SEQ ID NO: 62	SEQ ID NO: 63	AY103772.1	PCO133091	<i>Zea mays</i>
SEQ ID NO: 64	SEQ ID NO: 65	AJ010829.1 CAA09371.1	GRAB1 TACAA09371.1	<i>Triticum aestivum</i>
SEQ ID NO: 66	SEQ ID NO: 67	NM_186659.2 NP_911548.1	NAC3-like RiceNP_911548.1	<i>Oryza sativa</i>
SEQ ID NO: 68	SEQ ID NO: 69	DQ267442.1 ABB72844.1	NAC1-like elaeis	<i>Elaeis guineensis</i>
SEQ ID NO: 70	SEQ ID NO: 71	AB028183.1 BAA89798.1	NAC4-like OsNAC4	<i>Oryza sativa</i>
SEQ ID NO: 72	SEQ ID NO: 73	DQ028770.1 AAY46122.1	NAC2-like GmNAC2AAY46122.1	<i>Glycine max</i>
SEQ ID NO: 74	SEQ ID NO: 75	AY498713.1 AAR88435.1	NAC-like tomatoNAC	<i>Lycopersicon esculentum</i>
SEQ ID NO: 76	SEQ ID NO: 77	AY245883.1 AAP35052.1	NAC5-8 BrassicaNAC5-8"NAC-domain	<i>Brassica napus</i>

SEQ ID NO: 78	SEQ ID NO: 79	XM_475238.1 XP_475238.1	NAC48 AK068392"putative	<i>Oryza sativa</i>
SEQ ID NO: 80	SEQ ID NO: 81	AJ401151.1 CAC42087.1	NAC solanum"putative	<i>Solanum tuberosum</i>
SEQ ID NO: 82	SEQ ID NO: 83	NM_147856.2 NP_680161.1	ATAF2 AT5G08790"="ATAF2"NP_680161.1"	<i>Arabidopsis thaliana</i>
SEQ ID NO: 84	SEQ ID NO: 85	AF509873.1 AAM34773.1	NH10 PetuniaNH10="nam-like	<i>Petunia x hybrida</i>
SEQ ID NO: 86	SEQ ID NO: 87	AB218789 BAE48667.1	NAC PrunusPm74"NAC	<i>Prunus mume</i>
SEQ ID NO: 88	SEQ ID NO: 89	AY245885.1 AAP35054.1	NAC18 BnNAC18"NAC-domain	<i>Brassica napus</i>
SEQ ID NO: 90	SEQ ID NO: 91	NM_125774.3 NP_201184.2	ANAC102	<i>Arabidopsis thaliana</i>
SEQ ID NO: 92	SEQ ID NO: 93	AY714222.1 AAW48094.1	NAC CaNAC1	<i>Capsicum annuum</i>
SEQ ID NO: 94	SEQ ID NO: 95	NM_100054.2 NP_171677	ATAF1	<i>Arabidopsis thaliana</i>
SEQ ID NO: 96	SEQ ID NO: 97	AY573802.1 AAU43922.1	NAC-NOR LeNAC-NOR"transcription	<i>Lycopersicon esculentum</i>
SEQ ID NO: 98	SEQ ID NO: 99	NM_118875.2 NP_567773.1	RD26 Arabidopsis	<i>Arabidopsis thaliana</i>
SEQ ID NO: 100	SEQ ID NO: 101	DQ022843.1 AAY44098.1	NAC69-3 NAC69-3"TaNAC69-3""NAC	<i>Triticum aestivum</i>
SEQ ID NO: 102	SEQ ID NO: 103	A625682.1 AAU08785.1	NAC69-1 NAC69-1"TaNAC69""NAC	<i>Triticum aestivum</i>
SEQ ID NO: 104	SEQ ID NO: 105	AY742218.1 AAW62955.1	NAC23 Saccharum	<i>Saccharum officinarum</i>
SEQ ID NO: 106	SEQ ID NO: 107	AK063406.1	NAC10 ONAC10AK063406	<i>Oryza sativa</i>
SEQ ID NO:	SEQ ID NO:	AC145753.1	NAM	<i>Medicago</i>

108	109		medicagoNAClike	<i>truncatula</i>
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The invention is illustrated by transforming plants with the *Oryza sativa* sequence represented by SEQ ID NO: 1, encoding the polypeptide sequence of SEQ ID NO: 2, and with the *Oryza sativa* sequence represented by SEQ ID NO: 50, encoding the polypeptide sequence of SEQ ID NO: 51, and with the *Oryza sativa* sequence represented by SEQ ID NO: 52, encoding the polypeptide sequence of SEQ ID NO: 53, and with the *Oryza sativa* sequence represented by SEQ ID NO: 54, encoding the polypeptide of SEQ ID NO: 55, and with the *Oryza sativa* sequence represented by SEQ ID NO: 56, encoding the polypeptide of SEQ ID NO: 57, and with the *Oryza sativa* sequence represented by SEQ ID NO: 58, encoding the polypeptide of SEQ ID NO: 59, however performance of the invention is not restricted to these sequences. The methods of the invention may be performed using any nucleic acid encoding a NAC transcription factor as defined herein, such as any of the nucleic acid sequences given in Tables 3 and 4.

The NAC amino acid sequences given in Table 3 may be considered to be orthologues and paralogues of the NAC represented by SEQ ID NO: 2. The NAC amino acid sequences given in Table 4 may be considered to be orthologues and paralogues of the NAC represented by any one of SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55 SEQ ID NO: 57 and SEQ ID NO: 59.

Orthologues and paralogues may easily be found by performing a so-called reciprocal blast search as described in the "definitions" section herein. Where the query sequence is any of SEQ ID NO: 1 or SEQ ID NO: 2, or SEQ ID NO: 50 to SEQ ID NO: 59, the second BLAST would therefore be against *Oryza* sequences.

Table 3 gives examples of orthologues and paralogues of the NAC represented by SEQ ID NO 2. Table 4 gives examples of orthologues and paralogues of the NAC represented by SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55 SEQ ID NO: 57 and SEQ ID NO: 59. Further orthologues and paralogues may readily be identified using the BLAST procedure described above and by following the procedure given in the Examples section.

The NAC proteins are identifiable by the presence of a highly conserved N-terminal NAC domain (shown in Figure 5), accompanied by diverse C-terminal domains.

Specialist databases also exist for the identification of domains. The NAC domain in a NAC transcription factor may be identified as explained in the "definitions" section.

NAC domains may also be identified using routine techniques, such as by sequence alignment as explained in the "definitions" section herein.

The invention also provides hitherto unknown NAC-encoding nucleic acids and NAC polypeptides.

According to a further embodiment of the present invention, there is therefore provided an isolated nucleic acid molecule comprising:

- 5 (i) a nucleic acid represented by one of SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, or SEQ ID NO: 363;
- (ii) the complement of a nucleic acid represented by one of SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, or SEQ ID NO: 363;
- 10 (iii) a nucleic acid encoding a NAC polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, or SEQ ID NO: 364.

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According to a further embodiment of the present invention, there is also provided an isolated polypeptide comprising:

- (i) an amino acid sequence represented by one of SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, or SEQ ID NO: 364;
- 20 (ii) an amino acid sequence having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, or SEQ ID NO: 364;
- 25 (iii) derivatives of any of the amino acid sequences given in (i) or (ii) above.

Nucleic acids encoding NAC transcription factors defined herein need not be full-length nucleic acids, since performance of the methods of the invention does not rely on the use of full length nucleic acid sequences. Examples of nucleic acids suitable for use in performing the methods of the invention include the nucleic acid sequences given in Tables 3 and 4, but are not limited to those sequences. Nucleic acid variants may also be useful in practising the methods of the invention. Examples of such nucleic acid variants include portions of nucleic acids encoding a NAC transcription factor as defined herein, splice variants of nucleic acids encoding a NAC transcription factor as defined herein, allelic variants of nucleic acids encoding a NAC transcription factor as defined herein and variants of nucleic acids encoding a NAC transcription factor as defined herein that are obtained by gene shuffling. The terms portion, splice variant, allelic variant and gene shuffling will now be described.

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According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a portion of any one of the nucleic acid

sequences given in Tables 3 and 4, or a portion of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Tables 3 and 4.

Portions useful in the methods of the invention, encode a polypeptide falling within the definition of a NAC transcription factor as defined herein and having substantially the same biological activity as the NAC transcription factor represented by any of the amino acid sequences given in Tables 3 and 4. The portion is typically at least 600 consecutive nucleotides in length, preferably at least 700 consecutive nucleotides in length, more preferably at least 800 consecutive nucleotides in length and most preferably at least 900 consecutive nucleotides in length, the consecutive nucleotides being of any one of the nucleic acid sequences given in Tables 3 and 4. Preferably, the portion is a portion of any one of the nucleic acids given in Tables 3 and 4. Most preferably the portion is a portion of the nucleic acid of SEQ ID NO: 1, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58. Preferably, the portion encodes an amino acid sequence comprising any one or more of Motifs I to XI as defined herein.

A portion of a nucleic acid encoding a NAC transcription factor as defined herein may be prepared, for example, by making one or more deletions to the nucleic acid in question. The portions may be used in isolated form or they may be fused to other coding (or non coding) sequences in order to, for example, produce a protein that combines several activities. When fused to other coding sequences, the resultant polypeptide produced upon translation may be bigger than that predicted for the NAC transcription factor portion.

Another nucleic acid variant useful in the methods of the invention is a nucleic acid capable of hybridising, under reduced stringency conditions, preferably under stringent conditions, with a nucleic acid encoding a NAC transcription factor as defined herein, or with a portion as defined herein.

Hybridising sequences useful in the methods of the invention, encode a polypeptide having a NAC domain (as described above) and having substantially the same biological activity as the NAC transcription factor represented by any of the amino acid sequences given in Tables 3 and 4. The hybridising sequence is typically at least 600 consecutive nucleotides in length, preferably at least 700 consecutive nucleotides in length, more preferably at least 800 consecutive nucleotides in length and most preferably at least 900 consecutive nucleotides in length. Preferably, the hybridising sequence is one that is capable of hybridising to any of the nucleic acids given in Table 3 and 4, or to a portion of any of these sequences, a portion being as defined above. Most preferably, the hybridising sequence is capable of hybridising to a nucleic acid as represented by SEQ ID NO: 1, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58 capable of hybridising to a portion of any of the aforementioned sequences. Preferably, the sequence capable of hybridizing encodes a polypeptide comprising any one or more of Motifs I to XI as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a nucleic acid capable of hybridizing to any one of the nucleic acids given in Tables 3 and 4, or comprising introducing and expressing in a plant a nucleic acid capable of hybridising to a nucleic acid encoding an orthologue, paralogue or homologue of any of the nucleic acid sequences given in Tables 3 and 4.

Another nucleic acid variant useful in the methods of the invention is a splice variant encoding a NAC transcription factor as defined hereinabove.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a splice variant of any one of the nucleic acid sequences given in Tables 3 and 4, or a splice variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Tables 3 and 4.

Preferred splice variants are splice variants of a nucleic acid represented by any of SEQ ID NO: 1, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58, or splice variants encoding orthologues or paralogues of any of the amino acid sequences given in Tables 3 and 4. Preferably, the splice variants encode a polypeptide comprising any one or more of Motifs I to XI as defined herein.

Another nucleic acid variant useful in performing the methods of the invention is an allelic variant of a nucleic acid encoding a NAC transcription factor as defined hereinabove.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant an allelic variant of any one of the nucleic acids given in Tables 3 and 4, or comprising introducing and expressing in a plant an allelic variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Tables 3 and 4.

Preferably, the allelic variant is an allelic variant of SEQ ID NO: 1, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58, or an allelic variant of a nucleic acid encoding an orthologue or paralogue of any of the aforementioned SEQ ID NOs. Preferably, the allelic variant encodes a polypeptide comprising any one or more of Motifs I to XI as defined herein.

A further nucleic acid variant useful in the methods of the invention is a nucleic acid variant obtained by gene shuffling. Gene shuffling or directed evolution may also be used to generate variants of nucleic acids encoding NAC transcription factors as defined above.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a variant of any one of the nucleic acid sequences given in Tables 3 and 4, or comprising introducing and expressing in a plant a variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given
5 in Tables 3 and 4, which variant nucleic acid is obtained by gene shuffling. Preferably, the variants obtained by gene shuffling encode a polypeptide comprising any one or more of Motifs I to XI as defined herein.

Furthermore, nucleic acid variants may also be obtained by site-directed mutagenesis. Several methods
10 are available to achieve site-directed mutagenesis, the most common being PCR based methods (current protocols in molecular biology. Wiley Eds).

Also useful in the methods of the invention are nucleic acids encoding homologues of any one of the amino acid sequences given in Tables 3 and 4.

Also useful in the methods of the invention are nucleic acids encoding derivatives of any one of the amino acids given in Table 3 or orthologues or paralogues of any of the aforementioned SEQ ID NOs. Preferred derivatives are derivatives of the proteins represented by SEQ ID NO: 2, SEQ ID NO: 51, SEQ
15 ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59.

Furthermore, NAC transcription factors (at least in their native form) typically have DNA-binding activity and an activation domain. A person skilled in the art may easily determine the presence of an activation domain and DNA-binding activity using routine tools and techniques.

Nucleic acids encoding NAC transcription factors may be derived from any natural or artificial source. The nucleic acid may be modified from its native form in composition and/or genomic environment through deliberate human manipulation. Preferably the NAC transcription factor-encoding nucleic acid is from a plant, further preferably from a monocot, more preferably from the *Poaceae* family, most preferably the nucleic acid is from *Oryza sativa*.

Any reference herein to a NAC transcription factor is therefore taken to mean a NAC transcription factor as defined above. Any nucleic acid encoding such a NAC transcription factor is suitable for use in performing the methods of the invention.

The present invention also encompasses plants or parts thereof (including seeds) obtainable by the methods according to the present invention. The plants or parts thereof comprise a nucleic acid transgene encoding a NAC transcription factor as defined above.

The invention also provides genetic constructs and vectors to facilitate introduction and/or expression of the nucleic acid sequences useful in the methods according to the invention, in a plant.

Therefore, there is provided a gene construct comprising:

- 5 i. Any nucleic acid encoding a NAC transcription factor as defined hereinabove;
- ii. One or more control sequences operably linked to the nucleic acid of (i).

Constructs useful in the methods according to the present invention may be constructed using recombinant DNA technology well known to persons skilled in the art. The gene constructs may be
10 inserted into vectors, which may be commercially available, suitable for transforming into plants and suitable for expression of the gene of interest in the transformed cells. The invention therefore provides use of a gene construct as defined hereinabove in the methods of the invention.

Plants are transformed with a vector comprising the sequence of interest (i.e., a nucleic acid encoding a
15 NAC transcription factor). The skilled artisan is well aware of the genetic elements that must be present in the vector in order to successfully transform, select and propagate host cells containing the sequence of interest. The sequence of interest is operably linked to one or more control sequences (at least to a promoter).

20 According to one preferred feature of the invention, the nucleic acid encoding a NAC transcription factor is operably linked to a constitutive promoter. A constitutive promoter is transcriptionally active during most but not necessarily all phases of its growth and development and is substantially ubiquitously expressed. The constitutive promoter is preferably a GOS2 promoter, more preferably the constitutive promoter is a rice GOS2 promoter, further preferably the constitutive promoter is represented by a
25 nucleic acid sequence substantially similar to SEQ ID NO: 39 or SEQ ID NO: 339, most preferably the constitutive promoter is as represented by SEQ ID NO: 39 or SEQ ID NO: 339.

It should be clear that the applicability of the present invention is not restricted to the NAC transcription factor-encoding nucleic acid represented by SEQ ID NO: 1, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID
30 NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58, nor is the applicability of the invention restricted to expression of a such a NAC transcription factor-encoding nucleic acid when driven by a GOS2 promoter. Examples of other constitutive promoters which may also be used to perform the methods of the invention are shown in Table 2a in the "definitions" section herein.

35 According to another preferred feature of the invention, the nucleic acid encoding a NAC-type transcription factor is operably linked to a young green tissue-specific promoter. A young green tissue-specific promoter as defined herein is a promoter that is transcriptionally active predominantly in young green tissue, substantially to the exclusion of any other parts of a plant, whilst still allowing for any leaky expression in these other plant parts. The young green tissue-specific promoter is preferably a

protochlorophyllid reductase promoter, more preferably the protochlorophyllid reductase promoter represented by a nucleic acid sequence substantially similar to SEQ ID NO: 40, most preferably the promoter is as represented by SEQ ID NO: 40.

5 It should be clear that the applicability of the present invention is not restricted to the NAC transcription factor-encoding nucleic acid represented by SEQ ID NO: 1, nor is the applicability of the invention restricted to expression of a such a NAC transcription factor-encoding nucleic acid when driven by a protochlorophyllid reductase promoter.

10 Examples of other young green tissue-specific promoters which may also be used to perform the methods of the invention are shown in Table 2c above.

According to another preferred feature of the invention, the nucleic acid encoding a NAC-type transcription factor is operably linked to a root-specific promoter (internal reference pro0110). A root-specific promoter as defined herein is a promoter that is transcriptionally active predominantly in plant roots, substantially to the exclusion of any other parts of a plant, whilst still allowing for any leaky expression in these other plant parts. The root-specific promoter is preferably an RCc3 promoter (Plant Mol Biol. 1995 Jan;27(2):237-48), more preferably the RCc3 promoter is from rice, further preferably the RCc3 promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 110, most preferably the promoter is as represented by SEQ ID NO: 110.

It should be clear that the applicability of the present invention is not restricted to the NAC transcription factor-encoding nucleic acid represented by SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56 or SEQ ID NO: 58, nor is the applicability of the invention restricted to expression of a such a NAC transcription factor-encoding nucleic acid when driven by an RCc3 promoter.

Examples of other root-specific promoters which may also be used to perform the methods of the invention are shown in Table 2b above.

30 Optionally, one or more terminator sequences may be used in the construct introduced into a plant. Additional regulatory elements may include transcriptional as well as translational enhancers. Those skilled in the art will be aware of terminator and enhancer sequences that may be suitable for use in performing the invention. An intron sequence may also be added to the 5' untranslated region (UTR) or in the coding sequence to increase the amount of the mature message that accumulates in the cytosol, as described in the definitions section. Other control sequences (besides promoter, enhancer, silencer, intron sequences, 3'UTR and/or 5'UTR regions) may be protein and/or RNA stabilizing elements. Such sequences would be known or may readily be obtained by a person skilled in the art.

The genetic constructs of the invention may further include an origin of replication sequence that is required for maintenance and/or replication in a specific cell type. One example is when a genetic construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule). Preferred origins of replication include, but are not limited to, the f1-ori and colE1.

5 The genetic construct may optionally comprise a selectable marker gene. Selectable markers are described in more detail in the "definitions" section herein. The marker genes may be removed or excised from the transgenic cell once they are no longer needed. Techniques for marker removal are known in the art, useful techniques are described above in the definitions section.

10 The invention also provides a method for the production of transgenic plants having enhanced yield-related traits relative to control plants, comprising introduction and expression in a plant of any nucleic acid encoding a NAC transcription factor as defined hereinabove.

More specifically, the present invention provides a method for the production of transgenic plants having enhanced yield-related traits, which method comprises:

- 15
- i. introducing and expressing a nucleic acid encoding a NAC transcription factor (as defined herein) in a plant cell; and
 - ii. cultivating the plant cell under conditions promoting plant growth and development.

20 The nucleic acid may be introduced directly into a plant cell or into the plant itself (including introduction into a tissue, organ or any other part of a plant). According to a preferred feature of the present invention, the nucleic acid is preferably introduced into a plant by transformation.

The genetically modified plant cells can be regenerated via all methods with which the skilled worker is familiar. Suitable methods can be found in the abovementioned publications by S.D. Kung and R. Wu, Potrykus or Höfgen and Willmitzer.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant. To select transformed plants, the plant material obtained in the transformation is, as a rule, subjected to selective conditions so that transformed plants can be distinguished from untransformed plants. For example, the seeds obtained in the above-described manner can be planted and, after an initial growing period, subjected to a suitable selection by spraying. A further possibility consists in growing the seeds, if appropriate after sterilization, on agar plates using a suitable selection agent so that only the transformed seeds can grow into plants. Alternatively, the transformed plants are screened for the presence of a selectable marker such as the ones described above.

Following DNA transfer and regeneration, putatively transformed plants may also be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed and homozygous second-generation (or T2) transformants selected, and the T2 plants may then further be propagated through classical breeding techniques. The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

The present invention clearly extends to any plant cell or plant produced by any of the methods described herein, and to all plant parts and propagules thereof. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced by the parent in the methods according to the invention.

The invention also includes host cells containing an isolated nucleic acid encoding a NAC transcription factor as defined hereinabove. Preferred host cells according to the invention are plant cells.

The invention also extends to harvestable parts of a plant such as, but not limited to seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs. The invention furthermore relates to products derived, preferably directly derived, from a harvestable part of such a plant, such as dry pellets or powders, oil, fat and fatty acids, starch or proteins.

According to a preferred feature of the invention, the modulated expression is increased expression. Methods for increasing expression of nucleic acids or genes, or gene products, are well documented in the art. Examples of methods for increasing expression are given in the "definitions" section herein.

As mentioned above, a preferred method for modulating (preferably, increasing) expression of a nucleic acid encoding a NAC transcription factor is by introducing and expressing in a plant a nucleic acid encoding a NAC transcription factor; however the effects of performing the method, i.e. enhancing yield-related traits may also be achieved using other well known techniques, such as T-DNA activation,

TILLING, homologous recombination or directed evolution. A description of some of these techniques is given in the "definitions" section herein.

According to a preferred feature of the present invention, performance of the methods of the invention gives plants having an increased growth rate relative to control plants, particularly during the early stages of plant development (typically three weeks post germination in the case of rice and maize, but this will vary from species to species) leading to early vigour. Therefore, according to the present invention, there is provided a method for increasing the growth rate of plants, which method comprises modulating expression, preferably increasing expression, in a plant of a nucleic acid encoding a particular type of NAC transcription factor, as defined herein. The present invention also provides a method for obtaining plants having early vigour relative to control plants, which method comprises modulating, preferably increasing, expression in a plant of a nucleic acid encoding a NAC transcription factor as defined herein.

Early vigour may also result from or be manifested as increased plant fitness relative to control plants due to, for example, the plants being better adapted to their environment (i.e. being more able to cope with various abiotic or biotic stress factors). Plants having early vigour also show better establishment of the crop (with the crop growing in uniform manner, i.e. with the majority of plants reaching the various stages of development at substantially the same time), and show better growth and often better yield. Early vigour may be determined by measuring various factors, such as seedling growth rate, thousand kernel weight, percentage germination, percentage emergence, seedling height, root length and shoot biomass and many more.

Performance of the methods of the invention gives plants grown under non-stress conditions or under mild drought conditions increased yield relative to control plants grown under comparable conditions. Therefore, according to the present invention, there is provided a method for increasing yield in plants grown under non-stress conditions or under mild drought conditions, which method comprises increasing expression in a plant of a nucleic acid encoding a NAC transcription factor.

Performance of the methods of the invention gives plants grown under conditions of nutrient deficiency, particularly under conditions of nitrogen deficiency, increased yield relative to control plants grown under comparable conditions. Therefore, according to the present invention, there is provided a method for increasing yield in plants grown under conditions of nutrient deficiency, which method comprises increasing expression in a plant of a nucleic acid encoding a POI polypeptide. Nutrient deficiency may result from a lack of nutrients such as nitrogen, phosphates and other phosphorous-containing compounds, potassium, calcium, cadmium, magnesium, manganese, iron and boron, amongst others.

In the case of use in the methods of the invention of nucleic acids encoding NAC4 transcription factors (for example, SEQ ID NO: 52) and NAC4 transcription factors themselves (for example SEQ ID NO: 53),

an increase in yield and/or seed yield and/or growth rate was found to occur in plants grown under substantially non-stress conditions and under conditions of stress compared to control plants.

5 A "NAC4 transcription factor" as defined herein refers to any amino acid sequence which when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising an amino acid sequence represented by SEQ ID NO: 53 rather than with any other NAC group.

10 The NAC4 transcription factor may also comprise Motif XI: DSMPLRHADSSCSE, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif XI.

Motif XI is preferably DS M/V/I P R/K L/I/A H T/A/S D/E SS C/G SE.

15 Motif XI is typically found in NACs of SEQ ID NO: 53 and SEQ ID NO: 55 and in NACs clustering (in a phylogenetic tree) with the NACs represented by the aforementioned SEQ ID NOs rather than with any other NAC group. Motif XI may comprise one or more conservative amino acid substitution at any position.

20 Plants typically respond to exposure to stress by growing more slowly. In conditions of severe stress, the plant may even stop growing altogether. Mild stress on the other hand is defined herein as being any stress to which a plant is exposed which does not result in the plant ceasing to grow altogether without the capacity to resume growth. Mild stress in the sense of the invention leads to a reduction in the growth of the stressed plants of less than 40%, 35% or 30%, preferably less than 25%, 20% or 15%,
25 more preferably less than 14%, 13%, 12%, 11% or 10% or less in comparison to the control plant under non-stress conditions. Due to advances in agricultural practices (irrigation, fertilization, pesticide treatments) severe stresses are not often encountered in cultivated crop plants. As a consequence, the compromised growth induced by mild stress is often an undesirable feature for agriculture. Mild stresses are the typical stresses to which a plant may be exposed. These stresses may be the
30 everyday biotic and/or abiotic (environmental) stresses to which a plant is exposed. Typical abiotic or environmental stresses include temperature stresses caused by atypical hot or cold/freezing temperatures; salt stress; water stress (drought or excess water), anaerobic stress, chemical toxicity and oxidative stress. The abiotic stress may be an osmotic stress caused by a water stress (particularly due to drought), salt stress, oxidative stress or an ionic stress. Chemicals may also cause abiotic stresses
35 (for example too high or too low concentrations of minerals or nutrients). Biotic stresses are typically those stresses caused by pathogens, such as bacteria, viruses, fungi and insects. The term "non-stress conditions" as used herein are those environmental conditions that do not significantly go beyond the everyday climatic and other abiotic conditions that plants may encounter, and which allow optimal

growth of the plant. Persons skilled in the art are aware of normal soil conditions and climatic conditions for a given geographic location.

Abiotic stress leads to a series of morphological, physiological, biochemical and molecular changes that adversely affect plant growth and productivity (Wang *et al.* (Planta (2003) 218: 1-14). Drought, salinity, extreme temperatures and oxidative stress are known to be interconnected and may induce growth and cellular damage through similar mechanisms. For example, drought and/or salinisation are manifested primarily as osmotic stress, resulting in the disruption of homeostasis and ion distribution in the cell. Oxidative stress, which frequently accompanies high or low temperature, salinity or drought stress may cause denaturation of functional and structural proteins. As a consequence, these diverse environmental stresses often activate similar cell signaling pathways and cellular responses, such as the production of stress proteins, up-regulation of anti-oxidants, accumulation of compatible solutes and growth arrest.

Since diverse environmental stresses activate similar pathways, the exemplification of the present invention with drought stress (in the case of use of nucleic acids encoding NAC4 transcription factors, and NAC4 transcription factors themselves, in the methods of the invention) should not be seen as a limitation to drought stress, but more as a screen to indicate the involvement of NAC4-encoding nucleic acids and NAC4 transcription factors in abiotic stresses in general. Furthermore, the methods of the present invention may be performed under non-stress conditions or under conditions of mild drought to give plants having enhanced yield-related traits (particularly increased yield and seed yield) relative to control plants.

A particularly high degree of "cross talk" is reported between drought stress and high-salinity stress (Rabbani *et al.* (2003) Plant Physiol 133: 1755-1767). For example, drought and/or salinisation are manifested primarily as osmotic stress, resulting in the disruption of homeostasis and ion distribution in the cell. Therefore, it would be apparent that nucleic acids encoding NAC4 transcription factors, and NAC4 transcription factors themselves would, along with their usefulness in conferring drought-tolerance in plants, also find use in protecting the plant against various other osmotic stresses. Similarly, it would be apparent that nucleic acids encoding NAC4 transcription factors, and NAC4 transcription factors themselves would, along with their usefulness in conferring salt-tolerance in plants, also find use in protecting the plant against various other abiotic stresses. Furthermore, oxidative stress, which frequently accompanies high or low temperatures, salinity or drought stress, may cause denaturing of functional and structural proteins. As a consequence, these diverse environmental stresses often activate similar cell signaling pathways and cellular responses, such as the production of stress proteins, up-regulation of anti-oxidants, accumulation of compatible solutes and growth arrest. Furthermore, Rabbani *et al.* (2003, Plant Physiol 133: 1755-1767) report that similar molecular mechanisms of stress tolerance and responses exist between dicots and monocots. The methods of the invention are therefore advantageously applicable to any plant.

The term "abiotic stress" as defined herein is taken to mean any one or more of: water stress (due to drought or excess water), anaerobic stress, salt stress, nutrient stress, temperature stress (due to hot, cold or freezing temperatures), chemical toxicity stress and oxidative stress. According to one aspect of the invention, the abiotic stress is an osmotic stress, selected from water stress, salt stress, oxidative stress and ionic stress. Preferably, the water stress is drought stress. The term salt stress is not restricted to common salt (NaCl), but may be any one or more of: NaCl, KCl, LiCl, MgCl₂, CaCl₂, Phosphorous salts, amongst others. Nutrient stress may be caused by a lack or excess of nutrients such as nitrogen, phosphates and other phosphorous-containing compounds, potassium, calcium, cadmium, magnesium, manganese, iron and boron, amongst others.

Increased tolerance to abiotic stress is manifested by increased plant yield under abiotic stress conditions as defined above. Insofar as the invention concerns the use of NAC4 transcription factors and their encoding nucleic acids, such increased yield may include one or more of the following: increased seed size, increased seed weight, increased aboveground biomass, increased plant height, increased root biomass, increased number of flowers per panicle and increased number of first panicles, each relative to control plants.

According to the present invention, there is provided a method for enhancing yield-related traits in plants grown under abiotic stress conditions relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding a NAC4 transcription factor. According to one aspect of the invention, the abiotic stress is osmotic stress, selected from one or more of the following: water stress, salt stress, oxidative stress, nutrient stress and ionic stress. Preferably, the water stress is drought stress.

The methods of the invention are advantageously applicable to any plant.

Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs. According to a preferred embodiment of the present invention, the plant is a crop plant. Examples of crop plants include soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato and tobacco. Further preferably, the plant is a monocotyledonous plant. Examples of monocotyledonous plants include sugarcane. More preferably the plant is a cereal. Examples of cereals include rice, maize, wheat, barley, millet, triticale, rye, sorghum and oats. Plants in which early vigour is a particularly desirable trait include rice, maize, wheat, sunflower, sorghum.

The present invention also encompasses use of nucleic acids encoding NAC transcription factors and use of NAC transcription factor polypeptides in enhancing yield-related traits.

Nucleic acids encoding NAC transcription factors or NAC transcription factors themselves, may find use in breeding programmes in which a DNA marker is identified which may be genetically linked to a NAC transcription factor-encoding gene. The nucleic acids/genes, or the NAC transcription factors themselves may be used to define a molecular marker. This DNA or protein marker may then be used in breeding programmes to select plants having enhanced yield as defined hereinabove in the methods of the invention.

Allelic variants of NAC transcription factor-encoding nucleic acids/genes may also find use in marker-assisted breeding programmes. Such breeding programmes sometimes require introduction of allelic variation by mutagenic treatment of the plants, using for example EMS mutagenesis; alternatively, the programme may start with a collection of allelic variants of so called "natural" origin caused unintentionally. Identification of allelic variants then takes place, for example, by PCR. This is followed by a step for selection of superior allelic variants of the sequence in question and which give increased yield. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question. Growth performance may be monitored in a greenhouse or in the field. Further optional steps include crossing plants in which the superior allelic variant was identified with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

Nucleic acids encoding NAC transcription factors may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. Such use of NAC transcription factor encoding nucleic acids requires only a nucleic acid sequence of at least 15 nucleotides in length. The NAC transcription factor-encoding nucleic acids may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Sambrook J, Fritsch EF and Maniatis T (1989) Molecular Cloning, A Laboratory Manual) of restriction-digested plant genomic DNA may be probed with the NAC transcription factor-encoding nucleic acids. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander *et al.* (1987) Genomics 1: 174-181) in order to construct a genetic map. In addition, the nucleic acids may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the NAC transcription factor-encoding nucleic acid in the genetic map previously obtained using this population (Botstein *et al.* (1980) Am. J. Hum. Genet. 32:314-331).

The production and use of plant gene-derived probes for use in genetic mapping is described in Bematzky and Tanksley (1986) Plant Mol. Biol. Reporter 4: 37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near

isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

The nucleic acid probes may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel *et al.* *In: Non-mammalian Genomic Analysis: A Practical Guide*, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, the nucleic acid probes may be used in direct fluorescence *in situ* hybridisation (FISH) mapping (Trask (1991) *Trends Genet.* 7:149-154). Although current methods of FISH mapping favor use of large clones (several kb to several hundred kb; see Laan *et al.* (1995) *Genome Res.* 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

The present invention further provides a method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding an AP2-2 polypeptide.

A preferred method for modulating (preferably, increasing) expression of a nucleic acid encoding an AP2-2 polypeptide is by introducing and expressing in a plant a nucleic acid encoding an AP2-2 polypeptide.

The term "AP2-2 polypeptide" as defined herein refers to a transcription factor that classifies as an ERF protein, and more particularly as a member of Group VII of the ERF proteins, according to the definition by Nakano *et al.* (2006). Group VII of ERF proteins is, besides the presence of a single AP2/ERF domain, which is part of all ERF proteins, also characterised by other motifs, such as CMVII-1 to CMVII-8 (Nakano *et al.*, 2006). These CMVII motifs were delineated based on analysis of *Arabidopsis thaliana* and *Oryza sativa* sequences and are part of the *Arabidopsis* and/or rice sequences (Figure 2), but may also be present in Group VII ERF proteins of other species.

The AP2-2 polypeptide useful in the methods of the present invention comprises the conserved sequence Motif XII (SEQ ID NO: 133):

(R/I/V/L/K)(R/K/Q/D/E/A)(I/L)(R/Y/H)G(A/S/R/K/T/D/G/H/L/N)(K/T/R/N/G)A(K/R/E)(V/L/P/T)NF(P/V)

Preferably, motif XII is

(R/I/K)(R/K/Q/D/A)(I/L)(R/Y/H)G(A/S/R/K/T/D/E/G/H/L/N)(K/T/R/N/G)A(K/R/E)(V/L/P/T)NF(P/V/A)

Preferably, the AP2-2 polypeptide useful in the methods of the present invention furthermore also comprises one or more of the following motifs:

Motif XIII (SEQ ID NO: 134):

MCGG(A/S)(I/V/L)(I/L)(S/H/A/Y/G/P/E)(D/G/H/Y/E/Q/N)

Preferably, motif XIII is MCGG(A/S)I(I/L)(S/H/A/Y)(D/G/H/Y/E)

More preferably motif XIII is MCGG(A/S)I(I/L)(S/H)(D/G/H/E)

Motif XIV (SEQ ID NO: 135)

(K/N/R/S/H/M/Q/P/A/E)(R/K/H/A/G/E/V/P/M)(E/K/A/R/S/Q/T/V/G/H/P)(R/K/Q/S/G)(K/G/P/S/R/T/A/N)(T/N/R/S/A/Y/H/G)(L/Q/H/V/R/K/A/P/G)(Y/F)(R/W/K/L/M)G(I/V)(R/Q/H)(R/Q/W/K)R(P/K/T)

Preferably, motif XIV is:

5 (K/N/R/S/H/M)(R/K/H/A/G/E/V/P)(E/K/A/R/S/Q)(R/K/Q/S)(K/G/P/S/R/T)(T/N/R/S/A/Y/H/G)(L/Q/H/V/R/K/A/P/G/F/I)(Y/F/L)(R/W/K/L/M/H)G(I/V)(R/Q/H)(R/Q/W/K)R(P/K/T)

More preferably, motif XIV is:

(K/N/R/S)(R/K/H)(E/K/A/R)(R/K/Q)(K/G/P/S)(T/N/R/S/A)(L/Q/H/V/R/K)(Y/F)(R/W/K)G(I/V)R(R/Q)RP

Most preferably, motif XIV is:

10 (K/N)(R/H)KRKNQ(Y/F)RGIRQRP

Motif XV (SEQ ID NO: 136):

SD(Q/T/E/V)(G/S)SNSF(G/D/E/S/N)(C/S)S(D/E)(F/Y/L)(G/S)(W/Q/L)(E/G/S)(N/E/D)

Preferably, motif XV is:

SD(Q/T)(G/S/A)SNS(F/I)(G/D)(C/S)S(D/E)F(G/S)(W/Q/L)(E/S)(N/D)

15 Motif XVI (SEQ ID NO: 137):

(L/I/F/M)W(S/T/N/M)(F/Y/L/I)(D/E/Q/G)(N/D/H/E)(I/Y/F/S/M/L/V/D/H/N/E/G)

Preferably, motif XVI is

(L/I/M)W(S/T/M)(F/Y/L/I)(D/E/Q/G)(N/D/E)(I/Y/F/S/M/L/V/D)

More preferably, motif XVI is (L/I/M)W(S/M)(F/L/I)D(D/E)(I/M/L/V)

20 Motif XVII (SEQ ID NO: 138):

(D/E/S)(F/A/W/D)(E/A)(A/D/L)(D/A/G/E)(F/G/L)(N/E/R/G/Q/W)(E/G/V/D/R)F(E/K/V/Y/G/D/L/I)(V/R/D/S/N/A/E)(D/G/T/E/R/A/Y/L/F)

Preferably, motif XVII is

(D/E/S)(F/A/W/D)(E/A)(A/D)(D/A)(F/G)(E/R/Q/W)(E/G/D/R)F(E/K/Y/G/D/L/I)(V/R/D/S/N/A/E)(D/G/T/E/R)

25 Further preferably, motif XVII is

(D/E/S)(F/A)(E/A)(A/D)(D/A)F(E/R/Q/W)(E/G/D/R)F(E/K/Y/G/D)(V/R/D/S/N)(D/G/T/E)

More preferably, motif XVII is

(D/E/S)(F/A)(E/A)(A/D)DF(E/R/Q/W)(E/G)F(E/K/Y)(V/R/D/S)(D/G/T)

Most preferably, motif XVII is (D/E)FEADF(E/R/Q)EF(E/K)(V/R/D)(D/G)

30 These motifs were derived mainly from *Arabidopsis* and rice sequences, therefore, one or more conserved substitutions are allowed in these motifs for AP2-2 sequences from other plant species.

Furthermore, AP2-2 polypeptides (at least in their native form) may have DNA-binding activity. Tools and techniques for measuring DNA-binding activity are well known in the art.

35

The terms "domain" and "motif" are defined in the "definitions" section herein. Specialist databases exist for the identification of domains. Examples are given in the "definitions" section herein.

Analysis of the polypeptide sequence of SEQ ID NO: 132 in the SMART database, revealed there to be an AP2 domain (SMART entry SM00380, Fig. 2). This domain is plant specific and is known to play a role in protein-DNA interactions (binds to the GCC-box, essential for the response to ethylene).

- 5 The present invention is illustrated by transforming plants with the nucleic acid sequence represented by SEQ ID NO: 131, encoding the polypeptide sequence of SEQ ID NO: 132. However, performance of the invention is not restricted to these sequences; the methods of the invention may advantageously be performed using any AP2-2-encoding nucleic acid or AP2-2 polypeptides as defined herein.
- 10 Examples of nucleic acids encoding AP2-2 polypeptides are given in Table 14 of Example 9 herein. Such nucleic acids are useful in performing the methods of the invention. The amino acid sequences given in Table 14 of Example 9 are example sequences of orthologues and paralogues of the AP2-2 polypeptides represented by SEQ ID NO: 132, the terms "orthologues" and "paralogues" being as defined herein. Further orthologues and paralogues may readily be identified by performing a so-called
- 15 reciprocal blast search.

The invention also provides hitherto unknown AP2-2-encoding nucleic acids and AP2-2 polypeptides.

- 20 According to a further embodiment of the present invention, there is therefore provided an isolated nucleic acid molecule comprising:
- (i) a nucleic acid represented by one of SEQ ID NO: 341, SEQ ID NO: 343, or SEQ ID NO: 345;
 - (ii) the complement of a nucleic acid represented by one of SEQ ID NO: 341, SEQ ID NO: 343, or SEQ ID NO: 345;
 - (iii) a nucleic acid encoding a POI polypeptide having, in increasing order of preference, at least
- 25 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 342, SEQ ID NO: 344, or SEQ ID NO: 346.

- 30 According to a further embodiment of the present invention, there is also provided an isolated polypeptide comprising:
- (i) an amino acid sequence represented by one of SEQ ID NO: 342, SEQ ID NO: 344, or SEQ ID NO: 346;
 - (ii) an amino acid sequence having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino
- 35 acid sequence represented by one of SEQ ID NO: 342, SEQ ID NO: 344, or SEQ ID NO: 346;
- (iii) derivatives of any of the amino acid sequences given in (i) or (ii) above.

Nucleic acid variants may also be useful in practising the methods of the invention. Examples of such variants include nucleic acids encoding homologues and derivatives of any one of the amino acid

sequences given in Table 14 of Example 9, the terms "homologue" and "derivative" being as defined herein. Also useful in the methods of the invention are nucleic acids encoding homologues and derivatives of orthologues or paralogues of any one of the amino acid sequences given in Table 14 of Example 9. Homologues and derivatives useful in the methods of the present invention have
5 substantially the same biological and functional activity as the unmodified protein from which they are derived.

Further nucleic acid variants useful in practising the methods of the invention include portions of nucleic acids encoding AP2-2 polypeptides, nucleic acids hybridising to nucleic acids encoding AP2-2
10 polypeptides, splice variants of nucleic acids encoding AP2-2 polypeptides, allelic variants of nucleic acids encoding AP2-2 polypeptides and variants of nucleic acids encoding AP2-2 polypeptides obtained by gene shuffling. The terms hybridising sequence, splice variant, allelic variant and gene shuffling are as described herein.

Nucleic acids encoding AP2-2 polypeptides need not be full-length nucleic acids, since performance of the methods of the invention does not rely on the use of full-length nucleic acid sequences. According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a portion of any one of the nucleic acid sequences given in Table 14 of Example 9, or a portion of a nucleic acid encoding an orthologue, paralogue or
20 homologue of any of the amino acid sequences given in Table 14 of Example 9.

A portion of a nucleic acid may be prepared, for example, by making one or more deletions to the nucleic acid. The portions may be used in isolated form or they may be fused to other coding (or non-coding) sequences in order to, for example, produce a protein that combines several activities. When
25 fused to other coding sequences, the resultant polypeptide produced upon translation may be bigger than that predicted for the protein portion.

Portions useful in the methods of the invention, encode an AP2-2 polypeptide as defined herein, and have substantially the same biological activity as the amino acid sequences given in Table 14 of Example 9. Preferably, the portion is a portion of any one of the nucleic acids given in Table 14 of Example 9, or is a portion of a nucleic acid encoding an orthologue or paralogue of any one of the amino acid sequences given in Table 14 of Example 9. Preferably the portion is, in increasing order of preference at least 600, 800, 900 or 1000 consecutive nucleotides in length, the consecutive nucleotides being of any one of the nucleic acid sequences given in Table 14 of Example 9, or of a nucleic acid
35 encoding an orthologue or paralogue of any one of the amino acid sequences given in Table 14 of Example 9. Most preferably the portion is a portion of the nucleic acid of SEQ ID NO: 131. Preferably, the portion encodes an amino acid sequence comprising (any one or more of the domains or motifs defined herein). Preferably, the portion encodes an amino acid sequence which, when used in the

construction of a phylogenetic tree, tends to cluster with the group of AP2-2 polypeptides comprising the amino acid sequence represented by SEQ ID NO: 132 rather than with any other group.

Another nucleic acid variant useful in the methods of the invention is a nucleic acid capable of hybridising, under reduced stringency conditions, preferably under stringent conditions, with a nucleic acid encoding an AP2-2 polypeptide as defined herein, or with a portion as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a nucleic acid capable of hybridizing to any one of the nucleic acids given in Table 14 of Example 9, or comprising introducing and expressing in a plant a nucleic acid capable of hybridising to a nucleic acid encoding an orthologue, paralogue or homologue of any of the nucleic acid sequences given in Table 14 of Example 9.

Hybridising sequences useful in the methods of the invention encode an AP2-2 polypeptide as defined herein, and have substantially the same biological activity as the amino acid sequences given in Table 14 of Example 9. Preferably, the hybridising sequence is capable of hybridising to any one of the nucleic acids given in Table 14 of Example 9, or to a portion of any of these sequences, a portion being as defined above, or wherein the hybridising sequence is capable of hybridising to a nucleic acid encoding an orthologue or paralogue of any one of the amino acid sequences given in Table 14 of Example 9. Most preferably, the hybridising sequence is capable of hybridising to a nucleic acid as represented by SEQ ID NO: 131 or to a portion thereof. Preferably, the hybridising sequence encodes an amino acid sequence comprising any one or more of the motifs or domains as defined herein. Preferably, the hybridising sequence encodes an amino acid sequence which, when used in the construction of a phylogenetic tree, tends to cluster with the group of AP2-2 polypeptides comprising the amino acid sequence represented by SEQ ID NO: 132 rather than with any other group.

Another nucleic acid variant useful in the methods of the invention is a splice variant encoding an AP2-2 polypeptide as defined hereinabove, a splice variant being as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a splice variant of any one of the nucleic acid sequences given in Table 14 of Example 9, or a splice variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 14 of Example 9.

Preferred splice variants are splice variants of a nucleic acid represented by SEQ ID NO: 131, or a splice variant of a nucleic acid encoding an orthologue or paralogue of SEQ ID NO: 132. Preferably, the amino acid sequence encoded by the splice variant comprises any one or more of the motifs or domains as defined herein. Preferably, the amino acid sequence encoded by the splice variant, when used in the

construction of a phylogenetic tree, tends to cluster with the group of AP2-2 polypeptides comprising the amino acid sequence represented by SEQ ID NO: 132 rather than with any other group.

Another nucleic acid variant useful in performing the methods of the invention is an allelic variant of a nucleic acid encoding an AP2-2 polypeptide as defined hereinabove, an allelic variant being as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant an allelic variant of any one of the nucleic acids given in Table 14 of Example 9, or comprising introducing and expressing in a plant an allelic variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 14 of Example 9.

The allelic variants useful in the methods of the present invention have substantially the same biological activity as the AP2-2 polypeptide of SEQ ID NO: 132 and any of the amino acids depicted in Table 14 of Example 9. Allelic variants exist in nature, and encompassed within the methods of the present invention is the use of these natural alleles. Preferably, the allelic variant is an allelic variant of SEQ ID NO: 131 or an allelic variant of a nucleic acid encoding an orthologue or paralogue of SEQ ID NO: 132. Preferably, the amino acid encoded by the allelic variant comprises any one or more of the motifs or domains as defined herein. Preferably, the amino acid sequence encoded by the allelic variant, when used in the construction of a phylogenetic tree, tends to cluster with the group of AP2-2 polypeptides comprising the amino acid sequence represented by SEQ ID NO: 132 rather than with any other group.

Gene shuffling or directed evolution may also be used to generate variants of nucleic acids encoding AP2-2 polypeptides as defined above; the term "gene shuffling" being as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a variant of any one of the nucleic acid sequences given in Table 14 of Example 9, or comprising introducing and expressing in a plant a variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 14 of Example 9, which variant nucleic acid is obtained by gene shuffling.

Preferably, the variant nucleic acid obtained by gene shuffling encodes an amino acid sequence comprising any one or more of the motifs or domains as defined herein. Preferably, the amino acid sequence encoded by the variant nucleic acid obtained by gene shuffling, when used in the construction of a phylogenetic tree, tends to cluster with the group of AP2-2 polypeptides comprising the amino acid sequence represented by SEQ ID NO: 132 rather than with any other group.

Furthermore, nucleic acid variants may also be obtained by site-directed mutagenesis. Several methods are available to achieve site-directed mutagenesis, the most common being PCR based methods (Current Protocols in Molecular Biology. Wiley Eds.).

5 Nucleic acids encoding AP2-2 polypeptides may be derived from any natural or artificial source. The nucleic acid may be modified from its native form in composition and/or genomic environment through deliberate human manipulation. Preferably the AP2-2 polypeptide-encoding nucleic acid is from a plant, further preferably from a dicotyledonous plant, more preferably from the family Poaceae, more preferably from the genus *Oryza*, most preferably from *Oryza sativa*.

10 Performance of the methods of the invention gives plants having enhanced yield-related traits. In particular, performance of the methods of the invention gives plants having increased yield, especially increased seed yield relative to control plants. The terms "yield" and "seed yield" are described in more detail in the "definitions" section herein. However it should be noted that the term "yield-related traits"
15 does not encompass the metabolite content of plant cells and that the enhanced yield-related traits are not the result of increased stress resistance.

The present invention provides a method for increasing yield, especially seed yield of plants, relative to control plants, which method comprises modulating expression, preferably increasing expression, in a
20 plant of a nucleic acid encoding an AP2-2 polypeptide as defined herein.

According to a preferred feature of the present invention, performance of the methods of the invention gives plants having an increased growth rate relative to control plants. Therefore, according to the present invention, there is provided a method for increasing the growth rate of plants, which method
25 comprises modulating expression, preferably increasing expression, in a plant of a nucleic acid encoding an AP2-2 polypeptide as defined herein.

Performance of the methods of the invention gives plants grown under non-stress conditions or under mild drought conditions increased yield relative to suitable control plants grown under comparable
30 conditions. Therefore, according to the present invention, there is provided a method for increasing yield in plants grown under non-stress conditions, which method comprises increasing expression in a plant of a nucleic acid encoding an AP2-2 polypeptide.

Performance of the methods of the invention gives plants grown under conditions of nutrient deficiency, particularly under conditions of nitrogen deficiency, increased yield relative to control plants grown under
35 comparable conditions. Therefore, according to the present invention, there is provided a method for increasing yield in plants grown under conditions of nutrient deficiency, which method comprises increasing expression in a plant of a nucleic acid encoding a POI polypeptide. Nutrient deficiency may

result from a lack of nutrients such as nitrogen, phosphates and other phosphorous-containing compounds, potassium, calcium, cadmium, magnesium, manganese, iron and boron, amongst others.

The present invention encompasses plants or parts thereof (including seeds) obtainable by the methods according to the present invention. The plants or parts thereof comprise a nucleic acid transgene encoding an AP2-2 polypeptide as defined above.

The invention also provides genetic constructs and vectors to facilitate introduction and/or expression in plants of nucleic acids encoding AP2-2 polypeptides. The gene constructs may be inserted into vectors, which may be commercially available, suitable for transforming into plants and suitable for expression of the gene of interest in the transformed cells. The invention also provides use of a gene construct as defined herein in the methods of the invention.

More specifically, the present invention provides a construct comprising:

- (a) a nucleic acid encoding an AP2-2 polypeptide as defined above;
- (b) one or more control sequences capable of driving expression of the nucleic acid sequence of (a); and optionally
- (c) a transcription termination sequence.

The term "control sequence" and "termination sequence" are as defined herein.

Plants are transformed with a vector comprising any of the nucleic acids described above. The skilled artisan is well aware of the genetic elements that must be present on the vector in order to successfully transform, select and propagate host cells containing the sequence of interest. The sequence of interest is operably linked to one or more control sequences (at least to a promoter).

Advantageously, any type of promoter may be used to drive expression of the nucleic acid sequence. A constitutive promoter is particularly useful in the methods of the invention, preferably the constitutive promoter is a strong constitutive promoters. It should be clear that the applicability of the present invention is not restricted to the AP2-2 polypeptide-encoding nucleic acid represented by SEQ ID NO: 131, nor is the applicability of the invention restricted to expression of an AP2-2 polypeptide-encoding nucleic acid when driven by a constitutive promoter.

The constitutive promoter is preferably a GOS2 promoter, more preferably the rice GOS2 promoter. See Table 2a in the "definitions" section herein for further examples of constitutive promoters.

Other control sequences (besides promoter, enhancer, silencer, intron sequences, 3'UTR and/or 5'UTR regions) may be protein and/or RNA stabilizing elements. Such sequences would be known or may readily be obtained by a person skilled in the art.

The genetic constructs of the invention may further include an origin of replication sequence that is required for maintenance and/or replication in a specific cell type. One example is when a genetic construct is required to be maintained in a bacterial cell as an episomal genetic element (e.g. plasmid or cosmid molecule). Preferred origins of replication include, but are not limited to, the f1-ori and colE1.

5

For the detection of the successful transfer of the nucleic acid sequences as used in the methods of the invention and/or selection of transgenic plants comprising these nucleic acids, it is advantageous to use marker genes (or reporter genes). Therefore, the genetic construct may optionally comprise a selectable marker gene. Selectable markers are described in more detail in the "definitions" section
10 herein. The marker genes may be removed or excised from the transgenic cell once they are no longer needed. Techniques for marker removal are known in the art, useful techniques are described above in the definitions section.

15

The invention also provides a method for the production of transgenic plants having enhanced yield-related traits relative to control plants, comprising introduction and expression in a plant of any nucleic acid encoding an AP2-2 polypeptide as defined hereinabove.

More specifically, the present invention provides a method for the production of transgenic plants having increased yield, which method comprises:

20

- (i) introducing and expressing in a plant or plant cell an AP2-2 polypeptide-encoding nucleic acid; and
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

25

The nucleic acid may be introduced directly into a plant cell or into the plant itself (including introduction into a tissue, organ or any other part of a plant). According to a preferred feature of the present invention, the nucleic acid is preferably introduced into a plant by transformation. The term "transformation" is described in more detail in the "definitions" section herein.

30

The genetically modified plant cells can be regenerated via all methods with which the skilled worker is familiar. Suitable methods can be found in the abovementioned publications by S.D. Kung and R. Wu, Potrykus or Höfgen and Willmitzer.

35

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant. To select transformed plants, the plant material obtained in the transformation is, as a rule, subjected to selective conditions so that transformed plants can be distinguished from untransformed plants. For example, the seeds obtained in the above-described manner can be planted and, after an initial growing period, subjected to a suitable selection by spraying. A further possibility consists in growing the seeds, if appropriate after

sterilization, on agar plates using a suitable selection agent so that only the transformed seeds can grow into plants. Alternatively, the transformed plants are screened for the presence of a selectable marker such as the ones described above.

- 5 Following DNA transfer and regeneration, putatively transformed plants may also be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

10 The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed and homozygous second-generation (or T2) transformants selected, and the T2 plants may then further be propagated through classical breeding techniques. The generated transformed
15 organisms may take a variety of forms. For example, they may be chimeras of transformed cells and non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

- 20 The present invention clearly extends to any plant cell or plant produced by any of the methods described herein, and to all plant parts and propagules thereof. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced by the parent in the
25 methods according to the invention.

The invention also includes host cells containing an isolated nucleic acid encoding an AP2-2 polypeptide as defined hereinabove. Preferred host cells according to the invention are plant cells. Host plants for the nucleic acids or the vector used in the method according to the invention, the expression cassette or
30 construct or vector are, in principle, advantageously all plants, which are capable of synthesizing the polypeptides used in the inventive method.

The methods of the invention are advantageously applicable to any plant. Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in
35 particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs. According to a preferred embodiment of the present invention, the plant is a crop plant. Examples of crop plants include soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato and tobacco. Further preferably, the plant is a monocotyledonous plant.

Examples of monocotyledonous plants include sugarcane. More preferably the plant is a cereal. Examples of cereals include rice, maize, wheat, barley, millet, rye, triticale, sorghum and oats.

The invention also extends to harvestable parts of a plant such as, but not limited to seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs. The invention furthermore relates to products derived, preferably directly derived, from a harvestable part of such a plant, such as dry pellets or powders, oil, fat and fatty acids, starch or proteins.

According to a preferred feature of the invention, the modulated expression is increased expression.

Methods for increasing expression of nucleic acids or genes, or gene products, are well documented in the art. Examples of methods for increasing expression are given in the "definitions" section.

As mentioned above, a preferred method for modulating (preferably, increasing) expression of a nucleic acid encoding an AP2-2 polypeptide is by introducing and expressing in a plant a nucleic acid encoding an AP2-2 polypeptide; however the effects of performing the method, i.e. enhancing yield-related traits may also be achieved using other well known techniques. A description of some of these techniques will now follow.

The effects of the invention may also be reproduced using the technique of T-DNA activation or TILLING (Targeted Induced Local Lesions In Genomes); for a description of the same see the "definitions" section.

The effects of the invention may also be reproduced using homologous recombination; for a description of the same see the "definitions" section.

The present invention also encompasses use of nucleic acids encoding AP2-2 polypeptides as described herein and use of this AP2-2 polypeptide in enhancing any of the aforementioned yield-related traits in plants.

Nucleic acids encoding AP2-2 polypeptide described herein, or the AP2-2 polypeptides themselves, may find use in breeding programmes in which a DNA marker is identified which may be genetically linked to an AP2-2 polypeptide-encoding gene. The nucleic acids/genes, or the AP2-2 polypeptides themselves may be used to define a molecular marker. This DNA or protein marker may then be used in breeding programmes to select plants having enhanced yield-related traits as defined hereinabove in the methods of the invention.

Allelic variants of an AP2-2 polypeptide-encoding nucleic acid/gene may also find use in marker-assisted breeding programmes. Such breeding programmes sometimes require introduction of allelic variation by mutagenic treatment of the plants, using for example EMS mutagenesis; alternatively, the

programme may start with a collection of allelic variants of so called "natural" origin caused unintentionally. Identification of allelic variants then takes place, for example, by PCR. This is followed by a step for selection of superior allelic variants of the sequence in question and which give increased yield. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question. Growth performance may be monitored in a greenhouse or in the field. Further optional steps include crossing plants in which the superior allelic variant was identified with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

Nucleic acids encoding AP2-2 polypeptides may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. Such use of AP2-2 polypeptide-encoding nucleic acids requires only a nucleic acid sequence of at least 15 nucleotides in length. The AP2-2 polypeptide-encoding nucleic acids may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Sambrook J, Fritsch EF and Maniatis T (1989) *Molecular Cloning, A Laboratory Manual*) of restriction-digested plant genomic DNA may be probed with the AP2-2-encoding nucleic acids. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander et al. (1987) *Genomics* 1: 174-181) in order to construct a genetic map. In addition, the nucleic acids may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the AP2-2 polypeptide-encoding nucleic acid in the genetic map previously obtained using this population (Botstein et al. (1980) *Am. J. Hum. Genet.* 32:314-331).

The production and use of plant gene-derived probes for use in genetic mapping is described in Bernatzky and Tanksley (1986) *Plant Mol. Biol. Reporter* 4: 37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

The nucleic acid probes may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel et al. In: *Non-mammalian Genomic Analysis: A Practical Guide*, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, the nucleic acid probes may be used in direct fluorescence in situ hybridisation (FISH) mapping (Trask (1991) *Trends Genet.* 7:149-154). Although current methods of FISH mapping favour use of large clones (several kb to several hundred kb; see Laan et al. (1995) *Genome Res.* 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

A variety of nucleic acid amplification-based methods for genetic and physical mapping may be carried out using the nucleic acids. Examples can be found in the "definitions" section herein.

- 5 The present invention further provides a method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding an AP2-70-like polypeptide.

10 The invention also provides hitherto unknown AP2-70-like-encoding nucleic acids and AP2-70-like polypeptides.

According to a further embodiment of the present invention, there is therefore provided an isolated nucleic acid molecule comprising:

- 15 (i) a nucleic acid represented by SEQ ID NO: 257;
(ii) the complement of a nucleic acid represented by SEQ ID NO: 257;
(iii) a nucleic acid encoding an AP2-70-like polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by SEQ ID NO: 258, and having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 331: PFLMQWLNLLPLPVLDSWCPHFHNSDALP (which represents the C-terminal region of SEQ ID NO: 258).

25 According to a further embodiment of the present invention, there is also provided an isolated polypeptide comprising:

- (i) an amino acid sequence represented by SEQ ID NO: 258;
(ii) an amino acid sequence having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by SEQ ID NO: 258, and having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 331: PFLMQWLNLLPLPVLDSWCPHFHNSDALP (which represents the C-terminal region of SEQ ID NO: 258);
(iii) derivatives of any of the amino acid sequences given in (i) or (ii) above.

35 A preferred method for modulating (preferably, increasing) expression of a nucleic acid encoding an AP2-70-like polypeptide is by introducing and expressing in a plant a nucleic acid encoding an AP2-70-like polypeptide.

Any reference hereinafter to a "protein useful in the methods of the invention" is taken to mean an AP2-70-like polypeptide as defined herein. Any reference hereinafter to a "nucleic acid useful in the methods of the invention" is taken to mean a nucleic acid capable of encoding such an AP2-70-like polypeptide. The nucleic acid to be introduced into a plant (and therefore useful in performing the methods of the invention) is any nucleic acid encoding the type of protein which will now be described, hereafter also named "AP2-70-like nucleic acid" or "AP2-70-like gene".

AP2-70-like polypeptides as defined below fall within Group Ib (A-6) according to the classification of Nakano *et al.*, 2006.

An "AP2-70-like polypeptide" as defined herein refers to any polypeptide comprising the following:

- (i) An AP2 DNA-binding domain as represented by SEQ ID NO: 332: YRGVQRHWGKWVAEIRLPRNRTLWLGTFTDTEEAALAYDSAAFRLRGESARLNF, or a domain having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the domain represented by SEQ ID NO: 332; and
- (ii) Having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the (*Oryza sativa*) polypeptide sequence represented by SEQ ID NO: 258; and
- (iii) Comprising Motif XVIII represented by SEQ ID NO: 333: RLPXNX¹RXRXLWLT F/Y D/E T/S, where X is any amino acid and X¹ is zero, one or more, and up to 30, gaps; and
- (iv) Comprising Motif XIX represented by SEQ ID NO: 334: RG D/E.

In the AP2 DNA-binding domain described above under (i), YRG and LAYD, as highlighted below, are preferred specific boxes for DNA-binding.

SEQ ID NO: 332:

YRGVQRHWGKWVAEIRLPRNRTLWLGTFTDTEEAALLAYDSAAFRLRGESARLNF.

Preferably, the AP2 DNA-binding domain described above under (i) comprises at least residues LPRNRTLWLGTFTD.

Motif XVIII (SEQ ID NO: 333) is preferably RLP K/R/Q NX¹R T/V/M R L/V WLGT F/Y D/E T/S, where X¹ is zero, one or more, and up to 30, gaps.

More preferably, Motif XVIII (SEQ ID NO: 333) is RLPRNX¹RTRLWLGTFTD, wherein X¹ is zero, one or more, and up to 30, gaps.

AP2-70 polypeptides as defined herein may also comprise one or more of the following motifs:

Motif XX/SEQ ID NO: 335: WDESESFLLHKYPSLEIDWDAILS, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XX. Adapted from Nakano *et al.*, 2006 (CMI-1).

- 5 Motif XXI/SEQ ID NO: 336: GPPLHAAVDAKLHAICH, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XXI. Adapted from Nakano *et al.*, 2006 (CMI-2).

- 10 Motif XXII/SEQ ID NO: 337: GANYLTPAQVLHVQAQLQRLRRP, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XXII. Adapted from Nakano *et al.*, 2006 (CMI-3).

- 15 Motif XXIII/SEQ ID NO: 338: VDSKELMGALAPSMVSFSYPCSEQSASS, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XXIII. Adapted from Nakano *et al.*, 2006 (CMI-4).

Any of Motifs XVIII and XX to XXIII described above may comprise one, two or three conservative and/or non-conservative change and/or deletion at any position.

- 20 The term "domain" and "motif" is defined in the "definitions" section herein. Specialist databases exist for the identification of domains. Examples are given in the "definitions" section herein.

Furthermore, AP2-70-like polypeptides (at least in their native form) typically have DNA-binding activity. Tools and techniques for measuring DNA-binding activity are well known in the art.

- 25 The present invention is illustrated by transforming plants with the nucleic acid sequence represented by SEQ ID NO: 257, encoding the polypeptide sequence of SEQ ID NO: 258. However, performance of the invention is not restricted to these sequences; the methods of the invention may advantageously be performed using any AP2-70-like-encoding nucleic acid or AP2-70-like polypeptide as defined herein.

- 30 Examples of nucleic acids encoding AP2-70-like polypeptides are given in Table 18 of Example 18 herein. Such nucleic acids are useful in performing the methods of the invention. The amino acid sequences given in Table 18 of Example 18 are example sequences of orthologues and paralogues of the AP2-70-like polypeptide represented by SEQ ID NO: 258, the terms "orthologues" and "paralogues" being as defined herein.
- 35

Nucleic acid variants may also be useful in practising the methods of the invention. Examples of such variants include nucleic acids encoding homologues and derivatives of any one of the amino acid sequences given in Table 18 of Example 18, the terms "homologue" and "derivative" being as defined

herein. Also useful in the methods of the invention are nucleic acids encoding homologues and derivatives of orthologues or paralogues of any one of the amino acid sequences given in Table 18 of Example 18. Homologues and derivatives useful in the methods of the present invention have substantially the same biological and functional activity as the unmodified protein from which they are derived.

Further nucleic acid variants useful in practising the methods of the invention include portions of nucleic acids encoding AP2-70-like polypeptides, nucleic acids hybridising to nucleic acids encoding AP2-70-like polypeptides, splice variants of nucleic acids encoding AP2-70-like polypeptides, allelic variants of nucleic acids encoding AP2-70-like polypeptides and variants of nucleic acids encoding AP2-70-like polypeptides obtained by gene shuffling. The terms hybridising sequence, splice variant, allelic variant and gene shuffling are as described herein.

Nucleic acids encoding AP2-70-like polypeptides need not be full-length nucleic acids, since performance of the methods of the invention does not rely on the use of full-length nucleic acid sequences. According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a portion of any one of the nucleic acid sequences given in Table 18 of Example 18, or a portion of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 18 of Example 18.

A portion of a nucleic acid may be prepared, for example, by making one or more deletions to the nucleic acid. The portions may be used in isolated form or they may be fused to other coding (or non-coding) sequences in order to, for example, produce a protein that combines several activities. When fused to other coding sequences, the resultant polypeptide produced upon translation may be bigger than that predicted for the protein portion.

Portions useful in the methods of the invention, encode an AP2-70-like polypeptide as defined herein, and have substantially the same biological activity as the amino acid sequences given in Table 18 of Example 18. Preferably, the portion is a portion of any one of the nucleic acids given in Table 18 of Example 18, or is a portion of a nucleic acid encoding an orthologue or paralogue of any one of the amino acid sequences given in Table 18 of Example 18. Preferably the portion is, in increasing order of preference at least 600, 650, 700, 750 consecutive nucleotides in length, the consecutive nucleotides being of any one of the nucleic acid sequences given in Table 18 of Example 18, or of a nucleic acid encoding an orthologue or paralogue of any one of the amino acid sequences given in Table 18 of Example 18. Most preferably the portion is a portion of the nucleic acid of SEQ ID NO: 257. Preferably, the portion encodes an amino acid sequence which when used in the construction of a phylogenetic tree, such as the one depicted in Figures. 3 and 4, tends to cluster with the group of AP2-70-like polypeptides (Group I(A-6), specifically Group Ib: see Nakanao et al., 2006 for classification) comprising the amino acid sequence represented by SEQ ID NO: 258 rather than with any other group.

Another nucleic acid variant useful in the methods of the invention is a nucleic acid capable of hybridising, under reduced stringency conditions, preferably under stringent conditions, with a nucleic acid encoding an AP2-70-like polypeptide as defined herein, or with a portion as defined herein.

5 According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a nucleic acid capable of hybridizing to any one of the nucleic acids given in Table 18 of Example 18, or comprising introducing and expressing in a plant a nucleic acid capable of hybridising to a nucleic acid encoding an orthologue, paralogue or homologue
10 of any of the nucleic acid sequences given in Table 18 of Example 18.

Hybridising sequences useful in the methods of the invention encode an AP2-70-like polypeptide as defined herein, and have substantially the same biological activity as the amino acid sequences given in Table 18 of Example 18. Preferably, the hybridising sequence is capable of hybridising to any one of
15 the nucleic acids given in Table 18 of Example 18, or to a portion of any of these sequences, a portion being as defined above, or wherein the hybridising sequence is capable of hybridising to a nucleic acid encoding an orthologue or paralogue of any one of the amino acid sequences given in Table 18 of Example 18. Most preferably, the hybridising sequence is capable of hybridising to a nucleic acid as represented by SEQ ID NO: 257 or to a portion thereof.

20 Preferably, the hybridising sequence encodes an amino acid sequence which when used in the construction of a phylogenetic tree, such as the one depicted in Figures 3 and 4, tends to cluster with the group of AP2-70-like polypeptides (Group I(A-6), specifically Group Ib: see Nakanao *et al.*, 2006 for classification) comprising the amino acid sequence represented by SEQ ID NO: 258 rather than with any
25 other group.

Another nucleic acid variant useful in the methods of the invention is a splice variant encoding an AP2-70-like polypeptide as defined hereinabove, a splice variant being as defined herein.

30 According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a splice variant of any one of the nucleic acid sequences given in Table 18 of Example 18, or a splice variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 18 of Example 18.

35 Preferred splice variants are splice variants of a nucleic acid represented by SEQ ID NO: 257, or a splice variant of a nucleic acid encoding an orthologue or paralogue of SEQ ID NO: 258. Preferably, the amino acid sequence encoded by the splice variant, when used in the construction of a phylogenetic tree, such as the one depicted in Figures 3 and 4, tends to cluster with the group of AP2-70-like

polypeptides (Group I(A-6), specifically Group Ib: see Nakanao *et al.*, 2006 for classification) comprising the amino acid sequence represented by SEQ ID NO: 258 rather than with any other group.

Another nucleic acid variant useful in performing the methods of the invention is an allelic variant of a nucleic acid encoding an AP2-70-like polypeptide as defined hereinabove, an allelic variant being as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant an allelic variant of any one of the nucleic acids given in Table 18 of Example 18, or comprising introducing and expressing in a plant an allelic variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 18 of Example 18.

The allelic variants useful in the methods of the present invention have substantially the same biological activity as the AP2-70-like polypeptide of SEQ ID NO: 258 and any of the amino acids depicted in Table 18 of Example 18. Allelic variants exist in nature, and encompassed within the methods of the present invention is the use of these natural alleles. Preferably, the allelic variant is an allelic variant of SEQ ID NO: 257 or an allelic variant of a nucleic acid encoding an orthologue or paralogue of SEQ ID NO: 258. Preferably, the amino acid sequence encoded by the allelic variant, when used in the construction of a phylogenetic tree, such as the one depicted in Figures 3 and 4, tends to cluster with the AP2-70-like polypeptides (Group I(A-6), specifically Group Ib: see Nakanao *et al.*, 2006 for classification) comprising the amino acid sequence represented by SEQ ID NO: 258 rather than with any other group.

Gene shuffling or directed evolution may also be used to generate variants of nucleic acids encoding AP2-70-like polypeptides as defined above; the term "gene shuffling" being as defined herein.

According to the present invention, there is provided a method for enhancing yield-related traits in plants, comprising introducing and expressing in a plant a variant of any one of the nucleic acid sequences given in Table 18 of Example 18, or comprising introducing and expressing in a plant a variant of a nucleic acid encoding an orthologue, paralogue or homologue of any of the amino acid sequences given in Table 18 of Example 18, which variant nucleic acid is obtained by gene shuffling.

Preferably, the amino acid sequence encoded by the variant nucleic acid obtained by gene shuffling, when used in the construction of a phylogenetic tree such as the one depicted in Figures 3 and 4, tends to cluster with the group of AP2-70-like polypeptides (Group I(A-6), specifically Group Ib: see Nakanao *et al.*, 2006 for classification) comprising the amino acid sequence represented by SEQ ID NO: 258 rather than with any other group.

Furthermore, nucleic acid variants may also be obtained by site-directed mutagenesis. Several methods are available to achieve site-directed mutagenesis, the most common being PCR based methods (Current Protocols in Molecular Biology. Wiley Eds.).

5 Nucleic acids encoding AP2-70-like polypeptides may be derived from any natural or artificial source. The nucleic acid may be modified from its native form in composition and/or genomic environment through deliberate human manipulation. Preferably the AP2-70-like polypeptide-encoding nucleic acid is from a plant, further preferably from a monocotyledonous plant, more preferably from the family poaceae, most preferably the nucleic acid is from *Oryza sativa*.

10 Performance of the methods of the invention gives plants having enhanced yield-related traits. In particular performance of the methods of the invention gives plants having increased yield, especially increased seed yield relative to control plants. The terms "yield" and "seed yield" are described in more detail in the "definitions" section herein.

15 The present invention provides a method for increasing yield, especially seed yield of plants, relative to control plants, which method comprises modulating expression, preferably increasing expression, in a plant of a nucleic acid encoding an AP2-70-like polypeptide as defined herein.

20 According to a preferred feature of the present invention, performance of the methods of the invention gives plants having an increased growth rate relative to control plants. Therefore, according to the present invention, there is provided a method for increasing the growth rate of plants, which method comprises modulating expression, preferably increasing expression, in a plant of a nucleic acid encoding an AP2-70-like polypeptide as defined herein.

25 Performance of the methods of the invention gives plants grown under non-stress conditions or under mild drought conditions increased yield relative to suitable control plants grown under comparable conditions. Therefore, according to the present invention, there is provided a method for increasing yield in plants grown under non-stress conditions or under mild drought conditions, which method
30 comprises increasing expression in a plant of a nucleic acid encoding an AP2-70-like polypeptide.

Performance of the methods of the invention gives plants grown under conditions of nutrient deficiency, particularly under conditions of nitrogen deficiency, increased yield relative to control plants grown under comparable conditions. Therefore, according to the present invention, there is provided a method for
35 increasing yield in plants grown under conditions of nutrient deficiency, which method comprises increasing expression in a plant of a nucleic acid encoding an AP2-70-like polypeptide. Nutrient deficiency may result from a lack or excess of nutrients such as nitrogen, phosphates and other phosphorous-containing compounds, potassium, calcium, cadmium, magnesium, manganese, iron and boron, amongst others.

The present invention encompasses plants or parts thereof (including seeds) obtainable by the methods according to the present invention. The plants or parts thereof comprise a nucleic acid transgene encoding an AP2-70-like polypeptide as defined above.

5

The invention also provides genetic constructs and vectors to facilitate introduction and/or expression in plants of nucleic acids encoding AP2-70-like polypeptides. The gene constructs may be inserted into vectors, which may be commercially available, suitable for transforming into plants and suitable for expression of the gene of interest in the transformed cells. The invention also provides use of a gene

10

More specifically, the present invention provides a construct comprising:

- (d) a nucleic acid encoding an AP2-70-like polypeptide as defined above;
- (e) one or more control sequences capable of driving expression of the nucleic acid sequence of
- (a); and optionally
- (f) a transcription termination sequence.

15

Preferably, the nucleic acid encoding an AP2-70-like polypeptide is:

- (i) a nucleic acid represented by SEQ ID NO: 257;
- (ii) the complement of a nucleic acid represented by SEQ ID NO: 257;
- (iv) a nucleic acid encoding an AP2-70-like polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by SEQ ID NO: 258, and having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 331: PFLMQWLNLLPLPVLDSSSWCPEHFHNSDALP (which represents the C-terminal region of SEQ ID NO: 258).

20

25

The term "control sequence" and "termination sequence" are as defined herein.

30

Plants are transformed with a vector comprising any of the nucleic acids described above. The skilled artisan is well aware of the genetic elements that must be present on the vector in order to successfully transform, select and propagate host cells containing the sequence of interest. The sequence of interest is operably linked to one or more control sequences (at least to a promoter).

35

Advantageously, any type of promoter, whether natural or synthetic, may be used to drive expression of the nucleic acid sequence. A constitutive promoter is particularly useful in the methods. See the "Definitions" section herein for definitions of the various promoter types. Also useful in the methods of the invention is a root-specific promoter.

It should be clear that the applicability of the present invention is not restricted to the AP2-70-like polypeptide-encoding nucleic acid represented by SEQ ID NO: 257, nor is the applicability of the invention restricted to expression of an AP2-70-like polypeptide-encoding nucleic acid when driven by a constitutive promoter, or when driven by a root-specific promoter.

The constitutive promoter is preferably a GOS2 promoter, preferably a GOS2 promoter from rice. Further preferably the constitutive promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 39 or SEQ ID NO: 339 most preferably the constitutive promoter is as represented by SEQ ID NO: 39 or SEQ ID NO: 339. See Table 2a in the "Definitions" section herein for further examples of constitutive promoters.

According to another preferred feature of the invention, the nucleic acid encoding an AP2-70-like polypeptide is operably linked to a root-specific promoter. The root-specific promoter is preferably an RCc3 promoter (Plant Mol Biol. 1995 Jan;27(2):237-48), more preferably the RCc3 promoter is from rice, further preferably the RCc3 promoter is represented by a nucleic acid sequence substantially similar to SEQ ID NO: 110 or SEQ ID NO: 340, most preferably the promoter is as represented by SEQ ID NO: 110. Examples of other root-specific promoters which may also be used to perform the methods of the invention are shown in Table 2b herein.

For the detection of the successful transfer of the nucleic acid sequences as used in the methods of the invention and/or selection of transgenic plants comprising these nucleic acids, it is advantageous to use marker genes (or reporter genes). Therefore, the genetic construct may optionally comprise a selectable marker gene. Selectable markers are described in more detail in the "definitions" section herein.

The invention also provides a method for the production of transgenic plants having enhanced yield-related traits relative to control plants, comprising introduction and expression in a plant of any nucleic acid encoding an AP2-70-like polypeptide as defined hereinabove.

More specifically, the present invention provides a method for the production of transgenic plants having increased enhanced yield-related traits, particularly increased (seed) yield, which method comprises:

- (iii) introducing and expressing in a plant or plant cell an AP2-70-like polypeptide-encoding nucleic acid; and
- (iv) cultivating the plant cell under conditions promoting plant growth and development.

The nucleic acid of (i) may be any of the nucleic acids capable of encoding an AP2-70-like polypeptide as defined herein. Preferably, the nucleic acid is:

- (i) a nucleic acid represented by SEQ ID NO: 257;
- (ii) the complement of a nucleic acid represented by SEQ ID NO: 257;

- (iii) a nucleic acid encoding an AP2-70-like polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by SEQ ID NO: 258, and having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 331: PFLMQWLNLLPLPVLDSWCPPEHFHNSDALP (which represents the C-terminal region of SEQ ID NO: 258).

The nucleic acid may be introduced directly into a plant cell or into the plant itself (including introduction into a tissue, organ or any other part of a plant). According to a preferred feature of the present invention, the nucleic acid is preferably introduced into a plant by transformation. The term "transformation" is described in more detail in the "definitions" section herein.

The genetically modified plant cells can be regenerated via all methods with which the skilled worker is familiar. Suitable methods can be found in the abovementioned publications by S.D. Kung and R. Wu, Potrykus or Höfgen and Willmitzer.

Generally after transformation, plant cells or cell groupings are selected for the presence of one or more markers which are encoded by plant-expressible genes co-transferred with the gene of interest, following which the transformed material is regenerated into a whole plant. To select transformed plants, the plant material obtained in the transformation is, as a rule, subjected to selective conditions so that transformed plants can be distinguished from untransformed plants. For example, the seeds obtained in the above-described manner can be planted and, after an initial growing period, subjected to a suitable selection by spraying. A further possibility consists in growing the seeds, if appropriate after sterilization, on agar plates using a suitable selection agent so that only the transformed seeds can grow into plants. Alternatively, the transformed plants are screened for the presence of a selectable marker such as the ones described above.

Following DNA transfer and regeneration, putatively transformed plants may also be evaluated, for instance using Southern analysis, for the presence of the gene of interest, copy number and/or genomic organisation. Alternatively or additionally, expression levels of the newly introduced DNA may be monitored using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

The generated transformed plants may be propagated by a variety of means, such as by clonal propagation or classical breeding techniques. For example, a first generation (or T1) transformed plant may be selfed and homozygous second-generation (or T2) transformants selected, and the T2 plants may then further be propagated through classical breeding techniques. The generated transformed organisms may take a variety of forms. For example, they may be chimeras of transformed cells and

non-transformed cells; clonal transformants (e.g., all cells transformed to contain the expression cassette); grafts of transformed and untransformed tissues (e.g., in plants, a transformed rootstock grafted to an untransformed scion).

5 The present invention clearly extends to any plant cell or plant produced by any of the methods described herein, and to all plant parts and propagules thereof. The present invention extends further to encompass the progeny of a primary transformed or transfected cell, tissue, organ or whole plant that has been produced by any of the aforementioned methods, the only requirement being that progeny exhibit the same genotypic and/or phenotypic characteristic(s) as those produced by the parent in the
10 methods according to the invention.

The invention also includes host cells containing an isolated nucleic acid encoding a AP2-70-like polypeptide as defined hereinabove. Preferred host cells according to the invention are plant cells. Host plants for the nucleic acids or the vector used in the method according to the invention, the
15 expression cassette or construct or vector are, in principle, advantageously all plants, which are capable of synthesizing the polypeptides used in the inventive method.

The methods of the invention are advantageously applicable to any plant. Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in
20 particular monocotyledonous and dicotyledonous plants including fodder or forage legumes, ornamental plants, food crops, trees or shrubs. According to a preferred embodiment of the present invention, the plant is a crop plant. Examples of crop plants include soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato and tobacco. Further preferably, the plant is a monocotyledonous plant. Examples of monocotyledonous plants include sugarcane. More preferably the plant is a cereal.
25 Examples of cereals include rice, maize, wheat, barley, millet, rye, triticale, sorghum and oats.

The invention also extends to harvestable parts of a plant such as, but not limited to seeds, leaves, fruits, flowers, stems, rhizomes, tubers and bulbs. The invention furthermore relates to products derived, preferably directly derived, from a harvestable part of such a plant, such as dry pellets or
30 powders, oil, fat and fatty acids, starch or proteins.

According to a preferred feature of the invention, the modulated expression is increased expression. Methods for increasing expression of nucleic acids or genes, or gene products, are well documented in the art. Examples are given in the "definitions" section herein.
35

As mentioned above, a preferred method for modulating (preferably, increasing) expression of a nucleic acid encoding an AP2-70-like polypeptide is by introducing and expressing in a plant a nucleic acid encoding an AP2-70-like polypeptide; however the effects of performing the method, i.e. enhancing

yield-related traits may also be achieved using other well known techniques. A description of some of these techniques can be found in the "definitions" section.

The effects of the invention may also be reproduced using the technique of T-DNA activation or TILLING (Targeted Induced Local Lesions In Genomes); for a description of the same see the "definitions" section.

The effects of the invention may also be reproduced using homologous recombination; for a description of the same see the "definitions" section.

The present invention also encompasses use of nucleic acids encoding AP2-70-like polypeptides as described herein and use of these AP2-70-like polypeptide in enhancing any of the aforementioned yield-related traits in plants.

Nucleic acids encoding AP2-70-like polypeptide described herein, or the AP2-70-like polypeptides themselves, may find use in breeding programmes in which a DNA marker is identified which may be genetically linked to an AP2-70-like polypeptide-encoding gene. The nucleic acids/genes, or the AP2-70-like polypeptides themselves may be used to define a molecular marker. This DNA or protein marker may then be used in breeding programmes to select plants having enhanced yield-related traits as defined hereinabove in the methods of the invention.

Allelic variants of an AP2-70-like polypeptide-encoding nucleic acid/gene may also find use in marker-assisted breeding programmes. Such breeding programmes sometimes require introduction of allelic variation by mutagenic treatment of the plants, using for example EMS mutagenesis; alternatively, the programme may start with a collection of allelic variants of so called "natural" origin caused unintentionally. Identification of allelic variants then takes place, for example, by PCR. This is followed by a step for selection of superior allelic variants of the sequence in question and which give increased yield. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question. Growth performance may be monitored in a greenhouse or in the field. Further optional steps include crossing plants in which the superior allelic variant was identified with another plant. This could be used, for example, to make a combination of interesting phenotypic features.

Nucleic acids encoding AP2-70-like polypeptides may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. Such use of AP2-70-like polypeptide-encoding nucleic acids requires only a nucleic acid sequence of at least 15 nucleotides in length. The AP2-70-like polypeptide-encoding nucleic acids may be used as restriction fragment length polymorphism (RFLP) markers. Southern blots (Sambrook J, Fritsch EF and

Maniatis T (1989) Molecular Cloning, A Laboratory Manual) of restriction-digested plant genomic DNA may be probed with the AP2-70-like-encoding nucleic acids. The resulting banding patterns may then be subjected to genetic analyses using computer programs such as MapMaker (Lander et al. (1987) Genomics 1: 174-181) in order to construct a genetic map. In addition, the nucleic acids may be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. Segregation of the DNA polymorphisms is noted and used to calculate the position of the AP2-70-like polypeptide-encoding nucleic acid in the genetic map previously obtained using this population (Botstein et al. (1980) Am. J. Hum. Genet. 32:314-331).

The production and use of plant gene-derived probes for use in genetic mapping is described in Bernatzky and Tanksley (1986) Plant Mol. Biol. Reporter 4: 37-41. Numerous publications describe genetic mapping of specific cDNA clones using the methodology outlined above or variations thereof. For example, F2 intercross populations, backcross populations, randomly mated populations, near isogenic lines, and other sets of individuals may be used for mapping. Such methodologies are well known to those skilled in the art.

The nucleic acid probes may also be used for physical mapping (i.e., placement of sequences on physical maps; see Hoheisel et al. In: Non-mammalian Genomic Analysis: A Practical Guide, Academic press 1996, pp. 319-346, and references cited therein).

In another embodiment, the nucleic acid probes may be used in direct fluorescence in situ hybridisation (FISH) mapping (Trask (1991) Trends Genet. 7:149-154). Although current methods of FISH mapping favour use of large clones (several kb to several hundred kb; see Laan et al. (1995) Genome Res. 5:13-20), improvements in sensitivity may allow performance of FISH mapping using shorter probes.

The methods according to the present invention result in plants having enhanced yield-related traits, as described hereinbefore. These traits may also be combined with other economically advantageous traits, such as further yield-enhancing traits, tolerance to other abiotic and biotic stresses, traits modifying various architectural features and/or biochemical and/or physiological features.

Description of figures

The present invention will now be described with reference to the following figures in which:

Fig. 1 shows a phylogenetic tree taken from Ooka *et al.*, 2003 (DNA Research 10, 239-247). The dashed box 3rd from the bottom, marked "OsNAC7", is the group comprising the sequence of SEQ ID NO: 2. The cluster of NACs starting from ONAC022 until OsNAC3, represent the cluster comprising the sequences of SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 and SEQ ID NO: 59.

Amino acid sequences clustering in these groups (the amino acid sequences given in Tables 3 and 4, for example) are considered to be useful in the methods of the invention.

Fig. 2 shows the sequence of SEQ ID NO: 132 with (A): Putative nuclear localisation signal, (B): AP2/ERF DNA binding domain, (1): CMVII-1 motif, (3): CMVII-3 motif, (4): CMVII-4 motif, (5): CMVII-5 motif, (6): CMVII-6 motif, (7): CMVII-7 motif, (8): CMVII-8 motif. The CMVII motifs were identified according to Nakano et al. (2006).

Fig. 3 shows a phylogenetic tree taken from Nakano *et al.* (Plant Physiol. Vol. 140, 2006) in which the group indicated as I(A-6) includes the group of AP2-70-like polypeptides defined herein.

Fig. 4 shows a section of a phylogenetic tree comprising AP2-70-like polypeptide sequences defined herein and expanding the group indicated as Group I(A-6) in Nakano *et al.*, 2006. The phylogenetic tree was constructed using a neighbour-joining clustering algorithm as provided in the AlignX programme from the Vector NTI (Invitrogen).

Fig. 5 shows an alignment of NAC transcription factors as defined hereinabove. The sequences were aligned using AlignX program from Vector NTI suite (InforMax, Bethesda, MD). Multiple alignment was done with a gap opening penalty of 10 and a gap extension of 0.01. Minor manual editing was also carried out where necessary to better position some conserved regions. The NAC domain and Motifs I to III are indicated.

Fig. 6 shows an alignment of NAC transcription factors as defined hereinabove. The sequences were aligned using AlignX program from Vector NTI suite (InforMax, Bethesda, MD). Multiple alignment was done with a gap opening penalty of 10 and a gap extension of 0.01. Minor manual editing was also carried out where necessary to better position some conserved regions. The NAC domain and Motifs IV to XI are indicated.

Fig. 7 shows a CLUSTAL W multiple sequence alignment of AP2-2 polypeptides from *Arabidopsis* and rice. SEQ ID NO: 132 (Os06g09390) is indicated in bold and the conserved regions (motifs XII to XVII, SEQ ID NO: 133 to SEQ ID NO: 138) are underlined.

Fig. 8 shows an alignment of AP2-70-like polypeptides with Motifs XVIII and XIX indicated and with the AP2 DNA-binding domain also indicated.

Fig. 9 shows a binary vector p163, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC transcription factor-encoding nucleic acid under the control of a GOS2 promoter (internal reference PRO0129).

Fig. 10 shows a binary vector p164, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC1 (SEQ ID NO: 50) transcription factor-encoding nucleic acid under the control of a GOS2 promoter (internal reference PRO0129) for constitutive expression.

5 **Fig. 11** shows a binary vector p165, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC4 (SEQ ID NO: 52) transcription factor-encoding nucleic acid under the control of a GOS2 promoter (internal reference PRO0129) for constitutive expression.

10 **Fig. 12** shows a binary vector p166, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC4 (SEQ ID NO: 52) transcription factor-encoding nucleic acid under the control of an RCc3 promoter (internal reference PRO0110) for root-specific expression.

15 **Fig. 13** shows a binary vector p167, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC transcription factor-encoding nucleic acid under the control of a protochlorophyllid reductase promoter (internal reference PRO0123).

Fig. 14 shows a binary vector p167, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC6 (SEQ ID NO: 54) transcription factor-encoding nucleic acid under the control of an RCc3 promoter (internal reference PRO0110) for root-specific expression.

20 **Fig. 15** shows a binary vector p168, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC7 (SEQ ID NO: 56) transcription factor-encoding nucleic acid under the control of a GOS2 promoter (internal reference PRO0129) for constitutive expression.

25 **Fig. 16** shows a binary vector p169, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC3 (SEQ ID NO: 58) transcription factor-encoding nucleic acid under the control of an RCc3 promoter (internal reference PRO0110) for root-specific expression.

30 **Fig. 17** shows a binary vector pGOS2::NAC1, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC1 (SEQ ID NO: 50) transcription factor-encoding nucleic acid under the control of a GOS2 promoter for constitutive expression.

35 **Fig. 18** shows a binary vector pGOS2::NAC4, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC4 (SEQ ID NO: 52) transcription factor-encoding nucleic acid under the control of a GOS2 promoter for constitutive expression.

Fig. 19 shows a binary vector pRCc3::NAC4, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC4 (SEQ ID NO: 52) transcription factor-encoding nucleic acid under the control of an RCc3 promoter for root-specific expression.

Fig. 20 shows a binary vector pRCc3::NAC6, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC6 (SEQ ID NO: 54) transcription factor-encoding nucleic acid under the control of an RCc3 promoter for root-specific expression.

Fig. 21 shows a binary vector pGOS2::NAC7, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC7 (SEQ ID NO: 56) transcription factor-encoding nucleic acid under the control of a GOS2 promoter for constitutive expression.

Fig. 22 shows a binary vector pRCc3::NAC3, for increased expression in *Oryza sativa* of an *Oryza sativa* NAC3 (SEQ ID NO: 58) transcription factor-encoding nucleic acid under the control of an RCc3 promoter for root-specific expression.

Fig. 23 shows the binary vector for increased expression in *Oryza sativa* of a rice AP2-2 protein-encoding nucleic acid under the control of a GOS2 promoter.

Fig. 24 shows the binary vector for increased expression in *Oryza sativa* of an *Oryza sativa* AP2-70-like protein-encoding nucleic acid under the control of a rice RCC3 promoter (pRCC3).

Fig. 25 shows the binary vector for increased expression in *Oryza sativa* of an *Oryza sativa* AP2-70-like protein-encoding nucleic acid under the control of a rice GOS2 promoter (pGOS2).

Figs. 26 to 29 details examples of sequences useful in performing the methods according to the present invention.

Examples

The present invention will now be described with reference to the following examples, which are by way of illustration alone. The following examples are not intended to completely define or otherwise limit the scope of the invention.

A) OsNAM2

Example 1: Cloning of OsNAM2 cDNA

Total cellular RNA from 2-week-old rice seedlings was used to clone *OsNAM2* cDNA. RNA was extracted using an RNeasy Kit (Qiagen, Germany). *OsNAM2* cDNA was 1292bp long, from 5' UTR (untranslated region) to the stop codon. Two overlapping cDNAs were joined in the *OsNAM2* cDNA clone. A 5' cDNA of 1025 bp was obtained by 5' RACE-PCR using an adapter primer (5'-AAGCAGTGGTATCAACGCAGAGTACGCGGG-3') and the *OsNAM2* specific primer (*OsNAM2*-2) (5'-CTC TCC AGA GGC GGC ATC ATG TCG GA -3'). The 5' RACE-PCR was performed with the BD SMART[™] RACE cDNA Amplification Kit (Clontech, USA). The adapter primer (SMART II A Oligonucleotide) was as provided by the manufacturer. The 3' cDNA of 620bp was obtained by PCR

with two OsNAM2-specific primers (NAM2-1 (5' – TGA TCG GGA TGA GGA AGA C -3') and NAM2-3 (5'- GAT CAG TCT CGG TCA TCG ATG -3')). The first-stranded cDNA as PCR template was synthesized with the Oligotex mRNA kit (Qiagen, Valencia, CA). Candidate PCR products were gel-purified, subcloned into the pGEM-T Easy (Promega, USA), and confirmed by sequencing. The vector
5 harboring the 5' cDNA was cut with *HindIII* and ligated with a *HindIII* fragment of the 3' cDNA vector. The result was a 1292 bp OsNAM2 cDNA.

Example 2: Vector Construction

2.1 OsNAM2 under the control of a GOS2 promoter

10 The entry clone was subsequently used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the nucleic acid sequence of interest already cloned in the entry clone. A rice GOS2 promoter (SEQ ID NO: 39 or SEQ ID NO: 339) for constitutive expression (internal reference PRO0129)
15 was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector p163 (Figure 9) was transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described below.

2.2 OsNAM2 under the control of a protochlorophyllid reductase promoter

The entry clone was subsequently used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo*
25 recombination with the nucleic acid sequence of interest already cloned in the entry clone. A protochlorophyllid reductase promoter (SEQ ID NO: 40) for green tissue-specific expression (internal reference PRO0123) was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector p167 (Figure 13) was transformed into
30 *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described below.

Example 3: Evaluation procedure

3.1 Evaluation setup

35 Approximately 30 independent T0 rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T1 seed. Seven events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homozygotes) and approximately 10 T1 seedlings lacking the transgene (nullizygotes) were selected by

monitoring visual marker expression. The transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. Greenhouse conditions were of short days (12 hours light), 28°C in the light and 22°C in the dark, and a relative humidity of 70%. From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

3.2 Statistical analysis: t-test and F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and to verify an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the mere presence or position of the gene that is causing the differences in phenotype.

To check for an effect of the genes within an event, i.e., for a line-specific effect, a t-test was performed within each event using data sets from the transgenic plants and the corresponding null plants. "Null plants" or "null segregants" or "nullizygotes" are the plants treated in the same way as the transgenic plant, but from which the transgene has segregated. Null plants can also be described as the homozygous negative transformed plants. The threshold for significance for the t-test is set at 10% probability level. The results for some events can be above or below this threshold. This is based on the hypothesis that a gene might only have an effect in certain positions in the genome, and that the occurrence of this position-dependent effect is not uncommon. This kind of gene effect is also named herein a "line effect of the gene". The p-value is obtained by comparing the t-value to the t-distribution or alternatively, by comparing the F-value to the F-distribution. The p-value then gives the probability that the null hypothesis (i.e., that there is no effect of the transgene) is correct.

Example 4: Evaluation results

4.1 OsNAM2 under the control of a GOS2 promoter

There was an increase in aboveground area, number of panicles, the number of flowers per panicle and the total number of seeds for transgenic plants expressing an OsNAM2 gene under the control of a GOS2 promoter compared to nullizygotes. There was a significant increase in the number of flowers per panicle and the total number of seeds for transgenic plants compared to nullizygotes. There was a >12% increase (average for 4 events) in the number of flowers per panicle for transgenic plants compared to nullizygotes, with a significant p-value from the F-test of <0.0014. Furthermore, there was a 35% increase in the total number of seeds for transgenic plants compared to nullizygotes, with a significant p-value from the F-test of <0.0045.

4.2 OsNAM2 under the control of a protochlorophyllid reductase promoter

There was an increase in aboveground area, number of panicles and the total number of seeds for transgenic plants expressing an OsNAM2 gene under the control of a protochlorophyllid reductase promoter compared to nullizygotes. There was a >16% increase (average for 2 events) in the aboveground area for transgenic plants compared to nullizygotes, with a significant p-value from the F-test of <0.0014. There was a >16% increase in the number of panicles for transgenic plants compared to nullizygotes and a >18% increase in the total number of seeds for transgenic plants compared to nullizygotes.

B) OsNAC1, 3, 4, 6, and 7

Example 5: Cloning of OsNAC1, 3, 4, 6, and 7

Oryza sativa genes containing a NAC domain, OsNAC1 (Gene bank accession number AK067690), OsNAC3 (AK069257), OsNAC4 (AK068392), OsNAC6 (AK102475) and OsNAC7 (AK107330), were identified to be stress-inducible in rice by expression profiling conducted with the 60K Rice Whole Genome Microarray (GreenGene Biotech Inc., Korea). This microarray contained 70-mer oligonucleotide probes with sequences corresponding to 58,417 known or predicted ORFs covering the entire rice genome (Oh *et al.*, 2005 *Plant Physiology* **138**: 341-351). The full-length cDNAs of OsNAC1 and OsNAC3 were obtained from rice EST stocks generated by GreenGene Biotech Inc. These cDNAs were inserted into *EcoR*I and *Xho*I sites of Bluescript SKII (Stratagene). The full-length cDNAs of OsNAC4, OsNAC6 and OsNAC7 were amplified by PCR using as template an *Oryza sativa* seedling cDNA library (GreenGene Biotech, Korea). After reverse transcription of RNA extracted from 14-day-old seedlings that were treated with 400 mM NaCl for 6 hours, the cDNAs were cloned into Uni-ZAP XR (Stratagene). Average insert size of the library was 1.5 kb and original number of plaques was of the order of 1.10^6 pfu. Original titre was determined to be 2.10^9 pfu/ml after first amplification of 2.10^6 pfu/ml. 0.1 µg of cDNA library was used in each 50µl PCR mixture. PCR primers that were used for the amplification of the OsNAC genes are listed in Table 7. PCR amplifications were performed using *Pfu* DNA polymerase in standard conditions. The DNA fragments were amplified and purified also using standard methods. PCR products were ligated into *EcoR*I site of pBluescript SKII and sequenced.

Table 7. List of primers used for isolation of OsNACs.

Gene	Forward Primers	Reverse Primers
OsNAC4	5'CCAACACTAGTAGGATAAAG3'	5'ACCACTGGGCTAATTAATTA3'
OsNAC6	5'GGTCGACCCACGCGTCCGCT3'	5'AACTGAAGTACCCGTTCTTA3'
OsNAC7	5'ATCCTCCACAAGAGAAACTA3'	5'AGTACAGTGTAGCACAATAA3'

Example 6: Expression Vector Construction**6.1 GOS2 constructs**

The entry clone was subsequently used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the nucleic acid sequence of interest already cloned in the entry clone. A rice GOS2 promoter (SEQ ID NO: 39) for constitutive expression (internal reference PRO0129) was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vectors p164 (Figure 10), p165 (Figure 11) and p168 (Figure 15) were each transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described below.

6.2 RCc3 constructs

The entry clone was subsequently used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contains as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the nucleic acid sequence of interest already cloned in the entry clone. A rice RCc3 promoter (SEQ ID NO: 110) for root-specific expression (internal reference PRO0110) was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector p166 (Figure 12), p167 (Figure 14) and p169 (Figure 16) were each transformed into *Agrobacterium* strain LBA4044 and subsequently to *Oryza sativa* plants. Transformed rice plants were allowed to grow and were then examined for the parameters described below.

Example 7: Evaluation procedure**7.1 Evaluation setup**

Approximately 30 independent T0 rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T1 seed. Seven events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homozygotes) and approximately 10 T1 seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. The transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. Greenhouse conditions were of short days (12 hours light), 28°C in the light and 22°C in the dark, and a relative humidity of 70%. From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each

time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

Drought screen

- 5 Plants from five events (T2 seeds) were grown in potting soil under normal conditions until they approached the heading stage. They were then transferred to a "dry" section where irrigation was withheld. Humidity probes were inserted in randomly chosen pots to monitor the soil water content (SWC). When SWC went below certain thresholds, the plants were automatically re-watered continuously until a normal level was reached again. The plants were then re-transferred again to
- 10 normal conditions. The rest of the cultivation (plant maturation, seed harvest) was the same as for plants not grown under abiotic stress conditions. A confirmation round was performed consisting of repeating the screen with T2 seeds not harvested from plants of the first drought screen, but from plants grown under normal conditions.

15 Parameters measured

- The plant aboveground area (or leafy biomass) was determined by counting the total number of pixels on the digital images from aboveground plant parts discriminated from the background. This value was averaged for the pictures taken on the same time point from the different angles and was converted to a physical surface value expressed in square mm by calibration. Experiments show that the aboveground
- 20 plant area measured this way correlates with the biomass of plant parts above ground. The Areamax is the above ground area at the time point at which the plant had reached its maximal leafy biomass.

- The mature primary panicles were harvested, bagged, barcode-labelled and then dried for three days in the oven at 37°C. The panicles were then threshed and all the seeds collected. The filled husks were
- 25 separated from the empty ones using an air-blowing device. After separation, both seed lots were then counted using a commercially available counting machine. The empty husks were discarded. The filled husks were weighed on an analytical balance and the cross-sectional area of the seeds was measured using digital imaging. This procedure resulted in the set of the following seed-related parameters:

- 30 The flowers-per-panicle estimates the average number of florets per panicle on a plant, derived from the number of total seeds divided by the number of first panicles. The tallest panicle and all the panicles that overlapped with the tallest panicle when aligned vertically, were considered as first panicles and were counted manually. The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. The total seed yield (total seed weight) was measured by
- 35 weighing all filled husks harvested from a plant. Total seed number per plant was measured by counting the number of husks harvested from a plant and corresponds to the number of florets per plant. Thousand Kernel Weight (TKW) is extrapolated from the number of filled seeds counted and their total weight. Harvest index is defined as the ratio between the total seed weight and the above-ground area (mm²), multiplied by a factor 10⁶. The parameter EmerVigor is an indication of the seedling vigour. It is

calculated from the area (in mm²) covered by leafy biomass in the first imaging. The seed fill rate (fillrate) is an indication of the filling of the seeds. It is expressed as a proportion (in %) of the number of filled seeds over the number of florets (nrtotalseed).

5 These parameters were derived in an automated way from the digital images using image analysis software and were analysed statistically. Individual seed parameters (including width, length, area, weight) were measured using a custom-made device consisting of two main components, a weighing and imaging device, coupled to software for image analysis.

10 7.2 Statistical analysis: t-test and F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and to verify an overall effect of the
15 gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the mere presence or position of the gene that is causing the differences in phenotype.

20 To check for an effect of the genes within an event, i.e., for a line-specific effect, a t-test was performed within each event using data sets from the transgenic plants and the corresponding null plants. "Null plants" or "null segregants" or "nullizygotes" are the plants treated in the same way as the transgenic plant, but from which the transgene has segregated. Null plants can also be described as the homozygous negative transformed plants. The threshold for significance for the t-test is set at 10%
25 probability level. The results for some events can be above or below this threshold. This is based on the hypothesis that a gene might only have an effect in certain positions in the genome, and that the occurrence of this position-dependent effect is not uncommon. This kind of gene effect is also named herein a "line effect of the gene". The p-value was obtained by comparing the t-value to the t-distribution or alternatively, by comparing the F-value to the F-distribution. The p-value then gives the probability
30 that the null hypothesis (i.e., that there is no effect of the transgene) is correct.

Example 8: Evaluation results

8.1 NAC1 under the control of a GOS2 promoter

An increase in the following yield-related parameters was observed for transgenic plants overexpressing
35 NAC1 under the control of a GOS2 promoter. The p-value shown is from the t-test unless otherwise indicated. The percentage difference is for transgenic plants compared to nullizygotes. Although not shown in Table 8, an increase in root biomass was also observed, with the best event giving a 7% increase compared to nullizygotes.

Table 8: Results for NAC1 under the control of a GOS2 promoter

Trait	Positive events	Average difference	p value
Area max	6 events	13.70%	<0.077
		overall +11%	0 (F test)
Emergence vigour	5 events	29.60%	<0.225
		overall +16%	<0.0108 (F test)
TKW	5 events	5.40%	<0.097
		overall +3%	0 (F test)
First panicles	3 events	20.33%	<0.061
Total number seeds	2 events	16	<0.15

8.2 NAC4 under the control of a GOS2 promoter

An increase in the following yield-related parameters was observed for transgenic plants overexpressing NAC4 under the control of a GOS2 promoter. The p-value shown is from the t-test unless otherwise indicated. The percentage difference is for transgenic plants compared to nullizygotes. Although not shown in the Table 9a, an increase in seed weight was also observed, with the best event giving a 30% increase compared to nullizygotes. Table 9a shows the results obtained under non-stress conditions and Table 9b shows the results obtained under conditions of stress.

Table 9a: Results for NAC4 under the control of a GOS2 promoter

Trait	Positive events	Average difference	p value
Area max	3 events	18.33%	<0.051
		overall +9%	<0.0023 (F test)
Emergence vigor	3 events	30.67%	<0.38
Root max	2 events	10.50%	<0.088
TKW	4 events	6.50%	<0.042
		overall +4%	0 (F test)
First panicles	3 events	15.67%	<0.34
Total number seeds	3 events	13.33	<0.281
		overall +5%	<0.091 (F test)

Table 9b: Results for NAC4 under the control of a GOS2 promoter (drought screen)

Trait	Positive events	Average difference	p value
Area max	2 events	10.5 %	<0.0011
		overall +8 %	0 (F test)
Emergence vigor	3 events	42 %	<0.0007
TKW	3 events	4 %	<0.042

		overall +4.66 %	<0.0251 (F test)
First panicles	3 events	4.33 %	<0.091
		Overall + 2%	<0.00275 (F test)
Root thin	2 events	6 %	<0.0901

8.3 NAC4 under the control of an RCc3 promoter

An increase in the following yield-related parameters was observed for transgenic plants overexpressing NAC4 under the control of an RCc3 promoter. The p-value shown is from the t-test unless otherwise indicated. The percentage difference is for transgenic plants compared to nullizygotes. Although not shown in Table 10a, an increase in thousand kernel weight was also observed, with the best event giving a 4% increase compared to nullizygotes.

Table 10a: Results for NAC4 under the control of an RCc3 promoter

Trait	Positive events	Average difference	p value
Area max	2 events	13.00%	<0.0125
		overall + 4%	<0.0313 (F test)
Emergence vigour	2 events	13.50%	<0.288
		overall +7%	<0.11 (F test)
Root max	1 event	9.00%	<0.0597
		overall +4%	<0.0722 (F test)
Total seed yield	2 events	16.00%	<0.094
		overall +6%	<0.0733 (F test)
Total number seeds	2 events	14.5	<0.137

Table 10b: Results for NAC4 under the control of an RCc3 promoter (drought screen)

Trait	Positive events	Average difference	p value
Area max	2 events	8 %	<0.1077
Total seed yield	2 events	49 %	<0.018
		Overall +20%	0.002 (F test)
Number filled seeds	2 events	50.5 %	<0.0138
		Overall +20%	0.0017 (F test)
Fill rate	2 events	46.5%	<0.0418
		Overall + 16%	0.011 (F test)
Harvest Index	2 events	47%	<0.0168
		Overall +19%	0.0037
Height	2 events	6.5 %	<0.0103
Number total seeds	2 events	26 %	<0.0579

		Overall + 4%	0.1951 (F test)
Root max	2 events	6.5 %	<0.1038
Flower per panicle	2 events	17.5%	<0.1019

8.4 NAC6 under the control of an RCc3 promoter

An increase in the following yield-related parameters was observed for transgenic plants overexpressing NAC6 under the control of an RCc3 promoter. The p-value shown is from the t-test unless otherwise indicated. The percentage difference is for transgenic plants compared to nullizygotes. Although not shown in Table 11, an increase in the number of flowers per panicle was also observed, with the best event giving a 20% increase compared to nullizygotes. Furthermore, and also not shown in the table, an increase in the number of panicles was also observed, with the best event giving a 28% increase compared to nullizygotes.

Table 11: Results for NAC6 under the control of an RCc3 promoter

Trait	Positive events	Average difference	p value
Area max	2 events	17.50%	<0.0104
Emergence vigor	2 events	21.00%	<0.2385
Root max	3 events	13.33%	<0.0093
		overall + 5.00%	<0.0673 (F test)
rootshoot index	4events	64.00%	<0.1279
		overall + 37%	<0.0005 (F test)
Total seed yield	2 events	20.00%	<0.2378
Total number seeds	2 events	20%	<0.0323

8.5 NAC7 under the control of a GOS2 promoter

An increase in the following yield-related parameters was observed for transgenic plants overexpressing NAC7 under the control of a GOS2 promoter. The p-value shown is from the t-test unless otherwise indicated. The percentage difference is for transgenic plants compared to nullizygotes.

Table 12: Results for NAC7 under the control of a GOS2 promoter

Trait	Positive events	Average difference	p value
Area max	3 events	18.33%	<0.011
		overall +11%	0 (F test)
Emergence vigor	3 events	17.33%	<0.422
Root max	1 event	11.00%	<0.0249
		overall +4%	<0.0370 (F test)
Total seed yield	2 events	20.50%	<0.08

Flower per panicle	3 events	10%	<0.101
First panicles		19.00%	<0.0769
Total number seeds	2 events	15%	<0.177
		overall +5%	<0.0751 (F test)

8.6 NAC3 under the control of an RCc3 promoter

An increase in the following yield-related parameters was observed for transgenic plants overexpressing NAC3 under the control of an RCc3 promoter. The p-value shown is from the t-test unless otherwise indicated. The percentage difference is for transgenic plants compared to nullizygotes. Although not shown in Table 13, An increase in aboveground area was observed (with the best event giving a 19% increase), an increase in early vigour (with the best event giving a 20% increase), an increase in root biomass (with the best event giving a 15% increase), an increase in thousand kernel weight, an increase in harvest index (with the best event giving an increase of 26%), an increase in the number of panicles (with the best event giving an increase of 33%).

Table 13: Results for NAC3 under the control of an RCc3 promoter

Trait	Positive events	Average difference	p value
Total seed yield	2 events	29.00%	<0.00777
		overall + 6%	<0.00553 (F test)
Total number seeds	1 event	44%	<0.0001
		overall + 5%	<0.1084 (F test)

C) AP2-2 polypeptide

Example 9: Identification of sequences related to SEQ ID NO: 131 and SEQ ID NO: 132

Sequences (full length cDNA, ESTs or genomic) related to SEQ ID NO: 131 and/or protein sequences related to SEQ ID NO: 132 were identified amongst those maintained in the Entrez Nucleotides database at the National Center for Biotechnology Information (NCBI) using database sequence search tools, such as the Basic Local Alignment Tool (BLAST) (Altschul *et al.* (1990) J. Mol. Biol. 215:403-410; and Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402). The program was used to find regions of local similarity between sequences by comparing nucleic acid or polypeptide sequences to sequence databases and by calculating the statistical significance of matches. The polypeptide encoded by SEQ ID NO: 131 was used for the TBLASTN algorithm, with default settings and the filter to ignore low complexity sequences set off. The output of the analysis was viewed by pairwise comparison, and ranked according to the probability score (E-value), where the score reflects the probability that a particular alignment occurs by chance (the lower the E-value, the more significant the hit). In addition to E-values, comparisons were also scored by percentage identity. Percentage identity refers to the number of identical nucleotides (or amino acids) between the two compared nucleic acid (or

polypeptide) sequences over a particular length. In some instances, the default parameters may be adjusted to modify the stringency of the search.

Table 14 provides a list of nucleic acid and protein sequences related to the nucleic acid sequence as represented by SEQ ID NO: 131 and the protein sequence represented by SEQ ID NO: 132.

Table 14: Nucleic acid sequences encoding AP2-2 polypeptides and AP2-2 polypeptides.

Name/identifier	Source organism	Nucleic acid SEQ ID NO:	Poly-peptide SEQ ID NO:
AP2-EREBP	<i>Oryza sativa</i>	131	132
Os07g47790	<i>Oryza sativa</i>	139	140
AAX13280	<i>Triticum aestivum</i>	141	142
Os01g21120	<i>Oryza sativa</i>	143	144
Os03g08470	<i>Oryza sativa</i>	145	146
CAD56466	<i>Triticum aestivum</i>	147	148
AT2G47520.1	<i>Arabidopsis thaliana</i>	149	150
Os02g54160	<i>Oryza sativa</i>	151	152
Os09g26420	<i>Oryza sativa</i>	153	154
AAP32468	<i>Triticum aestivum</i>	155	156
AAP32467	<i>Triticum aestivum</i>	157	158
AT1G53910.1	<i>Arabidopsis thaliana</i>	159	160
AAM65746	<i>Arabidopsis thaliana</i>	161	162
AT3G14230.1	<i>Arabidopsis thaliana</i>	163	164
AT3G14230.2	<i>Arabidopsis thaliana</i>	165	166
AT3G14230.3	<i>Arabidopsis thaliana</i>	167	168
AT3G16770	<i>Arabidopsis thaliana</i>	169	170
Os07g42510	<i>Oryza sativa</i>	171	172
Os03g08490	<i>Oryza sativa</i>	173	174
Os03g08500	<i>Oryza sativa</i>	175	176
AT1G72360	<i>Arabidopsis thaliana</i>	177	178
Os03g08460	<i>Oryza sativa</i>	179	180
Os05g29810	<i>Oryza sativa</i>	181	182
Os03g22170	<i>Oryza sativa</i>	183	184
Os10g25170	<i>Oryza sativa</i>	185	186
Os09g11460	<i>Oryza sativa</i>	187	188
AAK95687	<i>Lycopersicon esculentum</i>	189	190

Os09g11480	<i>Oryza sativa</i>	191	192
AAQ91334	<i>Lycopersicon esculentum</i>	193	194
AAR87866	<i>Lycopersicon esculentum</i>	195	196
AT1G80580	<i>Arabidopsis thaliana</i>	197	198
AAP40022	<i>Nicotiana tabacum</i>	199	200
CAE54591	<i>Fagus sylvatica</i>	201	202
CAD21849	<i>Fagus sylvatica</i>	203	204
ABD65407	<i>Capsicum annuum</i>	205	206
AAP72289	<i>Capsicum annuum</i>	207	208
AAS20427	<i>Capsicum annuum</i>	209	210
AAX07458	<i>Gossypium hirsutum</i>	211	212
AAT77192	<i>Gossypium barbadense</i>	213	214
AAX20013	<i>Gossypium hirsutum</i>	215	216
AAX68526	<i>Gossypium hirsutum</i>	217	218
AAX68525	<i>Gossypium hirsutum</i>	219	220
AAT77191	<i>Gossypium barbadense</i>	221	222
AAV51937	<i>Gossypium hirsutum</i>	223	224
AAV85777	<i>Gossypium hirsutum</i>	225	226
AAX07460	<i>Gossypium hirsutum</i>	227	228
AAX84670	<i>Manihot esculenta</i>	229	230
AAW33881	<i>Populus alba</i> x <i>Populus tremula</i>	231	232
BAE71206	<i>Trifolium pratense</i>	233	234
AAQ10777	<i>Glycine max</i>	235	236
AAL67489	<i>Narcissus pseudonarcissus</i>	237	238
CAA05084	<i>Arabidopsis thaliana</i>	239	240
ABE84970	<i>Medicago truncatula</i>	241	242
ABE80536	<i>Medicago truncatula</i>	243	244
AAC29516	<i>Solanum tuberosum</i>	245	246
BAC56862	<i>Solanum tuberosum</i>	247	248
AAS01337	<i>Coffea canephora</i>	249	250
AAZ14085	<i>Hordeum vulgare</i>	251	252
BAD01556	<i>Cucumis melo</i>	253	254
BAF43419	<i>Malus</i> x <i>domestica</i>	255	256

Example 10: Alignment of AP2-2 polypeptide sequences

Alignment of polypeptide sequences was performed using the AlignX programme from the Vector NTI (Invitrogen) which is based on the popular Clustal algorithm of progressive alignment (Thompson *et al.* (1997) Nucleic Acids Res 25:4876-4882; Chenna *et al.* (2003). Nucleic Acids Res 31:3497-3500). Default values are for the gap open penalty of 10, for the gap extension penalty of 0,1 and the selected weight matrix is Blosom 62 (if polypeptides are aligned). Results in Figure 7 show that AP2-2 polypeptides share regions of high sequence conservation. Motifs XII to XVII are underlined for Os06g09390 (SEQ ID NO: 132).

Example 11: Calculation of global percentage identity between polypeptide sequences useful in performing the methods of the invention

Global percentages of similarity and identity between full length polypeptide sequences useful in performing the methods of the invention were determined using one of the methods available in the art, the MatGAT (Matrix Global Alignment Tool) software (BMC Bioinformatics. 2003 4:29. MatGAT: an application that generates similarity/identity matrices using protein or DNA sequences. Campanella JJ, Bitincka L, Smalley J; software hosted by Ledion Bitincka). MatGAT software generates similarity/identity matrices for DNA or protein sequences without needing pre-alignment of the data. The program performs a series of pair-wise alignments using the Myers and Miller global alignment algorithm (with a gap opening penalty of 12, and a gap extension penalty of 2), calculates similarity and identity using for example Blosom 62 (for polypeptides), and then places the results in a distance matrix. Sequence similarity is shown in the bottom half of the dividing line and sequence identity is shown in the top half of the diagonal dividing line.

Parameters used in the comparison were:

Scoring matrix: Blosom62

First Gap: 12

Extending gap: 2

Results of the software analysis are shown in Table 15 for the global similarity and identity over the full length of the polypeptide sequences (excluding the partial polypeptide sequences). Percentage identity is given above the diagonal and percentage similarity is given below the diagonal.

The percentage identity between the full length polypeptide sequences useful in performing the methods of the invention can be as low as 20 % amino acid identity compared to SEQ ID NO: 132. The sequence identity will be higher when specific domains, such as the AP2 domain are compared.

Table 15: MatGAT results for global similarity and identity over the full length of the polypeptide sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1. SEQID 132		27.7	63.3	29.8	38.3	62.4	24	59.5	40.8	61.1	58.2	37.2	37.2	37.1	37
2. SEQID 140	37.8		27.2	43.9	29.7	26.6	36.4	27.5	26.5	26.2	25.7	29.1	29.1	27.4	27.7
3. SEQID 142	76.5	35.8		29.9	33.1	90.8	24.5	55.9	39	94.6	88.5	35.9	35.9	36.7	37.3
4. SEQID 144	37.6	55.6	35.5		31.1	30.3	41.1	27.6	25	28.7	29.2	27.7	27.9	27.2	27.5
5. SEQID 146	50.6	37.7	48.2	39.5		32	24.9	36.1	33.2	30.7	30.2	34.3	34.3	32.1	32.4
6. SEQID 148	74.9	35.2	94.4	35.2	47		25.2	56.5	38.6	87.4	88	36.2	36.2	37.6	37.9
7. SEQID 150	31.8	48.1	32.1	52.7	34.1	32.1		23.6	22.2	23.9	24.7	26.3	26.3	24.8	25.3
8. SEQID 152	74.8	35.1	69.9	34.2	47.1	69	31.2		42.7	53.5	53.6	39.9	39.9	36.1	36.3
9. SEQID 154	54	33.6	51.5	32.6	45.7	51	28	56.1		37.3	36.1	36.8	36.8	35	35.3
10. SEQID 156	73.2	33.8	96.1	34.6	46.5	91.3	31.5	67.1	50		85.1	34.8	35.1	35.9	36.3
11. SEQID 158	70.7	34.6	89.9	36.1	45.8	90	34	66.6	48	86.8		32.5	32.5	34	34.4
12. SEQID 160	53.3	38.5	54.2	35.8	48	52.5	33	53.7	50	53.6	49.2		99.4	62.2	62.8
13. SEQID 162	53.3	38.5	54.2	35.8	48	52.5	33	53.7	50	53.6	49.2	100		62.2	62.8
14. SEQID 164	56.7	34.3	54.4	33.5	47.2	54.6	29.6	55.4	49.7	54.1	50.1	70.7	71		98.9
15. SEQID 166	57.1	34.7	54.7	33.9	47.7	54.9	30.4	55.7	49.7	54.7	50.7	71.7	72	98.9	
16. SEQID 168	57.2	34.8	54.8	34	47.9	55.1	30.2	55.6	51	54.8	50.8	71.9	72.2	98.7	99.7
17. SEQID 170	41.2	47.2	38.9	46.4	41.3	38.4	46.8	38.6	36.9	37.5	38.3	40.8	40.8	39.6	40
18. SEQID 172	51.9	34.8	52.1	38.9	52	54.4	32.2	50.4	43.9	49.9	52.9	46.6	46.6	44.3	43.7
19. SEQID 174	46.4	34.9	43.4	40.8	51.2	46.7	31.5	48.2	40.9	42.8	44	43.3	43.6	42.2	42.7
20. SEQID 176	50	38.6	49.6	40.1	52.7	49	32.8	48.2	44.7	47.6	45.5	48	48	44.6	45.1
21. SEQID 178	41.7	46.9	44.5	47.7	47	45	44.3	42.5	39.6	42.5	44.6	45	45.3	39.6	40.3
22. SEQID 180	47.5	36.5	40.8	35.9	44.9	42.1	32.8	44.1	38.1	39.4	42.8	46.6	46.6	42.7	42.4
23. SEQID 182	32.3	50	32.7	50.7	36.8	33.2	47	32.1	31.1	31.5	32.2	31.8	31.8	32.5	32.8
24. SEQID 184	39	55.1	37.2	53.5	43.1	39.8	44.9	37.3	36.9	36.6	39.8	36.3	36.3	34.3	34.7
25. SEQID 186	40.6	35.7	42	41.3	50.6	42.1	32	44.4	42.7	42.5	40.7	39.7	39.7	40.1	39.5
26. SEQID 188	31.8	37.9	34.1	41.4	39.2	33.8	38.4	32.1	33.1	33	35.8	34.1	34.1	33	33.6
27. SEQID 190	60.2	34.1	59.1	36.8	48.1	59.4	33.6	58.9	54.3	57.5	54.6	59.7	59.7	60.7	61.3
28. SEQID 192	39.5	41.2	38	42	38.6	39.8	38	38.9	37.4	36.9	39.5	39.4	39.4	38	39.5
29. SEQID 194	53.9	37	54.6	38.2	47.9	55.3	34.9	50.1	46.7	53.2	53.6	57.5	57.5	58.3	57.6
30. SEQID 196	44.2	48.8	44.5	51.2	41.3	43.8	49.2	40.5	37.6	41.4	41.9	39.1	39.1	41.2	40
31. SEQID 198	29.6	35.5	33.5	34	33.2	32.7	32	32.3	29.5	34.1	35.2	33.8	33.8	31.1	31.5
32. SEQID 200	56.6	32.8	55.6	37	49.9	55.3	33.3	56.1	52.3	54	51.4	61.5	61.5	62.8	62.8
33. SEQID 202	56.6	34.9	57.4	37.6	49.7	57.9	31	60.8	56.8	55.3	53.4	63.8	64	64.1	64.3
34. SEQID 204	56.5	34.1	57.6	37.6	49.3	57.6	30.7	60.5	55.1	56.3	53.3	62.7	62.9	62.8	63.5
35. SEQID 206	60	34.1	57.9	36.5	50.4	58.9	32.5	57.6	52.5	56.5	53.3	59.5	59.5	59.6	60.3

36. SEQID 208	59.1	32.8	56.6	35.2	49.3	57.7	32	56.6	51.3	55.3	52	58.5	58.5	58.6	59.2
37. SEQID 210	44.2	48.5	43.4	52.3	42.8	43.3	45.8	42.7	39.6	40.8	42.5	43.6	43.6	41.7	41.3
38. SEQID 212	55.4	34.9	51.8	34.6	50	53.3	33.1	57.4	57.6	50	47.7	64.6	64.9	65.6	65.4
39. SEQID 214	50.3	37	49.6	38.6	46.1	51.3	37	48.8	44.9	47.3	52.1	54.2	54.5	53.6	54.1
40. SEQID 216	53.5	30.8	50.8	34.1	49	51.8	33.1	52.8	55.6	49.2	48.2	59.8	60.1	59.8	59.6
41. SEQID 218	39	43.3	40	45.6	41.6	37.2	42.1	40	37.9	37.7	41	39.9	39.7	39.3	38.4
42. SEQID 220	38.7	45.3	42	47.3	42.5	40.4	46.5	37.5	40.7	37.2	40.4	40.5	40.5	40.4	40
43. SEQID 222	32.6	47.7	32.7	49.3	35.3	33	51.5	32.9	31.3	30.4	31.3	33.2	33.2	33.5	34.7
44. SEQID 224	39.2	45.9	40.8	45.1	40.4	39.5	45.9	38.9	39.4	39.4	37.7	41.1	41.1	38.8	38.9
45. SEQID 228	40.6	43.5	39.4	45.4	41.9	40.1	42.4	40.8	38.9	37.5	39.8	39.1	39.1	39.8	40.5
46. SEQID 230	58	34.1	53.5	38.1	48	57	32	59.3	59.3	51.7	53.5	64.8	64.8	64.6	64.6
47. SEQID 232	56.6	33.9	51.3	36.1	47.4	51.6	31.8	56.1	53.8	52.1	49.2	60.3	60	61.3	61.1
48. SEQID 234	56.9	35.1	52.7	35.3	48.1	53.2	31.7	53.8	54.5	50.9	50.6	57.4	57.4	61	61.3
49. SEQID 236	55.7	35.2	52.9	35.4	45.8	53.1	33.3	57	56.8	49.7	50.8	55.7	56	59.4	59.1
50. SEQID 240	40.6	46.3	42.5	47.2	40.4	41.3	46.3	39.5	36.9	39.4	41.3	39.7	39.7	39.8	40.3
51. SEQID 242	42.5	40.7	44.8	43.9	40.7	44.7	43	42.2	37.6	43.1	43.4	44.1	44.1	43	43.7
52. SEQID 244	33.4	40.8	29.6	38.3	32.9	32.1	41.7	32.9	27.8	28.7	31.9	35.2	35.5	32.5	32.8
53. SEQID 246	46.1	42.6	41.4	47.3	42.8	41.3	41.6	41.6	39.4	41.7	40.4	41.6	41.1	40.6	40.8
54. SEQID 248	42.3	46.6	40.6	45.1	42.2	40.7	43.6	37.8	37.9	39.2	39.8	42.2	42.2	41.2	41.1
55. SEQID 250	43.4	40.1	44.8	43.2	48.5	45.6	37.7	45.5	42.7	43.7	44.3	43	43	42.5	42.9
56. SEQID 252	46.7	38.4	47.3	39.6	60.5	47.9	34.1	47.9	42.4	45.9	48.5	44.7	45.8	42.5	42.9
57. SEQID 254	43.4	49.5	44.2	51.6	44.9	43.8	46.2	40.5	40.2	42.5	44	43	43	40.1	40
58. SEQID 256	36.2	44.8	38.3	45.6	40.4	39.5	45.2	36.4	36.6	36.3	38.9	38.3	38.3	38	38.7

	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1. SEQID 132	37.6	29.6	38.3	30.1	34	26.5	29.6	26	27.2	27.9	23.7	41.4	27.7	38.4	32.2
2. SEQID 140	27.8	34.1	28.7	27.7	27.6	34.1	26.1	40.3	45.8	28.5	26.6	26.9	32.5	28.7	36.7
3. SEQID 142	37.4	28.5	35.2	30.7	32.4	29.1	26.6	25.8	28.2	27.8	23.5	40.1	25.3	36.7	32.8
4. SEQID 144	27.5	35.9	30.6	32	31.3	33	29.8	41.6	39.3	31.4	28.8	29.4	30.2	31.2	43.5
5. SEQID 146	32.5	29.3	36.3	35.7	37.5	29.5	30.2	27.5	30.3	35.9	27.6	35.4	29.7	35.4	30.3
6. SEQID 148	38	28.4	36.9	31.6	32	30.3	26.9	26.9	28.7	29.3	23.5	40.9	26.5	38	33.3
7. SEQID 150	25.7	33.3	25.1	24	24.6	31.7	21.8	36.7	31	24.2	26.9	28	28	25.4	38.1
8. SEQID 152	36.4	28.3	37.2	32	31.6	30.1	27.9	25.8	28.6	32.2	23.4	42	28.7	37.5	31.1
9. SEQID-154	35.7	25.3	31.7	30.1	31	26.2	23.8	24.7	28.8	28.1	23.6	37.8	26.2	33.6	27.5
10. SEQID 156	36.4	27.3	33.2	30.2	31.4	27.7	24.6	24.7	24.5	26.2	22.4	39	24.2	35.3	30.5
11. SEQID 158	34.5	28	33.7	29.3	28.3	29.1	25.3	25.8	27.8	26.6	23.6	37.1	25.9	34.9	30.1

12. SEQID 160	63	28.5	32.4	28	30.2	31.3	27.3	24.9	25.7	27.2	24.9	43.4	29.1	42.9	28.9
13. SEQID 162	63	28.5	32.4	28.2	30.2	31	27.3	24.9	25.7	27.2	24.7	43.7	29.1	42.9	28.9
14. SEQID 164	98.7	29.3	32.6	27.9	29.9	27.7	26.1	24.5	26.3	27.1	24.1	42.5	27.9	44	29.1
15. SEQID 166	99.7	29.6	31.9	28.2	30.2	28.3	26.4	24.8	26.6	27.9	24.9	42.9	29.6	43.9	28.3
16. SEQID 168		29.7	31.9	28.3	30.3	28.1	26.7	24.9	26.7	28.5	23.9	43	29.4	44.8	29.5
17. SEQID 170	40.1		30.7	29.6	29.3	31.6	24.8	36.1	35.6	28.5	26.5	28.9	30.4	31.6	34.9
18. SEQID 172	43.6	40.6		31.4	32.6	30.1	28.3	28.8	28.5	32.5	24.4	33.8	26.4	32.5	28.1
19. SEQID 174	42.8	42.7	46.2		47.1	30.5	30.9	30.5	28.9	35.3	24.5	29.3	28.8	27.4	28.7
20. SEQID 176	45.2	41.3	50.3	59.3		28.9	30.3	27.9	29.2	34.3	24.6	29.8	28.5	29.9	29.7
21. SEQID 178	40.1	45	45.6	44.5	45.9		27	30.2	28.6	26.1	27.9	31.4	28.4	31.2	33.7
22. SEQID 180	42.8	38	42.1	47.2	47.1	41.4		25.8	25	26.5	26.1	28	27.5	30	24.7
23. SEQID 182	32.9	46.8	39.2	38	37.7	42.7	35		37.4	27.6	28.6	23.9	33.5	26.6	31.3
24. SEQID 184	34.5	48.8	38.6	40.5	38.6	43.1	37.1	44.4		30.6	27.2	24.6	30.6	28.3	35.4
25. SEQID 186	39.6	40.7	45	51.2	50.2	39.8	38	33.9	37.9		26.9	29.2	28.5	27.3	26.6
26. SEQID 188	33.7	44	33	37.4	36.8	41.6	35.3	37.9	39.5	39.8		23.3	41.3	25.7	25.2
27. SEQID 190	61.5	39.2	49.7	44.9	45.2	46.2	45.4	32.5	34.7	43	33.9		27.1	52.8	32.8
28. SEQID 192	39.6	43.2	37.1	39.9	39.8	47.7	41.4	40.8	43.6	37.6	56.4	37.4		29.5	26.5
29. SEQID 194	59.1	42.2	45.3	47.1	46.5	45.3	45	36.4	38.8	43.1	37	66.9	41.9		31
30. SEQID 196	41.4	51.2	39.8	41.4	42.2	53.1	39.6	41.5	50.8	38.2	42.7	45.4	44.6	43.4	
31. SEQID 198	31.6	43.8	33.9	35.2	30.4	42	34	36.3	40.6	33.5	39.5	34.4	41	32.1	41.5
32. SEQID 200	62	40.8	47.8	41.3	44.4	44.2	45	32.6	32.6	40.3	33.9	80.4	37.5	73.9	42.4
33. SEQID 202	64.3	38.4	47.9	45.8	47.9	44.7	46.6	32.5	36.8	41.3	35.2	71.7	35.2	62.2	44.7
34. SEQID 204	63.5	38.1	48.3	45.6	47.5	43.5	45.9	31.7	36	41.1	33.6	71.7	35.7	61.3	45.1
35. SEQID 206	60.3	41.9	50.7	44	46.4	45.1	44.8	33.9	36	39.7	36.3	90.7	38.4	66.7	46.1
36. SEQID 208	59.4	41.7	49.6	43.9	47.4	45.5	46.1	34.4	36.3	40.1	36.6	89.2	38.8	67.8	46.1
37. SEQID 210	42.2	55.7	43	43.6	43.2	50.8	40.5	41.3	51.1	37.9	40.5	45.7	46.2	43.4	81.4
38. SEQID 212	65.9	40.3	47.4	43.1	45.9	43.6	43.1	33.3	33.8	41.3	33.3	67.2	35.4	57.4	44.4
39. SEQID 214	54.3	40.8	44.7	43.9	44.1	47.6	41.1	34.5	37	41.9	32.9	58.9	36.7	53.5	48.6
40. SEQID 216	59.8	35.6	49.2	43.4	45.7	42.7	42.2	30.3	32.6	39.9	33.1	63.9	35.9	55.1	41.4
41. SEQID 218	38.2	62.5	39.2	39.9	41.6	50.8	44.5	44.4	40.6	37.9	41.8	40.1	42.5	44.3	50.6
42. SEQID 220	40.6	59.4	38	38.6	40.1	48.1	40.5	47.3	45.3	38.5	44.1	38.4	43	43.4	50.8
43. SEQID 222	34.5	50.8	32.5	30.8	35	42.7	35.9	51	40.7	34.5	44.4	32.5	41.2	38.5	41.9
44. SEQID 224	38.8	60.4	38	39.6	40.4	47.3	41.4	45.9	45.9	38.2	42	38.2	43.9	42.5	50
45. SEQID 228	40.4	62.6	40.1	39.6	41.3	50.4	42.3	44.3	42	39.8	43.5	41.1	42.7	45	51.1
46. SEQID 230	64.3	39.9	50.4	45.1	46.5	45.9	44.4	33.3	34.9	42	36	69.3	36.2	61.2	43.6
47. SEQID 232	61.8	39.2	46.3	40.8	43.4	43.7	43.4	31.3	35.8	38.4	32.6	67.4	36.8	56.8	42.1

48. SEQID 234	61.3	39	43.9	42.3	47	44.2	47.3	32.5	36.1	39	33	63.4	37.7	54.3	42.3
49. SEQID 236	59.4	39.6	45.6	44.5	46.9	43.2	41.9	33.3	37	39.1	33.6	63.5	35.4	53.1	41.9
50. SEQID 240	40.4	94.4	39.8	40.2	42.9	44.7	40.5	45.9	50	37.6	43.1	41.1	42	43.4	51.9
51. SEQID 242	43.6	47.2	43.6	42.1	41.3	44.9	43.3	37.4	42.3	37.9	34.1	48.4	39	48.3	58
52. SEQID 244	31.8	47.6	29.5	33.3	33.1	45	33.1	35.4	39.1	32.3	42.9	33.6	39.6	36.4	41.2
53. SEQID-246	41.2	46	41.8	41.7	41.9	47.7	44.5	35.2	43.6	37.6	37.6	48.4	41.6	45	81.2
54. SEQID 248	40.4	62.1	43	39.6	42.2	51.1	43.6	46.2	47	41.3	42.4	41.9	47	47.1	53.8
55. SEQID 250	43	45.9	47.4	45.3	45	42.6	44.4	37.7	43.8	44.7	35.6	50.5	40.4	48	55.3
56. SEQID 252	43.9	40.9	47.7	45.4	51.4	46	43.9	36.6	40.2	45.7	35.4	46.8	39.9	46.6	41.8
57. SEQID 154	40.4	55.7	41.8	44.2	43.2	52	41.1	41	46.9	38.2	38.5	45.2	42.9	42.8	63.7
58. SEQID-156	39.3	58.3	37.4	38.6	41.3	46.2	40.8	44	46	40.4	40.9	36.8	42.5	42.8	50

	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
1. SEQID 132	20.3	41.3	41.2	41	40.3	39.4	31.4	42	34.5	38.4	26.8	29.5	24.2	28.2	27
2. SEQID 140	24	25.8	27	26.4	25.1	26.3	36.6	26.9	26.8	25.5	33.1	33.3	35.4	33.1	33.7
3. SEQID 142	21.5	40.3	41.2	40.5	38.7	37	29.9	38.4	34.3	35.7	26.3	28	24	27.9	26.2
4. SEQID 144	24.1	30.1	30.4	30.2	28.9	28.5	42.8	27.8	29.4	27.3	34.2	37.5	33.9	37	34.8
5. SEQID 146	21.5	36.8	34.5	33.8	36.9	36.2	29.7	35	29.4	34.9	29.3	29.1	25.1	28.3	27.8
6. SEQID 148	21.2	41.3	43.1	42	40.6	38.9	31.2	39.9	35.6	37.2	27.4	27.8	24.4	27.7	27.2
7. SEQID 150	23	26.9	26.1	25.8	26.7	26.3	39.4	25.6	26.3	25.3	33.7	34.8	35.8	34.8	32.8
8. SEQID 152	21	41.1	43	43	41.1	40.1	29.8	43.2	35.9	39.7	27	29.1	25.2	28	27.2
9. SEQID 154	20.8	37.1	40	38.7	35.9	35.5	28.3	38.8	30.8	38.1	27.2	29.4	23.5	27.9	26.7
10. SEQID156	21.3	39.5	39.9	39.5	38.5	36.8	28	36.9	32.5	34.6	25.8	26.2	22.6	27.6	25.1
11. SEQID 158	23.7	38.1	40	38.8	36.8	35.1	29.6	35.4	35.7	34.2	25.7	26.8	22.7	26.5	26.5
12. SEQID 160	23.2	47.2	48.8	47.9	44.3	43.6	32.2	52.1	39.1	46.6	28.4	30.7	25.4	30.1	28.4
13. SEQID 162	23.2	46.9	48.8	47.6	44.1	43.3	32.2	52.1	39.1	46.6	28.4	30.9	25.4	30.4	28.4
14. SEQID 164	21.8	45.8	47	45.3	43.9	43.9	29.8	50.9	38.2	45.8	28.5	30.3	24.8	30	29
15. SEQID166	21.5	46	47.3	45.5	43.8	43.8	30.1	51.1	38.8	46	28	30.1	24.3	29.8	28.3
16. SEQID 168	21.3	45.9	47.6	45.9	44.4	44.4	30.2	52.5	39.2	46.6	28.3	31	24.3	29.9	28.3
17. SEQID 170	24.5	30.8	28.1	28.3	30.8	30.2	36.9	28.5	27.3	26.1	45	44.1	39.2	44.3	45.2
18. SEQID172	21.6	34.3	32.2	32.2	34	33.2	28.9	34.3	28.8	36.2	27	28.4	25.6	25.4	27.5
19. SEQID 174	23.5	26.9	30.2	29.9	28.3	27.8	28.4	28	24.9	27.8	25	25.9	22	27.9	24.9
20. SEQID 176	19	30.4	31.2	31.3	29.7	29.8	28.5	30.1	25.9	30.3	25.2	26.7	23.1	28	25.8
21. SEQID178	23.9	32.5	33.2	33.2	31.4	31.9	32.7	32	31.5	31.5	33.9	31	28.6	31.4	33.1
22. SEQID 180	20.5	27.9	29.8	29.2	27.6	28.3	24.8	27.3	22.1	25.2	27.2	26.4	23	26.1	25.8
23. SEQID 182	24.2	24	24.3	24.5	24.8	25.1	32	24.4	24.5	23.7	35.2	37.5	33.2	37.4	35.5

24. SEQID 184	24.9	24.5	27.1	26.5	24.9	25.6	36	25.4	25.4	24.4	29.6	30.5	26.8	31	29.4
25. SEQID 186	23.1	27.6	28	27.7	27.3	26.2	25.2	28.5	24.2	27.9	25.8	24.8	23.1	25.5	25.5
26. SEQID 188	23.8	24.7	23.3	22	24.9	25.3	25.1	24.3	20.9	23.6	28.2	27.8	26.9	25.6	27
27. SEQID 190	21	69.5	54.9	54.5	84.3	82.1	33.6	51.3	44.6	49.5	28.7	27.6	23.9	28.2	29
28. SEQID 192	26.7	26.7	25.2	25.2	26.5	27.2	27.1	26.1	23.5	27	27.4	29.1	27.9	28.4	27
29. SEQID 194	21.3	68.5	48.7	48.3	54.5	55.4	31.7	44.9	35.9	44.2	30.4	31.6	28.4	31.3	30.7
30. SEQID 196	21.9	32.3	32.5	32.7	35.2	34	72.7	32.3	34.2	28.9	32.3	33.9	28.7	33	32.9
31. SEQID 198		20.9	18.9	18.8	20.2	20.5	23	22.1	21	20.9	24.3	24.4	26.5	24.9	25.3
32. SEQID 200	31.5		59.9	59.5	69.4	67.4	32.3	55.1	45.4	52.9	28.1	28.8	23.5	28.5	27.3
33. SEQID 202	30.7	72.9		96.3	56.1	55.1	33.2	66.1	54	58.6	30.5	28.5	24.1	28.9	30.7
34. SEQID204	30.7	71.8	97.1		55.8	54.7	33.5	65.1	53	57.1	29.7	28.9	24.3	27.7	30.4
35. SEQID 206	32	81.1	72.2	72		97.3	34.4	53.5	45.8	49.5	28.8	28.9	25.3	27.2	28.8
36. SEQID-208	32.8	79.1	70.6	70.4	97.9		33.5	52.5	44.7	48	28.4	28.1	24.7	27.1	28.4
37. SEQID 210	43.6	43.2	43.7	43.2	45.9	46.6		32.1	32	30.6	35.8	36.5	32.5	32.4	36
38. SEQID 212	31.8	69	79.7	78.7	68.7	67.4	42.8		75.1	69.5	27.9	29	25.4	29.2	29.5
39. SEQID 214	33.5	56.1	66.9	66.1	58.7	58.3	46.4	77.7		52.9	25.4	26.9	23.4	25.9	26.7
40. SEQID 216	32.3	64.9	72.5	70.7	63.9	61.6	40.9	83.1	64.4		27	29.5	24	29.2	27.5
41. SEQID 218	43.7	42.6	41.3	40	40.5	39.3	51.1	40.3	40.1	37.6		62.8	65.8	61.9	95.8
42. SEQID 220	41.8	40.6	37.8	38.1	41.1	39	54.5	36.9	39.2	36.4	74.3		47.3	94.1	64.2
43. SEQID 222	38.7	35.1	33.1	33.3	33.1	33.3	44.3	34.1	33.2	32.8	69	54.3		46.5	68.8
44. SEQID 224	40.6	40.3	39.4	38.1	36.8	37.4	49.2	37.9	38.9	36.9	72.8	96.9	54.1		62.4
45. SEQID 228	42.4	43.2	42.9	41.9	40.3	38.8	52.3	41.8	41.1	38.6	97.3	74.8	70.2	73.3	
46. SEQID 230	31.5	72.1	79.5	76.9	70.1	68	44.4	77.7	65.1	70.5	39.6	39.1	34.4	36.5	40.9
47. SEQID 232	30.5	68.2	74.5	72.9	68.2	66.3	42.4	74.1	62.6	65.4	38.4	40.5	31.6	38.9	40.5
48. SEQID 234	28.8	65.6	68.3	66.5	63.4	61.3	43.9	65.9	54.5	64.4	39.7	41.6	33	38.7	39.7
49. SEQID 236	28.6	63.8	69.8	67.2	65.4	63.5	44.5	70.3	57.8	64.6	40.4	40.1	34.4	39.6	41.9
50. SEQID 240	42.6	39.5	38.4	38.7	42.4	42.3	54.5	37.2	40.4	36.4	61.3	58.2	52	60.8	63.4
51. SEQID 242	36.1	47.3	45.5	45.3	46.7	46.6	59	46.9	46.7	43.4	45.6	45.9	37	45.2	45.6
52. SEQID 244	40.2	32.6	31	31.2	33.9	33.9	42.8	31.5	35.1	31.1	42.9	43.8	40.8	42.4	40.8
53. SEQID 246	39.3	42.9	44.4	44.5	47.5	47.4	75.5	46.7	51.4	42.9	43.3	47	37.9	46.3	45
54. SEQID248	40.2	42.9	40.2	39.5	41.3	40.7	55.3	40.3	44.2	37.4	56.1	62.1	49.2	61.4	58
55. SEQID 250	34.3	46.8	45.2	46.9	46.9	46.3	55.6	46.7	47.4	43.4	43.2	43.8	34	41.9	42.6
56. SEQID 252	36	43.7	45.8	43.2	45.1	45	40.9	41.5	43	43.4	38.7	39	29.9	39.9	36.6
57. SEQID254	39.9	42.9	45.5	45.1	46.1	45.5	64.1	44.4	47	43.2	48	49.1	38.5	48	48.7
58. SEQID 256	41.8	39.3	41.3	41.3	37.3	37.4	51.9	40	39.8	38.1	62.5	66	50.4	67.5	61.1

	46	47	48	49	50	51	52	53	54	55	56	57	58
1. SEQID 132	41	41.4	40.8	41.6	28.6	29.8	21.5	33.4	27.9	32.1	33.3	31.5	26.6
2. SEQID 140	28.1	27.1	26.8	27	36.4	31.3	26.8	31.8	36.4	31.1	28.4	37.8	33.2
3. SEQID 142	38.8	38.3	38.6	36.2	30.3	30.5	20.2	27.2	29	30.2	31.3	32.4	26.8
4. SEQID 144	31.3	28.4	29.2	31.1	35.1	33.7	23.5	37.8	34.6	35	30.5	43.8	36.2
5. SEQID 146	34.8	34.4	35.8	34.5	27.8	30.4	21.5	28.1	28.1	31.9	49.7	31.5	29.6
6. SEQID 148	43.4	39.7	39.8	37.9	29.5	32.2	21.5	29.4	28.9	30.3	31	34.5	26.7
7. SEQID 150	26.2	25	24.9	25.3	33.2	33.7	29.1	34.1	35.1	31	25.5	37.7	35.7
8. SEQID 152	45.3	42.4	40.8	39.5	28.3	30.4	22.1	28.6	28.1	30.7	35.7	31	25.4
9. SEQID 154	43.1	37.4	36.8	39.7	26	27.8	19.8	27.1	27.3	30.6	30.2	28.7	27.8
10. SEQID 156	39.2	37.9	37.5	34.5	28.7	27.7	19.9	27.4	27	29.1	28.8	30.8	26.8
11. SEQID 158	40.9	37	38.6	37	29.5	29.8	21.1	27	27.4	29.2	31	32.9	26.5
12. SEQID 160	49.3	46.3	44.8	44.4	28.3	30.8	24.1	29.9	29.7	29.3	31.1	32.2	27
13. SEQID 162	49.3	46	45.1	44.4	28.3	30.8	24.4	29.1	30	29.3	31.6	32.5	27
14. SEQID 164	46.6	42.3	43.2	42.6	29.7	31	22.6	28.3	29.2	29.9	30.6	29.8	28.8
15. SEQID 166	47.1	42.7	43.6	42.8	30.1	31.8	21.8	28.8	29.3	30.2	30.8	29.6	28.8
16. SEQID 168	46.7	42.7	44	43.1	30.1	31.4	21.7	28.6	28.8	30.3	31.9	30.2	28.6
17. SEQID 170	30.2	29.1	29.1	28.4	90.8	32.5	29	34.3	41.2	31.4	27.5	35.4	42.8
18. SEQID 172	34.9	31.7	31.5	33.5	29.8	28.7	19.5	26.9	29.7	31.5	36	30.1	27.9
19. SEQID 174	31.1	28	28	30.8	29	28.3	21.1	26.9	29.4	28.8	32.4	25.5	28.6
20. SEQID 176	31.6	29.9	32.2	33	28.7	26.5	22.5	28	25.5	27.1	35.9	30.8	27.7
21. SEQID 178	35.5	33.3	31.4	32.2	31.2	28.9	26.6	30.1	31.4	29.3	30	35	30.6
22. SEQID 180	28.2	26.4	29.6	29	26.7	27.1	19.6	24.1	25.7	24.1	27.4	26.8	27.5
23. SEQID 182	24.1	24.5	25.7	26.8	36.2	28.9	23.6	27	33	28	27.7	33.3	35.2
24. SEQID 184	27.4	25.7	25.6	26.2	34.9	31.8	23.7	32.8	33.6	30.6	29.8	34.2	33
25. SEQID 186	30	28.3	27	29	28.2	25.4	22.6	25.6	25.8	28	32.4	26.9	28.3
26. SEQID 188	23.6	21.3	22.1	24.8	27.5	23.1	27.9	23	29.1	23.2	25.8	23.4	28.3
27. SEQID 190	52	49.7	46.2	45.1	28.6	37.1	22.2	32.2	28.9	36.1	32.2	35.1	27.2
28. SEQID 192	27.5	26.1	27.8	26.9	29.1	26.4	24.7	24.6	30.4	24.9	28.7	27.4	29.2
29. SEQID 194	46.2	45.3	41.8	40.1	31.5	32.8	26.6	31.3	33.2	30.9	32.6	31.4	30.7
30. SEQID 196	34.1	31.4	31	30.9	37.3	44.6	26.2	77.7	33.2	46.2	28.8	51.1	34.9
31. SEQID 198	18.9	19.2	19.9	19.9	23.7	20	24.9	21.4	22.5	23.7	22.8	22.1	25.1
32. SEQID 200	57.4	55.4	48.4	46.9	30.1	35.5	22.1	32.4	31.5	34.5	32	34.5	29.7
33. SEQID 202	67.1	59.2	53.5	54.4	28.6	33.8	20.4	31.5	30.3	33.2	31.1	35	31
34. SEQID 204	66	58	51.1	52.5	28.8	31.1	20.3	31.2	28.6	34	30.5	34.6	31
35. SEQID 206	51.8	49	45.6	45.3	30.2	34.7	22.3	33.5	29.5	34.5	30.7	36.8	28.3

36. SEQID 208	50.3	47.8	44.2	44.2	29.6	34.8	22.4	32.7	28.9	33.4	30.6	36	28.7
37. SEQID 210	33.6	31.4	33.9	34	38.2	44.3	26.8	67.9	37.6	46.3	29.5	48.6	33.9
38. SEQID 212	63.7	57	49.9	52.2	28	34	22.3	31.6	28.4	33.8	31.2	34.3	29.6
39. SEQID 214	50.8	48.2	40.3	43.5	26.1	32.4	20.4	30.6	28.4	31	25.6	34	25.4
40. SEQID 216	57.9	53.2	49.5	48.5	27.3	32.3	19.9	29.9	27.7	31.8	31.6	31	27.4
41. SEQID 218	28.6	26.6	28.8	30.1	44.4	31.5	26.3	29.1	44.6	29.4	25.3	32.2	50
42. SEQID 220	30.4	30.2	30.1	31.2	45.8	32.3	25	31.5	48	30.6	27.9	32.4	52.1
43. SEQID 222	26.5	24.5	24.9	25.6	37.7	26.9	28.8	25.3	37.5	25.6	21	27.1	41.8
44. SEQID 224	28.1	29.1	29.3	29.6	44.5	31.1	24.7	29.9	46.9	29.5	27.5	30.5	51.3
45. SEQID 228	29.4	27.6	29.3	30.7	45.3	31	24.8	29.7	45	30.3	24.9	31.8	49.4
46. SEQID 230		68.5	52.9	51.9	30.8	33.3	22.1	31.9	31.4	35.1	32.9	36	29.1
47. SEQID 232	80.1		46	47.6	27.8	29.5	20.5	30	29.7	35.6	32.9	32.8	27.4
48. SEQID 234	68.3	62.6		69.4	27.5	34	20.3	31.7	28.4	32.5	29.7	32.9	26
49. SEQID 236	69.8	66.4	80.5		28.6	31.9	21.2	30.8	29.4	33.9	30.8	33.1	27.8
50. SEQID 240	39.9	37.9	37.4	41.1		31.3	28.6	33.9	42	32.3	28.4	36.6	40.4
51. SEQID 242	45.4	42.4	46	43.8	45.9		22.3	41.3	33.2	41.7	25.4	52.8	31.3
52. SEQID 244	31.8	31.1	31.9	31.3	47.2	38		23.3	27	23.3	22.2	23.2	28
53. SEQID 246	45.9	41.1	44.2	43	49.3	60.7	38.9		32.8	43.1	26	47.5	31.1
54. SEQID 248	44.6	40	39.5	40.9	60.2	47.2	39.4	48.7		30.5	29.3	33.2	39.9
55. SEQID 250	44.9	48.7	44.9	47.1	44.4	53.8	33.7	56.5	42.9		29.2	46.7	30.2
56. SEQID 252	47.2	45.8	39.5	43.5	40.2	40.9	32.6	42.4	41.8	44.4		26.5	26.9
57. SEQID 254	45.4	41.6	43.1	44.5	57.9	63.6	39.6	61.1	49.8	56.5	38.4		31.9
58. SEQID 256	39.6	36.6	37.1	35.9	58.3	46.9	42.1	45	54.2	41.9	39.9	46.5	

Example 12: Identification of domains comprised in polypeptide sequences useful in performing the methods of the invention

The Integrated Resource of Protein Families, Domains and Sites (InterPro) database is an integrated interface for the commonly used signature databases for text- and sequence-based searches. The InterPro database combines these databases, which use different methodologies and varying degrees of biological information about well-characterized proteins to derive protein signatures. Collaborating databases include SWISS-PROT, PROSITE, TrEMBL, PRINTS, ProDom and Pfam, Smart and TIGRFAMs. Interpro is hosted at the European Bioinformatics Institute in the United Kingdom.

The results of the InterPro scan of the polypeptide sequence as represented by SEQ ID NO: 132 resented in Table 16.

Table 16: InterPro scan results of the polypeptide sequence as represented by SEQ ID NO: 132

Database	Accession number	Accession name
PRODOM	PD001423	Q9SP16_ORYSA_Q9SP16;
PRINTS	PR00367	ETHRSPELEMNT
GENE3D	G3DSA:3.30.730.10	no description
PFAM	PF00847	AP2
SMART	SM00380	AP2
PROFILE	PS51032	AP2_ERF
SUPERFAMILY	SSF54171	DNA binding domain

Example 13: Topology prediction of the polypeptide sequences useful in performing the methods of the invention (subcellular localization, transmembrane...)

TargetP 1.1 predicts the subcellular location of eukaryotic proteins. The location assignment is based on the predicted presence of any of the N-terminal pre-sequences: chloroplast transit peptide (cTP), mitochondrial targeting peptide (mTP) or secretory pathway signal peptide (SP). Scores on which the final prediction is based are not really probabilities, and they do not necessarily add to one. However, the location with the highest score is the most likely according to TargetP, and the relationship between the scores (the reliability class) may be an indication of how certain the prediction is. The reliability class (RC) ranges from 1 to 5, where 1 indicates the strongest prediction. TargetP is maintained at the server of the Technical University of Denmark.

For the sequences predicted to contain an N-terminal presequence a potential cleavage site can also be predicted.

A number of parameters were selected, such as organism group (non-plant or plant), cutoff sets (none, predefined set of cutoffs, or user-specified set of cutoffs), and the calculation of prediction of cleavage sites (yes or no).

The results of TargetP 1.1 analysis of the polypeptide sequence as represented by SEQ ID NO: 132 are presented Table 17. The "plant" organism group has been selected, no cutoffs defined, and the predicted length of the transit peptide requested. The subcellular localization of the polypeptide sequence as represented by SEQ ID NO: 132 may be the cytoplasm or nucleus, no transit peptide is predicted.

Table 17: TargetP 1.1 analysis of the polypeptide sequence as represented by SEQ ID NO: 132

Length (AA)	130
Chloroplastic transit peptide	0.098
Mitochondrial transit peptide	0.339
Secretory pathway signal peptide	0.035
Other subcellular targeting	0.797

Predicted Location	/
Reliability class	3
Predicted transit peptide length	/

Many other algorithms can be used to perform such analyses, including:

- ChloroP 1.1 hosted on the server of the Technical University of Denmark;
- Protein Prowler Subcellular Localisation Predictor version 1.2 hosted on the server of the Institute for Molecular Bioscience, University of Queensland, Brisbane, Australia;
- PENCE Proteome Analyst PA-GOSUB 2.5 hosted on the server of the University of Alberta, Edmonton, Alberta, Canada;
- TMHMM, hosted on the server of the Technical University of Denmark

Example 14: Expression vector construction using the nucleic acid sequence as represented by SEQ ID NO: 131

Unless otherwise stated, recombinant DNA techniques are performed according to standard protocols described in (Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York) or in Volumes 1 and 2 of Ausubel et al. (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D. Croy, published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

The *Oryza sativa* AP2-2 gene was amplified by PCR from a rice cDNA library. The PCR fragment of the expected length was purified and subsequently cloned in a Gateway® vector using standard technology. The entry clone comprising SEQ ID NO: 131 was then used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contained as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the nucleic acid sequence of interest already cloned in the entry clone. A rice GOS2 promoter (SEQ ID NO: 39) for root specific expression was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector pGOS2::AP2-2 (Figure 23) was transformed into *Agrobacterium* strain LBA4044 according to methods well known in the art.

Example 15: Plant transformation

Rice transformation

The *Agrobacterium* containing the expression vector was used to transform *Oryza sativa* plants. Mature dry seeds of the rice japonica cultivar Nipponbare were dehusked. Sterilization was carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2% HgCl₂, followed by a 6 times 15 minutes wash with sterile distilled water. The sterile seeds were then germinated on a medium

containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli were excised and propagated on the same medium. After two weeks, the calli were multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces were sub-cultured on fresh medium 3 days before co-cultivation (to boost cell division activity).

Agrobacterium strain LBA4404 containing the expression vector was used for co-cultivation. *Agrobacterium* was inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28°C. The bacteria were then collected and suspended in liquid co-cultivation medium to a density (OD₆₀₀) of about 1. The suspension was then transferred to a Petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues were then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25°C. Co-cultivated calli were grown on 2,4-D-containing medium for 4 weeks in the dark at 28°C in the presence of a selection agent. During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential was released and shoots developed in the next four to five weeks. Shoots were excised from the calli and incubated for 2 to 3 weeks on an auxin-containing medium from which they were transferred to soil. Hardened shoots were grown under high humidity and short days in a greenhouse.

Approximately 35 independent T0 rice transformants were generated for one construct. The primary transformants were transferred from a tissue culture chamber to a greenhouse. After a quantitative PCR analysis to verify copy number of the T-DNA insert, only single copy transgenic plants that exhibit tolerance to the selection agent were kept for harvest of T1 seed. Seeds were then harvested three to five months after transplanting. The method yielded single locus transformants at a rate of over 50 % (Aldemita and Hodges1996, Chan *et al.* 1993, Hiei *et al.* 1994).

Corn transformation

Transformation of maize (*Zea mays*) is performed with a modification of the method described by Ishida *et al.* (1996) Nature Biotech 14(6): 745-50. Transformation is genotype-dependent in corn and only specific genotypes are amenable to transformation and regeneration. The inbred line A188 (University of Minnesota) or hybrids with A188 as a parent are good sources of donor material for transformation, but other genotypes can be used successfully as well. Ears are harvested from corn plant approximately 11 days after pollination (DAP) when the length of the immature embryo is about 1 to 1.2 mm. Immature embryos are cocultivated with *Agrobacterium tumefaciens* containing the expression vector, and transgenic plants are recovered through organogenesis. Excised embryos are grown on callus induction medium, then maize regeneration medium, containing the selection agent (for example imidazolinone but various selection markers can be used). The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to maize rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to

soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Wheat transformation

- 5 Transformation of wheat is performed with the method described by Ishida et al. (1996) Nature Biotech 14(6): 745-50. The cultivar Bobwhite (available from CIMMYT, Mexico) is commonly used in transformation. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* containing the expression vector, and transgenic plants are recovered through organogenesis. After incubation with *Agrobacterium*, the embryos are grown *in vitro* on callus induction medium, then regeneration medium,
10 containing the selection agent (for example imidazolinone but various selection markers can be used). The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA
15 insert.

Soybean transformation

- Soybean is transformed according to a modification of the method described in the Texas A&M patent US 5,164,310. Several commercial soybean varieties are amenable to transformation by this method.
20 The cultivar Jack (available from the Illinois Seed foundation) is commonly used for transformation. Soybean seeds are sterilised for *in vitro* sowing. The hypocotyl, the radicle and one cotyledon are excised from seven-day old young seedlings. The epicotyl and the remaining cotyledon are further grown to develop axillary nodes. These axillary nodes are excised and incubated with *Agrobacterium tumefaciens* containing the expression vector. After the cocultivation treatment, the explants are washed
25 and transferred to selection media. Regenerated shoots are excised and placed on a shoot elongation medium. Shoots no longer than 1 cm are placed on rooting medium until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Rapeseed/canola transformation

- Cotyledonary petioles and hypocotyls of 5-6 day old young seedling are used as explants for tissue culture and transformed according to Babic et al. (1998, Plant Cell Rep 17: 183-188). The commercial cultivar Westar (Agriculture Canada) is the standard variety used for transformation, but other varieties can also be used. Canola seeds are surface-sterilized for *in vitro* sowing. The cotyledon petiole explants
35 with the cotyledon attached are excised from the *in vitro* seedlings, and inoculated with *Agrobacterium* (containing the expression vector) by dipping the cut end of the petiole explant into the bacterial suspension. The explants are then cultured for 2 days on MSBAP-3 medium containing 3 mg/l BAP, 3 % sucrose, 0.7 % Phytagar at 23 °C, 16 hr light. After two days of co-cultivation with *Agrobacterium*, the petiole explants are transferred to MSBAP-3 medium containing 3 mg/l BAP, cefotaxime, carbenicillin, or

timentin (300 mg/l) for 7 days, and then cultured on MSBAP-3 medium with cefotaxime, carbenicillin, or timentin and selection agent until shoot regeneration. When the shoots are 5 – 10 mm in length, they are cut and transferred to shoot elongation medium (MSBAP-0.5, containing 0.5 mg/l BAP). Shoots of about 2 cm in length are transferred to the rooting medium (MS0) for root induction. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Alfalfa transformation

A regenerating clone of alfalfa (*Medicago sativa*) is transformed using the method of (McKersie et al., 1999 Plant Physiol 119: 839–847). Regeneration and transformation of alfalfa is genotype dependent and therefore a regenerating plant is required. Methods to obtain regenerating plants have been described. For example, these can be selected from the cultivar Rangelander (Agriculture Canada) or any other commercial alfalfa variety as described by Brown DCW and A Atanassov (1985. Plant Cell Tissue Organ Culture 4: 111-112). Alternatively, the RA3 variety (University of Wisconsin) has been selected for use in tissue culture (Walker et al., 1978 Am J Bot 65:654-659). Petiole explants are cocultivated with an overnight culture of *Agrobacterium tumefaciens* C58C1 pMP90 (McKersie et al., 1999 Plant Physiol 119: 839–847) or LBA4404 containing the expression vector. The explants are cocultivated for 3 d in the dark on SH induction medium containing 288 mg/ L Pro, 53 mg/ L thioproline, 4.35 g/ L K₂SO₄, and 100 µm acetosyringinone. The explants are washed in half-strength Murashige-Skoog medium (Murashige and Skoog, 1962) and plated on the same SH induction medium without acetosyringinone but with a suitable selection agent and suitable antibiotic to inhibit *Agrobacterium* growth. After several weeks, somatic embryos are transferred to BOi2Y development medium containing no growth regulators, no antibiotics, and 50 g/ L sucrose. Somatic embryos are subsequently germinated on half-strength Murashige-Skoog medium. Rooted seedlings were transplanted into pots and grown in a greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Example 16: Phenotypic evaluation procedure

16.1 Evaluation setup

Approximately 35 independent T0 rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T1 seed. Six events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homozygotes) and approximately 10 T1 seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. The transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. Greenhouse conditions were of shorts days (12 hours light), 28°C in the light and 22°C in the dark, and a relative humidity of 70%.

Four T1 events were further evaluated in the T2 generation following the same evaluation procedure as for the T1 generation but with more individuals per event. From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

16.2 Statistical analysis: F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and to verify for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the mere presence or position of the gene that is causing the differences in phenotype.

16.3 Parameters measured

Biomass-related parameter measurement

From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

The plant aboveground area (or leafy biomass) was determined by counting the total number of pixels on the digital images from aboveground plant parts discriminated from the background. This value was averaged for the pictures taken on the same time point from the different angles and was converted to a physical surface value expressed in square mm by calibration. Experiments show that the aboveground plant area measured this way correlates with the biomass of plant parts above ground. The above ground area is the area measured at the time point at which the plant had reached its maximal leafy biomass. The early vigour is the plant (seedling) aboveground area three weeks post-germination. Increase in root biomass is expressed as an increase in total root biomass (measured as maximum biomass of roots observed during the lifespan of a plant); or as an increase in the root/shoot index (measured as the ratio between root mass and shoot mass in the period of active growth of root and shoot).

Seed-related parameter measurements

The mature primary panicles were harvested, counted, bagged, barcode-labelled and then dried for three days in an oven at 37°C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. The number of filled seeds was determined by counting the number of filled husks

that remained after the separation step. The total seed yield was measured by weighing all filled husks harvested from a plant. Total seed number per plant was measured by counting the number of husks harvested from a plant. Thousand Kernel Weight (TKW) is extrapolated from the number of filled seeds counted and their total weight. The Harvest Index (HI) in the present invention is defined as the ratio between the total seed yield and the above ground area (mm^2), multiplied by a factor 10^6 . The total number of flowers per panicle as defined in the present invention is the ratio between the total number of seeds and the number of mature primary panicles. The seed fill rate as defined in the present invention is the proportion (expressed as a %) of the number of filled seeds over the total number of seeds (or florets).

Example 17: Results of the phenotypic evaluation of the transgenic plants

The results of the evaluation of transgenic rice plants expressing the AP2-2 nucleic acid are as follows.

There was an increase in yield compared to corresponding nullizygotes (controls), in particular seed yield, expressed as Thousand Kernel Weight and Harvest Index, was statistically significant increased compared to the control plants. For the TKW, an overall increase of 2% in T1 and of 3.4% in T2 was observed compared to control plants. In the case of harvest index, the overall increase compared to control plants was respectively 9.2% (T1) and 36.2% (T2).

D) APETELA2-70-like (AP2-70-like) polypeptide

Example 18: Identification of AP2-70-like sequences

Sequences (full length cDNA, ESTs or genomic) related to SEQ ID NO: 257 and/or protein sequences related to SEQ ID NO: 258 were identified amongst those maintained in the Entrez Nucleotides database at the National Center for Biotechnology Information (NCBI) using database sequence search tools, such as the Basic Local Alignment Tool (BLAST) (Altschul *et al.* (1990) J. Mol. Biol. 215:403-410; and Altschul *et al.* (1997) Nucleic Acids Res. 25:3389-3402). The program was used to find regions of local similarity between sequences by comparing nucleic acid or polypeptide sequences to sequence databases and by calculating the statistical significance of matches. The polypeptide encoded by SEQ ID NO: 257 was used for the TBLASTN algorithm, with default settings and the filter to ignore low complexity sequences set off. The output of the analysis was viewed by pairwise comparison, and ranked according to the probability score (E-value), where the score reflects the probability that a particular alignment occurs by chance (the lower the E-value, the more significant the hit). In addition to E-values, comparisons were also scored by percentage identity. Percentage identity refers to the number of identical nucleotides (or amino acids) between the two compared nucleic acid (or polypeptide) sequences over a particular length. In some instances, the default parameters may be adjusted to modify the stringency of the search.

Table 18 provides a list of nucleic acid and protein sequences related to the nucleic acid sequence as represented by SEQ ID NO: 257 and the protein sequence represented by SEQ ID NO: 258.

Table 18: AP2-70-encoding nucleic acid sequences and AP2-70 polypeptides useful in the methods of the present invention.

Name	Source organism	Nucleic acid SEQ ID NO:	Poly-peptide SEQ ID NO:	Status
	<i>Oryza sativa</i>	257	258	Full length
	<i>Oryza sativa</i>	259	260	Full length
NP_001049235.1	<i>Oryza sativa</i>	261	262	full length
ABB90886.1	<i>Triticum aestivum</i>	263	264	Full length
AAZ08560.1	<i>Triticum aestivum</i>	265	266	Full length
AAX13274.1	<i>Triticum aestivum</i>	267	268	Full length
NM_001054677.1	<i>Oryza sativa</i>	269	270	Full length
ABK28776.1	<i>Arabidopsis thaliana</i>	271	272	Full length
BAD37688.1	<i>Oryza sativa</i>	273	274	Full length
ABB89754.1	<i>Asparagus officinalis</i>	275	276	Full length
ABJ09421.1	<i>Aloe vera</i>	277	278	Full length
AAT39542.1	<i>Gossypium hirsutum</i>	279	280	Full length
AAF17691.1	<i>Arabidopsis thaliana</i>	281	282	Full length
NP_177931.1	<i>Arabidopsis thaliana</i>	283	284	Full length
NP_195688.1	<i>Arabidopsis thaliana</i>	285	286	Full length
AAM08622.1	<i>Oryza sativa</i>	287	288	Full length
ABB89755.1	<i>Broussonetia papyrifera</i>	289	290	Full length
AAZ14831.1	<i>Jatropha curcas</i>	291	292	Full length
AAC49770.1	<i>Arabidopsis thaliana</i>	293	294	Full length
NP_001063013.1	<i>Oryza sativa</i>	295	296	Full length
NP_001061779.1	<i>Oryza sativa</i>	297	298	Full length
AAO13360.1	<i>Lycopersicon esculentum</i>	299	300	Full length
AAM80486.1	<i>Zea mays</i>	301	302	Full length
AAP56252.1	<i>Oryza sativa</i>	303	304	Full length
AAF76898.1	<i>Atriplex hortensis</i>	305	306	Full length
NP_173638.1	<i>Arabidopsis thaliana</i>	307	308	Full length
NP_179810.1	<i>Arabidopsis thaliana</i>	309	310	Full length
AAZ03388.1	<i>Glycine max</i>	311	312	Full length
NP_564468.1	<i>Arabidopsis thaliana</i>	313	314	Full length
NP_179685.1	<i>Arabidopsis thaliana</i>	315	316	Full length
NP_193098.1	<i>Arabidopsis thaliana</i>	317	318	Full length
BAD25342.1	<i>Oryza sativa</i>	319	320	Full length

NP_001053379.1	Oryza sativa	321	322	Full length
CAD41199.2	Oryza sativa	323	324	Full length
NP_176620.1	Arabidopsis thaliana	325	326	Full length
11978.m07152	Oryza sativa	327	328	Full length
11975.m09040	Oryza sativa	329	330	Full length

Example 19: Alignment of AP2-70-like polypeptide sequences

Alignment of polypeptide sequences was performed using the AlignX programme from the Vector NTI (Invitrogen) which is based on the popular Clustal algorithm of progressive alignment (Thompson *et al.* (1997) Nucleic Acids Res 25:4876-4882; Chenna *et al.* (2003). Nucleic Acids Res 31:3497-3500). Default values are for the gap open penalty of 10, for the gap extension penalty of 0,1 and the selected weight matrix is Blosum 62 (if polypeptides are aligned).

A phylogenetic tree of AP2-70-like polypeptides was constructed using a neighbour-joining clustering algorithm as provided in the AlignX programme from the Vector NTI (Invitrogen).

Example 20: Cloning and vector construction

Unless otherwise stated, recombinant DNA techniques are performed according to standard protocols described in (Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York) or in Volumes 1 and 2 of Ausubel *et al.* (1994), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D. Croy, published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

The *Oryza sativa* AP2-70 gene was amplified by PCR from a rice cDNA library. The PCR fragment of the expected length was purified and subsequently cloned in a Gateway® vector using standard technology. The entry clone comprising SEQ ID NO: 257 was then used in an LR reaction with a destination vector used for *Oryza sativa* transformation. This vector contained as functional elements within the T-DNA borders: a plant selectable marker; a screenable marker expression cassette; and a Gateway cassette intended for LR *in vivo* recombination with the nucleic acid sequence of interest already cloned in the entry clone. A rice GOS2 promoter (SEQ ID NO: 39) for constitutive expression was located upstream of this Gateway cassette.

After the LR recombination step, the resulting expression vector pGOS2::AP2-70 (Figure 25) was transformed into *Agrobacterium* strain LBA4044 according to methods well known in the art.

A second vector identical to above except comprising an RCc3 promoter (SEQ ID NO: 110) for root-specific expression was also made. Again, after the LR recombination step, the resulting expression

vector pRCc3::AP2-70 (Figure 24) was transformed into *Agrobacterium* strain LBA4044 according to methods well known in the art.

Example 21: Plant transformation

Rice transformation

The *Agrobacterium* containing the expression vector was used to transform *Oryza sativa* plants. Mature dry seeds of the rice japonica cultivar Nipponbare were dehusked. Sterilization was carried out by incubating for one minute in 70% ethanol, followed by 30 minutes in 0.2% HgCl₂, followed by a 6 times 15 minutes wash with sterile distilled water. The sterile seeds were then germinated on a medium containing 2,4-D (callus induction medium). After incubation in the dark for four weeks, embryogenic, scutellum-derived calli were excised and propagated on the same medium. After two weeks, the calli were multiplied or propagated by subculture on the same medium for another 2 weeks. Embryogenic callus pieces were sub-cultured on fresh medium 3 days before co-cultivation (to boost cell division activity).

Agrobacterium strain LBA4404 containing the expression vector was used for co-cultivation. *Agrobacterium* was inoculated on AB medium with the appropriate antibiotics and cultured for 3 days at 28°C. The bacteria were then collected and suspended in liquid co-cultivation medium to a density (OD₆₀₀) of about 1. The suspension was then transferred to a Petri dish and the calli immersed in the suspension for 15 minutes. The callus tissues were then blotted dry on a filter paper and transferred to solidified, co-cultivation medium and incubated for 3 days in the dark at 25°C. Co-cultivated calli were grown on 2,4-D-containing medium for 4 weeks in the dark at 28°C in the presence of a selection agent. During this period, rapidly growing resistant callus islands developed. After transfer of this material to a regeneration medium and incubation in the light, the embryogenic potential was released and shoots developed in the next four to five weeks. Shoots were excised from the calli and incubated for 2 to 3 weeks on an auxin-containing medium from which they were transferred to soil. Hardened shoots were grown under high humidity and short days in a greenhouse.

Approximately 35 independent T0 rice transformants were generated for one construct. The primary transformants were transferred from a tissue culture chamber to a greenhouse. After a quantitative PCR analysis to verify copy number of the T-DNA insert, only single copy transgenic plants that exhibit tolerance to the selection agent were kept for harvest of T1 seed. Seeds were then harvested three to five months after transplanting. The method yielded single locus transformants at a rate of over 50 % (Aldemita and Hodges 1996, Chan *et al.* 1993, Hiei *et al.* 1994).

Corn transformation

Transformation of maize (*Zea mays*) is performed with a modification of the method described by Ishida *et al.* (1996) Nature Biotech 14(6): 745-50. Transformation is genotype-dependent in corn and only specific genotypes are amenable to transformation and regeneration. The inbred line A188 (University of

Minnesota) or hybrids with A188 as a parent are good sources of donor material for transformation, but other genotypes can be used successfully as well. Ears are harvested from corn plant approximately 11 days after pollination (DAP) when the length of the immature embryo is about 1 to 1.2 mm. Immature embryos are cocultivated with *Agrobacterium tumefaciens* containing the expression vector, and transgenic plants are recovered through organogenesis. Excised embryos are grown on callus induction medium, then maize regeneration medium, containing the selection agent (for example imidazolinone but various selection markers can be used). The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to maize rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Wheat transformation

Transformation of wheat is performed with the method described by Ishida et al. (1996) Nature Biotech 14(6): 745-50. The cultivar Bobwhite (available from CIMMYT, Mexico) is commonly used in transformation. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* containing the expression vector, and transgenic plants are recovered through organogenesis. After incubation with *Agrobacterium*, the embryos are grown *in vitro* on callus induction medium, then regeneration medium, containing the selection agent (for example imidazolinone but various selection markers can be used). The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Soybean transformation

Soybean is transformed according to a modification of the method described in the Texas A&M patent US 5,164,310. Several commercial soybean varieties are amenable to transformation by this method. The cultivar Jack (available from the Illinois Seed foundation) is commonly used for transformation. Soybean seeds are sterilised for *in vitro* sowing. The hypocotyl, the radicle and one cotyledon are excised from seven-day old young seedlings. The epicotyl and the remaining cotyledon are further grown to develop axillary nodes. These axillary nodes are excised and incubated with *Agrobacterium tumefaciens* containing the expression vector. After the cocultivation treatment, the explants are washed and transferred to selection media. Regenerated shoots are excised and placed on a shoot elongation medium. Shoots no longer than 1 cm are placed on rooting medium until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Rapeseed/canola transformation

Cotyledonary petioles and hypocotyls of 5-6 day old young seedling are used as explants for tissue culture and transformed according to Babic et al. (1998, Plant Cell Rep 17: 183-188). The commercial cultivar Westar (Agriculture Canada) is the standard variety used for transformation, but other varieties can also be used. Canola seeds are surface-sterilized for *in vitro* sowing. The cotyledon petiole explants with the cotyledon attached are excised from the *in vitro* seedlings, and inoculated with *Agrobacterium* (containing the expression vector) by dipping the cut end of the petiole explant into the bacterial suspension. The explants are then cultured for 2 days on MSBAP-3 medium containing 3 mg/l BAP, 3 % sucrose, 0.7 % Phytagar at 23 °C, 16 hr light. After two days of co-cultivation with *Agrobacterium*, the petiole explants are transferred to MSBAP-3 medium containing 3 mg/l BAP, cefotaxime, carbenicillin, or timentin (300 mg/l) for 7 days, and then cultured on MSBAP-3 medium with cefotaxime, carbenicillin, or timentin and selection agent until shoot regeneration. When the shoots are 5 – 10 mm in length, they are cut and transferred to shoot elongation medium (MSBAP-0.5, containing 0.5 mg/l BAP). Shoots of about 2 cm in length are transferred to the rooting medium (MS0) for root induction. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Alfalfa transformation

A regenerating clone of alfalfa (*Medicago sativa*) is transformed using the method of (McKersie et al., 1999 Plant Physiol 119: 839–847). Regeneration and transformation of alfalfa is genotype dependent and therefore a regenerating plant is required. Methods to obtain regenerating plants have been described. For example, these can be selected from the cultivar Rangelander (Agriculture Canada) or any other commercial alfalfa variety as described by Brown DCW and A Atanassov (1985. Plant Cell Tissue Organ Culture 4: 111-112). Alternatively, the RA3 variety (University of Wisconsin) has been selected for use in tissue culture (Walker et al., 1978 Am J Bot 65:654-659). Petiole explants are cocultivated with an overnight culture of *Agrobacterium tumefaciens* C58C1 pMP90 (McKersie et al., 1999 Plant Physiol 119: 839–847) or LBA4404 containing the expression vector. The explants are cocultivated for 3 d in the dark on SH induction medium containing 288 mg/ L Pro, 53 mg/ L thioproline, 4.35 g/ L K₂SO₄, and 100 µm acetosyringinone. The explants are washed in half-strength Murashige-Skoog medium (Murashige and Skoog, 1962) and plated on the same SH induction medium without acetosyringinone but with a suitable selection agent and suitable antibiotic to inhibit *Agrobacterium* growth. After several weeks, somatic embryos are transferred to BOi2Y development medium containing no growth regulators, no antibiotics, and 50 g/ L sucrose. Somatic embryos are subsequently germinated on half-strength Murashige-Skoog medium. Rooted seedlings were transplanted into pots and grown in a greenhouse. T1 seeds are produced from plants that exhibit tolerance to the selection agent and that contain a single copy of the T-DNA insert.

Example 22: Phenotypic evaluation procedure**22.1 Evaluation setup**

Approximately 35 independent T0 rice transformants were generated. The primary transformants were transferred from a tissue culture chamber to a greenhouse for growing and harvest of T1 seed. Six events, of which the T1 progeny segregated 3:1 for presence/absence of the transgene, were retained. For each of these events, approximately 10 T1 seedlings containing the transgene (hetero- and homozygotes) and approximately 10 T1 seedlings lacking the transgene (nullizygotes) were selected by monitoring visual marker expression. The transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. Greenhouse conditions were of short days (12 hours light), 28°C in the light and 22°C in the dark, and a relative humidity of 70%.

Four T1 events were further evaluated in the T2 generation following the same evaluation procedure as for the T1 generation but with more individuals per event. From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

22.2 Statistical analysis: F-test

A two factor ANOVA (analysis of variants) was used as a statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured of all the plants of all the events transformed with the gene of the present invention. The F-test was carried out to check for an effect of the gene over all the transformation events and to verify for an overall effect of the gene, also known as a global gene effect. The threshold for significance for a true global gene effect was set at a 5% probability level for the F-test. A significant F-test value points to a gene effect, meaning that it is not only the mere presence or position of the gene that is causing the differences in phenotype.

22.3 Parameters measured**Biomass-related parameter measurement**

From the stage of sowing until the stage of maturity the plants were passed several times through a digital imaging cabinet. At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles.

The plant aboveground area (or leafy biomass) was determined by counting the total number of pixels on the digital images from aboveground plant parts discriminated from the background. This value was averaged for the pictures taken on the same time point from the different angles and was converted to a physical surface value expressed in square mm by calibration. Experiments show that the aboveground plant area measured this way correlates with the biomass of plant parts above ground. The above ground area is the area measured at the time point at which the plant had reached its maximal leafy biomass. The early vigour is the plant (seedling) aboveground area three weeks post-germination.

Increase in root biomass is expressed as an increase in total root biomass (measured as maximum biomass of roots observed during the lifespan of a plant); or as an increase in the root/shoot index (measured as the ratio between root mass and shoot mass in the period of active growth of root and shoot).

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Seed-related parameter measurements

The mature primary panicles were harvested, counted, bagged, barcode-labelled and then dried for three days in an oven at 37°C. The panicles were then threshed and all the seeds were collected and counted. The filled husks were separated from the empty ones using an air-blowing device. The empty husks were discarded and the remaining fraction was counted again. The filled husks were weighed on an analytical balance. The number of filled seeds was determined by counting the number of filled husks that remained after the separation step. The total seed yield was measured by weighing all filled husks harvested from a plant. Total seed number per plant was measured by counting the number of husks harvested from a plant. Thousand Kernel Weight (TKW) is extrapolated from the number of filled seeds counted and their total weight. The Harvest Index (HI) in the present invention is defined as the ratio between the total seed yield and the above ground area (mm²), multiplied by a factor 10⁶. The total number of flowers per panicle as defined in the present invention is the ratio between the total number of seeds and the number of mature primary panicles. The seed fill rate as defined in the present invention is the proportion (expressed as a %) of the number of filled seeds over the total number of seeds (or florets).

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Example 23: Results of the phenotypic evaluation of the transgenic plants

The results of the evaluation of transgenic rice plants expressing an AP2-70 nucleic acid are presented below. The percentage difference between the transgenics and the corresponding nullizygotes is also shown.

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Table 19a results of expression of pGOS2::AP2-70

Trait	Positive events	Average difference
Root Shoot Index	3 events	21.3 %
		overall + 14%
Total Seed Yield	2 events	27 %
Fill rate	3 events	27 %
TKW	4 events	8.75 %
		overall + 6%
Harvest Index	4 events	30.5 %
		overall + 16%
Root thick	2 events	10.5 %
Height	2 events	8 %
		overall + 4%

30

Table 19b results of expression of pRCc3::AP2-70

Trait	Positive events	Average difference
Area max	2 events	16.5 %
		Overall + 7%
Total seed yield	2 events	233 %
		Overall + 89%
Number filled seed	2 events	184.5 %
		Overall + 68%
Fill rate	2 events	206%
		Overall + 87%
Harvest Index	2 events	238.5%
		Overall + 86%
TKW	3 events	11.3 %
		Overall + 7%
Height	2 events	12.5 %
		Overall + 7%

Claims

1. A method for enhancing yield-related traits in plants, comprising modulating expression in a plant of a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 2, rather than with any other NAC group.

2. Method according to claim 1, wherein said NAC transcription factor comprises any one or more of the following motifs:

Motif I: KIDLDIIQELD, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif I;

Motif II: CKYGXGHGGDEQTEW, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif II, where 'X' is taken to be any amino acid or a gap;

Motif III: GWVVCRAFQKP, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif III.

3. Method according to claim 1 or 2, wherein said nucleic acid encoding a NAC transcription factor is any one of the nucleic acid SEQ ID NOs given in Table 3 or a portion thereof or a sequence capable of hybridising with any one of the nucleic acids SEQ ID NOs given in Table 3.

4. Method according to any one of claims 1 to 3, wherein said modulated expression is effected by any one or more of T-DNA activation tagging, TILLING, or homologous recombination.

5. Method according to any one of claims 1 to 3, wherein said modulated expression is effected by introducing and expressing in a plant a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 2 rather than with any other NAC group.

6. Method according to any one of claims 1 to 5, wherein said enhanced yield-related trait is increased aboveground area.

7. Method according to any one of claims 1 to 6, wherein said enhanced yield-related trait is increased seed yield.

8. Method according to any one of claims 5 to 7, wherein said nucleic acid is operably linked to a green tissue-specific promoter, preferably to a protochlorophyllid reductase promoter.

9. Method according to any one of claims 5 to 7, wherein said nucleic acid is operably linked to a constitutive promoter, preferably to a GOS2 promoter.

10. A method for enhancing yield-related traits in plants, comprising modulating expression in a plant of a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with any other NAC group.

11. A method for enhancing yield-related traits in plants grown under abiotic stress conditions, comprising modulating expression in a plant of a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 53 rather than with any other NAC group.

12. Method according to claim 10, wherein said NAC transcription factor comprises any one or more of the following motifs:

Motif IV: PVPIIA, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif IV;

Motif V: NGSRPN, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif V;

Motif VI: CRLYNKK, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif VI;

Motif VII: NEWEKMQ, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif VII;

Motif VIII: WGETRTPESE, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence Motif VIII;

Motif IX: VPKESMDDA, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif IX;

Motif X: SYDDIQGMYS, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif X; and

Motif XI: DSMPLRHADSSCSE, or a motif having in increasing order of preference at least 50%, 60%, 70%, 80% or 90% sequence identity to the sequence of Motif XI.

13. Method according to claim 10 or 12, wherein said nucleic acid encoding a NAC transcription factor is any one of the nucleic acid SEQ ID NOs given in Table 4 or a portion thereof or a sequence capable of hybridising with any one of the nucleic acids SEQ ID NOs given in Table 4.

14. Method according to any one of claims 10 to 13, wherein said modulated expression is effected by any one or more of T-DNA activation tagging, TILLING, or homologous recombination.

15. Method according to any one of claims 10 to 13, wherein said modulated expression is effected by introducing and expressing in a plant a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with any other NAC group.

16. Method according to any one of claims 10 to 15, wherein said enhanced yield-related trait is increased aboveground area.

17. Method according to any one of claims 10 to 16, wherein said enhanced yield-related trait is increased seed yield.

18. Method according to any one of claims 10 to 17, wherein said enhanced yield-related trait is increased early vigour.

19. Method according to any one of claims 15 to 18, wherein said nucleic acid is operably linked to a root -specific promoter, preferably to an RCc3 promoter.

20. Method according to any one of claims 15 to 18, wherein said nucleic acid is operably linked to a constitutive promoter, preferably to a GOS2 promoter.

21. Method according to any one of claims 1 to 20, wherein said nucleic acid encoding a NAC transcription factor is of plant origin, preferably from a monocotyledonous plant, further preferably from the family Poaceae, more preferably from the genus *Oryza*, most preferably from *Oryza sativa*.

22. Plant or part thereof including seeds obtainable by a method according to any one of claims 1 to 21, wherein said plant or part thereof comprises a nucleic acid encoding a NAC transcription factor.

23. Construct comprising:

(a) Nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted

in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 2 rather than with any other NAC group;

(b) One or more control sequences capable of driving expression of the nucleic acid sequence of (a); and optionally

5 (c) A transcription termination sequence.

24. Construct according to claim 23, wherein said one or more control sequences is at least a green tissue-specific promoter, preferably a protochlorophyllid reductase promoter.

10 25. Construct comprising:

(a) Nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with
15 any other NAC group;

(b) One or more control sequences capable of driving expression of the nucleic acid sequence of (a); and optionally

(c) A transcription termination sequence.

20 26. Construct according to claim 25, wherein said one or more control sequences is at least a root -specific promoter, preferably an RCc3 promoter.

27. Construct according to claim 23 or 25, wherein said one or more control sequences is at least a constitutive promoter, preferably a GOS2 promoter.

25 28. Use of a construct according to any one of claims 23 to 27 for making plants having enhanced yield-related traits, particularly increased seed yield and/or increased aboveground area, relative to control plants.

30 29. Plant, plant part or plant cell transformed with a construct according to any one of claims 23 to 27.

30. Method for the production of a transgenic plant having enhanced yield-related traits relative to control plants, which method comprises:

35 (i) introducing and expressing in a plant a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 2, SEQ ID

NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with any other NAC group; and

- (ii) cultivating the plant cell under conditions promoting plant growth and development.

5 31. Transgenic plant having increased yield relative to suitable control plants, said increased yield resulting from increased expression of a nucleic acid encoding a NAC transcription factor, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 2, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 10 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with any other NAC group.

32. Transgenic plant according to claim 22, 29 or 31, wherein said plant is a crop plant or a monocot or a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum and oats.

15 33. Harvestable parts of a plant according to any one of claims 22, 29, 31 or 32, wherein said harvestable parts are preferably seeds.

34. Products derived from a plant according to claim 32 and/or from harvestable parts of a plant according to claim 33.

20 35. Use of a nucleic acid encoding a NAC transcription factor in enhancing yield-related traits in plants, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence e represented by SEQ ID NO: 2, SEQ ID NO: 51, SEQ ID NO: 53, 25 SEQ ID NO: 55, SEQ ID NO: 57 or SEQ ID NO: 59 rather than with any other NAC group.

36. Use of a nucleic acid encoding a NAC4 transcription factor in enhancing yield-related traits in plants grown under abiotic stress conditions, wherein the amino acid sequence of said NAC transcription factor, when used in the construction of a NAC phylogenetic tree, such as the one depicted 30 in Fig. 1, tends to cluster with the group of NACs comprising the amino acid sequence represented by SEQ ID NO: 53 rather than with any other NAC group

37. Use according to claim 35 or 36, wherein said enhanced yield-related trait is increased seed yield and/or increased aboveground area and/or early vigour relative to control plants.

35 38. A method for enhancing yield-related traits in plants relative to control plants, comprising modulating expression in a plant of a nucleic acid encoding an AP2-2 polypeptide, which AP2-2 polypeptide comprises motif XII (SEQ ID NO: 133) and preferably also one or more of: motif XIII (SEQ

ID NO: 134), motif XIV (SEQ ID NO: 135), motif XV (SEQ ID NO: 136), motif XVI (SEQ ID NO: 137), and motif XVII (SEQ ID NO: 138).

39. Method according to claim 38, wherein said AP2-2 polypeptide has, in increasing order of preference, at least 20, 25, 30, 35, 40, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the AP2-2 polypeptide represented by SEQ ID NO: 132.

40. Method according to claim 38 or 39, wherein said nucleic acid encoding an AP2-2 polypeptide is represented by any one of the nucleic acid SEQ ID NOs given in Table 14 or a portion thereof, or a sequence capable of hybridising with any one of the nucleic acids SEQ ID NOs given in Table 14.

41. Method according to any of claims 38 to 40, wherein said nucleic acid sequence encodes an orthologue or paralogue of any of the SEQ ID NOs given in Table 14.

42. Method according to any of claims 38 to 41, wherein said modulated expression is effected by introducing and expressing in a plant a nucleic acid encoding an AP2-2 polypeptide.

43. Method according to any of claims 38 to 42, wherein said enhanced yield-related trait is increased yield, preferably increased seed yield relative to control plants.

44. Method according to claim 42 or 43, wherein said nucleic acid is operably linked to a constitutive promoter, preferably to a GOS2 promoter.

45. Method according to any of claims 38 to 44, wherein said nucleic acid encoding an AP2-2 polypeptide is of plant origin, preferably from a dicotyledonous plant, further preferably from the family Poaceae, more preferably from the genus *Oryza*, most preferably from *Oryza sativa*.

46. Plant or part thereof, including seeds, obtainable by a method according to any of claims 38 to 45, wherein said plant or part thereof comprises a recombinant nucleic acid encoding an AP2-2 polypeptide.

47. Construct comprising:

- (a) nucleic acid encoding an AP2-2 polypeptide as defined in any one of claims 38 to 41;
- (b) one or more control sequences capable of driving expression of the nucleic acid sequence of (a); and optionally
- (c) a transcription termination sequence.

48. Construct according to claim 47, wherein said one or more control sequences is a constitutive promoter, preferably a GOS2 promoter.

49. Use of a construct according to claims 47 or 48 in a method for making plants having increased yield, particularly increased seed yield relative to control plants.

50. Plant, plant part or plant cell transformed with a construct according to claim 47 or 48.

51. Method for the production of a transgenic plant having increased yield, particularly increased seed yield relative to control plants, comprising:

- (i) introducing and expressing in a plant a nucleic acid encoding an AP2-2 polypeptide as defined in any one of claims 38 to 41; and
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

52. Transgenic plant having increased yield, particularly increased seed yield, relative to control plants, resulting from increased expression of a nucleic acid encoding an AP2-2 polypeptide as defined in any one of claims 38 to 41, or a transgenic plant cell derived from said transgenic plant.

53. Transgenic plant according to claim 46, 50 or 52, wherein said plant is a crop plant or a monocot or a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum and oats, or a transgenic plant cell derived from said transgenic plant.

54. Harvestable parts of a plant according to claim 53, wherein said harvestable parts are preferably seeds.

55. Products derived from a plant according to claim 53 and/or from harvestable parts of a plant according to claim 54.

56. Use of a nucleic acid encoding an AP2-2 polypeptide as defined in any one of claims to 41 in increasing yield, particularly in increasing seed yield, in plants relative to control plants.

57. A method for enhancing yield-related traits in plants relative to control plants, comprising (i) modulating expression in a plant of a nucleic acid encoding an APETELA2-70-like (AP2-70-like) polypeptide comprising:

- (i) An AP2 DNA-binding domain as represented by SEQ ID NO: 332: YRGVRQRHWGKWVAEIRLPNRTRLWLGTFTDTEEAALAYDSAAFRLRGESARLNF, or a domain having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the domain represented by SEQ ID NO: 332; and

- (ii) Having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to the *Oryza sativa* polypeptide sequence represented by SEQ ID NO: 258; and
- (iii) Comprising Motif I represented by SEQ ID NO: 333: RLPXNX¹RXRXLGT F/Y D/E T/S, where X is any amino acid and X¹ is zero, one or more, and up to 30, gaps; and
- (iv) Comprising Motif XIX represented by SEQ ID NO: 334: RG D/E.

58. Method according to claim 57, wherein said AP2-70-like polypeptide further comprises one or more of the following motifs:

- (i) SEQ ID NO: 335/Motif XX: WDESESFLHKYPSLEIDWDAILS, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XX; and/or
- (ii) SEQ ID NO: 336/Motif XXI: GPPLHAAVDAKLHAICH, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XXI; and/or
- (iii) SEQ ID NO: 337/Motif XXII: GANYLTPAQVLHVQAQLQLRRP, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XXII; and/or
- (iv) SEQ ID NO: 338/Motif XXIII: VDSKELMGALAPSMVSFSYPCSEQSASS, or a motif having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more sequence identity to Motif XXIII.

59. Method according to claim 57 or 58, wherein said modulated expression is effected by introducing and expressing in a plant a nucleic acid encoding an AP2-70-like polypeptide.

60. Method according to any of claims 57 to 59, wherein said nucleic acid encoding an AP2-70-like polypeptide is represented by any one of the nucleic acid SEQ ID NOs given in Table 18 or a portion thereof, or a sequence capable of hybridising with any one of the nucleic acids SEQ ID NOs given in Table 18.

61. Method according to any of claims 57 to 60, wherein said nucleic acid sequence encodes an orthologue or paralogue of any of the SEQ ID NOs given in Table 18.

62. Method according to any of claims 57 to 61, wherein said enhanced yield-related trait is increased yield, preferably increased seed yield relative to control plants.

63. Method according to any one of claims 59 to 62, wherein said nucleic acid is operably linked to a constitutive promoter, preferably to a GOS2 promoter, most preferably to a GOS2 promoter from rice.

64. Method according to any one of claims 59 to 52, wherein said nucleic acid is operably linked to a root-specific promoter, preferably to an RCC3 promoter, most preferably to an RCC3 promoter from rice.

5

65. Method according to any of claims 57 to 64, wherein said nucleic acid encoding an AP2-70-like polypeptide is of plant origin, preferably from a Monocotyledonous plant, further preferably from the family Poaceae more preferably from the genus *Oryza*, most preferably from *oryza sativa*.

10 66. Plant or part thereof, including seeds, obtainable by a method according to any of claims 57 to 65, wherein said plant or part thereof comprises a recombinant nucleic acid encoding an AP2-70-like polypeptide.

67. An isolated nucleic acid molecule comprising:

- 15 (a) a nucleic acid represented by SEQ ID NO: 257;
(b) the complement of a nucleic acid represented by SEQ ID NO: 257;
(c) a nucleic acid encoding an AP2-70-like polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by SEQ ID NO: 258, and having in
20 increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NO: 331: PFLMQWLNLLPLPVLDSWCEHFHNSDALP.

68. An isolated polypeptide comprising:

- 25 (a) an amino acid sequence represented by SEQ ID NO: 258;
(b) an amino acid sequence having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by SEQ ID NO: 258, and having in increasing order of preference at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%,
30 99% or more sequence identity to SEQ ID NO: 331: PFLMQWLNLLPLPVLDSWCEHFHNSDALP;
(c) derivatives of any of the amino acid sequences given in (i) or (ii) above.

69. Construct comprising:

- 35 (a) nucleic acid encoding an AP2-70-like polypeptide as defined in claim 57, 58 or 67; one or more control sequences capable of driving expression of the nucleic acid sequence of (a); and optionally
(b) a transcription termination sequence.

70. Construct according to claim 69, wherein said one or more control sequences is selected from:

- (i) a constitutive promoter, preferably a GOS2 promoter, most preferably to a GOS2 promoter from rice; or
- (ii) a root-specific promoter, preferably to an RCC3 promoter, most preferably to an RCC3 promoter from rice.

71. Use of a construct according to claim 69 or 70 in a method for making plants having increased yield, particularly increased seed yield relative to control plants.

72. Plant, plant part or plant cell transformed with a construct according to claims 69 or 70.

73. Method for the production of a transgenic plant having increased yield, particularly increased seed yield relative to control plants, comprising:

- (i) introducing and expressing in a plant a nucleic acid encoding an AP2-70-like polypeptide as defined in claim 57, 58 or 67; and
- (ii) cultivating the plant cell under conditions promoting plant growth and development.

74. Transgenic plant having increased yield, particularly increased seed yield, relative to control plants, resulting from increased expression of a nucleic acid encoding an AP2-70-like polypeptide as defined in claim 57, 58 or 67 or a transgenic plant cell derived from said transgenic plant.

75. Transgenic plant according to claim 66, 72 or 74, wherein said plant is a crop plant or a monocot or a cereal, such as rice, maize, wheat, barley, millet, rye, sorghum and oats, or a transgenic plant cell derived from said transgenic plant.

76. Harvestable parts of a plant according to claim 75, wherein said harvestable parts are preferably seeds.

77. Products derived from a plant according to claim 75 and/or from harvestable parts of a plant according to claim 76.

78. Use of a nucleic acid encoding an AP2-70-like polypeptide in increasing yield, particularly in increasing seed yield, in plants relative to control plants.

79. An isolated nucleic acid molecule comprising:

- (i) a nucleic acid represented by one of SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, or SEQ ID NO: 363;

- (ii) the complement of a nucleic acid represented by one of SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, or SEQ ID NO: 363;
- (iii) a nucleic acid encoding a NAC polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, or SEQ ID NO: 364.

80. An isolated polypeptide comprising:

- (i) an amino acid sequence represented by one of SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, or SEQ ID NO: 364;
- (ii) an amino acid sequence having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, or SEQ ID NO: 364;
- (iii) derivatives of any of the amino acid sequences given in (i) or (ii) above.

81. An isolated nucleic acid molecule comprising:

- (i) a nucleic acid represented by one of SEQ ID NO: 341, SEQ ID NO: 343, or SEQ ID NO: 345;
- (ii) the complement of a nucleic acid represented by one of SEQ ID NO: 341, SEQ ID NO: 343, or SEQ ID NO: 345;
- (iii) a nucleic acid encoding a POI polypeptide having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 342, SEQ ID NO: 344, or SEQ ID NO: 346.

82. An isolated polypeptide comprising:

- (i) an amino acid sequence represented by one of SEQ ID NO: 342, SEQ ID NO: 344, or SEQ ID NO: 346;
- (ii) an amino acid sequence having, in increasing order of preference, at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence represented by one of SEQ ID NO: 342, SEQ ID NO: 344, or SEQ ID NO: 346;
- (iii) derivatives of any of the amino acid sequences given in (i) or (ii) above.

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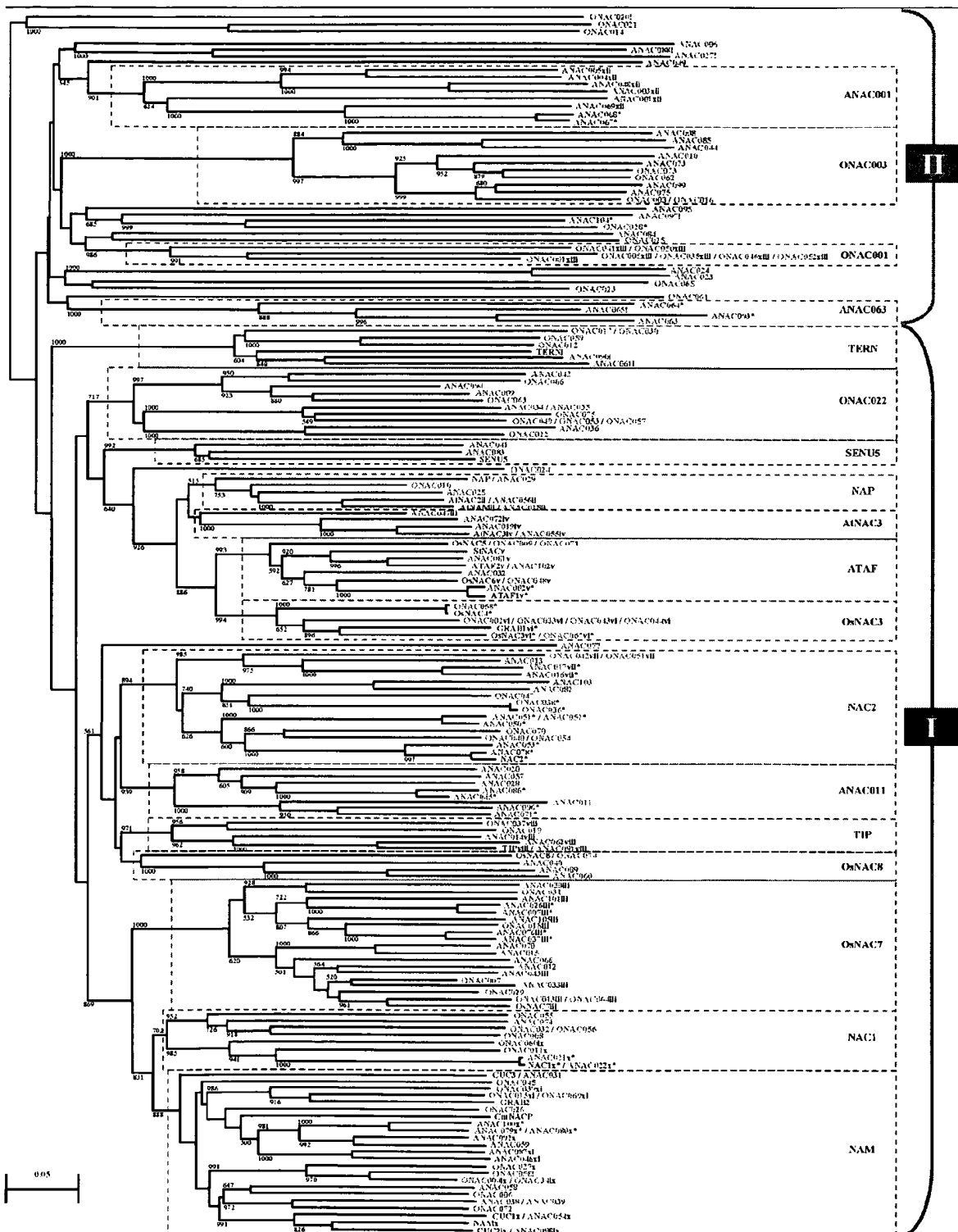


FIGURE 1

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|-----1-----| |-----6-----|
MCGGAILSDLIPPPRRVTAGDLWLEKTKKQQQKKKNKGARRLPLRQEEEDDFEADFEEFEV
| -A- |

--6-----| |-----3-----|
DSGEWEVESDADEAKPLAAPRSGFAKGGLKNTTVAGADGPAARSAKRKRKNQFRGIRQRPWG
| -A- | |-----B-|

KWAAEIRDPRKGVRVWLGTFNSPEEAARAYDAEARRIRGKKAKVNFDPGAPVASQRSHAEPS
-----B-----|

|-----7-----|
SMNMPAFSIEEKPAVMSAGNKTMYNTNAYAYPAVEYTLQEPFVQIQNVSFVPAMNAIEDTFV

-----7-----|
NLSSDQGSNSFGCSDFSQENDIKTPDITSMLAPTMTGVDDSAFLQNNASDAMVPPVPMGNASI
|-----4-----|

DLADLEPYMKFLIDGGSDESIDTLLSSDGSQDVASSMDLWSFDDMPVSAEFY
|-----8-----| |5|

FIGURE 2

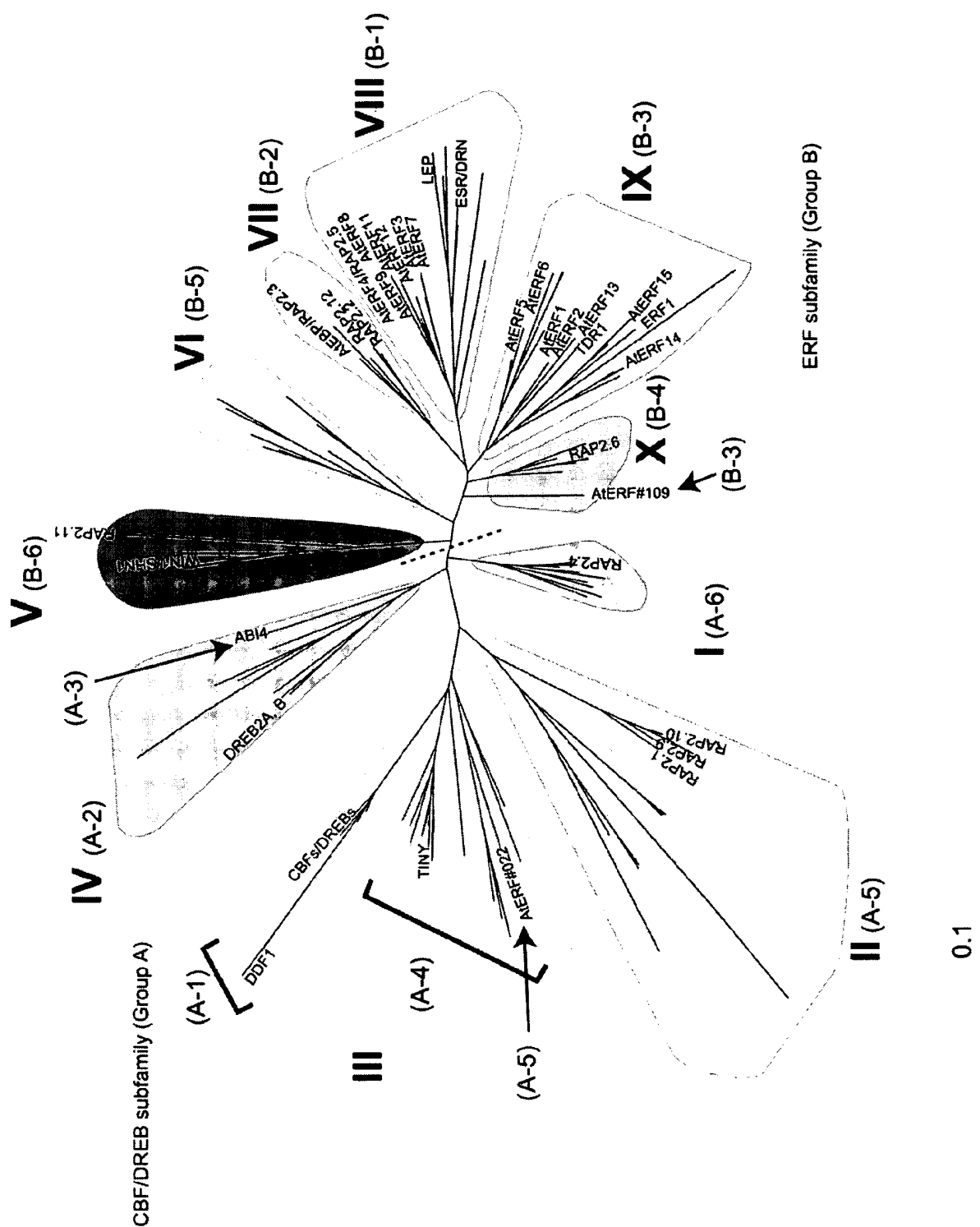


FIGURE 3

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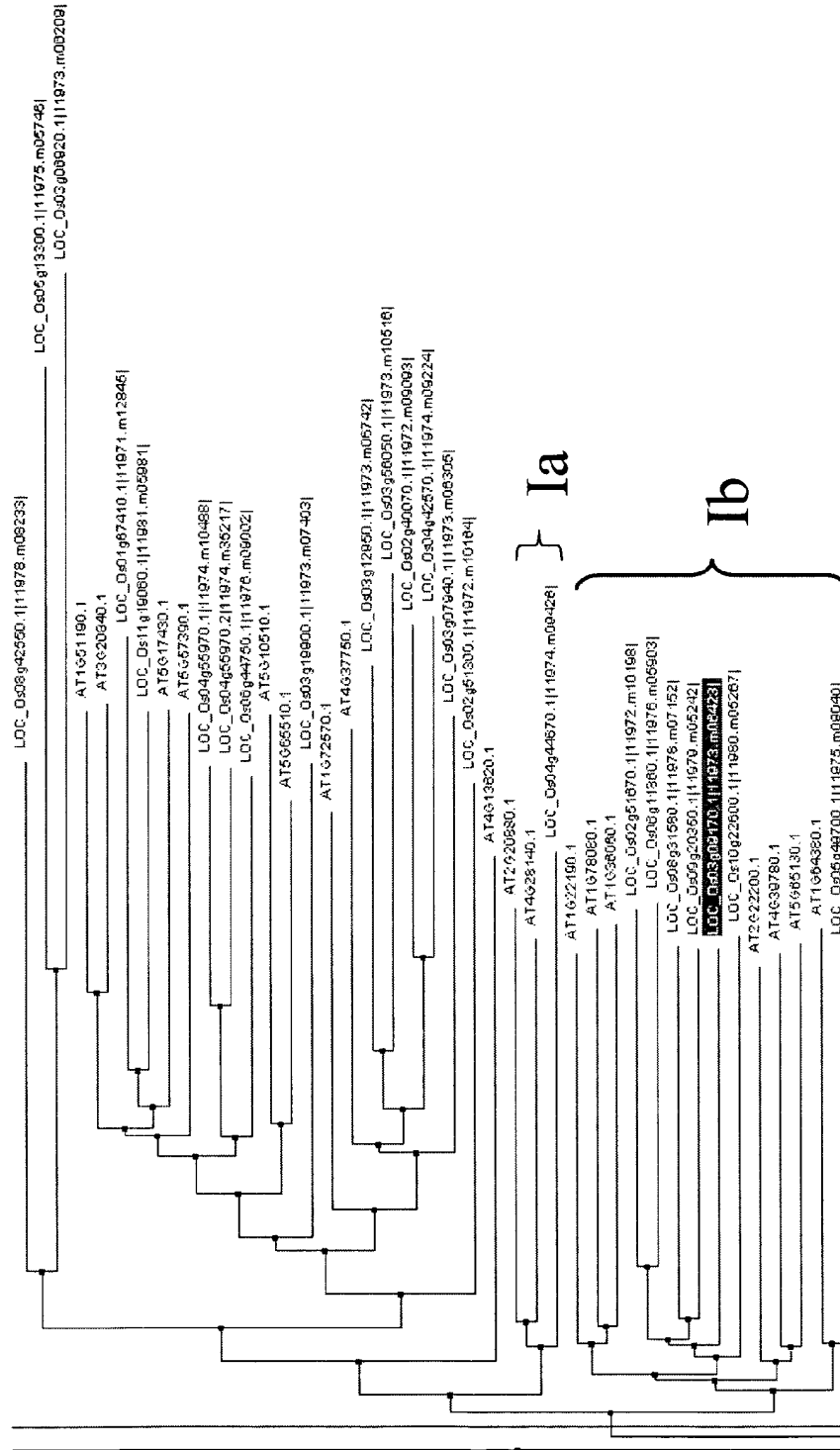


FIGURE 4

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11980.m06650
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11973.m05887
OJ1015F07.11"
ANAC037"AT2G18060"NP_179397.1"
ANAC076"AT4G36160"NP_195339.1"
medicagoABE89364.1|
Ze567"NAC-domain
ANAC105"At5g66300"AAU94387.1"
Maizenac6CAH56056.1
ANAC030"AT1G71930"
CDS4054
11978.m04282
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-----MNS-- 3
-----M 1
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-----MEPME 5
-----MESVD 5
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-----MDRHEEE 7
-----MDRHEEE 7
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ANAC026"AT1G62700"
11980.m06650
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ANAC076"AT4G36160"NP_195339.1"
medicagoABE89364.1|
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Maizenac6CAH56056.1
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QSS-CTVPPGFRFHPTDEELVGYYLRKKVASCKIDLDVIKDIDLYRIEPW 54
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MOTIF I

NAC domain

FIGURE 5

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 DLQERCR----IGNEEQHEWYFFSHKDKKYPTGTRTNRATMAGFWKATGR 95
 DLIERCR----IGYEEQNEWYFFSHKDKKYPTGTRTNRATMAGFWKATGR 100
 DLQERCR----IGYEEQTEWYFFSHRDKKYPTGTRTNRATVAGFWKATGR 101
 DLKERCK----IGTGPNNEWYFFSHKDKKYPTGTRTNRATTAGFWKATGR 99
 DIQARCK----LGEEQNEWYFFSHKDKKYPTGTRTNRATAAGFWKATGR 98
 DLQERCKYG-GHGGDEQTEWYFFSYKDRKYPSGTRTNRATAAGFWKATGR 106
 DLQERCKYG-GHGGDEQTEWYFFSYKDRKYPSGTRTNRATAAGFWKATGR 106

MOTIF II

NAC domain

OSJNBa0075G19.15"NAM-like
 ANAC101"AT5G62380" id="NP_20104
 11972.m09332
 OSJNBb0020011.1protein_id="XP_
 ANAC007/EMB2749"
 ANAC026"AT1G62700"
 11980.m06650
 OSJNBa0053C23.15"NP_922493.1"N
 11973.m05887
 OJ1015F07.11"
 ANAC037"AT2G18060"NP_179397.1"
 ANAC076"AT4G36160"NP_195339.1"
 medicagoABE89364.1|
 Ze567"NAC-domain
 ANAC105"At5g66300"AAU94387.1"
 Maizenac6CAH56056.1
 ANAC030"AT1G71930"
 CDS4054
 11978.m04282
 translationAK071064sense

DKPIYATKQHSLLVGMKRKTLVYYRGRAPNGHKSDWIMHEYR-LETTETAP 159
 DKAIYSKQE---LVGMKRKTLVYKGRAPNGQKSDWIMHEYR-LETDENGP 142
 DKPIYARSC---LVGMKRKTLVYKGRAPNGQKSDWIMHEYR-LETNENGT 142
 DKPIYVKN---LVGMKRKTLVYRGRAPNGQKSDWIMHEYR-LETNEYGA 187
 DKAIYLRHS---LIGMRKTLVYKGRAPNGQKSDWIMHEYR-LETDENGT 142
 DKAIYIRHS---LIGMRKTLVYKGRAPNGQKSDWIMHEYR-LETSNGT 142
 DKAVRERSR---LIGMRKTLVYKGRAPNGHKTDWIVHEYR-LESDENAP 143

 DKAVHDKSR---LIGMRKTLVYKGRAPNGQKTDWIMHEYR-LETDENAP 140
 DKAVHDKSR---LIGMRKTLVYKGRAPNGQKTDWIMHEYR-LETDENAP 140
 DKAVYDKTK---LIGMRKTLVYKGRAPNGKSDWIMHEYR-LESDENAP 144
 DKAVYDKSK---LIGMRKTLVYKGRAPNGQKTDWIMHEYR-LESDENAP 145
 DKSVYERTK---LIGMRKTLVYKGRAPNGQKTDWIMHEYR-LETVENAP 141
 DKAVYEKL---LIGMRKTLVYKGRAPNGQKTDWIMHEYR-LESEENGP 146
 DKAVYLSNK---LIGMRKTLVYRGRAPNGQKSDWIIHEYYSLESHQNSP 148
 DKAIFLGSAR---RIGLRKTLVYIIGRAPHGKKTEWIMHEYR--LDEENVE 145
 DKAVLSKNS---VIGMRKTLVYKGRAPNGRKSQSDWIMHEYR-LQNSELAP 144
 DKPVLSSPSTR-VIGMRKTLVYKGRAPNGRKTWIIHEYR-LQSNEHAP 154
 DKPVLSSPSTR-VIGMRKTLVYKGRAPNGRKTWIIHEYR-LQSNEHAP 154

NAC domain

FIGURE 5 (continued)

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OSJNBa0075G19.15"NAM-like
 ANAC101"AT5G62380" id="NP_20104
 11972.m09332
 OSJNBb0020011.1protein_id="XP_
 ANAC007/EMB2749"
 ANAC026"AT1G62700"
 11980.m06650
 OSJNBa0053C23.15"NP_922493.1"N
 11973.m05887
 OJ1015F07.11"
 ANAC037"AT2G18060"NP_179397.1"
 ANAC076"AT4G36160"NP_195339.1"
 medicagoABE89364.1|
 Ze567"NAC-domain
 ANAC105"At5g66300"AAU94387.1"
 Maizenac6CAH56056.1
 ANAC030"AT1G71930"
 CDS4054
 11978.m04282
 translationAK071064sense

PQ--EEGWVVCRAFKKRLPTTRRDSHDAPCGSWYVDEDAPGAFMSPMMI 207
 PH--EEGWVVCRAFKKKLTMTMNYN-NPRTMMGSSSGQESN--WFTQQMDV 187
 TP--EEGWVVCRAFKKRVAT-VRRMA--DG--SPCWFDHGAAGAFMPDL 185
 PQ--EEGWVVCRAFKKRVAA-VQRAAG-DGGDSPFWFNEHVAFMAPAGL 233
 PQ--EEGWVVCRAFKKRLAA-VRRMGDYDSSPS-HWYDDQLSFMASELET 188
 PQ--EEGWVVCRAFKKRLAATVRKMGDYHSSPSQHWYDDQLSFMASEIIS 190
 PQ--EEGWVVCRAFKKRLTMQPPRSSIGAWIAS-----YSYHDPVAVFVG 185
 -----MQPPRSSIGAWIAS-----YSYHDPVAVFVG 26
 PQ--EEGWVVCRAFKKRLTAYPARSMVETWDYSLHERNIMSAAAAAFAADP 188
 PQ--EEGWVVCRAFKKRLTAYPARSMVETWDYSLHERNIMSAAAAAFAADP 188
 PQ--EEGWVVCRAFKKRLATGQAKNTETWSS-SYFYDEVAPNGVNSVMDP 190
 PQ--EEGWVVCRAFKKRLPMTGQAKNTETWSS-SYFYDELPSGVRVSTEP 191
 PQASEEGWVVCRAFKKRLTSVQAKNTETWSS-SYFYDELPSGVRVSTEP 188
 PQ--EEGWVVCRAFKKRLATGQTRTTTAWES-NYFLDESS--LLTSTMD- 189
 PQ--EEGWVVCRAFKKRLTTIPTKRRQLWDPNCLFYDDAT---LLEPLDK 192
 IQ--EDGWVVCRAFKKRL---NYEQRGHNMALDDELDQPFVTPVVP 189
 VQ--EEGWVVCRAFKKRLPNQRPLGYEPWQNLQYHVESNNYSSSVTMT 192
 TQ--EEGWVVCRAFKKRLMPNQQQHRLSYGCI PGSYGAGAYAAVPDNYSL 202
 TQ--EEGWVVCRAFKKRLMPNQQQHRLSYGCI PGSYGAGAYAAVPDNYSL 202
 MQ--EEGWVVCRAFKKRLMPNQQQHRLSYGCI PGSYGAGAYAAVPDNYSL 48

MOTIF III

NAC domain

OSJNBa0075G19.15"NAM-like
 ANAC101"AT5G62380" id="NP_20104
 11972.m09332
 OSJNBb0020011.1protein_id="XP_
 ANAC007/EMB2749"
 ANAC026"AT1G62700"
 11980.m06650
 OSJNBa0053C23.15"NP_922493.1"N
 11973.m05887
 OJ1015F07.11"
 ANAC037"AT2G18060"NP_179397.1"
 ANAC076"AT4G36160"NP_195339.1"
 medicagoABE89364.1|
 Ze567"NAC-domain
 ANAC105"At5g66300"AAU94387.1"
 Maizenac6CAH56056.1
 ANAC030"AT1G71930"
 CDS4054
 11978.m04282
 translationAK071064sense

TRSSILRPHQHAG-----ITLQEQHLHTTYK-----HRD 237
 GNG-----NYHYL-----PDLESPRMFQSS-----SSS 211
 SSPRQLLPHHHHHPGSSAALYHGHHHQQQLQMYG-----HCKPE 225
 DSP-----YHGHRSHP-----CKLE 249
 NGQRILPNHHQQQ-----QHEHQHMPYGLNASAYALNNPNLQCKQE 231
 SSPRQLPNHHYN-----RHHHQTLPCLN--AFNNNNPNLQCKQE 230
 GEHFKQEAAAE-----LDG-----VAAAA-----GANA 208
 GEHFKQEAAAE-----LDG-----VAAAA-----GANA 49
 SAAYAQMRRQH-----RSGRFKQEAELDG-----AATA 216
 SAAYAQMRRQH-----RSGRFKQEAELDG-----AATA 216
 IDYISKQQHNI-FG-----KGLMCKQELEGMV-----DGIN 220
 LNYVSKQKQNV-FA-----QDLMFQKQLEGS-----IGLN 221
 IDLILRQPQRI-SA-----QNFMYKQIEAEA-----DTLL 218
 -DYTTTQPSNIPLT-----SSFMCQKQLEAS-----ENLN 218
 RARHNPDTATPFK-----QELLSEASHVQDG-----DFGS 223
 AGTSSLPTTDHKN-----PHLMQYDFPSFDP-----SMQ 219
 SHHIGASSSSHN-----QMLMSNNHYNPNN-----TSSS 223
 LHHDNPSFAGRPLMSAAASALFANNNNNSVVDHSN-----ILSSE 242
 LHHDNPSFAGRPLMSAAASALFANNNNNSVVDHSN-----ILSSE 242
 LHHDNPSFAGRPLMSAAASALFANNNNNSVVDHSN-----ILSSE 88

FIGURE 5 (continued)

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OSJNBa0075G19.15"NAM-like
ANAC101"AT5G62380"ID="NP_20104
11972.m09332
OSJNBb0020011.lprotein_id="XP_
ANAC007/EMB2749"
ANAC026"AT1G62700"
11980.m06650
OSJNBa0053C23.15"NP_922493.1"N
11973.m05887
OJ1015F07.11"
ANAC037"AT2G18060"NP_179397.1"
ANAC076"AT4G36160"NP_195339.1"
medicagoABE89364.1|
Ze567"NAC-domain
ANAC105"AT5g66300"AAU94387.1"
Maizenac6CAH56056.1
ANAC030"AT1G71930"
CDS4054
11978.m04282
translationAK071064sense

LTTKIQ-----QLQVP-AAGHLLNTMPHDLES----- 264
LSSLHQ-----NDQDPYGVVLSTINATPTTIMQ----- 239
LEYHH-----LLPQEAFLQHLPLESPKPPPPPPAAAAYIGG- 262
VEYHHH-----LLPQEAAPFMHLPRLESPKLP-----AADII--- 281
LELHYNHLVQR---NHLLDESHLSFLQLPLESPKIQDNSNCNSLPYGT 278
LELHYNQMVFHQQQNHHLRES--MFLQLPLESP-----TSNCN----- 267
FLRYST-----RLAELPLESP----- 225
FLRYST-----RLAELPLESP----- 66
LLHYSS-----HLAELPLESPSAAA----- 237
LLHYSS-----HLAELPLESPSAAA----- 237
-YIQSN-----QFIQLPLQLQSPSLPL----- 240
-FIHCD-----QFIQLPLESPSLPL----- 241
RFMHSE-----QLVPLPLQLQSPS--L----- 237
-FIHCD-----QFIQLPHLESPSLQS----- 238
MYLQCID-----DDQFSQLPLESPSLPS----- 247
LPQLMS-----ADQFVPTLFPSHPGV----- 240
MHQYGN-----IELPQLDSPSLSP----- 242
SKLHFS-----DMMPPLESPTIVDGEgyvsQASSCV 273
SKLHFS-----DMMPPLESPTIVDGEgyvsQASSCV 273
SKLHFS-----DMMPPLESPTIVDGEgyvsQASSCV 119

----STSSFHSLVSPDHHQINMHHAQADPFFDDMHAVDQA----- 301
----RDD--GHVITNDDDHMMIMNTSTGDHHQSGLLVNDHDN-----D 276
----HLGSSSSTALTTHDDEASGSAAQQPPSLEAVYMAGAGVG--IGVDA 307
----VATAASSALQP----CGHTTAQQLQLQIEPVYVT-----ADA 314
SNIDNNSSHNANLQQS-NIAHEEQNLQGNQNFSSLYMNSGNE---QVMD 323
SDNNNNTRNISNLQKSSNISHEEQQLQGNQSFSSLYYDQGV-----QMT- 312
--PLPSQGSQAASAVVDG--EEDNADSSRRPGGG-----GGAAAA 261
--PLPSQGSQAASAVVDG--EEDNADSSRRPGGG-----GGAAAA 102
-APLQPNPSQLATAGEDDDCKGDNNGRRRAKKARA-----AGDKVA 276
-APLQPNPSQLATAGEDDDCKGDNNGRRRAKKARA-----AGDKVA 276
-MKRPSSSMSITSMDNNYN-YKLFLADEE-SFESFIR-GEDRRKKKKQVM 286
-TKRPVSLTSITSLEKNKNIYKRHLIEEDVSFNALISSGNKDKKKKTSV 290
-TKRQNS-----MPIISEK----- 250
-IKRPISSILYEHDQEDDQITKRITNNVRSKDE----- 271
-EITPHSTTFSENSSRKDD----MSSEK----- 270
-ATAMSSSIDVECSQNLTLTSLTNGSDGMLHVRAGGAGAG----VDRFA 284
-----SLGTNKDQNESFEQEEKSFN----- 263
DVDQQAGIVDWNLLTSLPPPAHQLFHHLPSAS---SSKN----- 310
DVDQQAGIVDWNLLTSLPPPAHQLFHHLPSAS---SSKN----- 310
DVDQQAGIVDWNLLTSLPPPAHQLFHHLPSASGVITSRVRGD--GAAAA 167

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FIGURE 5 (continued)

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OSJNBa0075G19.15"NAM-like	TTTDWRVLDKFVASQLSN-----DATNKPAD-----HYTDEG	333
ANAC101"AT5G62380" id="NP_20104	QVMDWQTLDFKVASQLIMSQEEEEVNKDPSD-----NSSNE-	312
11972.m09332	SVTDWRLLDKFVASQLLSKE---SMSSYGS-----HPAQV	339
OSJNBb0020011.1protein_id="XP_	SAADWRDLDFKVASQFGHGD---STAKEPSY-----CNPVQV	348
ANAC007/EMB2749"	QVTDWRVLDKFVASQLSNEE---AATASASI-----QNNAK-	356
ANAC026"AT1G62700"	--TDWRVLDKFVASQLSNDEEAAAVVSSSSH-----QNNVKI	347
11980.m06650	VTTDWRADFDFKVASQLSPPEQHTCRAT-----D	289
OSJNBa0053C23.15"NP_922493.1"N	VTTDWRADFDFKVASQLSPPEQHTCRAT-----D	130
11973.m05887	TTTDWRALDKFVASQLSPGECGSMEATAEAAAA-----AVAGVSSPLDHG	321
OJ1015F07.11"	TTTDWRALDKFVASQLSPGECGSMEATAEAAAA-----AVAGVSSPLDHG	321
ANAC037"AT2G18060"NP_179397.1"	MTGNWRELDFKVASQLMSQEDNGTSSSFAGHH-----IVNEDKNNN-	326
ANAC076"AT4G36160"NP_195339.1"	MTTDWRALDKFVASQLMSQED-GVSGFGGHHEEDNNKIGHYNNEESNKG	339
medicagoABE89364.1	-VTDWRDLDFKVASQLS-----QEDHRHET	274
Ze567"NAC-domain	-VRDWRDLDFKVASQLSQEEEEIRCVEEG-----FSTNFQENI	307
ANAC105"AT5g66300"AAU94387.1"	RITDWRVLDKFVASQFL-----	287
Maizenac6CAH56056.1	GTTDWSILDKLLASHQNLGQLFHGKVTAASASP-----MAPYHQQLMEL	328
ANAC030"AT1G71930"	-CVDWRTLDTLLETQVIHPHN-----PNIL	287
CDS4054	-----SNNISSSGF	319
11978.m04282	-----SNNISSSGF	319
translationAK071064sense	AAAGWRGRGTGWRPSGPWPSGASTPSAPPPTAAP-----IPSRASGTGS	211
OSJNBa0075G19.15"NAM-like	DILQVSDKQQEV-----AAADYASTSTSSSQIDPWK-	364
ANAC101"AT5G62380" id="NP_20104	TFHHLSEEQAAAT-----MVSMNASSSSSPCSFYSWAQ	344
11972.m09332	FQAADGGKHHEA-----LDYAS--TSAGSGGGEADLWK-	370
OSJNBb0020011.1protein_id="XP_	FQVE--GKQEDS-----LDYVS--TSASCGG-EEDLWK-	376
ANAC007/EMB2749"	DTSNAEYQVDEE-----KDPKRASDMGEEYT---ASTSSSQIDLWK-	395
ANAC026"AT1G62700"	DTNRNTGYHVIDEGINLPENDSERVVEMGEEYSNAHAASTSSSQIDL---	394
11980.m06650	DDDMAALLLLDGGGQEDDAGRWLGSAGLLSAVAADATTDGCLGTSCVPGD	339
OSJNBa0053C23.15"NP_922493.1"N	DDDMAALLLLDGGGQEDDAGRWLGSAGLLSAVAADATTDGCLGTSCVPGD	180
11973.m05887	DDDMAALLFLNSD-ERDEVDRWTG---LLGSGAGASGVGDGLG-ICVFDK	366
OJ1015F07.11"	DDDMAALLFLNSD-ERDEVDRWTG---LLGSGAGASGVGDGLG-ICVFDK	366
ANAC037"AT2G18060"NP_179397.1"	DVEMDSSMFLSERE-----EENRFVSEFLSTNS--DYDIG-ICVFDN	365
ANAC076"AT4G36160"NP_195339.1"	SVETASSTLLSDRE-----EENRFISGLLCSNL--DYDLY-RDLHV-	377
medicagoABE89364.1	SSDMSLFLQLSSKD-----DEENKLSSFLTTRS--DCDIG-ICVFEN	313
Ze567"NAC-domain	DHSTSLSHMFNYQDIEEYSGCDKGGKLNGLSSTSSDHFVDG-ICIFDK	356
ANAC105"AT5g66300"AAU94387.1"	-----MSGED-----	292
Maizenac6CAH56056.1	GWLVVVVVLAEASTAVPQRRDRSPQVPQVIIGSTSSLATLLSSDHIRIL	378
ANAC030"AT1G71930"	MFETQSYNPAPSPF-----SMHQSYNEVEANIHSLGCFPDS--	324
CDS4054	IDD-----RD-----	324
11978.m04282	IDD-----RD-----	324
translationAK071064sense	LPNPNPPLLRDRHREALSQIIRQFDPNPCRYSVEKARYVYVGLFPPEGR	261
OSJNBa0075G19.15"NAM-like	-----	
ANAC101"AT5G62380" id="NP_20104	NTHT-----	348
11972.m09332	-----	
OSJNBb0020011.1protein_id="XP_	-----	
ANAC007/EMB2749"	-----	
ANAC026"AT1G62700"	-----	
11980.m06650	IN-----	341
OSJNBa0053C23.15"NP_922493.1"N	IN-----	182
11973.m05887	-----	
OJ1015F07.11"	-----	
ANAC037"AT2G18060"NP_179397.1"	-----	
ANAC076"AT4G36160"NP_195339.1"	-----	
medicagoABE89364.1	-----	
Ze567"NAC-domain	L-----	357
ANAC105"AT5g66300"AAU94387.1"	-----	
Maizenac6CAH56056.1	VDY-----	381
ANAC030"AT1G71930"	-----	
CDS4054	-----	
11978.m04282	-----	

FIGURE 5 (continued)

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CDS4035 -----MG--MGMRERDAEAEELNL 17
AY103772.1zeamaystranslation -----MGQPVTTRRRERDAEAEELDL 19
taNAC2 -----MGMPAVRRRRERDAEAEELNL 19
TAGRAB1CAA09371.1" -----MVMAAAER--RDAEAEELNL 17
riceNP_911548.1" -----MAAAKRRVRDAEADNL 17
elaeis -----MGSRRRDAEAEELNL 14
OsNAC4 -----MAAAVGGSGRRDAEAEELNL 19
GmNAC2"AAY46122.1" -----MASELEL 7
PetuniaNH10="nam-like -----MTTAEQL 8
BnNAC18"NAC-domain -----MSEL-QL 6
ATAF1 -----MSELLQL 7
PrunusPm74"NAC -----MSSDDLQL 8
OsNAC6"protein_id="BAA89800.1" -----MSGG-----QDLQL 9
Saccharum -----MSGGG-----QDLQL 10
AK068392"putative -----MSGGGEGAAAAERQELQL 18
OsNAC5"BAA89799.1" -----MECGGALQL 9
tomatoNAC -----MNKGANGNQLEL 13
solanum"putative -----MNKGATGNQLEL 13
CaNAC1 -----MIKGIVGNQQLGL 13
BrassicaNAC5-8"NAC-domain -----MKAGLNL 7
AT5G08790="ATAF2"NP_680161.1" -----MKSELNL 7
ANAC102 MDFALFSSISIFEINHKKDPPIRRFIKTQNRILSTRKQQGTFPKMKAEELNL 50
NAC69-3"TaNAC69-3"NAC -----MPMGSSSAAMPAL 13
NAC69-1"TaNAC69"NAC -----MPMG-SSAAMPAL 12
CDS4034translationNAC3 -----MPSSGGAMPAL 11
medicagoNAClike -----MGTPQTNL 8
LeNAC-NOR"transcription -----MESTDSSTGTRHQPL 16
ONAC10AK063406 -----MESPDSSSGSAPPRVLRQQQPGSAPEL 29
Arabidopsis -----MGVREKDFLAQLSL 14
ONAC24 -----MAMQLSLPVL 10

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CDS4035 PPGRFRHPTDDELVEHYLCRKAAGQRLVPVPIIAEVDLYKFDPWDLPERAL 67
AY103772.1zeamaystranslation PPGRFRHPTDDELVEHYLCRKAAGQRLVPVPIIAEVDLYRFDPWDLPERAL 69
taNAC2 PPGRFRHPTDDELVEHYLCRKAAGQRLVPVPIIAEVDLYRFDPWALPDRLAL 69
TAGRAB1CAA09371.1" PPGRFRHPTDEELVADYLCARAAGRAPPVPIIAEVDLYRFDPWELPERAL 67
riceNP_911548.1" PPGRFRHPTDEELVAHYLCPRAAAGRAAPVPIIAEVDLYRHDWDLPHRAL 67
elaeis PPGRFRHPTDEELVVHYLCCKKACQRLVPVPIIAEVDLYKDPWDLPEKAL 64
OsNAC4 PPGRFRHPTDEELVVHYLCRKVARQPLVPVPIIAEVDLYKDPWDLPEKAL 69
GmNAC2"AAY46122.1" PPGRFRHPTDEELVLHYLCRKASQPIAVPIIAEIDLYKDPWDLPLGLAT 57
PetuniaNH10="nam-like PPGRFRHPTDEELVMHYLCRKASQPIAVPIIAEIDLYKDPWDLPLDAL 58
BnNAC18"NAC-domain PPGRFRHPTDEELVMHYLCRKASQSIAPVPIIAEIDLYKDPWELPGLAL 56
ATAF1 PPGRFRHPTDEELVMHYLCRKASQSIAPVPIIAEIDLYKDPWELPGLAL 57
PrunusPm74"NAC PPGRFRHPTDEELVKHYLCRKCSQPIAVPIIAEIDLYKYNPWLPLGLAL 58
OsNAC6"protein_id="BAA89800.1" PPGRFRHPTDEELVMHYLCRRACGLPIAVPIIAEIDLYKFDWQLPRMAL 59
Saccharum PPGRFRHPTDEELVMHYLCRRACSLPIAVPIIAEIDLYKFDWQLPRMAL 60
AK068392"putative PPGRFRHPTDEELVMHYLCRRACGLPIAVPIIAEVDLYKFDWHLPRMAL 68
OsNAC5"BAA89799.1" PPGRFRHPTDDELVMYYLCRKCGGLPLAAPVIAEVDLYKFNWDLPERAM 59
tomatoNAC PAGFRFHPTDDELVQHYLCRKACGQSIAPVPIIAEIDLYKFDWQLPEKAL 63
solanum"putative PAGFRFHPTDDELVQHYLCRKACGQPIAVSIITEIDLYKFDWQLPEKAL 63
CaNAC1 PAGFRFHPTDDELVQHYLCRKACGQSIAPVPIIAEIDLYKFDWQLPEKAL 63
BrassicaNAC5-8"NAC-domain PAGFRFHPTDEELVQHYLCRKACSEIAPVIAEIDLYKFNWELPEMSL 57
AT5G08790="ATAF2"NP_680161.1" PAGFRFHPTDEELVKFYLCRKACSEIAPVIAEIDLYKFNWELPEMSL 57
ANAC102 PAGFRFHPTDEELVKFYLCRRACSEPINVPVIAEIDLYKFNWELPEMAL 100
NAC69-3"TaNAC69-3"NAC PPGRFRHPTDEELIVHYLGRQAASMPSPVPIIAEVDNIYKCNPDWLPKAL 62
NAC69-1"TaNAC69"NAC PPGRFRHPTDEELIVHYLRRQAASMPSPVPIIAEVDNIYKCNPDWLPKAL 62
CDS4034translationNAC3 PPGRFRHPTDEELIVHYLMNQAAASVKCPVPIIAEVDNIYKCNPDWLPKAL 61
medicagoNAClike PPGRFRHPTDAELILHYLRKKIASIPLVPSIIAEVDIYKLDWDLPAKAS 58
LeNAC-NOR"transcription PPGRFRHPTDEELIVHYLKKRVAGAPIVDIIGEIDLYKFDWELPAKAI 66
ONAC10AK063406 PPGRFRHPTDEELVVHYLKKKAASVPLVPTIIAEVDLYKFDWDLPEKAN 79
Arabidopsis PTGFRFHPTDEELLVQYLCRKVAGYHFSLQVIGDIDLYKFDWDLPSKAL 64
ONAC24 PTGFRFHPTDEELVINYLQRRATGLSCPIPIADVEIYNFNWELPSMAL 60

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*,****:*** **: * : * : * : * : *

MOTIF IV

NAC DOMAIN

FIGURE 6

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CDS4035      FGAREWYFFTPDRDKYPNGSRPNRAAGNGYWKATGADKPVAPRG----- 111
AY103772.1zeamaystranslation  FGAREWYFFTPDRDKYPNGSRPNRAAGDGYWKATGADKPVAPRAAAD-- 117
taNAC2      FGTREWYFFTPDRDKYPNGSRPNRAAGNGYWKATGADKPVAPRG----- 113
TAGRAB1CAA09371.1"  FGAREWYFFTPDRDKYPNGSRPNRAAGCGYWKATGADRPVARAG----- 111
riceNP_911548.1"  FGRREWYFFTPDRDKYPNGSRPNRAAASGYWKATGADKPVVHNG----- 111
elaeis      FGLKEWYFFTPDRDKYPNGSRPNRAAGRGYWKATGADKPVTPKGS----- 109
OsNAC4      FGRKEWYFFTPDRDKYPNGSRPNRAAGRGYWKATGADKPVAPKGS----- 114
GmNAC2"AA46122.1"  YGEKEWYFFSPDRDKYPNGSRPNRAAGTGYWKATGADKPIGQPK----- 101
PetuniaNH10="nam-like  YGEKEWYFFSPDRDKYPNGSRPNRAAGTGYWKATGADKPIGHPK----- 102
BnNAC18"NAC-domain  YGEKEWYFFSPDRDKYPNGSRPNRSAGSGYWKATGADKPIGLPK----- 100
ATAF1      YGEKEWYFFSPDRDKYPNGSRPNRSAGSGYWKATGADKPIGLPK----- 101
PrunusPm74"NAC    YGEKEWYFFSPDRDKYPNGSRPNRAAGSGYWKATGADKPIGSPK----- 102
OsNAC6"protein_id="BAA89800.1"  YGEKEWYFFSPDRDKYPNGSRPNRAAGSGYWKATGADKPVGSPK----- 103
Saccharum    YGEKEWYFFSPDRDKYPNGSRPNRAACSGYWKATGADKPVGTPK----- 104
AK068392"putative  YGEKEWYFFSPDRDKYPNGSRPNRAAGSGYWKATGADKPVGTPR----- 112
OsNAC5"BAA89799.1"  GGEKEWYFFSPDRDKYPNGQRPNRAAGTGYWKATGADKPVGSPR----- 103
tomatoNAC    YGEKEWYFFSPDRDKYPNGSRPNRAAGTGYWKATGADKPVGKPK----- 107
solanum"putative  YGEKEWYFFSPDRDKYPNGSRPNRAAGTGYWKATGADKPVGKPK----- 107
CaNAC1      YGEKEWYFFSQEDRKYPNGSRPNRAAGTGYWKATGADKPVGKPK----- 107
BrassicaNAC5-8"NAC-domain  YGEKEWYFFSPDRDKYPNGSRPNRAAGTGYWKATGADKPIGKPK----- 101
AT5G08790"="ATAF2"NP_680161.1"  YGEKEWYFFSPDRDKYPNGSRPNRAAGTGYWKATGADKPIGKPK----- 101
ANAC102     YGEKEWYFFSHRDRKYPNGSRPNRAAGTGYWKATGADKPIGKPK----- 144
NAC69-3"TaNAC69-3"NAC  FGENEWYFFSPDRDKYPNGARPNRAAGSGYWKATGTDKAILSTPANES-- 111
NAC69-1"TaNAC69"NAC  FGENEWYFFSPDRDKYPNGARPNRAAGSGYWKATGTDKAILSTPANES-- 110
CDS4034translationNAC3  FGENEWYFFSPDRDKYPNGARPNRAAGSGYWKATGTDKISILSTPTSDN-- 109
medicagoNAClike  FGEKEWYFFSPDRDKYPNGARPNRAAASGYWKATGTDKTIIVASLPCGGGR 108
LeNAC-NOR"transcription  FGEQEWFFSPDRDKYPNGARPNRAATSGYWKATGTDKPVFTSGGTQK-- 114
ONAC10AK063406  FGEQEWYFFSPDRDKYPNGARPNRAATSGYWKATGTDKPIVMSGSTR--- 126
Arabidopsis  FGEKEWYFFSPDRDKYPNGSRPNRVAGSGYWKATGTDKIITADGR----- 109
ONAC24      FGEHEWYFFTLRDHRYPNVSRPSRSAASGFWKATGTDKPVQVANMQST-- 108
* .*:*: : .*:*: : .*:*: : .*:*: : .*:*: : .*:*: : .*:*: :

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MOTIF V

NAC DOMAIN

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CDS4035      ---RTLGIKKALVFYAGKAPRGVKTDWIMHEYRLA----DAGRA----- 148
AY103772.1zeamaystranslation  --ARTLGIKKALVFYAGKAPRGVKTDWIMHEYRLA----DAG----- 153
taNAC2      --GRTMGIKKALVFYAGKAPRGVKTDWIMHEYRLA----DAGR----- 150
TAGRAB1CAA09371.1"  ---RTVGIKKALVFYHGRPSAGVKTDWIMHEYRLA----GADGR----- 148
riceNP_911548.1"  ---RTAGIKKALVFYHKGPPRGVKTDWIMHEYRLA----KKGGA----- 148
elaeis      --SRPLGIKKALVFYSGKAPRGVKTDWIMHEYRLA----DTNR----- 146
OsNAC4      ---ARTVGIKKALVFYSGKAPRGVKTDWIMHEYRLA----DADR----- 151
GmNAC2"AA46122.1"  ---PVGIKKALVFYAGKAPKGDKNWIMHEYRLA----DVDRS----- 137
PetuniaNH10="nam-like  ---AVGIKKALVFYAGKAPKGEKTNWIMHEYRLA----DVDRS----- 138
BnNAC18"NAC-domain  ---PVGIKKALVFYAGKAPKGEKTNWIMHEYRLA----DVDRS-----A 138
ATAF1      ---PVGIKKALVFYAGKAPKGEKTNWIMHEYRLA----DVDRS----- 137
PrunusPm74"NAC    ---PVGIKKALVFYAGKAPKGEKTNWIMHEYRLA----DVDRS----- 138
OsNAC6"protein_id="BAA89800.1"  ---PVAIKKALVFYAGKAPKGEKTNWIMHEYRLA----DVDRS----- 139
Saccharum    ---PLAIKKALVFYAGKAPKGEKTNWIMHEYRLA----DVDRS----- 140
AK068392"putative  ---PVAIKKALVFYAGKAPKGDKNWIMHEYRLA----DVDRS----- 148
OsNAC5"BAA89799.1"  ---AVAIKKALVFYAGKPPKGVKTNWIMHEYRLA----DVDRSA-----A 141
tomatoNAC    ---TLGIKKALVFYAGKAPRGIKTNWIMHEYRLA----NVDRS----- 143
solanum"putative  ---TLGIKKALVFYAGKAPRGIKTNWIMHEYRLA----NVDRS----- 143
CaNAC1      ---TLGIKKALVFYAGKAPRGIKTNWIMHEYRLA----NVDRS----- 143
BrassicaNAC5-8"NAC-domain  ---TLGIKKALVFYAGKAPKGIKTNWIMHEYRLA----NVDRS----- 137
AT5G08790"="ATAF2"NP_680161.1"  ---TLGIKKALVFYAGKAPKGIKTNWIMHEYRLA----NVDRS----- 137
ANAC102     ---TLGIKKALVFYAGKAPKGIKTNWIMHEYRLA----NVDRS----- 180
NAC69-3"TaNAC69-3"NAC  -----IGVKKALVFYRGKPPKGVKTDWIMHEYRLT---AADNRT-----T 148
NAC69-1"TaNAC69"NAC  -----IGVKKALVFYRGKPPKGVKTDWIMHEYRLT---AADNRT-----T 147
CDS4034translationNAC3  -----IGVKKALVFYKGPVKGVKTDWIMHEYRLTGTSTANSTTT-----T 149
medicagoNAClike  SQENIIGVKKALVFYKGPVKGIKTNWIMHEYRLV---DNNKP-----I 149
LeNAC-NOR"transcription  -----VGKKALVFYGGKPPKGVKTNWIMHEYRVVENKTNNKPLGCDNIV 159
ONAC10AK063406  ---EKVGKKALVFYRGKPPKGVKTNWIMHEYRLT---DTSSSAAAVAT 169
Arabidopsis  ---RVGIKKALVFYAGKAPKGTKNWIMHEYRLI---EHSRS----- 145
ONAC24      ---PVAMKKALVFYVGRPPMETKTTWIMHEYRLT---NTGGSTASHPS 150
.:***** *:.. *: *****:

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NAC DOMAIN

FIGURE 6 (continued)

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CDS4035
AY103772.1zeamaystranslation
taNAC2
TAGRAB1CAA09371.1"
riceNP_911548.1"
elaeis
OsNAC4
GmNAC2"AAY46122.1"
PetuniaNH10="nam-like
BnNAC18"NAC-domain
ATAF1
PrunusPm74"NAC
OsNAC6"protein_id="BAA89800.1"
Saccharum
AK068392"putative
OsNAC5"BAA89799.1"
tomatoNAC
solanum"putative
CaNAC1
BrassicaNAC5-8"NAC-domain
AT5G08790"="ATAF2"NP_680161.1"
ANAC102
NAC69-3"TaNAC69-3"NAC
NAC69-1"TaNAC69"NAC
CDS4034translationNAC3
medicagoNAClike
LeNAC-NOR"transcription
ONAC10AK063406
Arabidopsis
ONAC24

AAGAKK-----GSLRLDDWVLCRLYNKK-----EWEKMQQ-- 180
-GRAKK-----GSLRLDDWVLCRLYNKK-----EWEKMRG-- 184
AAASKK-----GSLRLDDWVLCRLYNKK-----EWEKMQQ-- 182
AAKNG-----GTLRLDEWVLCRLYNKK-----QWEKMQQ-- 179
AAAAGA-----GALRLDDWVLCRLYNKK-----EWEKMQSR-- 180
AAN-KK-----GSLRLDDWVLCRLYNKK-----TWEKMQQ-- 176
APGGKK-----GSQKLDEWVLCRLYNKK-----NWEKVKLE-- 183
VRKKN-----TLRLDDWVLCRIYNKK-----TIEKLQ-- 166
ARKNN-----SLRLDDWVLCRIYNKK-----SIEKNQ-- 168
ARKKKN-----SLRLDDWVLCRIYNKK-----AIEKRG-- 167
VRKKKN-----SLRLDDWVLCRIYNKK-----ATERRG-- 166
PRKKSS-----SLRLDDWVLCRIYNKK-----TVEKQQQ-- 169
ARKKN-----SLRLDDWVLCRIYNKK-----GLEKPPAAV 171
ARKKN-----SLRLDDWVLCRIYNKK-----GLEKP-- 167
ARKKN-----TLRLDDWVLCRIYNKK-----GVEKP-- 175
ARKLSKSSH-----NALRLDDWVLCRIYNKK-----VIERKD-- 174
AGKN-----NNLRLDDWVLCRIYNKK-----TLEKHYN-- 172
AGKN-----NNLRLDDWVLCRIYNKK-----TLEKHYN-- 172
AGKS-----NNLRLDDWVLCRIYNKKCH-----TLRSITM-- 173
ASVKK-----NNLRLDDWVLCRIYNKK-----TMEKYYP-- 168
ASVKK-----NNLRLDDWVLCRIYNKK-----TMEKYFP-- 168
ASTNKK-----NNLRLDDWVLCRIYNKK-----TMEKYL-- 211
KRRGSS-----MRLDDWVLCRIHKKCNLHNFSSSDQEQEHE-- 185
KRRGSS-----MRLDDWVLCRIHKKCGNLPNFSSSDQEQEHE-- 184
KQRRASS-----MTMRLDDWVLCRIHKKSNDFN--SSDQHDQEP-- 187
KLKDS-----MRLDDWVLCRIYKKS-----KCALSTESS-- 180
ANKKS-----LRLDDWVLCRIYKKN-----NTQSIDL-- 189
TRRPPPPITGGSGAVSLRLDDWVLCRIYKKTWKAGAGQSRMECEDVED 219
-HGSS-----KLDDWVLCRIYKKT-----GSQRQAT-- 172
LSSSTAHP-----SVKLDEWVLCIFNKS-----EPDNTAPP-- 183

:***:::*

MOTIF VI

MOTIF VII

NAC DOMAIN

MOTIF VIII

CDS4035
AY103772.1zeamaystranslation
taNAC2
TAGRAB1CAA09371.1"
riceNP_911548.1"
elaeis
OsNAC4
GmNAC2"AAY46122.1"
PetuniaNH10="nam-like
BnNAC18"NAC-domain
ATAF1
PrunusPm74"NAC
OsNAC6"protein_id="BAA89800.1"
Saccharum
AK068392"putative
OsNAC5"BAA89799.1"
tomatoNAC
solanum"putative
CaNAC1
BrassicaNAC5-8"NAC-domain
AT5G08790"="ATAF2"NP_680161.1"
ANAC102
NAC69-3"TaNAC69-3"NAC
NAC69-1"TaNAC69"NAC
CDS4034translationNAC3
medicagoNAClike
LeNAC-NOR"transcription
ONAC10AK063406
Arabidopsis
ONAC24

-----K-----EVK-----EEASDMVT-----SQSHSHTHSWG 203
-----KGAAAGAVKE-----EEAMDMST-----SHSQ-ITHSWG 212
-----QQGEEETMMEPKAENTASDMVTVSHSHSQSQSHSHSWG 220
-----R-----QEEEAANK-----AAASQSVSWG 198
-----K-----EEEEAMAA-----AQSG-----WG 194
-----Q-----KEAASFGE-----TMDS-VDDTGS 195
-----Q-----QDVASVAA-----AAPRNHHQNG 203
-----SSD-VAHSRNIES--SEIEDRKPEILKSGGGCLPPAPVPAPQ 207
-----NNKKIMNTSYMDMTVSSEEDRKPEIL-----PPLPPQAPQ 205
-----PPPTPVVYGDEVVEEKPRLSEMG-----PPP-----PVM 197
-----PPP-PVVYGDIEEKKPKVTEMV-----PPP-----PQ 195
-----QQQQQQTTSRMSSGSEFEDRK-----ENLAC-----PPPPAAVAPTR 208
AAAGMVSSGGGVQRKPMV--GVNAAVSSPPEQKPVV--AGP-AFP-- 211
AAA--SSG--DHKPMV--FAAGAVSSPPEQKPFV--ATPGGLPPAF 206
-----SGGGGGERSNMMSHGETASACSPPEQKPAV--LPPPPPPYAAA 216
-----TVDAGEDVKAAPAAAAAKGGRIGGGGAAAMKVELSDYGFYDQE 218
-----VDNKETTSFGFEDEEIKPKILPTQLA--PMP--PRPR 205
-----VDNKETASFGFEDEEIKPKILPTQLA--QMP--PRPR 205
-----WASKRGESFGFEDEEIKPKIFPTQLA--PAPGQWPPRPQ 210
-----ADEK-----PMTV 176
-----ADEK-----PRTT 176
-----AAAE-----KPTE 219
-----QESSTTVEDSHNNHTVSSPKSEAFDGDGDDQLQLQFRPMAI 227
-----QESS-TVEDSQNNHTVSSPKSEAFDGDGDDHLQLQFRPMAI 225
-----ESTVEQLEDIHNN--SSEQPPAPADMNNQSDQFQPMTASM 227
-----ETMVGVEHAEETQ-----FQETLFPITKNTSPLQNT--LMS 216
-----HDMLGSIQNVNPN-----ILQGIKPSNYGTILLENESNMYD 226
-----AVAAYAPSSQQAATAAGMAGSDGAGGVAAAHGGDYSSLLH 260
-----PVQACREEHSTNGSSSSSSOLD 195
-----SNVVSRLQCSPLPPPAAPPGN 205

FIGURE 6 (continued)

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	MOTIF VIII	MOTIF XI	
CDS4035	ETRTPESEIVD-----NDPFPELDSFPAPQPAPPPATA-----	236	
AY103772.1zeamaystranslation	ETRTPESEIVD-----ND-----LPFPDPA-----	232	
taNAC2	EARTPESEIVD-----NDPSLFQQATAAAFOAQSFAAAAAHOEMM----	260	
TAGRAB1CAA09371.1"	ETRTPESD-VD-----NDPFPELDSLP---EFQTANAS-----	227	
riceNP_911548.1"	ETRTPESEIVD-----SDAFPEMDYSL---PAASFDDA-----	224	
elaeis	DSFRTPESID-----NDVMEFEDDDMAQVGAHPPQAFNGMQGVR----	235	
OsNAC4	EWMDAFAADTM-----SDSFQTHSDIDNASAC---LRHGCGGGG----	241	
GmNAC2"AAAY46122.1"	ATAKTDYMYFD-----PSDSIPKLHT-DSSCSECVVSPGFASE-----	244	
PetuniaNH10="nam-like	QQVYNDFFYLD-----PSDSVPKIHS-DSSCSECVVSPEFTCER-----	243	
BnNAC18"NAC-domain	P---NDFVYFD-----TSDSVPKLHTTESSCSECVVSPEFTSE-----	232	
ATAF1	T---SEFAYFD-----TSDSVPKLHTDSSCSECVVSPEFTSE-----	230	
PrunusPm74"NAC	P---NDYVYFD-----TSDSVPRLHT-DSSCSECVVSPEFTCE-----	242	
OsNAC6"protein_id="BAA89800.1"	----DLAAYYD-----RPSDSMPRLH-ADSSCSECVLSP-EFAC-----	244	
Saccharum	T--ADLAAYYD-----RPSDSMPRLH-ADSSCSECVLSPEQLACD-----	243	
AK068392"putative	APFSELAIFYDV-----RPSDSVPRAHGADSSCSECVLTTSASSGGVV---E	260	
OsNAC5"BAA89799.1"	P--ESEMCLCFDRSGSADRDSMPRLHT-DSSGSEHVLSPSPSPDPFGGGD	265	
tomatoNAC	STPANDYFYFE-----SSESMT--RMHTTNSSSGSE-HVLSPCD-----	241	
solanum"putative	STPTNDYFHE-----SSESMT--RMHTTNSSSGSE-HVLSPCD-----	241	
CaNAC1	STPASDYFNFE-----TSESMTTTRMHTTNSSSGSE-HVLSLCD-----	248	
BrassicaNAC5-8"NAC-domain	TAA---SSPFD-----ASDSTYPTLQEDDSSSSSGGR--VVSPDA-----	210	
AT5G08790"="ATAF2"NP_680161.1"	TMAEQSSSPFD-----TSDSTYPTLQEDDSSSSSGHGHVVSVDV-----	215	
ANAC102	KMS-----TSDSRCSSHVISPD-----VTCSDN-----	242	
NAC69-3"TaNAC69-3"NAC	AKSCSLTDLNLT---VDYAALSHLLLDGAGAGASSSDAGADYQLPPENP	273	
NAC69-1"TaNAC69"NAC	AKSCSLTDLNLT---VDYAALSHLLLD--GAGASSSDAGADYQLPPENP	269	
CDS4034translationNAC3	SKSCSLTDLNLT---IDCAALSQFLD-----GSSDAIAEPPAPP-SP	266	
medicagoNAClike	QKSVSFSNLLDA---MDYSMLSSFLSE-----NSNPNPSGIGTSSGFNT	256	
LeNAC-NOR"transcription	GIMNNTNDIINN---NNRSIPQISSKR---TMHGGLYWNNDATTTTT	268	
ONAC10AK063406	HDSHEDTFLVNG--LLTAEDAAGLSTGASSLSQLAAAAAAATPCDATKQ	308	
Arabidopsis	DVLDSEFPEIKD-----QSFNLRPMNSLRTIILGNFDWASLAGLN-----	234	
ONAC24	YPPLPVGATND-----GGVFACAGDMLFTIOEHQEGTPSMLPP-----	243	

	MOTIF IX	MOTIF X	
CDS4035	----MIVPKKESMDDATAAAAAAATI----	PRNNSSLFVDISYDDIQ---	275
AY103772.1zeamaystranslation	----MIVPKKERVDDGGSAR-----	TSDLFVDISYDDIQ---	262
taNAC2	--ATLMIVPKKEAADEAG-----	RNDLFVDISYDDIQ---	289
TAGRAB1CAA09371.1"	----LKPKEEVQELGN-----	DDWLMGSLDLDLQ---	252
riceNP_911548.1"	----LKPKEEARD-----	DDWLMGSLDLDLQ---	246
elaeis	--VNNITGYQPATEQRPKEE-----	NDWFTDLNLDLDFH---	266
OsNAC4	--FGDVAPPNRGFVT-VKED-----	NDWFTGLNFDELQ---	271
GmNAC2"AAAY46122.1"	---VQSEPK--WNEWEKS-----	LEFPFNYVDAT---	268
PetuniaNH10="nam-like	--EVQSEAK--LSEWEKAA-----	LDLPFNYMDATTGAT	273
BnNAC18"NAC-domain	---VQSEPK--WKDWSGE-----	KSSLDGFGFNYIDAT---	259
ATAF1	---VQSEPK--WKDWSAVSN-----	DNNNTLDGFGFNYIDATV---	262
PrunusPm74"NAC	---VQSEPK--WKEWEKA-----	LDFNINYMDTSV---	267
OsNAC6"protein_id="BAA89800.1"	--EVQSQPK--ISEWERT-----	FATVG---PINPAA---	269
Saccharum	--REVQSQPK--ISEWERT-----	FASD---PVNPAG---	268
AK068392"putative	RPEVQSQPK--IAEWERT-----	FAGAAAPAGAVSTAG---	291
OsNAC5"BAA89799.1"	HDYAESQPSGGCGGWPGVD-----	WAAVGDDGFFVIDSSL---	299
tomatoNAC	-KEVQSAPK--WDEDHR-----	NTLDFQLNYLDGLL---	269
solanum"putative	-KEVQSAPK--WDEDHR-----	NTLDFQLNYLDGLL---	269
CaNAC1	-KEVQSAPK--WDDLGT-----	AALDFQINYLDGLL---	276
BrassicaNAC5-8"NAC-domain	-REVQSEPK--WGEFEN-----	AFDASMFGGGSMDLLQ---	240
AT5G08790"="ATAF2"NP_680161.1"	-LEVQSEPK--WGELEDAL-----	EAFDTSMFG-SSMELLQ---	247
ANAC102	-WEVESEPK--WINLEDAL-----	EAFNDDTSMFSSIGLLQ---	275
NAC69-3"TaNAC69-3"NAC	LIYSQP-PWQQTLYHNNNNN-----	GYVNIIDTID---	301
NAC69-1"TaNAC69"NAC	LIYSQP-PWQQTLYHNNNNN-----	GYVNNETID---	296
CDS4034translationNAC3	LIYTPHPNYQTLNYNINSNSSMPHAFESRLDHHGQYVNNYNVNGLRKR		316
medicagoNAClike	ENFNQQ---QSSHINTCNN-----	YMSQKNPQ---	280
LeNAC-NOR"transcription	TIDRNHSPNTRKFLVENNED-----	DGLNMNNIS---	297
ONAC10AK063406	LLAPSPPTFNWFEAFLPRAKEFPSG----	LSRSSRDIGDMSLSSTVDRS	353
Arabidopsis	-PIPELAPTNGLPSYGG-----	YDAFRAAEEGAES---	263
ONAC24	--IPNLEPPAATIGNSSSLNG-----	TAAAAAADGHHG---	273

FIGURE 6 (continued)

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	MOTIF X	
CDS4035	---GMYSGLDMLPP-GDDF-----YSSL	294
AY103772.1zeamaystranslation	---GMYSGLDMLPPAGEDL-----YSSL	282
taNAC2	---SMYNGLDMMPPGDDLL-----YSSL	309
TAGRAB1CAA09371.1"	---GPGS---IMLPWDDSY-----AASF	269
riceNP_911548.1"	---GLGS---LLQADD-----LSM	259
elaeis	---STCMAFGSTPALDMS-----DHDYYS	288
OsNAC4	---PPYMMNLQHMQMVMNPAAPGH-----DGGYLS	300
GmNAC2"AA46122.1"	---LNNSFM-AQFQGNQMLS-----	285
PetuniaNH10="nam-like	TLDNSLLGSQFQSSYQMS-----	291
BnNAC18"NAC-domain	---AFGGG-GGSNQLF-----	271
ATAF1	---DNAFGGG-GSSNQMF-----	276
PrunusPm74"NAC	---ENGFGPQFQSANQMS-----	282
OsNAC6"protein_id="BAA89800.1"	---SIL---DPAGSGGLGGLGGG-----S	288
Saccharum	---SML---VDPVVGGHAG-----	281
AK068392"putative	---PILGQLDPAAVAGG-----G	307
OsNAC5"BAA89799.1"	---FELPSPAAFSRAAGDG-----	315
tomatoNAC	---NEPFETQMQQQICN-FDQFN-----	288
solanum"putative	---NEPFETQMQQQSCN-FDQFN-----	288
CaNAC1	---NDPFETQMQQQNCN-IDQFN-----	295
BrassicaNAC5-8"NAC-domain	---SEDFVPQFLYQPSYDFNSWQE-----D	262
AT5G08790"="ATAF2"NP_680161.1"	---PDAFVPQFLYQSDY-FTSFQ-----D	267
ANAC102	---NDAFVPQFQYQSSDFVDSFQ-----D	296
NAC69-3"TaNAC69-3"NAC	VPQIPPEARVDDYGMNGDRYNGMKRK-----RSS--GSLYCS-QLQLP	340
NAC69-1"TaNAC69"NAC	VPQIPPEARVDDYGMNGDRYNGMKRK-----RSS--GSLYCS-QLQLP	335
CDS4034translationNAC3	MMACSATSFDDGSSSNDVFHAVVKKPQLLPDSRGSFGGGYCNQQLSET	366
medicagoNAClike	---SNTLKHQLSNVDEDMLYPSKKY-----LSS-----SCNFPNINS	314
LeNAC-NOR"transcription	---RITNHEQSSSIANFLSQFPQN-----PS-----IQQQQQQOE	329
ONAC10AK063406	LSEAGAVAIDTGAANGANTMPAFINPLG---VQGATYQQHQAIMGASLP	400
Arabidopsis	---GHVNRQNNSSGLTQSGF-----	280
ONAC24	-----RLEEEDTSAYTFTD-----	287
CDS4035	FASPRVKGTTPRAGAGMGMVVF----	316
AY103772.1zeamaystranslation	FASPRVRGNQPTGPAXLG--PF----	302
taNAC2	FASPRVRGSQP-GAGGMP-APF----	329
TAGRAB1CAA09371.1"	LSPVATMKMEQDVSPFFF-----	287
riceNP_911548.1"	LAPPPAAKTEPLGAPFF-----	276
elaeis	N-LPQLRSNQSDLLPF-----	303
OsNAC4	ISSPQMKMWQTILPFF-----	316
GmNAC2"AA46122.1"	--PLQDMFMYWPNKSF-----	299
PetuniaNH10="nam-like	--PLQDMFMHL-HKPF-----	304
BnNAC18"NAC-domain	--PLQDMFMYNMPKPY-----	285
ATAF1	--PLQDMFMY-MQKPY-----	289
PrunusPm74"NAC	--PLQDIFMY-LQKPY-----	295
OsNAC6"protein_id="BAA89800.1"	DPLLQDILMY-WGKPF-----	303
Saccharum	DPLLQDILMY-WGKPF-----	296
AK068392"putative	DPLLQDILMY-WGKPF-----	322
OsNAC5"BAA89799.1"	--AAFQDMFTY-LQKPF-----	329
tomatoNAC	--NFQDMFLY-MQKPY-----	301
solanum"putative	--NFQDMFFY-MQKPY-----	301
CaNAC1	--TFQDMFLY-MQKPY-----	307
BrassicaNAC5-8"NAC-domain	PPEQKPFLLNW-SFAPQG-----	278
AT5G08790"="ATAF2"NP_680161.1"	PPEQKPFLLNW-SFAPQG-----	283
ANAC102	PPEQKPFLLNW-NFAPQG-----	312
NAC69-3"TaNAC69-3"NAC	AD----QYSGMLIHPP-LSQQLHM--	359
NAC69-1"TaNAC69"NAC	AD----QYSGMLIHPP-LSQQLHM--	354
CDS4034translationNAC3	ATGFQFQNGNLLSHFFPLNNHLQMQ-	391
medicagoNAClike	QYENYLMKQSLMNQQLLLGPHHQYQG	340
LeNAC-NOR"transcription	EVLGSLNDGVVFRQPYNQVTGMNWYS	355
ONAC10AK063406	SESAAAAACNFQHPFQLSRVNWDS-	425
Arabidopsis	-YSSSGFGVSGQTFEFRQ-----	297
ONAC24	-QEMEQLMLDMDQDFGNDQPQE--	310

FIGURE 6 (continued)

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LOC_Os07g47790.1 11977.m08994	-----MCGG	4
LOC_Os07g47790.2 11977.m29326	-----MCGG	4
LOC_Os01g21120.1 11971.m08596	-----MCGG	4
LOC_Os03g08470.1 11973.m06355	-----MCGG	4
LOC_Os03g08470.2 11973.m34802	-----MCGG	4
AT2G47520.1	-----MCGG	4
LOC_Os02g54160.1 11972.m10445	-----MCGG	4
LOC_Os06g09390.1 11976.m05658 	-----MCGG	4
LOC_Os09g26420.1 11979.m05794	-----MCGG	4
LOC_Os09g26420.2 11979.m21992	-----MCGG	4
LOC_Os09g26420.3 11979.m22092	-----MCGG	4
AT1G53910.1	-----MCGG	4
AT1G53910.2	-----MCGG	4
AT3G14230.1	-----MCGG	4
AT3G14230.2	-----MCGG	4
AT3G14230.3	-----MCGG	4
AT3G16770.1	-----MCGG	4
LOC_Os07g42510.1 11977.m08483	-----MCGG	4
LOC_Os03g08490.1 11973.m06357	-----MCGG	4
LOC_Os03g08500.1 11973.m06358	-----MCGG	4
AT1G72360.1	-----MSQS	4
LOC_Os03g08460.1 11973.m06354	-----MCGG	4
LOC_Os05g29810.1 11975.m07218	-----MCGG	4
LOC_Os03g22170.1 11973.m07620	-----MCGG	4
LOC_Os10g25170.1 11980.m05467	-----MCGG	4
LOC_Os09g11460.1 11979.m04408	-----MCGG	4
LOC_Os09g11460.2 11979.m21977	-----MCGG	4
LOC_Os09g11480.1 11979.m04410	-----MCGG	4
LOC_Os12g41030.1 11982.m07885	-----MCGG	4
LOC_Os12g41060.1 11982.m07888	-----MCGG	4
AT1G80580.1	-----MENS	4

FIGURE 7

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LOC_Os07g47790.1|11977.m08994|
 LOC_Os07g47790.2|11977.m29326|
 LOC_Os01g21120.1|11971.m08596|
 LOC_Os03g08470.1|11973.m06355|
 LOC_Os03g08470.2|11973.m34802|
 AT2G47520.1
 LOC_Os02g54160.1|11972.m10445|
LOC_Os06g09390.1|11976.m05658|
 LOC_Os09g26420.1|11979.m05794|
 LOC_Os09g26420.2|11979.m21992|
 LOC_Os09g26420.3|11979.m22092|
 AT1G53910.1
 AT1G53910.2
 AT3G14230.1
 AT3G14230.2
 AT3G14230.3
 AT3G16770.1
 LOC_Os07g42510.1|11977.m08483|
 LOC_Os03g08490.1|11973.m06357|
 LOC_Os03g08500.1|11973.m06358|
 AT1G72360.1
 LOC_Os03g08460.1|11973.m06354|
 LOC_Os05g29810.1|11975.m07218|
 LOC_Os03g22170.1|11973.m07620|
 LOC_Os10g25170.1|11980.m05467|
 LOC_Os09g11460.1|11979.m04408|
 LOC_Os09g11460.2|11979.m21977|
 LOC_Os09g11480.1|11979.m04410|
 LOC_Os12g41030.1|11982.m07885|
 LOC_Os12g41060.1|11982.m07888|
 AT1G80580.1

AIIISDFIPQREAHRAATG--SK-----RALCASDFWPSASQEA 40
 AIIISDFIPQREAHRAATG--SK-----RALCASDFWPSASQEA 40
 AIIYDIYPAR-----RRLCASDFWP---DA 26
 AIIAEFIPAPSRAAAATKRVT-----SHLWPAGSKNAARGKS 42
 AIIAEFIPAPSRAAAATKRVT-----SHLWPAGSKNAARGKS 42
 AIIISDFIWSK-----ESEPSQLG-S 24
 AIIHHLKGHEGSRRATEGLLWPEKK-----PRWGGGRRHFGGFVEE 48
AIIISDLIPPP--RRVTAGDLWLEKTKKQQ--QKKKNKGARRLP-LRQE 48
 AIIISGFIPPS--AAAAAAAVAKKQGGRRVT--ADVLWPGMLRKG-KAAA 49
 AIIISGFIPPS--AAAAAAAVAKKQGGRRVT--ADVLWPGMLRKG-KAAA 49
 AIIISGFIPPS--AAAAAAAVAKKQGGRRVT--ADVLWPGMLRKG-KAAA 49
 AIIISGFIPPS--AAAAAAAVAKKQGGRRVT--ADVLWPGMLRKG-KAAA 49
 AIIISDFIPPPRRRVTSEFIWPDLLKKNLK-----GSKKSSKNRSNFFD 47
 AIIISDFIPPPRRRVTSEFIWPDLLKKNLK-----GSKKSSKNRSNFFD 47
 AIIISDFIPPPRRSLRVTFNEFIWPDLLKKNVK-----ASKKRSNKRSDFFD 47
 AIIISDFIPPPRRSLRVTFNEFIWPDLLKKNVK-----ASKKRSNKRSDFFD 47
 AIIISDFIPPPRRSLRVTFNEFIWPDLLKKNVK-----ASKKRSNKRSDFFD 47
 AIIISDYAP-----LVTAK-----GRKLTAEEL--WSE 30
 SILGDLHLPVRRTVNAGDLWGDAGKGRDGDGLKKRKGSSWDFDVCDDDD 54
 AIIANIIIPATPP-RPATAAHVWPG-----DGEKRRKVGGGG 40
 AIIAELIPSAAPAARRVTAGHVWPG-----DANKAKKKGAR- 39
 FELYPWLG-----DANKAKKKGAR- 12
 AIIADFTPARVPRRLTAAELLPVTPTPPAAERTTRKRKSDVDFEAEFEL 54
 AIIADFVPPAGARRAAASDIS----- 25
 AIP--LISSRGPG-----KRSLSAADELWP 28
 AIIADLIPSPRSGGHTKKN-----KRRRISDDEDEFEA 59
 -----RVSSSSSSSSSSP-----ARHKKARRSRRLA 31
 -----RVSSSSSSSSSSP-----ARHKKARRSRRLA 31
 ALIPNDYGDKPPPPPPSESEWD-----ATTKMKKKKKRGGG 40

 GPDNHHAITVAADLPPPPPSVVAVEMAPP-----RGHRPGKEVEYNEEE 48
 YTVDGHRLQSVPLSSMHETSQNSSETYGL-----SKESPLVCMPLFETN 48

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	ADEFHLTAPCTFT-----PDQA-----	57
LOC_Os07g47790.2 11977.m29326	ADEFHLTAPCTFT-----PDQ-----	56
LOC_Os01g21120.1 11971.m08596	DDSD---PHTPA-----PEK-----	38
LOC_Os03g08470.1 11973.m06355	KSKRQRSFADVDDFEAAFEQFDDSDSDFDAAEEDEGHFV-----	82
LOC_Os03g08470.2 11973.m34802	KSKRQRSFADVDDFEAAFEQFDDSDSDFDAAEEDEGHFV-----	82
AT2G47520.1	VSSRKKRPVSVS-----EERD-----	41
LOC_Os02g54160.1 11972.m10445	DDEDFEADFEFEVDSGSDLELG---EEDDDDVVEIKP-----	84
LOC_Os06g09390.1 11976.m05658 	EEDDFEADFEFEVDSGEWEVES-----DADEAKP-----	78
LOC_Os09g26420.1 11979.m05794	AEEDFEADFEFERGMSDDAEAGGGGEEEEEDDDVVVVPPPAARFVVVR	99
LOC_Os09g26420.2 11979.m21992	AEEDFEADFEFERGMSDDAEAGGGGEEEEEDDDVVVVPPPAARFVVVR	99
LOC_Os09g26420.3 11979.m22092	AEEDFEADFEFERGMSDDAEAGGGGEEEEEDDDVVVVPPPAARFVVVR	99
AT1G53910.1	FDAEFEADFGFKDDSSIDCDDDFDVGDFADVKPFVFTSTPKPAVSAAA	97
AT1G53910.2	FDAEFEADFGFKDDSSIDCDDDFDVGDFADVKPFVFTSTPKPAVSAAA	97
AT3G14230.1	LDDDFEADFGFKDDSAFDCEDD---DDFVNVKPFVFTATTKPVASAFV	94
AT3G14230.2	LDDDFEADFGFKDDSAFDCEDD---DDFVNVKPFVFTATTKPVASAFV	94
AT3G14230.3	LDDDFEADFGFKDDSAFDCEDD---DDFVNVKPFVFTATTKPVASAFV	94
AT3G16770.1	LDASAADDFWGFYSTSKLHPTNQ-----VNVK-----	57
LOC_Os07g42510.1 11977.m08483	DDDDFEADFEFEEDDYGDDDDVGFGDDDDQESDMNGLKLAG-----	94
LOC_Os03g08490.1 11973.m06357	CDDDFEAAFERFGRE--DSEMEEEVEEVVG-----	70
LOC_Os03g08500.1 11973.m06358	-ADDFEAAFRDFDNDSDDEEMMVVEAEAEATSEH-----	73
AT1G72360.1	-----	
LOC_Os03g08460.1 11973.m06354	FEDDDDDDEFELSDDGDESIAVSCVSSPKSKAVPSFSFSS-----	94
LOC_Os05g29810.1 11975.m07218	-----DNAVLSAAGAGDESFAAAKAPAP-----	48
LOC_Os03g22170.1 11973.m07620	PPPQHASDDPAEQAAADEEEQE-----	51
LOC_Os10g25170.1 11980.m05467	AFEEFDAGDDSDSDSESEEVDEYDVVVDDDDSDGCVVL-----	99
LOC_Os09g11460.1 11979.m04408	VDEDWEAFAREFLSRDHDDDDDDHGDGHVVVAPLIRGSDKCVHGHEVVAS	81
LOC_Os09g11460.2 11979.m21977	VDEDWEAFAREFLSRDHDDDDDDHGDGHVVVAPLIRGSDKCVHGHEVVAS	81
LOC_Os09g11480.1 11979.m04410	GDDDDWEAFAREFIAGDDDDDDG-----GVSMFPGAGTMTTTEVAPAAA	85
LOC_Os12g41030.1 11982.m07885	-----MTMP-----	5
LOC_Os12g41060.1 11982.m07888	EDDDDEYDGRFEFEFEFLRFMSMVDEEDDDGDDDEVEVEIIAVVSPPHRP	98
AT1G80580.1	TTSFDISSLSFNPKPEPENTHRVMDDS-----	76

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	-----AEEP	61
LOC_Os07g47790.2 11977.m29326	-----EEP	59
LOC_Os01g21120.1 11971.m08596	-----PP	40
LOC_Os03g08470.1 11973.m06355	-----FASKSRVVAGHDGAAAARA	101
LOC_Os03g08470.2 11973.m34802	-----FASKSRVVAGHDGAAAARA	101
AT2G47520.1	-----	
LOC_Os02g54160.1 11972.m10445	-----ALSRDNLSTITTAGFDGPAAK	110
LOC_Os06g09390.1 11976.m05658 	----- GFAKGGLKNTTVAGADGPAAR	105
LOC_Os09g26420.1 11979.m05794	-----PPTADGMLTTKLQVQHDGPTAR	126
LOC_Os09g26420.2 11979.m21992	-----PPTADGMLTTKLQVQHDGPTAR	126
LOC_Os09g26420.3 11979.m22092	-----PPTADGMLTTKLQVQHDGPTAR	126
AT1G53910.1	-----SVFGKKVTGLDGAEK	115
AT1G53910.2	-----SVFGKKVTGLDGAEK	115
AT3G14230.1	-----LVGSAYAKKTVESAEQAEK	118
AT3G14230.2	-----VGSAYAKKTVESAEQAEK	114
AT3G14230.3	-----GSAYAKKTVESAEQAEK	113
AT3G16770.1	-----EEAVKKEQATEP	69
LOC_Os07g42510.1 11977.m08483	-----FSTTKLGL	102
LOC_Os03g08490.1 11973.m06357	-----KKAAVRRRRRATPAA	84
LOC_Os03g08500.1 11973.m06358	-----KPFVFRACKKAAAA	87
AT1G72360.1	-----SAS	15
LOC_Os03g08460.1 11973.m06354	-----DVSSSSRPRRRVAAAAAG	112
LOC_Os05g29810.1 11975.m07218	-----G	49
LOC_Os03g22170.1 11973.m07620	-----QPAARR	57
LOC_Os10g25170.1 11980.m05467	-----PPPPPPPPVIPH	111
LOC_Os09g11460.1 11979.m04408	-----ASGRRRRADDDGERRRR	104
LOC_Os09g11460.2 11979.m21977	-----ASGRRRRADDDGERRRR	104
LOC_Os09g11480.1 11979.m04410	-----ERPRR	92
LOC_Os12g41030.1 11982.m07885	-----SGGARVRA	14
LOC_Os12g41060.1 11982.m07888	-----LVGARGTTSAVESVTNLQARTSPLPNPVVPQTGTAKSKRGDSGAKAKPAA	148
AT1G80580.1	-----IAAVVGENVLFQDKNKVS DHLTKEGGV KRG	106

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	TKKRERKTLR---GIRRRP-----WGKWAEEIRD-PA	90
LOC_Os07g47790.2 11977.m29326	TKKRERKTLR---GIRRRP-----WGKWAEEIRD-PA	88
LOC_Os01g21120.1 11971.m08596	RAKREKKNQYR---GIRQRP-----WGKWAEEIRD-PV	69
LOC_Os03g08470.1 11973.m06355	ASKKKRGRHFR---GIRQRP-----WGKWAEEIRD-PH	130
LOC_Os03g08470.2 11973.m34802	ASKKKRGRHFR---GIRQRP-----WGKWAEEIRD-PH	130
AT2G47520.1	-GKERKNLYR---GIRQRP-----WGKWAEEIRD-PS	69
LOC_Os02g54160.1 11972.m10445	SAKRRKNQFR---GIRQRP-----WGKWAEEIRD-PR	139
LOC_Os06g09390.1 11976.m05658 	SAKRRKNQFR---GIRQRP-----WGKWAEEIRD-PR	134
LOC_Os09g26420.1 11979.m05794	SAKHRRKNQYR---GIRQRP-----WGKWAEEIRD-PS	155
LOC_Os09g26420.2 11979.m21992	SAKHRRKNQYR---GIRQRP-----WGKWAEEIRD-PS	155
LOC_Os09g26420.3 11979.m22092	SAKHRRKNQYR---GIRQRP-----WGKWAEEIRD-PS	155
AT1G53910.1	SANRRKNQYR---GIRQRP-----WGKWAEEIRD-PR	144
AT1G53910.2	SANRRKNQYR---GIRQRP-----WGKWAEEIRD-PR	144
AT3G14230.1	SSKRRKNQYR---GIRQRP-----WGKWAEEIRD-PR	147
AT3G14230.2	SSKRRKNQYR---GIRQRP-----WGKWAEEIRD-PR	143
AT3G14230.3	SSKRRKNQYR---GIRQRP-----WGKWAEEIRD-PR	142
AT3G16770.1	GKRRRKNVYR---GIRKRP-----WGKWAEEIRD-PR	98
LOC_Os07g42510.1 11977.m08483	GGSRKRKTRYR---GIRQRP-----WGKWAEEIRD-PR	131
LOC_Os03g08490.1 11973.m06357	G-RRARPSKYW---GVRRRP-----WGKWAEEIRD-PV	112
LOC_Os03g08500.1 11973.m06358	SSRRRKPQYR---GVRRRP-----WGKWAEEIRD-PV	116
AT1G72360.1	DGKKKQSSRYK---GIRRRP-----WGRWAAEIRD-PI	44
LOC_Os03g08460.1 11973.m06354	RRKASKKSKYR---GVRRRP-----SGRFAAEIRD-PK	141
LOC_Os05g29810.1 11975.m07218	R-----KTAYR---GIRRRP-----WGRWAAEIRD-PR	73
LOC_Os03g22170.1 11973.m07620	QRRGERRTLYR---GIRRRP-----WGKWAEEIRD-PA	86
LOC_Os10g25170.1 11980.m05467	ERHGARR--FR---GVRKRP-----WGKWAEEIRD-PV	138
LOC_Os09g11460.1 11979.m04408	RRREKRSYPYR---GIRQRP-----WGRWASEIRD-PV	133
LOC_Os09g11460.2 11979.m21977	RRREKRSYPYR---GIRQRP-----WGRWASEIRD-PV	133
LOC_Os09g11480.1 11979.m04410	RRRVRRSYPYR---GVRQRP-----WGRWASEIRD-PV	121
LOC_Os12g41030.1 11982.m07885	H-----FR---GVQWRK-----SGRWSAEIRS-RG	35
LOC_Os12g41060.1 11982.m07888	AKRRRSKHGFL---GVHQRT-----YGRWSAEIRD-NV	177
AT1G80580.1	RKMPQKTGGFM---GVRKRP-----WGRWSAEIRD-RI	135

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	KGAR-----VWLGTATAEAARAYDRAA	114
LOC_Os07g47790.2 11977.m29326	KGAR-----VWLGTATAEAARAYDRAA	112
LOC_Os01g21120.1 11971.m08596	KGVR-----VWLGTPTAEAAARAYDRAA	93
LOC_Os03g08470.1 11973.m06355	KGTR-----VWLGTFTNTPEEAARAYDVEA	154
LOC_Os03g08470.2 11973.m34802	KGTR-----VWLGTFTNTPEEAARAYDVEA	154
AT2G47520.1	KGVR-----VWLGTFTKTADEAARAYDVA	93
LOC_Os02g54160.1 11972.m10445	KGVR-----VWLGTFTNSAEAAARAYDAEA	163
LOC_Os06g09390.1 11976.m05658 	KGVR-----VWLGTFTNSPEEAARAYDAEA	158
LOC_Os09g26420.1 11979.m05794	KGVR-----VWLGTFTNTAEAAARAYDAEA	179
LOC_Os09g26420.2 11979.m21992	KGVR-----VWLGTFTNTAEAAARAYDAEA	179
LOC_Os09g26420.3 11979.m22092	KGVR-----VWLGTFTNTAEAAARAYDAEA	179
AT1G53910.1	EGAR-----IWLGTFTKTAEEAARAYDAAA	168
AT1G53910.2	EGAR-----IWLGTFTKTAEEAARAYDAAA	168
AT3G14230.1	KGSR-----EWLGTFTDAEEAARAYDAAA	171
AT3G14230.2	KGSR-----EWLGTFTDAEEAARAYDAAA	167
AT3G14230.3	KGSR-----EWLGTFTDAEEAARAYDAAA	166
AT3G16770.1	KGVR-----VWLGTFTNTAEAAAMAYDVAA	122
LOC_Os07g42510.1 11977.m08483	KGVR-----VWLGTFTGTAEEAAMAYDVEA	155
LOC_Os03g08490.1 11973.m06357	EGVR-----VWLGTATAEAHAHAYDAAA	136
LOC_Os03g08500.1 11973.m06358	KGIR-----VWLGTFTNAEAAALAYDDAA	140
AT1G72360.1	KGVR-----VWLGTFTNTAEAAARAYDLEA	68
LOC_Os03g08460.1 11973.m06354	KGRR-----VWLGTGSAEEAAMAYDREA	165
LOC_Os05g29810.1 11975.m07218	KGAR-----VWLGTATAEAARAYDVAA	97
LOC_Os03g22170.1 11973.m07620	KGAR-----VWLGTATAEAARAYDRAA	110
LOC_Os10g25170.1 11980.m05467	RGVR-----VWLGTFTPTAEAAARAYDAAA	162
LOC_Os09g11460.1 11979.m04408	KGIR-----VWLGTFTDAEGAARAYDDEV	157
LOC_Os09g11460.2 11979.m21977	KGIR-----VWLGTFTDAEGAARAYDDEV	157
LOC_Os09g11480.1 11979.m04410	KGAR-----VWLGTFTDAVEAARAYDAEA	145
LOC_Os12g41030.1 11982.m07885	AWGR--R-----RRLWIGTYDTAEAAARAYDAEA	62
LOC_Os12g41060.1 11982.m07888	IKGS-----RFGWIGTFDTALDAALAYDAVS	202
AT1G80580.1	GRCR-----HWLGTFTDAEEAARAYDAAA	159

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	RRIRG-----AKAKVNFNEDPPLDDP-----	136
LOC_Os07g47790.2 11977.m29326	RRIRG-----AKAKVNFNEDPPLDDP-----	134
LOC_Os01g21120.1 11971.m08596	RRIRG-----AKAKVNFNDFGAAP-----	115
LOC_Os03g08470.1 11973.m06355	RRLRG-----SKAKVNFATPAAARPRRGTRATAVPPP-----	188
LOC_Os03g08470.2 11973.m34802	RRLRG-----SKAKVNFATPAAARPRRGTRATAVPPP-----	188
AT2G47520.1	IKIRG-----RKAKLNFNT-----	108
LOC_Os02g54160.1 11972.m10445	RRIRG-----KKAKVNFPE-APTTAQRRAGSTTAKAPKSSV-----	199
LOC_Os06g09390.1 11976.m05658 	RRIRG-----KKAKVNFDPGAPVASQSHAEFSSNMPPAFSI-----	195
LOC_Os09g26420.1 11979.m05794	RKIRG-----KKAKVNFDP-EPAVAQKLSLKQNAAKQEK-----	212
LOC_Os09g26420.2 11979.m21992	RKIRG-----KKAKVNFDP-EPAVAQKLSLKQNAAKQEK-----	212
LOC_Os09g26420.3 11979.m22092	RKIRG-----KKAKVNFDP-EPAVAQKLSLKQNAAKQEK-----	212
AT1G53910.1	RRIRG-----SKAKVNFPEE-NMKANSQKR-SVKAN-LQKPV-----	202
AT1G53910.2	RRIRG-----SKAKVNFPEE-NMKANSQKR-SVKAN-LQKPV-----	202
AT3G14230.1	RRIRG-----TKAKVNFPEEKNPSVVSQKRPSAKTNNLQKSV-----	208
AT3G14230.2	RRIRG-----TKAKVNFPEEKNPSVVSQKRPSAKTNNLQKSV-----	204
AT3G14230.3	RRIRG-----TKAKVNFPEEKNPSVVSQKRPSAKTNNLQKSV-----	203
AT3G16770.1	KQIRG-----DKAKLNFDDLHPPPPNYTPPPSSPRSTDQPP-----	159
LOC_Os07g42510.1 11977.m08483	RRIRG-----KKAKVNFPDAAAAPKRPRRSSAKHSPQQK-----	191
LOC_Os03g08490.1 11973.m06357	RDLRG-----ATAKLNFPSSSS-STAAATPRPRKCRPTTATAT-----	172
LOC_Os03g08500.1 11973.m06358	RAIRG-----DRAKLNFPSATTPDTRKGRATAAAAAPAVKAT-----	177
AT1G72360.1	KRIIRG-----AKAKLNFNNESSGKRKAKAKT-----	94
LOC_Os03g08460.1 11973.m06354	RRIRG-----KGARLNFPRDGDGSPRRSNDRPCWTIDLNL-----	201
LOC_Os05g29810.1 1197.m07218	RDIRG-----AKAKLNF-----	110
LOC_Os03g22170.1 11973.m07620	RRIRG-----TKAKVNFNEDNAFAAAPPYHLAAYGDAS-----	146
LOC_Os10g25170.1 11980.m05467	RRLRG-----AKAKPNFPSPAPPPSAAAHRRKKRAHAATRS-----	198
LOC_Os09g11460.1 11979.m04408	RRIYG-----GNAKTNFPSP-PPTPPPEK-----	181
LOC_Os09g11460.2 11979.m21977	RRIYG-----GNAKTNFPSP-PPTPPPEK-----	181
LOC_Os09g11480.1 11979.m04410	RRIHG-----HKARTNFPPEPPLPAPSQAPFCFLDDDDDD-----	181
LOC_Os12g41030.1 11982.m07885	RRLHG-----AKAKTNFP-----PPPPPTAVHDDHVDL-----	90
LOC_Os12g41060.1 11982.m07888	RRLYG-----LNKTNFPAAAGEDDLPPPPPPAKPCSTKR-----	238
AT1G80580.1	RRLRG-----TKAKTNFVIP-----PLFPKEIAQAQEDNR-----	189

FIGURE 7 (continued)

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LOC_Os07g47790.1|11977.m08994|
 LOC_Os07g47790.2|11977.m29326|
 LOC_Os01g21120.1|11971.m08596|
 LOC_Os03g08470.1|11973.m06355|
 LOC_Os03g08470.2|11973.m34802|
 AT2G47520.1
 LOC_Os02g54160.1|11972.m10445|
LOC_Os06g09390.1|11976.m05658|
 LOC_Os09g26420.1|11979.m05794|
 LOC_Os09g26420.2|11979.m21992|
 LOC_Os09g26420.3|11979.m22092|
 AT1G53910.1
 AT1G53910.2
 AT3G14230.1
 AT3G14230.2
 AT3G14230.3
 AT3G16770.1
 LOC_Os07g42510.1|11977.m08483|
 LOC_Os03g08490.1|11973.m06357|
 LOC_Os03g08500.1|11973.m06358|
 AT1G72360.1
 LOC_Os03g08460.1|11973.m06354|
 LOC_Os05g29810.1|11975.m07218|
 LOC_Os03g22170.1|11973.m07620|
 LOC_Os10g25170.1|11980.m05467|
 LOC_Os09g11460.1|11979.m04408|
 LOC_Os09g11460.2|11979.m21977|
 LOC_Os09g11480.1|11979.m04410|
 LOC_Os12g41030.1|11982.m07885|
 LOC_Os12g41060.1|11982.m07888|
 AT1G80580.1

-----AADGSHGGA-- 146
 -----AADGSHGGA-- 144
 -----AAAAKAVPR-- 125
 -----ATAPAAAPPRGLKREFSPPAETALPFTNGFVDLTTAAAPPPAM-- 232
 -----ATAPAAAPPRGLKREFSPPAETALPFTNGFVDLTTAAAPPPAM-- 232

 -----EQKPTVKPAFNN-LANANAFVYPSANFTSNKPFVQPDNMPFVPA-- 242
 -----**EEKPAVMSAGNKTMYNTNAYAPAVEYTLQEPFVQIQNVSVFPA-- 239**
 -----LAPPLKTCGDDAFFQLNSSDNDLFAMLAKEVPKPAEPVDLMPP-- 255
 -----LAPPLKTCGDDAFFQLNSSDNDLFAMLAKEVPKPAEPVDLMPP-- 255
 -----LAPPLKTCGDDAFFQLNSSDNDLFAMLAKEVPKPAEPVDLMPP-- 255
 -----AKPN-----PNPSPALVQNSNISFEN-----MCFMEEKHQVSNNNN 238
 -----AKPN-----PNPSPALVQNSNISFEN-----MCFMEEKHQVSNNNN 238
 -----AKPNKSVTLVQQPHTLSQQYCNSFDNSFGDMSFMEKEKPMYNN-- 252
 -----AKPNKSVTLVQQPHTLSQQYCNSFDNSFGDMSFMEKEKPMYNN-- 248
 -----AKPNKSVTLVQQPHTLSQQYCNSFDNSFGDMSFMEKEKPMYNN-- 247
 -----AKKVCVVS--QSESELSQP-----SFPVEICIGFNG-- 188
 -----ARSSSSSPASLNASDAVSKSNNNRVSSAGSSSTDATAAIAIDG-- 235
 -----P-----KATTPNVVVVNLVDKEAEVSESSGASSALPDFSWQG-- 211
 -----PVINLVEEEDDEEVAAMASIKYEPETSESS--ESNALPDFSWQG-- 220
 -----VQVVEENHEADLDVAVVSSAPSSSCLDFLWE-- 125
 -----AAAVSGDDDDAMAVDAADADAGSAGRAAAYADQE-- 235
 -----PTIGAAAPPPPKRRKAAAAAN-- 133
 -----STSYLYPMAMTPAAAGLR----- 164
 -----PSSPPATSEVTAASASASSDVPAPAFASFVGE-- 231
 -----PAAERSP----- 188
 -----PAAERSP----- 188
 -----DGVARGNSPASSAPDRASAC-- 203
 -----EAHIKFLSEVELD-- 103
 -----PKCNTSGDLGAA-- 251
 -----MRQKQKKKKKKV-- 202

FIGURE 7 (continued)

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LOC_Os07g47790.1|11977.m08994|
 LOC_Os07g47790.2|11977.m29326|
 LOC_Os01g21120.1|11971.m08596|
 LOC_Os03g08470.1|11973.m06355|
 LOC_Os03g08470.2|11973.m34802|
 AT2G47520.1
 LOC_Os02g54160.1|11972.m10445|
LOC_Os06g09390.1|11976.m05658|
 LOC_Os09g26420.1|11979.m05794|
 LOC_Os09g26420.2|11979.m21992|
 LOC_Os09g26420.3|11979.m22092|
 AT1G53910.1
 AT1G53910.2
 AT3G14230.1
 AT3G14230.2
 AT3G14230.3
 AT3G16770.1
 LOC_Os07g42510.1|11977.m08483|
 LOC_Os03g08490.1|11973.m06357|
 LOC_Os03g08500.1|11973.m06358|
 AT1G72360.1
 LOC_Os03g08460.1|11973.m06354|
 LOC_Os05g29810.1|11975.m07218|
 LOC_Os03g22170.1|11973.m07620|
 LOC_Os10g25170.1|11980.m05467|
 LOC_Os09g11460.1|11979.m04408|
 LOC_Os09g11460.2|11979.m21977|
 LOC_Os09g11480.1|11979.m04410|
 LOC_Os12g41030.1|11982.m07885|
 LOC_Os12g41060.1|11982.m07888|
 AT1G80580.1

-----AIPCREFMDYDAVMAGFFHQPYVV-----ADGVPAPV----- 178
 -----AIPCREFMDYDAVMAGFFHQPYVV-----ADGVPAPV----- 176
 -----VAPTPAVLPPPKMEAVSEGAGACS-----SDEVKELS----- 157
 -----MMTSSFTDSVATSESGGSPAKKAR-----SDDVDSSEGS----- 266
 -----MMTSSFTDSVATSESGGSPAKKAR-----SDDVDSSEGS----- 266
 -----QVEEADTKPGNQNELIS-----ENQVESLS----- 135
 -----MNSAAPIEDPIIN--SDQGSNFGCSDFGWENDTKTPDITSAP 284
 -----MN---AIEDTFVNLSSDQGSNFGCSDFSQENDIKTPDITSMIA 280
 -----VKPLASTETFEMNMLSDTSSNSFGSSDFGWEDDTLTPDYTSVFV 299
 -----VKPLASTETFEMNMLSDTSSNSFGSSDFGWEDDTLTPDYTSVFV 299
 -----VKPLASTETFEMNMLSDTSSNSFGSSDFGWEDDTLTPDYTSVFV 299
 NQFGMTNSVDAG-CNGYQYFSSDQGSNSFDCSEFGWSDAQITPDISS-- 285
 NQFGMTNSVDAG-CNGYQYFSSDQGSNSFDCSEFGWSDAQITPDISS-- 285
 -QFGLTNSFDAGGNNGYQYFSSDQGSNSFDCSEFGWSDHGPKTPEISS-- 299
 -QFGLTNSFDAGGNNGYQYFSSDQGSNSFDCSEFGWSDHGPKTPEISS-- 295
 -QFGLTNSFDAGGNNGYQYFSSDQGSNSFDCSEFGWSDHGPKTPEISS-- 294
 -----DEFQNL-----YGFEPDYDLKQISSLE 212
 -----VKLELLSETDPSPPMAAAAAALDAFELNDLDGSRCKDNAFD-- 277
 -----MSASDDDDAAQQALLDAAG-GAKKRPRSEPHVTSDDDEVLP- 251
 -----MSASDEFVAAAAALSLSDDDLAKKRPRTEPEDTDS----- 257
 -----ENNPDTLLIDTQWLEDIIMGDANKKHEPNDEEANN----- 161
 -----ALSAACKKIKQCPRDEQMASATPELMEEDASSSRNMVP--- 273
 -----HHHHHHQJESSGS-----SSASSLPPTPP--- 157
 -----EQQLMTTTAVEYSVNDADVAVSVYFQPPPAVAYEFS----- 201
 -----GHGGAKSMPITTSQAPPATVASENVDDPEVDPYDVHGGI- 274
 -----STPTTTTSDGSRILIECCSDDLMSLLAAAFDMTT--- 225
 -----STPTTTTSDGSRILIECCSDDLMSLLAAAFDMTT--- 225
 -----TTSSTVASGERGDELILLECCSDDVMDLSLLAGFDVSS--- 240
 -----GDQ---ETPPESQVGGDQ-----AGGQHQQHHG----- 128
 -----AAPQAVDTPAAAAAGVELTSLCSVAAQAQEVSDG----- 287
 -----SVRKCCKVTSVAQLFDDANFINSSSIKGNVISSIDN----- 238

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	-----	
LOC_Os07g47790.2 11977.m29326	-----	
LOC_Os01g21120.1 11971.m08596	-----	
LOC_Os03g08470.1 11973.m06355	-----	
LOC_Os03g08470.2 11973.m34802	-----	
AT2G47520.1	-----	
LOC_Os02g54160.1 11972.m10445	IS-TIAEVDESAFIKS-STNPM-----	304
LOC_Os06g09390.1 11976.m05658 	P--TMTGVDDSAFLQNNASDAM-----	300
LOC_Os09g26420.1 11979.m05794	PNAAMPAYGEPAYLTGGAPKRMNNYG-----	326
LOC_Os09g26420.2 11979.m21992	PNAAMPAYGEPAYLTGGAPKRMNNYG-----	326
LOC_Os09g26420.3 11979.m22092	PNAAMPAYGEPAYLTGGAPKRMNNYG-----	326
AT1G53910.1	AVINNNNSALFFEEANPAKKLK-----	307
AT1G53910.2	AVINNNNSALFFEEANPAKKLK-----	307
AT3G14230.1	MLVNNNE--ASFVEETNAAKKLP-----	321
AT3G14230.2	MLVNNNE--ASFVEETNAAKKLP-----	317
AT3G14230.3	MLVNNNE--ASFVEETNAAKKLP-----	316
AT3G16770.1	SFLELDG-----	219
LOC_Os07g42510.1 11977.m08483	-----	
LOC_Os03g08490.1 11973.m06357	-----	
LOC_Os03g08500.1 11973.m06358	-----	
AT1G72360.1	-----	
LOC_Os03g08460.1 11973.m06354	-----	
LOC_Os05g29810.1 11975.m07218	-----	
LOC_Os03g22170.1 11973.m07620	-----	
LOC_Os10g25170.1 11980.m05467	-----	
LOC_Os09g11460.1 11979.m04408	-----	
LOC_Os09g11460.2 11979.m21977	-----	
LOC_Os09g11480.1 11979.m04410	-----	
LOC_Os12g41030.1 11982.m07885	-----	
LOC_Os12g41060.1 11982.m07888	-----	
AT1G80580.1	-----	

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	-----AEEAPTVAVVH-----HLPPQPQ-----	197
LOC_Os07g47790.2 11977.m29326	-----AEEAPTVAVVH-----HLPPQPQ-----	195
LOC_Os01g21120.1 11971.m08596	-----EELLAYENYSF-----LGIPYME-----	176
LOC_Os03g08470.1 11973.m06355	-----VGGSDTLGFTDELEFPFMLFQLPYSDGYESI-----	299
LOC_Os03g08470.2 11973.m34802	-----VGGSDTLGFTDELEFPFMLFQLPYSDGYESI-----	299
AT2G47520.1	-----EDIMALEDYMR-----YQIPVAD-----	154
LOC_Os02g54160.1 11972.m10445	-----VPP-----VMENSAVDLPLEPYMRFL-----LDDGAGD-----	333
LOC_Os06g09390.1 11976.m05658 	----- VPP-----VMGNASIDIADLEPYMKFL-----IDGSDE-----	329
LOC_Os09g26420.1 11979.m05794	-----IAPQGNMGNLAQNMPFTDPKMYLPLPYVESSSDE-----	363
LOC_Os09g26420.2 11979.m21992	-----IAPQGNMGNLAQNMPFTDPKMYLPLPYVESSSDE-----	363
LOC_Os09g26420.3 11979.m22092	-----IAPQGNMGNLAQNMPFTDPKMYLPLPYVESSSDE-----	363
AT1G53910.1	-----SMDFETPYNTEW-----DASLD-----	325
AT1G53910.2	-----SMDFETPYNTEW-----DASLD-----	325
AT3G14230.1	-----NSDESDDL MAYLDNALW-----DTPLEVE-----	345
AT3G14230.2	-----NSDESDDL MAYLDNALW-----DTPLEVE-----	341
AT3G14230.3	-----NSDESDDL MAYLDNALW-----DTPLEVE-----	340
AT3G16770.1	-----NTAEQ-----PSQLD-----	229
LOC_Os07g42510.1 11977.m08483	-----HQIHKVEAAVADEFAYFYDDPSYMLGYQLD-----	307
LOC_Os03g08490.1 11973.m06357	-----ASFSDNNTAAAGLLPLDDPFLFGDQFGDLNGGAFASL-----	289
LOC_Os03g08500.1 11973.m06358	-----GSGDDTDA-----LFDALLFADQYNHFNNGGAYES-----	286
AT1G72360.1	-----VDASLLSEELLAFENQTEYFSQMPFTEGNCDSSTS-----	196
LOC_Os03g08460.1 11973.m06354	-----LSMALQLQYAAAMIAECDREMEEIAA-----	298
LOC_Os05g29810.1 11975.m07218	-----PAAEHQLR-----ECMSGLEAFGLG-----	176
LOC_Os03g22170.1 11973.m07620	-----AVGGGAVVVPVSAPV-----AMTYGQSQE-----	226
LOC_Os10g25170.1 11980.m05467	-----ASYFAGGAYESLESLEFAHGGDSAAVDQAASD-----	305
LOC_Os09g11460.1 11979.m04408	-----	
LOC_Os09g11460.2 11979.m21977	-----	
LOC_Os09g11480.1 11979.m04410	-----	
LOC_Os12g41030.1 11982.m07885	-----CRLDHLMLMCN-----	140
LOC_Os12g41060.1 11982.m07888	-----WEFIQELLGGSVSPLDYINGQELAG-----	314
AT1G80580.1	-----LEKMGLELDLSIGLLSRK-----	256

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	-----QDAG-----LELWSFDNI	210
LOC_Os07g47790.2 11977.m29326	-----QDAG-----LELWSFDNI	208
LOC_Os01g21120.1 11971.m08596	-----GGAASAAAGAEAAAPAGLWTFEDY	200
LOC_Os03g08470.1 11973.m06355	-----SLFAAGDANSANTDMNAG-----VNLWSFDDF	327
LOC_Os03g08470.2 11973.m34802	-----SLFAAGDANSANTDMNAG-----VNLWSFDDF	327
AT2G47520.1	-----DQSATDIG-----NLWSYQDS	170
LOC_Os02g54160.1 11972.m10445	-----SIDSLNLGDSQDVVSNMDLWSFDDM	359
LOC_Os06g09390.1 11976.m05658 	----- SIDTLSSDGSQDVASSMDLWSFDDM	355
LOC_Os09g26420.1 11979.m05794	-----SMDNLLQNDATQDGASNEGIWSLDEL	389
LOC_Os09g26420.2 11979.m21992	-----SMDNLLQNDATQDGASNEGIWSLDEL	389
LOC_Os09g26420.3 11979.m22092	-----SMDNLLQNDATQDGASNEGIWSLDEL	389
AT1G53910.1	-----FLNEDAVTTQDNGANPMDLWSIDEI	350
AT1G53910.2	-----FLNEDAVTTQDNGANPMDLWSIDEI	350
AT3G14230.1	-----AMLGADAGAVTQEEENPVELWSLDEI	371
AT3G14230.2	-----AMLGADAGAVTQEEENPVELWSLDEI	367
AT3G14230.3	-----AMLGADAGAVTQEEENPVELWSLDEI	366
AT3G16770.1	-----ESVSEVDMWMLDDV	243
LOC_Os07g42510.1 11977.m08483	-----QGNSYENIDALFGGEAVNIGLWSFDDM	335
LOC_Os03g08490.1 11973.m06357	-----MDGLFAAG-----EANVAGESVGLWSFGD-	313
LOC_Os03g08500.1 11973.m06358	-----LDSLFSADAVQTAAAAAADQGMGLWSFDDG	317
AT1G72360.1	-----LSSLFDGG-----NDMGLWS----	211
LOC_Os03g08460.1 11973.m06354	-----VERDLERRRRQVFERRGHLVRQASL	323
LOC_Os05g29810.1 11975.m07218	-----LEEEEDDGG-----AGEPWDVDM	195
LOC_Os03g22170.1 11973.m07620	-----VAAPIWMWNFDDI	238
LOC_Os10g25170.1 11980.m05467	-----HWPAAALWSFADD	317
LOC_Os09g11460.1 11979.m04408	-----GDMRFWS----	232
LOC_Os09g11460.2 11979.m21977	-----GDMRFWS----	232
LOC_Os09g11480.1 11979.m04410	-----EPRSVLGMVN-	250
LOC_Os12g41030.1 11982.m07885	-----	
LOC_Os12g41060.1 11982.m07888	-----AAVGDLWSF----	323
AT1G80580.1	-----	

FIGURE 7 (continued)

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LOC_Os07g47790.1 11977.m08994	HTAVPM-----	216
LOC_Os07g47790.2 11977.m29326	HTAVPM-----	214
LOC_Os01g21120.1 11971.m08596	ELPSLAL-----	207
LOC_Os03g08470.1 11973.m06355	PIDGALF-----	334
LOC_Os03g08470.2 11973.m34802	PIDGALF-----	334
AT2G47520.1	N-----	171
LOC_Os02g54160.1 11972.m10445	PVS-DFY-----	365
LOC_Os06g09390.1 11976.m05658 	PVSAEFY-----	362
LOC_Os09g26420.1 11979.m05794	LMAAGAY-----	396
LOC_Os09g26420.2 11979.m21992	LMAAGAY-----	396
LOC_Os09g26420.3 11979.m22092	LMAAGAY-----	396
AT1G53910.1	HSMIGGVF-----	358
AT1G53910.2	HSMIGGVF-----	358
AT3G14230.1	NFMLEGDF-----	379
AT3G14230.2	NFMLEGDF-----	375
AT3G14230.3	NFMLEGDF-----	374
AT3G16770.1	IASYE-----	248
LOC_Os07g42510.1 11977.m08483	PMEFRAY-----	342
LOC_Os03g08490.1 11973.m06357	---DFLNASY-----	321
LOC_Os03g08500.1 11973.m06358	CCLVDVEASLSF-----	329
AT1G72360.1	-----	---
LOC_Os03g08460.1 11973.m06354	LLD-----	326
LOC_Os05g29810.1 11975.m07218	MLE-----	198
LOC_Os03g22170.1 11973.m07620	TAMPM-----	243
LOC_Os10g25170.1 11980.m05467	GSFCF-----	322
LOC_Os09g11460.1 11979.m04408	-----	---
LOC_Os09g11460.2 11979.m21977	-----	---
LOC_Os09g11480.1 11979.m04410	-----	---
LOC_Os12g41030.1 11982.m07885	-----	---
LOC_Os12g41060.1 11982.m07888	-----	---
AT1G80580.1	-----	---

FIGURE 7 (continued)

LOC_Os02g51670.1 11972.m10198	-----MAAAIDMYKYN-TSTHQIASSDQELMKAL--EPFIRSASSSSAS	41
LOC_Os06g11860.1 11976.m05903	-----MAAIDLKYQLSSSSSSSDQELMKAL--EPFIRSASPTSTS	41
LOC_Os08g31580.1 11978.m07152	-----MAAAIEGN-----LMRALGEAPSPQMOKIA---	25
LOC_Os09g20350.1 11979.m05242	-----MAAAIDLSGEE-----LMRAL--EPFIRDASGS---	26
LOC_Os03g09170.1 11973.m06423	-----MATTVDCGRG-----SNLP-AAMYDMVVDs---	25
AT2G22200.1	-----	
AT4G39780.1	-----MAAIDMFNSN-----TDPFQEELMKALQP	24
AT5G65130.1	--MALNMNAYVDEFMEA-----LEPFMKVTSSSSTS	29
AT1G22190.1	-----MTTSMDFYN-----KTFQSQDPFGGELMEALLPFIK----	36
AT1G78080.1	-----MAAAMNLYTCS-----RSFQDS--GGELMDALVPFIKSVSDSPSS	38
AT1G36060.1	-----MADLFGG-----GHGGELMEALQPFYKSASTSASN	30
LOC_Os10g22600.1 11980.m05267	DRQWRCLAAAASTSGNS-----KLPLPMALGGAVEYGQ	35
LOC_Os05g49700.1 11975.m09040	DASLRTLPPA-----IFP--GEVRSVSS	23
AT1G64380.1	EESNDIFQNN-----FSPKISEIRASLSQ	25
LOC_Os02g51670.1 11972.m10198	SPCHYYSSS-----PSMSQDSYMPPTSYPTSSIT--TAAA	75
LOC_Os06g11860.1 11976.m05903	TSTPLFYSSSSISTTTTPFYSYSSPLPQESYYLPASSSYAAIVPPPTTT	91
LOC_Os08g31580.1 11978.m07152	-----	
LOC_Os09g20350.1 11979.m05242	-----	
LOC_Os03g09170.1 11973.m06423	-----	
AT2G22200.1	-----	
AT4G39780.1	-----	
AT5G65130.1	-----	
AT1G22190.1	-----	
AT1G78080.1	-----	
AT1G36060.1	-----	
LOC_Os10g22600.1 11980.m05267	DS-----	38
LOC_Os05g49700.1 11975.m09040	SS-----	40
AT1G64380.1	PA-----	32
	LVHG-----	39
	LL-----	25
	II-----	27

FIGURE 8

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LOC_Os02g51670.1 11972.m10198	TTTSSFSQLPPLYSSQYHAA-----SPAASATN	103
LOC_Os06g11860.1 11976.m05903	NTTTSFSELPLPPSSSFA-----SPANAAA-	118
LOC_Os08g31580.1 11978.m07152	--PPFHPGLPPAPANFSSA-----GVHGFHY-	50
LOC_Os09g20350.1 11979.m05242	--PVVCSQFSPTSPFSFPHA-----FAYGGGL-	51
LOC_Os03g09170.1 11973.m06423	---KELMGALAPSMVSFSYP-----CSEQSASS	50
AT2G22200.1	---METASLSF---PVPNT-----SFGVN-KS	20
AT4G39780.1	--YTNTDSSP---TYSNT-----VGFEN-QT	46
AT5G65130.1	--NSSNPKPLTPNFI PNNDQ-----VLPVSNQT	55
AT1G22190.1	--SAFA-----FSLP-----AP	48
AT1G78080.1	--AASASAFLHPSAFSLPPLPGYY-----PDSTFLTQP	71
AT1G36060.1	--FASSNDAFASAPNDLFSSSSYYNPHASLFPSHSTSYPDYSGSMTYP	80
LOC_Os10g22600.1 11980.m05267	-AAPVAPFFVDAEQQLSP-----ATAMVLGA	66
LOC_Os05g49700.1 11975.m09040	--LSPGGSALDTVFSLPP-----PVTI	46
AT1G64380.1	--LAGGPNLTDSIFSLTSPSSVESATTS-----FNTHNPPPP	62
LOC_Os02g51670.1 11972.m10198	GPMGLTHLGPAQ-----IQQIQAQFLAQQQ-QQRALAG--	135
LOC_Os06g11860.1 11976.m05903	--VGLAHLGPEQ-----IQQIQVQFLMQQLQQRGMAASA	151
LOC_Os08g31580.1 11978.m07152	--MGPAQLSPAQ-----IQRVQAQLHMQRQ-----AQSG--	77
LOC_Os09g20350.1 11979.m05242	--AQQPELSPAQ-----MHYIQAARLHLQRQ-----AAQAG-	79
LOC_Os03g09170.1 11973.m06423	LLAGANYLTPAQ-----VLHVQAQLQLRRLR--PGAASG--	81
AT2G22200.1	MPLGLNQLTPYQ-----IHQIQNQLNHR-----RSTIS--	48
AT4G39780.1	TSLGLNQLTPYQ-----IHQIQNQLNQR-----RNIISP-	75
AT5G65130.1	GPIGLNQLTPTQ-----ILQIQTELHLRQNQSRRRAGSH-	89
AT1G22190.1	ISYGSDLH-----SFSHH-	61
AT1G78080.1	FSYGSDLQQTGSLIGLNNLSSSIHQIQSIHHPLPPTHNNNNFSNL-	120
AT1G36060.1	SSFGSDLQQPEN-----YQSQFHYQNTITYTHQDNNTCMLNF-	117
LOC_Os10g22600.1 11980.m05267	GWYNYNLVTPSQ-----AAQLHHLRLRAVGAAPCSMKRCG	101
LOC_Os05g49700.1 11975.m09040	PPIGSSVYYRQS-----ELLRHFAS-----	67
AT1G64380.1	PQIGSSVYLQR-----DIEKFHLQNRAISTPHPPPLFS	96

FIGURE 8 (conitued)

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-----AFLPRGQPMKQSGSPPRAGPFAAVAGA----- 163
 SASAAASYLGPRAQPMKQAG-----AAAAA----- 177
 -----LGPRAQPMKP-----ASAAAAPAAAAAR----- 99
 -----PLGPRAQPMKASSSSASAAAGAAATPPR----- 106
 -----CLAAAPPLPMKRHG-----AVAVAAAAAAR----- 106
 -----NLSPNRIRMKNLTP-----STS----- 65
 -----NLAPKVPMPKNMT-----AT----- 88
 -----LLTAKPTSMKKIDV-----AT----- 105
 -----LSP-KPVSMMKQTGTS-----AA----- 77
 -----LSP-KPLLMKQSGVAGSCFAYGSGVPS----- 146
 -----IEPSQPGFMTQGPS-----SGSVS----- 137
 -----GMAAAAAGRLALVG-----PAP----- 118
 -----QAAQAQSATAAASSSSAAAAAGLDDG----- 92
 STYDHHQTSELMQLQAAAGSPAAAFAAALAAGRVT----- 130

LOC_Os02g51670.1|11972.m10198|
 LOC_Os06g11860.1|11976.m05903|
 LOC_Os08g31580.1|11978.m07152|
 LOC_Os09g20350.1|11979.m05242|
 LOC_Os03g09170.1|11973.m06423|
 AT2G22200.1
 AT4G39780.1
 AT5G65130.1
 AT1G22190.1
 AT1G78080.1
 AT1G36060.1
 LOC_Os10g22600.1|11980.m05267|
 LOC_Os05g49700.1|11975.m09040|
 AT1G64380.1

-----AQSKLYR-----GVRQRH-----WGKWVAEIRLPKN 189
 -----AGKMYR-----GVRQRH-----WGKWVAEIRLPKN 203
 -----AQ-KLYR-----GVRQRH-----WGKWVAEIRLPKN 124
 -----PQ-KLYR-----GVRQRH-----WGKWVAEIRLPKN 131
 -----APVKLYR-----GVRQRH-----WGKWVAEIRLPKN 132
 -----KTKNLYR-----GVRQRH-----WGKWVAEIRLPKN 91
 -----AQKLYR-----GVRQRH-----WGKWVAEIRLPKN 113
 -----KPVKLYR-----GVRQRQ-----WGKWVAEIRLPKN 131
 -----KPTKLYR-----GVRQRH-----WGKWVAEIRLPKN 103
 -----KPTKLYR-----GVRQRH-----WGKWVAEIRLPKN 172
 -----KPAKLYR-----GVRQRH-----WGKWVAEIRLPKN 163
 -----VQAKLYR-----GVRQRH-----WGKWVAEIRLPKN 144
 -----APRKLYR-----GVRQRQ-----WGKWVAEIRLPQN 118
 -----KKKKLYR-----GVRQRH-----WGKWVAEIRLPQN 156

LOC_Os02g51670.1|11972.m10198|
 LOC_Os06g11860.1|11976.m05903|
 LOC_Os08g31580.1|11978.m07152|
 LOC_Os09g20350.1|11979.m05242|
 LOC_Os03g09170.1|11973.m06423|
 AT2G22200.1
 AT4G39780.1
 AT5G65130.1
 AT1G22190.1
 AT1G78080.1
 AT1G36060.1
 LOC_Os10g22600.1|11980.m05267|
 LOC_Os05g49700.1|11975.m09040|
 AT1G64380.1

MOTIF XVIII

AP2 DNA-binding domain

FIGURE 8 (conitued)

LOC_Os02g51670.1 11972.m10198	RT-----	RLWLGTFDTAEDAAALAYDKAA	212
LOC_Os06g11860.1 11976.m05903	RT-----	RLWLGTFDTAEDAAALAYDKAA	226
LOC_Os08g31580.1 11978.m07152	RT-----	RLWLGTFDTAEEAALTYDQAA	147
LOC_Os09g20350.1 11979.m05242	RT-----	RLWLGTFDTAEEAALAYDQAA	154
LOC_Os03g09170.1 11973.m06423	RT-----	RLWLGTFDTAEEAALAYDSAA	155
AT2G22200.1	RT-----	RLWLGTFETAKEKAALAYDQAA	114
AT4G39780.1	RT-----	RLWLGTFDTAEEAAMAYDLAA	136
AT5G65130.1	RT-----	RLWLGTFETAQEAALAYDQAA	154
AT1G22190.1	RT-----	RLWLGTFDTAEEAALAYDKAA	126
AT1G78080.1	RT-----	RLWLGTFDTAEEAALAYDKAA	195
AT1G36060.1	RT-----	RLWLGTFDTAEEAALAYDRAA	186
LOC_Os10g22600.1 11980.m05267	RT-----	RLWLGTYDTAEDAAALAYDGAA	167
LOC_Os05g49700.1 11975.m09040	RV-----	RVWLGTYDSPETAHAHAYDRAA	141
AT1G64380.1	RM-----	RVWLGTYDTAEEAAAYAYDRAA	179
	MOTIF XVIII		
	AP2 DNA-binding domain		
LOC_Os02g51670.1 11972.m10198	FRLRGDL-----	ARLNFPTRLRRGGAHL-----	234
LOC_Os06g11860.1 11976.m05903	FRLRGDA-----	ARLNFPTRLRRGGAHL-----	248
LOC_Os08g31580.1 11978.m07152	YRLRGDA-----	ARLNFP-----DNAAS-----	165
LOC_Os09g20350.1 11979.m05242	YRLRGDA-----	ARLNFP-----DNAAS-----	172
LOC_Os03g09170.1 11973.m06423	FRLRGES-----	ARLNFPPELRRGGAHL-----	177
AT2G22200.1	FQLRGDI-----	AKLNFPNLIHED-----	133
AT4G39780.1	YKLRGEF-----	ARLNFPQFRHEDGYG-GG-----SC-----	163
AT5G65130.1	HKIRGDN-----	ARLNFPDIVRQG-----HY-----	175
AT1G22190.1	YKLRGDF-----	ARLNFPDLRHN-----DE-----	146
AT1G78080.1	YKLRGDF-----	ARLNFPNLRHNGSHIG-GDF-----GE-----	223
AT1G36060.1	FKLRGDS-----	ARLNFPALRYQTGSSP-SDT-----GE-----	214
LOC_Os10g22600.1 11980.m05267	FRLRGDA-----	ARLNFPPELRRGGRHH-----	189
LOC_Os05g49700.1 11975.m09040	FKLRGEY-----	ARLNFPGVMD-----GRDCP-----DN-----	165
AT1G64380.1	YKLRGEX-----	ARLNFPNLKDPSELLGLGDS-----SK-----	208
	MOTIF XIX		
	AP2 DNA-binding domain		

FIGURE 8 (conitued)

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LOC_Os02g51670.1 11972.m10198	-----AGPLHASVDAKLTAICQSLATSSSKNTPA	263	ESAA-----AAEPESPKCSAST-----EG	283
LOC_Os06g11860.1 11976.m05903	-----AGPLHASIDAKLTAICHSLAAAPASS-K	276	KAAAA-----AAHPDSPKGSASTTTTSEG	301
LOC_Os08g31580.1 11978.m07152	-----RGPLDAAVDAKLQAICDTIAASKNASSRS	194	RGGAG-----RAMPINAPLVAAASSSSGSD	219
LOC_Os09g20350.1 11979.m05242	-----RGPLHASVDAKLQTLQCNIAAAKNAK-KS	200	SVSAS-----AAATSSAPTSNCSSPSSDDA	225
LOC_Os03g09170.1 11973.m06423	-----GPPLHAAVDAKLHAICHGMDLPQPQPTQ	206	SNATT-----TTMSTTATNTSPFFSSESP	231
AT2G22200.1	-----MNPLPSSVDTKLQAICKSLRKTEECVS	162	DQKEYSVSVSDKTEL-----FLPKAELFLPKREHLETNELSNESPRSD	207
AT4G39780.1	-----FNPLHSSVDAKLQELCQSLRKTEDIDLPC	192	SET-----ELFPKTEYQES---EYGFRLSD	215
AT5G65130.1	-----KQILSPSINAKIESICNSS-----DLPLPQ	200	IEK-----QNKTEEVLS-----GFSKPE	218
AT1G22190.1	-----YQPLQSSVDAKLEAICQNLAEETQKQVRS	175	TKKSS-----SRKR---SSTVAVKLPEED	196
AT1G78080.1	-----YKPLHSSVDAKLEAICKSMAET-QKQDKS	251	TKSSK-----KREKKVSSPDLSEKVKAE	275
AT1G36060.1	-----YGPIQAAVDAKLEAI---LAEPKNQPGKT	240	ERTSR-----KRAK-----AAASSAEQ	257
LOC_Os10g22600.1 11980.m05267	-----APALSASVDAKILQATTTTADTAAAAAP	218	ASTNTTPPPSPRVVKT-----PGCCSVSEASTTTTADAADVSTGSSPS	263
LOC_Os05g49700.1 11975.m09040	-----LRQLRDAVDAKIQAIRVRMARKRARARRQ	194	REESK-----KSQRAEDAKAATPSRPVASER	220
AT1G64380.1	-----LIAALKNAVDGKIQISICQVRKE--RAKKS	235	VKVS-----NSSATADSSCLS-SPEILSSS	260
LOC_Os02g51670.1 11972.m10198				
LOC_Os06g11860.1 11976.m05903				
LOC_Os08g31580.1 11978.m07152				
LOC_Os09g20350.1 11979.m05242				
LOC_Os03g09170.1 11973.m06423				
AT2G22200.1				
AT4G39780.1				
AT5G65130.1				
AT1G22190.1				
AT1G78080.1				
AT1G36060.1				
LOC_Os10g22600.1 11980.m05267				
LOC_Os05g49700.1 11975.m09040				
AT1G64380.1				

FIGURE 8 (conitued)

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LOC_Os02g51670.1 11972.m10198	-EDSVS-----	293
LOC_Os06g11860.1 11976.m05903	DESAIS-----	312
LOC_Os08g31580.1 11978.m07152	HSGGGD-----	230
LOC_Os09g20350.1 11979.m05242	SSCLES-----	236
LOC_Os03g09170.1 11973.m06423	VVKSEP-----	242
AT2G22200.1	-ETSL-----	217
AT4G39780.1	-ENSFS-----	225
AT5G65130.1	KEPEFG-----	229
AT1G22190.1	YS-SAG-----	206
AT1G78080.1	NSVSI-----	286
AT1G36060.1	PS-----	264
LOC_Os10g22600.1 11980.m05267	PTSSNQ-----	274
LOC_Os05g49700.1 11975.m09040	AASETT-----	231
AT1G64380.1	PVTTTT-----	271
LOC_Os02g51670.1 11972.m10198	PPTPLSPP-----	321
LOC_Os06g11860.1 11976.m05903	LPPPPPPP-----	343
LOC_Os08g31580.1 11978.m07152	TSSSSAAS-----	260
LOC_Os09g20350.1 11979.m05242	SLSPSSAATTAET--	272
LOC_Os03g09170.1 11973.m06423	ESSSADGDVSSSTGSSDVVPEMQLLDFSEAPWD-ESESF-----	280
AT2G22200.1	EYS-SSD-----	240
AT4G39780.1	ESS-SPESG-----	251
AT5G65130.1	GYSGSSPES-----	257
AT1G22190.1	TESYSGSGS-----	238
AT1G78080.1	TEFEESTAG-----	317
AT1G36060.1	SGGESDGS-----	297
LOC_Os10g22600.1 11980.m05267	PPAPRPPPP-----	304
LOC_Os05g49700.1 11975.m09040	TSSSYGSPD-----	255
AT1G64380.1	EDSYWVSPM-----	308

FIGURE 8 (conitued)

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LOC_Os02g51670.1 11972.m10198	-----HLRKPSWEI	331
LOC_Os06g11860.1 11976.m05903	-----HLYKCPSWEI	353
LOC_Os08g31580.1 11978.m07152	-----ALTKYPSYEI	270
LOC_Os09g20350.1 11979.m05242	-----ALTKYPSYEI	282
LOC_Os03g09170.1 11973.m06423	-----LLHKYPSLEI	290
AT2G22200.1	-----GLRKFPSVEI	250
AT4G39780.1	-----GLEKFPSVEI	261
AT5G65130.1	-----MGLHKYPSLEI	268
AT1G22190.1	-----ALEKYPSYEI	248
AT1G78080.1	-----SLEKYPSYEI	327
AT1G36060.1	-----MLGKCPSYEI	307
LOC_Os10g22600.1 11980.m05267	-----ALRRYPSWEI	314
LOC_Os05g49700.1 11975.m09040	-----LERMPSFDP	264
AT1G64380.1	-----DTDGFLARMPFDP	326
	MGV-----	
LOC_Os02g51670.1 11972.m10198	DWDSILS-----	338
LOC_Os06g11860.1 11976.m05903	DWDSILS-----	360
LOC_Os08g31580.1 11978.m07152	DWDSLNNNN-----	280
LOC_Os09g20350.1 11979.m05242	DWDSLLAAN-----	291
LOC_Os03g09170.1 11973.m06423	DWDAILS-----	297
AT2G22200.1	DWDAISKLANS-----	261
AT4G39780.1	DWDAISKLSSES-----	272
AT5G65130.1	DWDAIEKLF-----	277
AT1G22190.1	DWDSILQCSSLVN-----	261
AT1G78080.1	DWDSILA-----	334
AT1G36060.1	DWASILS-----	314
LOC_Os10g22600.1 11980.m05267	DWDAILS-----	321
LOC_Os05g49700.1 11975.m09040	ELIWEMLNF-----	273
AT1G64380.1	ELIWEVLAN-----	335

FIGURE 8 (conitued)

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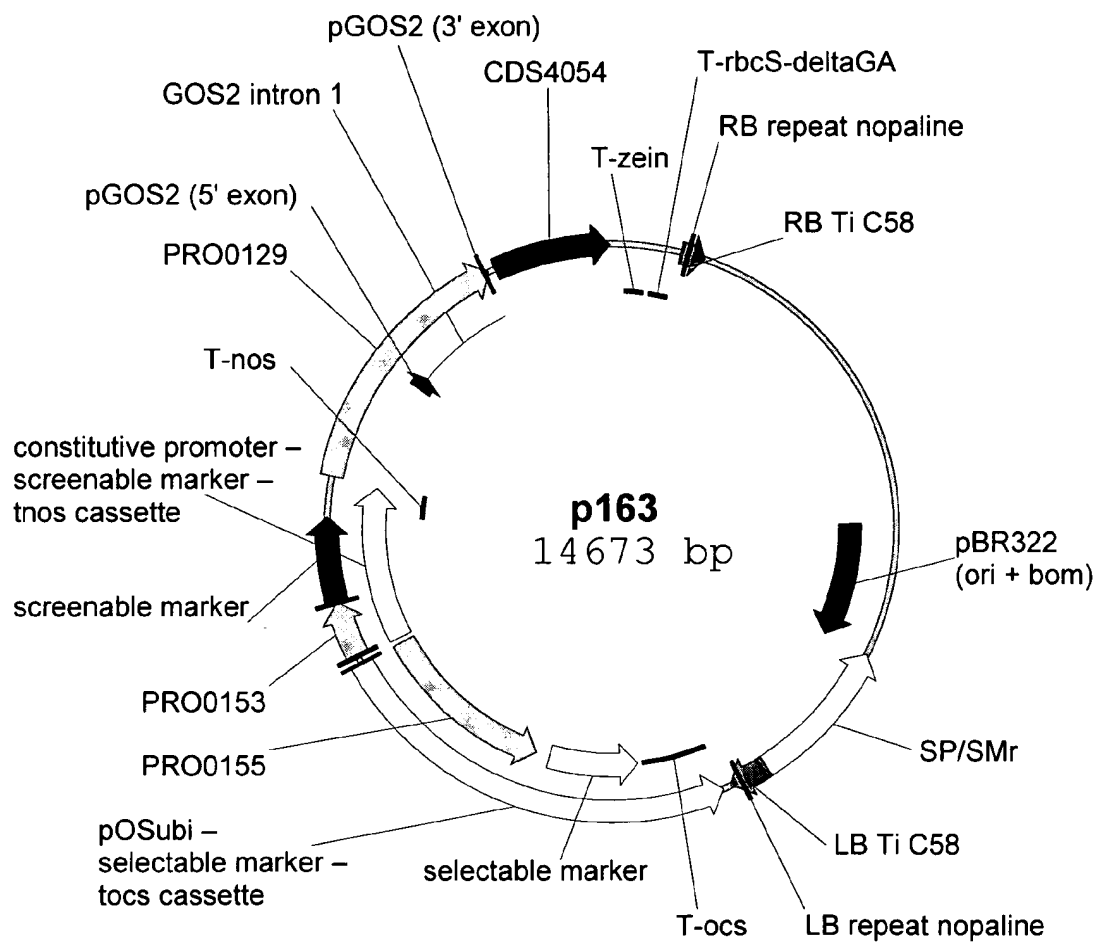


FIGURE 9

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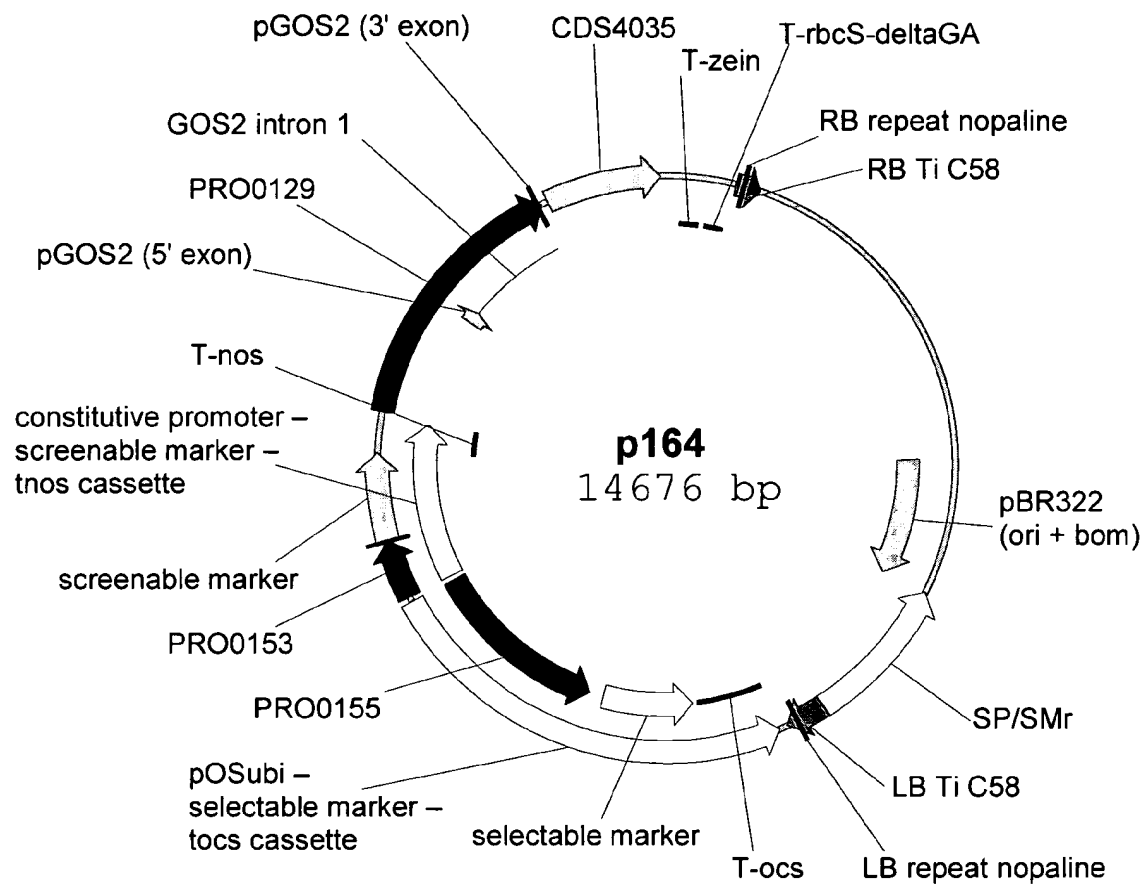


FIGURE 10

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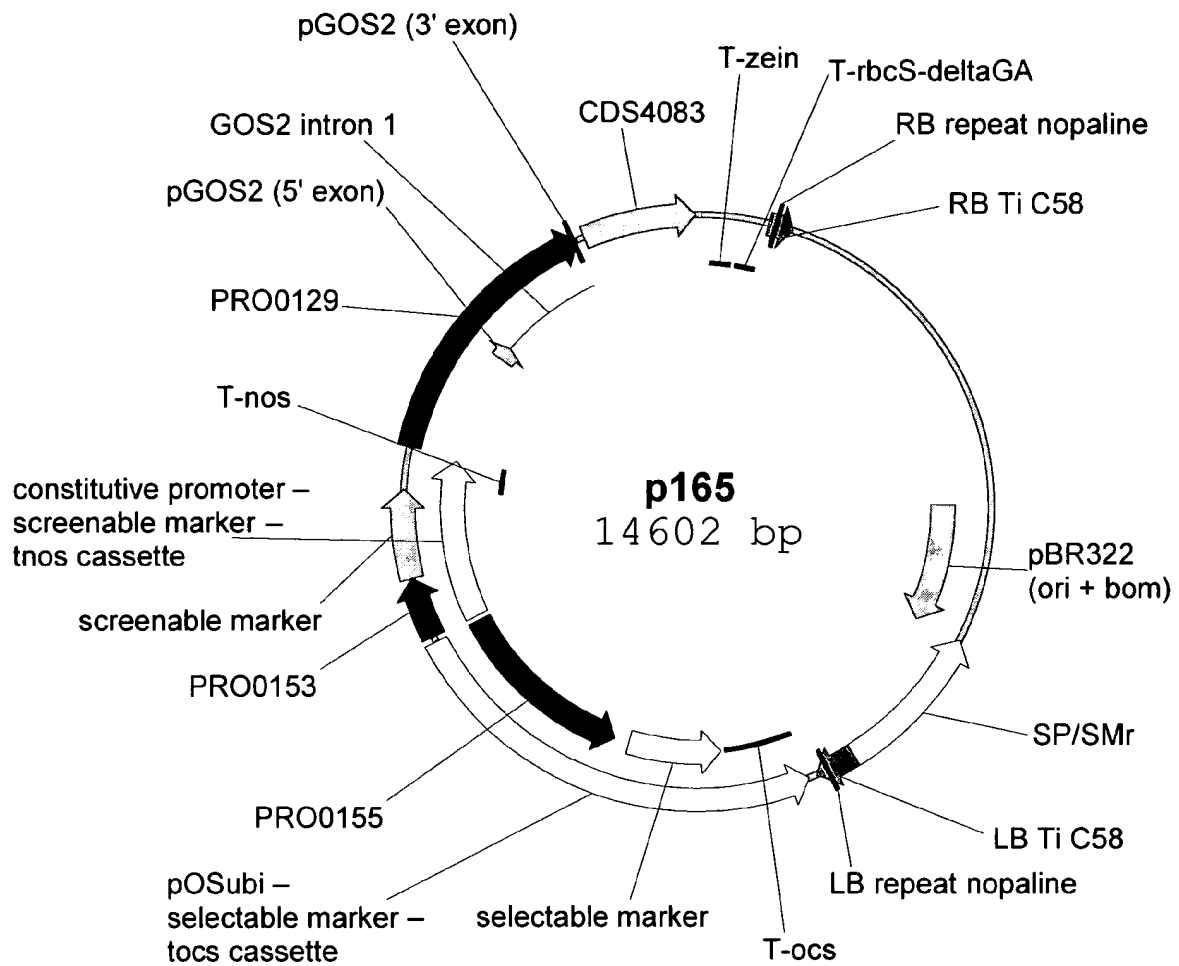


FIGURE 11

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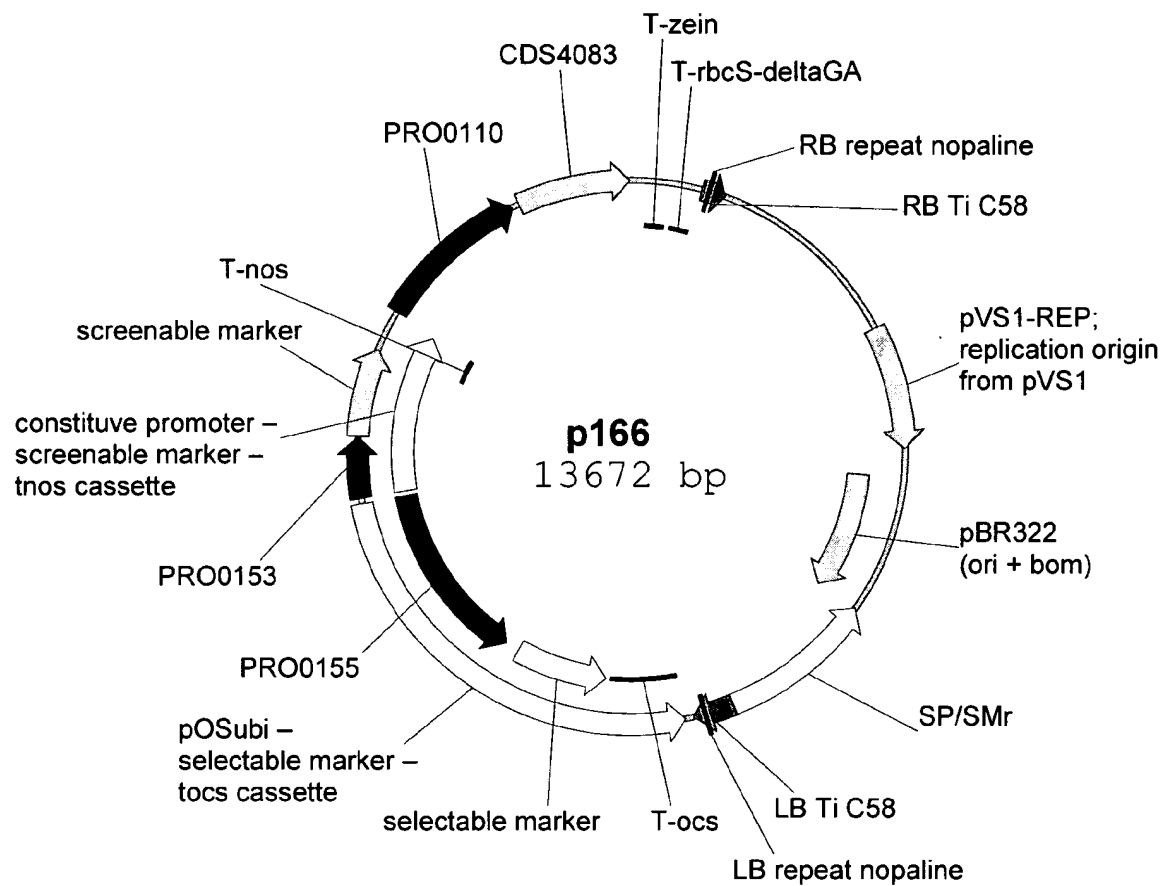


FIGURE 12

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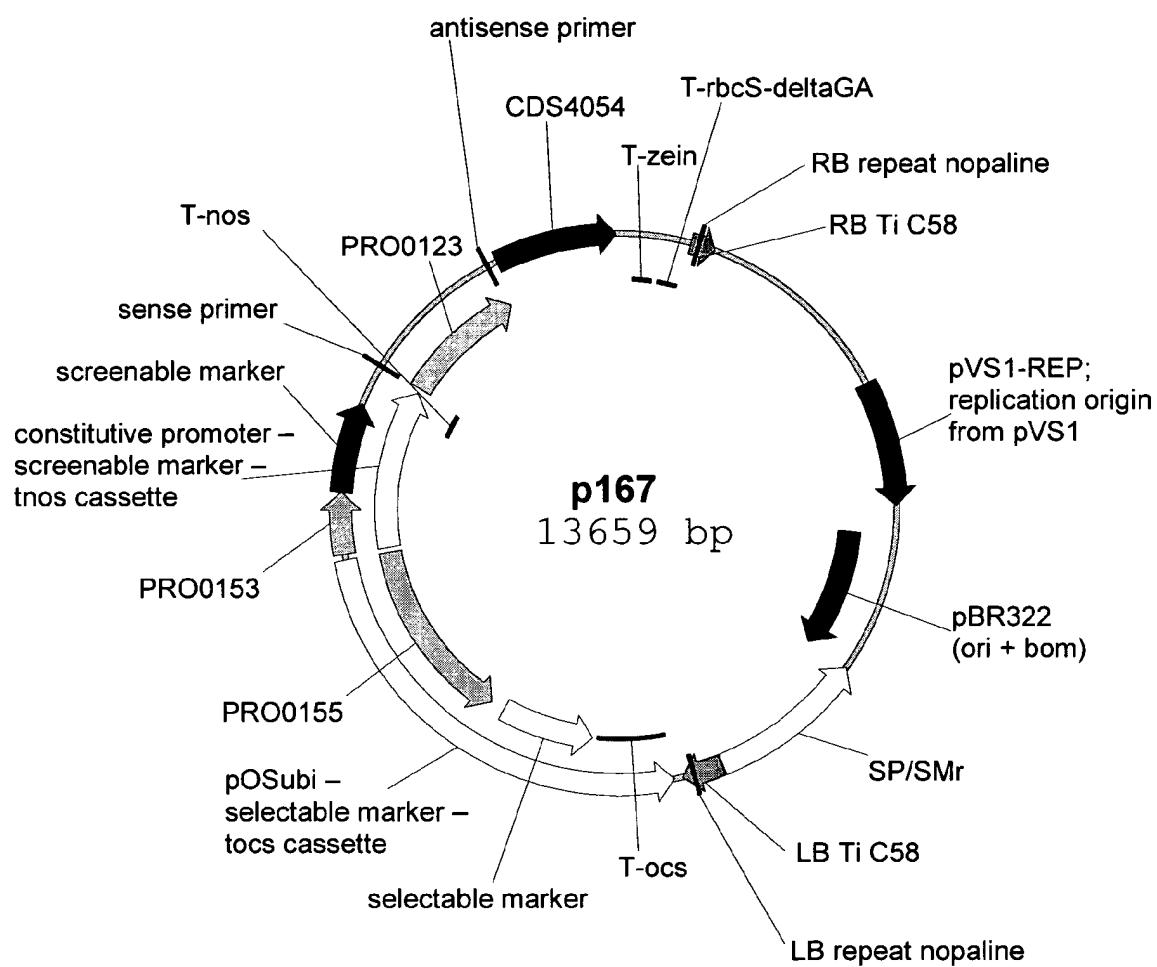


FIGURE 13

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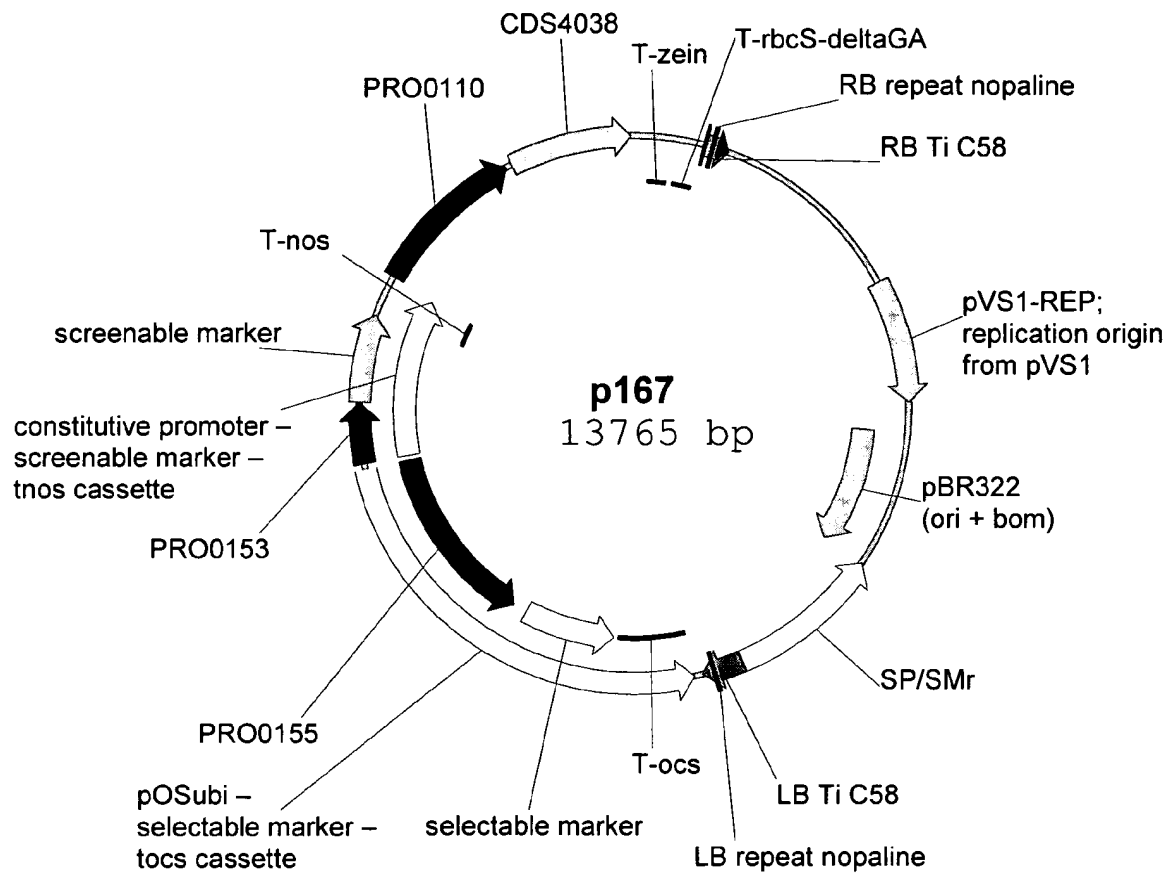


FIGURE 14

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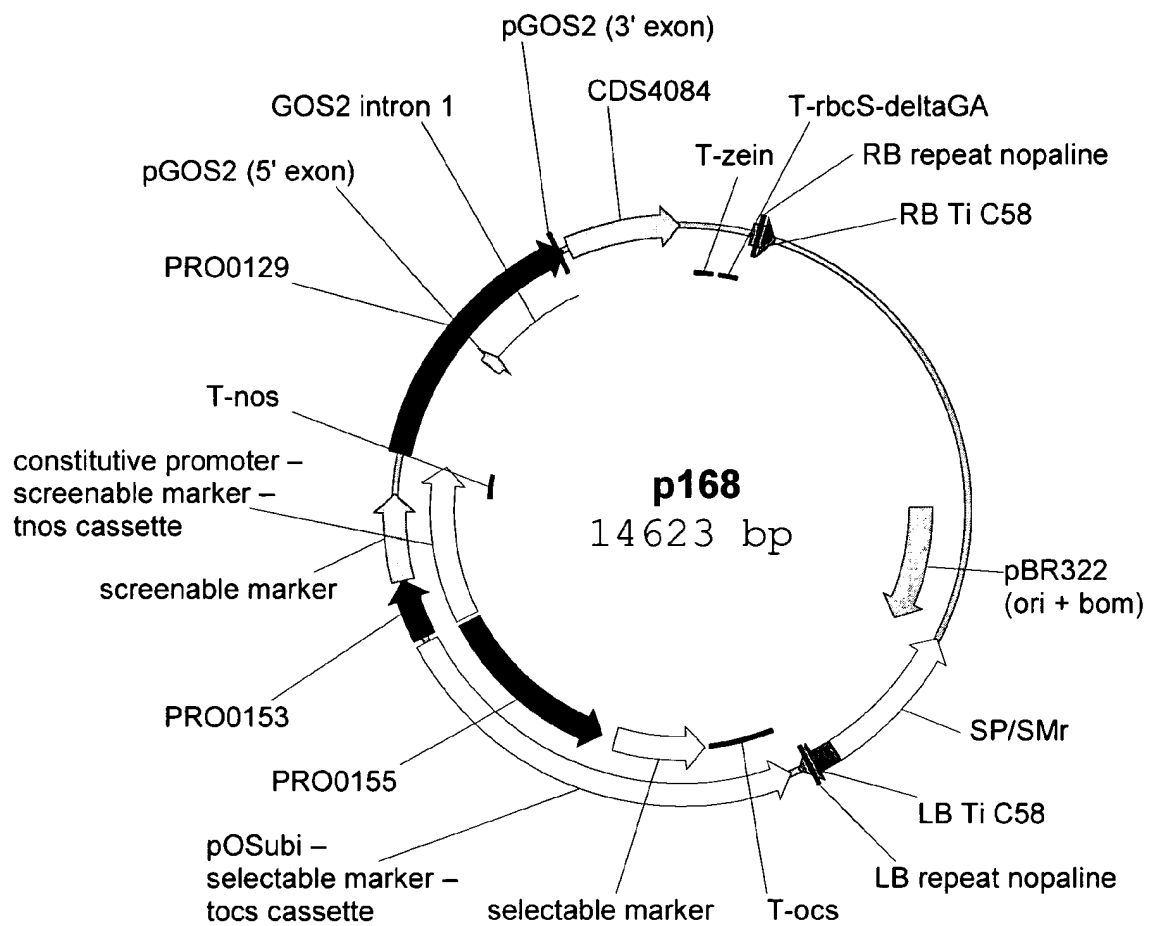


FIGURE 15

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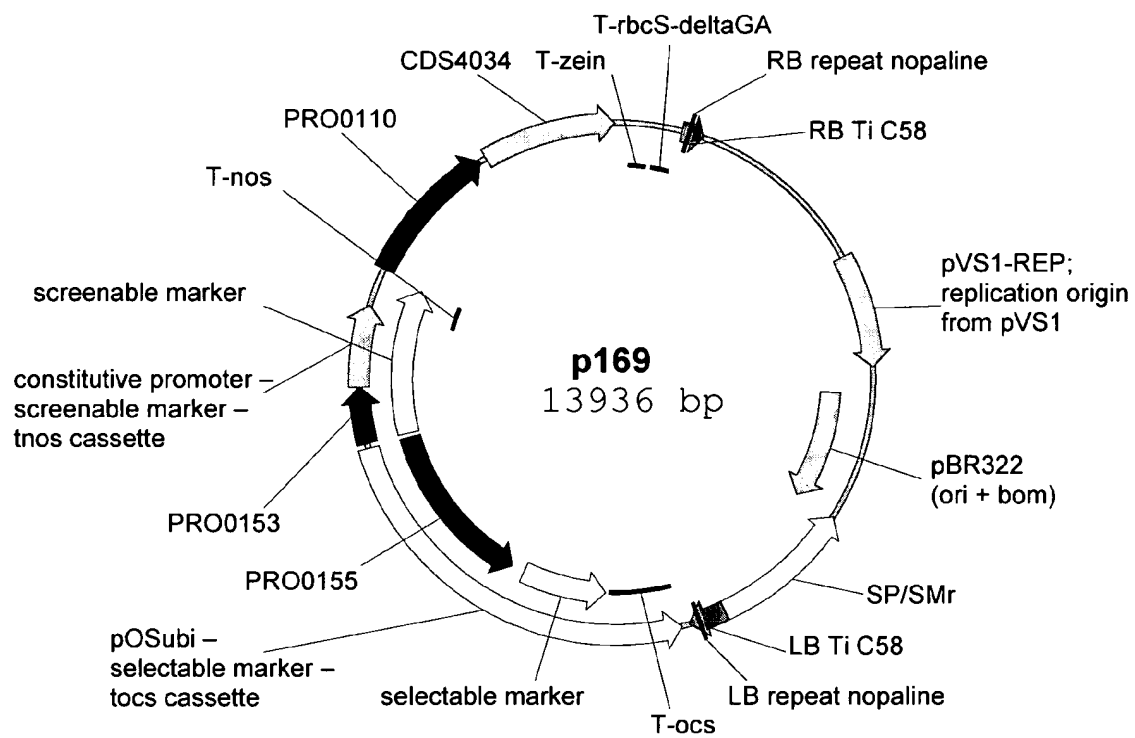


FIGURE 16

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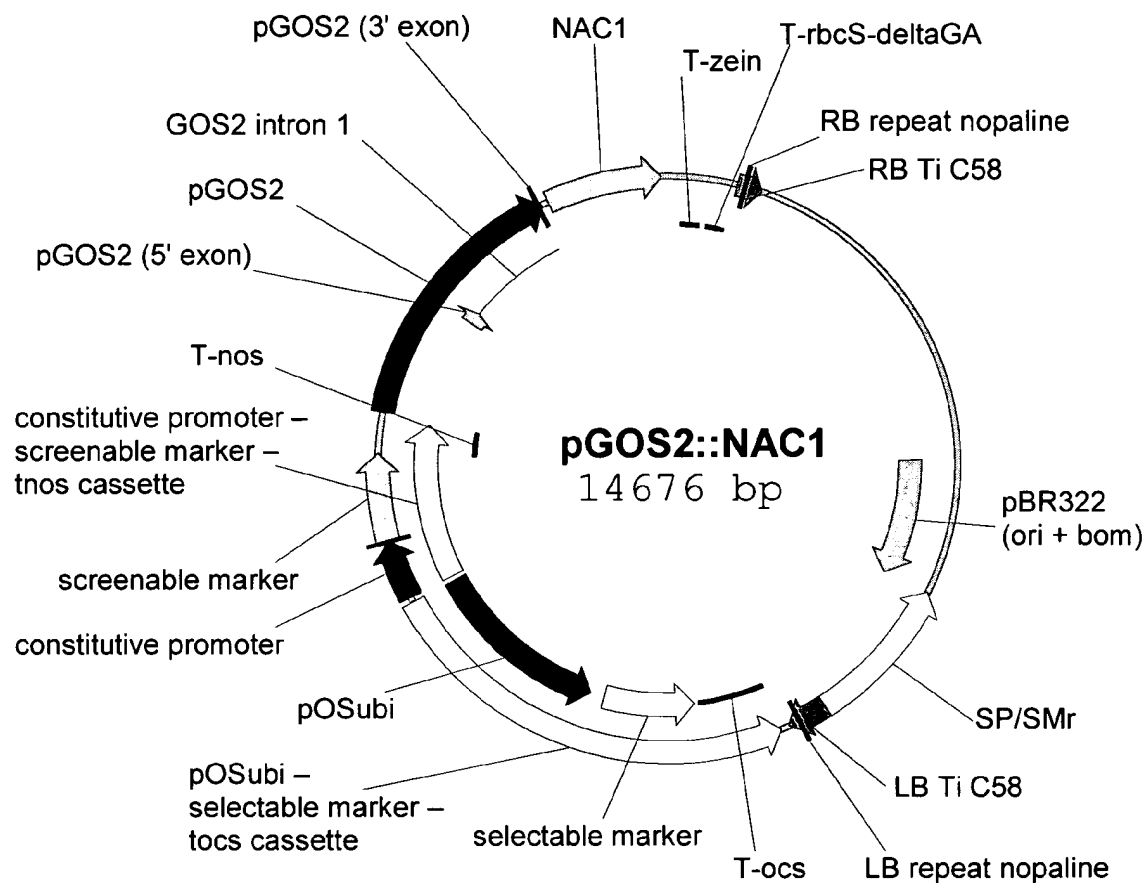


FIGURE 17

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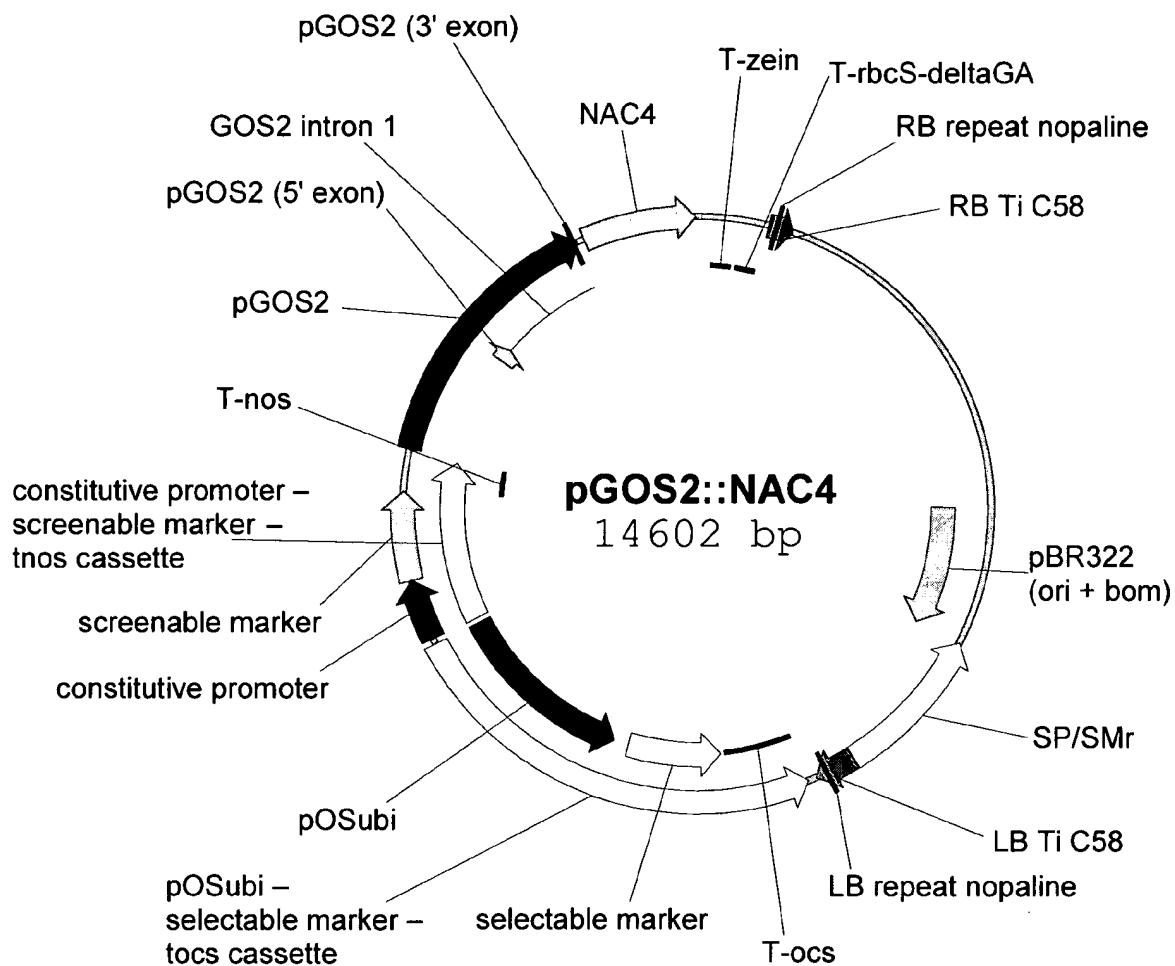


FIGURE 18

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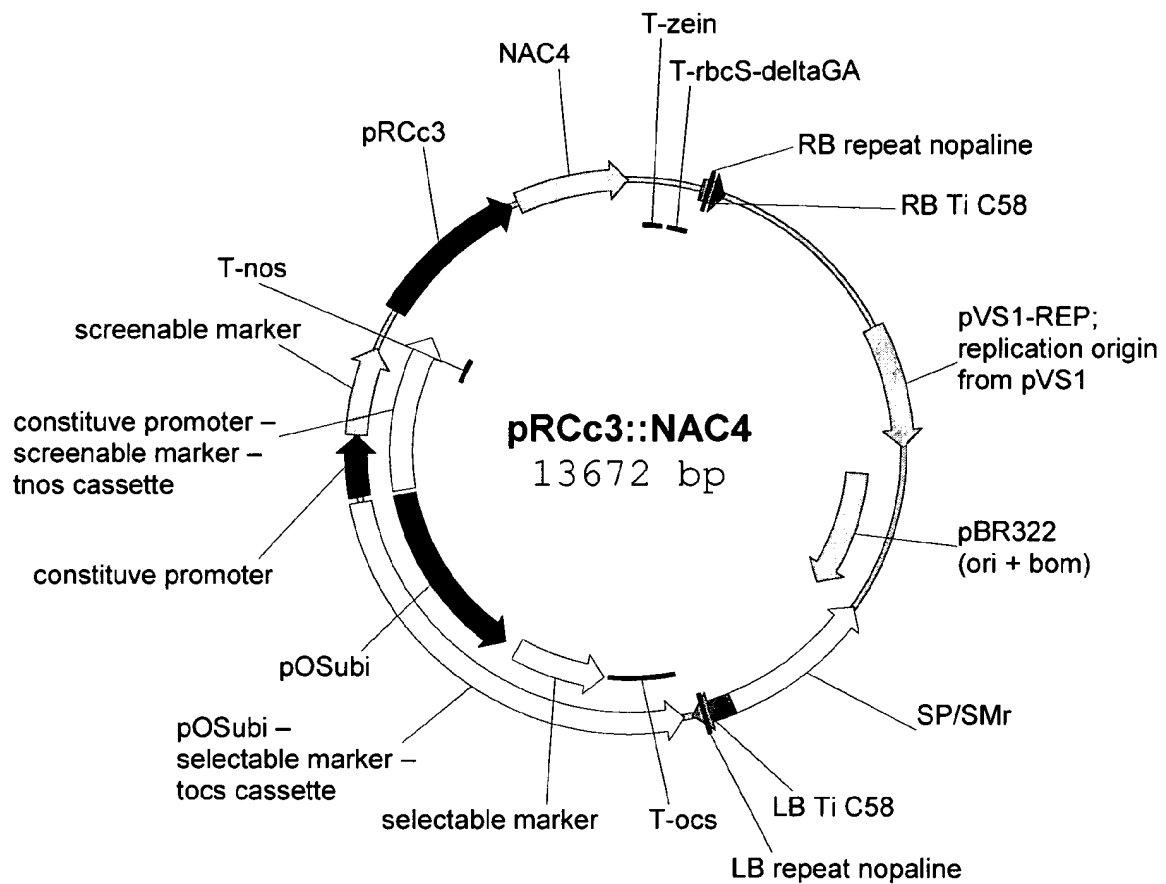


FIGURE 19

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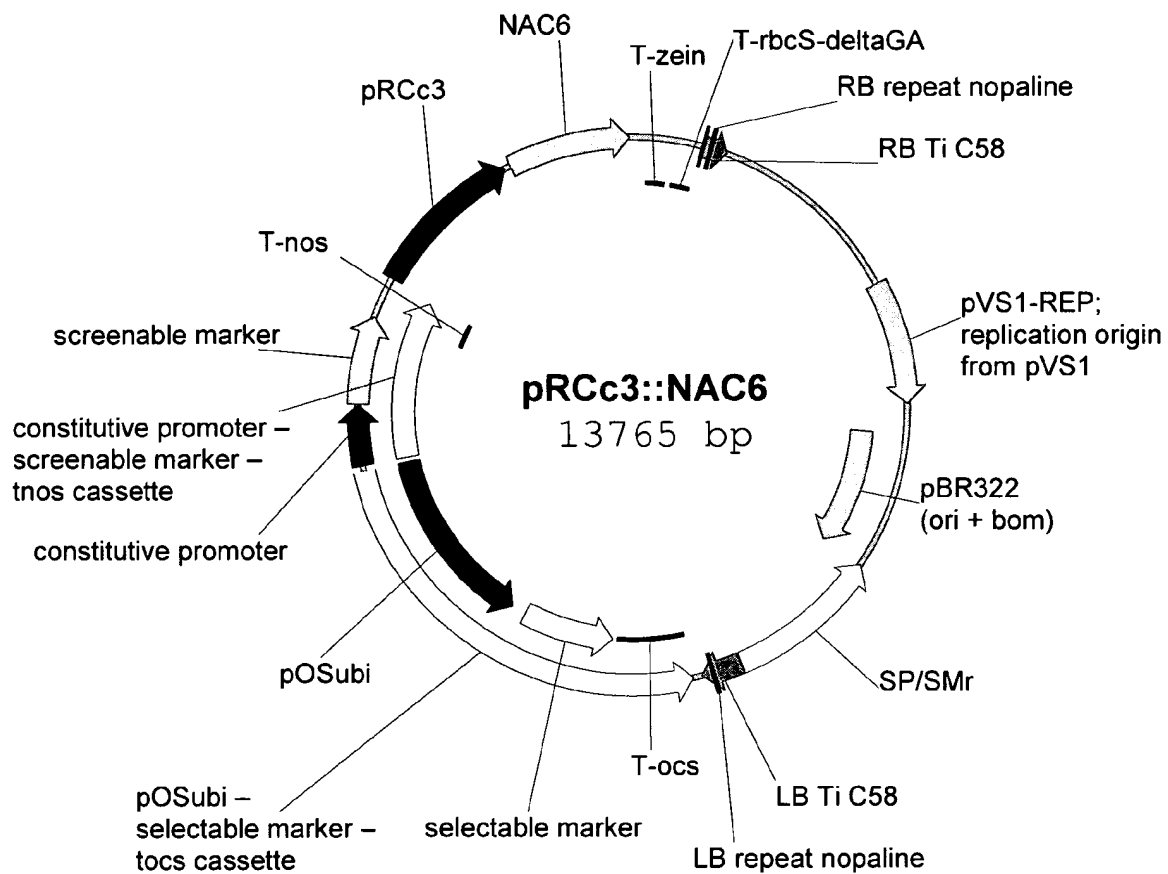


FIGURE 20

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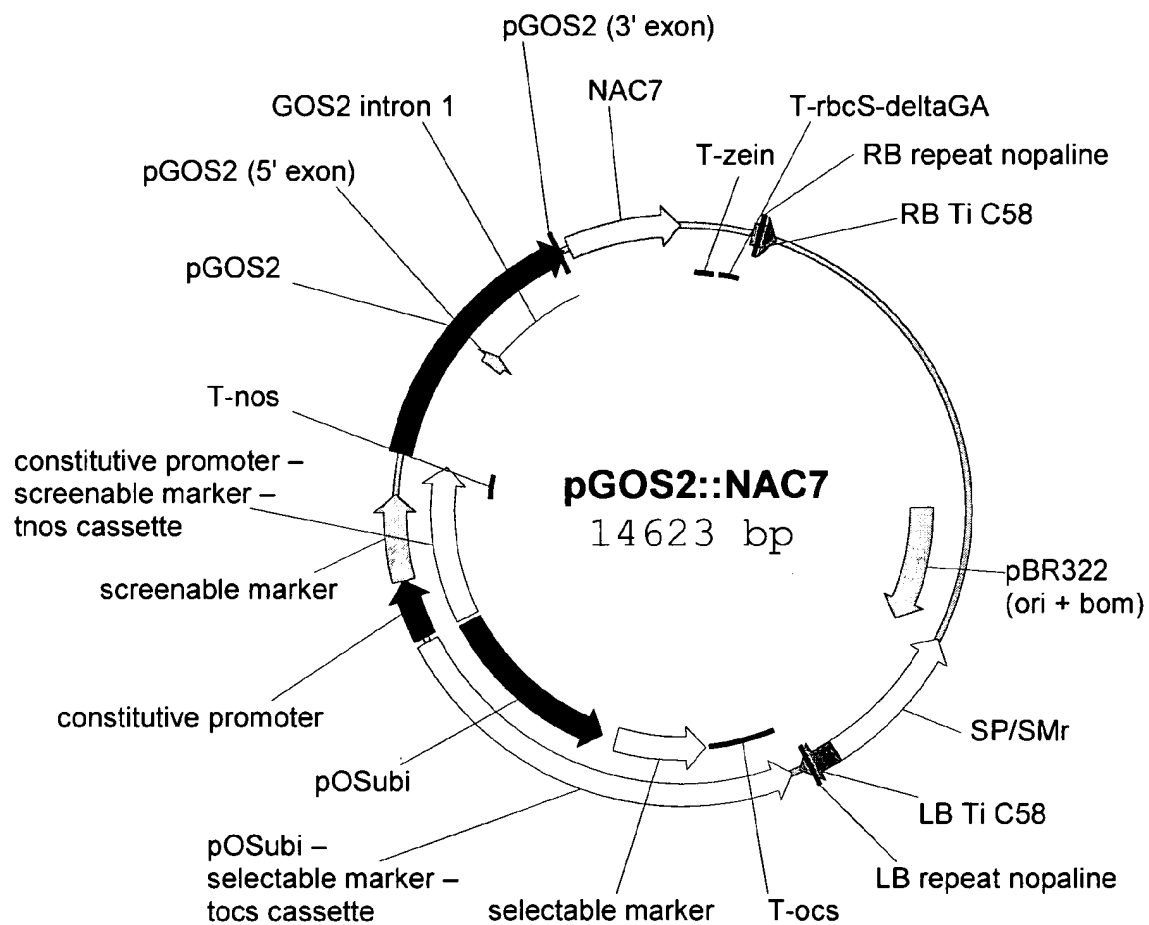


FIGURE 21

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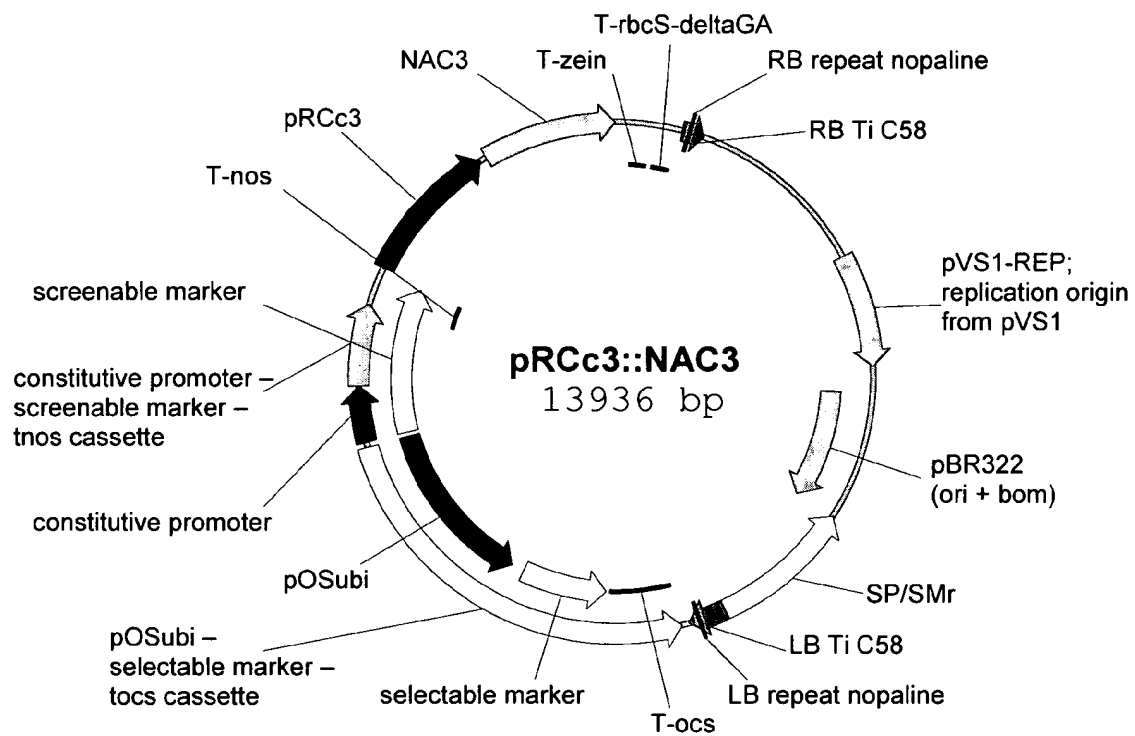


FIGURE 22

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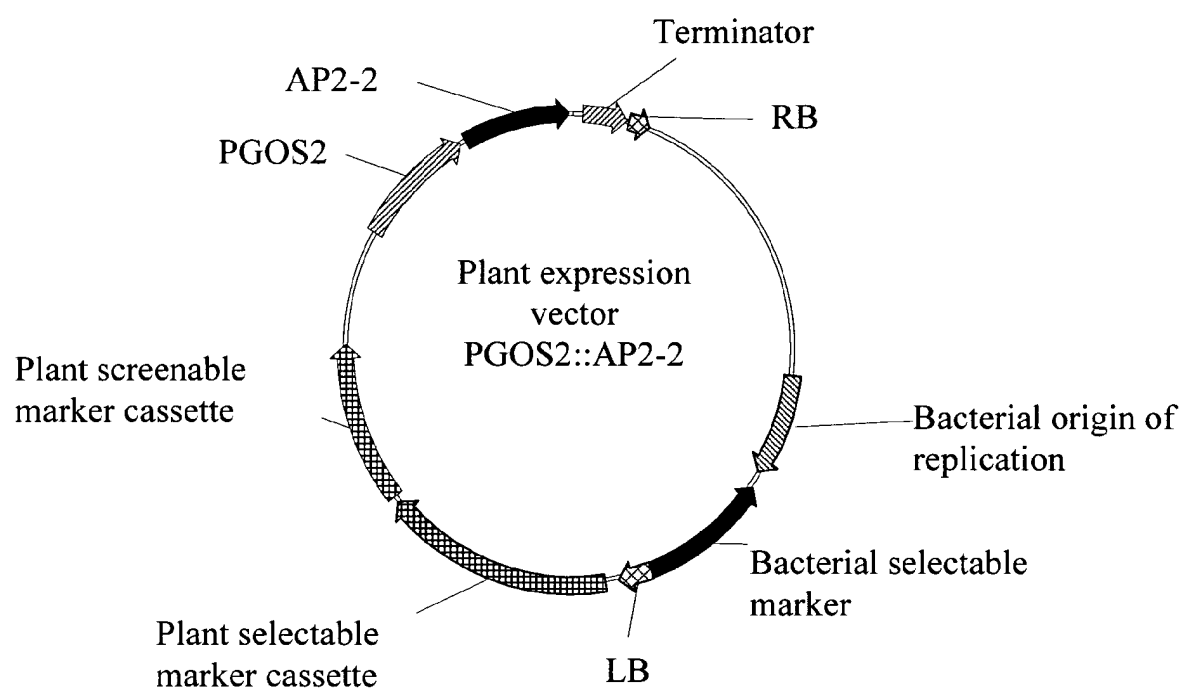


FIGURE 23

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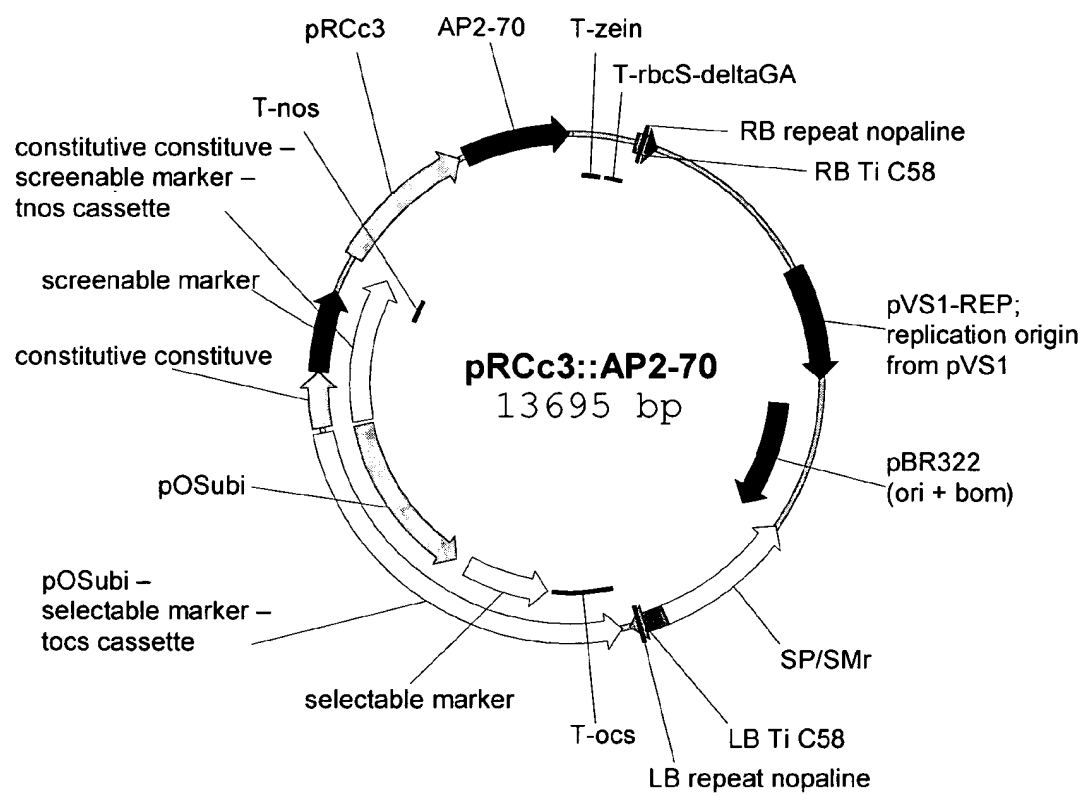


FIGURE 24

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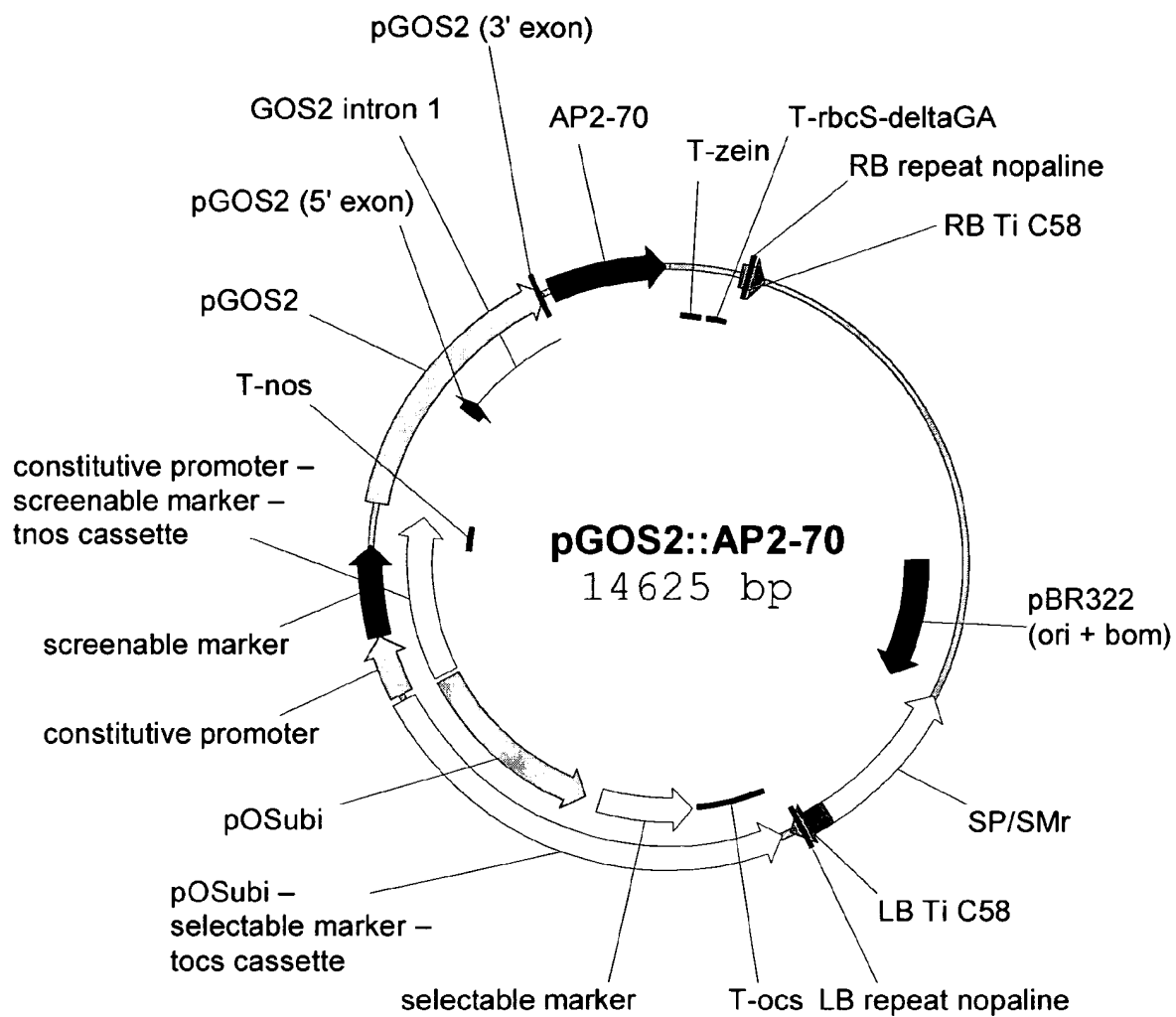


FIGURE 25

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SEQ ID NO: 1 - XM_479673.1| *Oryza sativa* (japonica cultivar-group) mRNA

ATCCAGATGCGCTTGCACTTGCACTTGCACTGCAGTTCATTGCTCTAGCTATAGGCTATAGCTACTATA
CACTCATGAGAATCTGAGATTGGGCTGAAAATTGATGAGCATCGATCTGAAGAAGACATATATATAGC
TGATGATGATATAGCTTTTTCTGCATATGCTTGTTTTGATCTGCAGCCAATCGATCGAGGCATAGAGA
GTCACCAGGCAATCAAATTTCCAACCATCCATCAGCTAGATATATATACAGCAAAGATCACGATACTCC
TAGCTAGCTAGCTAGAAGAATTGATCGGTTCGATCGGAGGAAATAGCAATGGATCGGCATGAGGAGGAG
GCAGGAGAGTCTCCATGTGTGCCGCCGGGGTTTCAGGTTTCACCCGACGGAGGAGGAGCTGGTGGGCTA
CTACCTCGCCAGGAAGGTGGCCTCCCAGAAGATCGATCTCGACATCATCCAGGAGCTCGATCTCTACA
GGATCGAGCCATGGGATCTGCAAGAGCGTTGCAAGTACGGTGGGCATGGCGGCGATGAGCAGACGGAG
TGGTACTTCTTCAGCTACAAGGACCGCAAGTACCCGACGGGACGAGGACCAACCGCGCCACGGCGGC
GGGCTTCTGGAAGGCCACCGGCCGCGACAAGCCGGTGCTCTCGTCGCCGTCGACGAGGGTGATCGGGA
TGAGGAAGACGCTGGTGTCTACAAGGGTCGCGCCCCAACGGCCGGAAGACCGACTGGATCATCCAC
GAGTACCGCCTCCAATCAAACGAACACGCCCTACTCAGGAGGAAGGTTGGGTGGTTTGCCGCGCGTT
TCAGAAGCCGATGCCCCAACCAGCAGCAGCACAGGCTGTCCTACGGCTGCATCCCCGGCAGCTACGGCG
CCGGAGCCTACGCCGCCGTCCCCGACAACCTACAGCTTGCTGCTGCACCACGACAACCCTAGCTTCGCC
GGGCGGCCATTGATGAGCGCCGCTGCCTCAGCTCTCTTCGCCAACAACAACAATAACAGCGTCGTCTGA
CCACAGCAACATTCTGAGTTCAGAGTCCAAGCTTCACTTCTCCGACATGATGCCGCCTCTGGAGAGCC
CCACCATCGTCGACGGCGAGGGCTACGTCTCGCAGGCTAGCAGCTGCGTCGACGTCGATCAGCAAGCC
GGCATCGTCGACTGGAACCTGCTCACCAGCTTGCTGCCGCCGCCGGCGCATCAGCTCTTCCACCACCT
GCCTTCCGCTTCTAGCTCCAAGAACAGCAACAACATTTCTTCGTCAGGCTTCATCGATGACCGAGACT
GATCGATCGATCCAGATCGATTATTATCAATTGACAATTCATTCATCATATATATGCATGAATTTCTTA
CAAATACGCACAATTAAACGATCGAGTGTACTATTAATTAGTTGATTACTCCGTCTCCATGATGTATA
CATTAATTTGACCACTGGCCATCATCAGGCCATCTGCATGCTTACTATCTAGCTTATGTCAGTACACG
GTTGTTAGTTCATTCTTAATTAATTAGCTACTAGTGTGAGTGTGTGTATCTATCGGTTGTTTCGTCTTT
TGACCTCATTGCTGAGAGAGGTTTGTAAGTATGATGATTAAGTTAGCTAGCATTTAATTAGGTGCTA
TATATACACATATATATGCACTATCACTATATACATCATATATATGTATACATATATATCGTTGTCTGCT
TAATGTGTACACCACCTCTCTGCAGTATATATAGTATTGATCAATTAATTTGT

SEQ ID NO: 2 - CDS4054 NAM2

MDRHEEEAGESPCVPPGFRFHPTEEELVGYYLARKVASQKIDLDIIQELDLYRIEPWDLQERCKYGGH
GGDEQTEWYFFSYKDRKYPSTRTNRATAAGFWKATGRDKPVLSSPSTRVIGMRKTLVFKGRAPNGR
KTDWIIHEYRLQSNEHAPTQEEGWVVCRAFQKPMNPQQHRLSYGCI PGSYGAGAYAAVPDNYSLLLH
HDNPSFAGRPLMSAAASALFANNNNSVVDHSNILSSESKLHFSDMMPPLESPTIVDGEYVSQASSC
VDVDQQAGIVDWNLLTSLLPFAHQLFHHLPSASSSKNSNNISSSGFIDDRD

FIGURE 26

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SEQ ID NO: 3 - AK106313.1| *Oryza sativa* (japonica cultivar-group)

AATTTGCTTCTCATCTTTCTTCTCTACTCCTCTCAAATACAAGAGCTCACACTGCTCCCTAGCTTCCT
TCTTCATCCCTTGAAGTAGTTGTGCTAGCTACTGACCAGCCTGAAGATAGATGCTAGTTTGTGTAGAGAA
TTCGATCTTCTGAGGCGTATGGTGATCATGGAGTCATGTGTGCCTCCTGGGTTTAGGTTCCACCCAC
CGACGAGGAGCTCGTCGGCTACTACCTCCGGAAGAAGGTGGCCTCGCAGAAGATCGACCTCGACGTCA
TCCGCGACGTCGACCTCTACCGCATCGAGCCATGGGATCTCCAAGAGCATTTGCAGGATAGGGTACGAG
GAGCAGAGCGAGTGCTTCTTTCAGCTACAAGGACAGGAAGTACCCGACGGGGACGAGGACGAACAG
GGCGACGATGACGGGGTTCTGGAAGGCGACGGGGAGGGACAAGGCGGTGCGTGAGAGGAGCAGGCTCA
TCGGGATGAGGAAGACGCTCGTCTTCTACAAGGGCAGGGCACCCAACGGCCACAAGACCGACTGGATT
GTCCACGAGTACCGCCTCGAGTCCGACGAGAACGCCCCGCCTCAGGAAGAAGGCTGGGTGGTGTCCG
CGCGTTCAAGAAGCGAACCATGCAGCCGCCGCGGAGCTCCATCGGAGCATGGGAGGCGAGCTACTCCT
ACCACGACCCCGCCGTCTTCGTGCGCGGGGGAACACTTCAAGCAAGAGGCGCGGCCGAGCTGGAC
GGCGTCGCGCGCCGCCGCGGAGCTAACGCCTTCTGCGGTACTCCACCCGCCTGGCCGAGCTCCCGCA
GCTGGAGAGCCCGCCGCTGCCAAGCCAGGGGAGCCAGGCGGCCTCGGCCGTGCTCGACGGCGAGGAAG
ATAACGCCGATTCTAGCAGGCGCCCTGGCGGCGGCGGCGGCCGCCGCCGCGGTGACCACGGACTGG
AGGGCGTTTCGACAAGTTCGTGCGCTCCAGCTCAGCCCCGAGGAGCAGCACACCTGCCGGGCCACCGA
CGACGACGACATGGCAGCGCTGCTGCTCCTCGACGGCGGCGGCGAGGAGGACGACGCCGGGAGGTGGC
TGGGCTCCGCCGGGTGCTGAGCGCCGTGGCGGCCGACGCGACGACGGACTGCGGCCTCGGCACCAGC
TGCGTGCCCTGGCGACATCAACTGATTGAGGGCCAAGCCGATCGAGCTCTCACTTCTCCTTAGCATAAA
GTGTGAGATATCTACGAATTGTATGGATGGCTATATACGTACGCCTATACATATGTAGCTGGTCAA
AGCATCGTTTCAGTTTCAGTTTCAGTTCTTGGAAGTCAATGGATGTTGACCATT

SEQ ID NO: 4 - 11980.m06650 protein no apical meristem, AK106313

MVIMESCVPPGFRFHPTDEELVGYLRRKVASQKIDLDVIRDVDLYRIEPWDLQEHCRIGYEEQSEWY
FFSYKDRKYPTGTRTNRATMTGFWKATGRDKAVRERSRLIGMRKTLVFYKGRAPNGHKTDWIVHEYRL
ESDENAPPQEEGWVVCRAFFKKRTMQPPRSSIGAWESYSYHDPVAVFVGGGEHFKQEAALDGVAAAA
GANAFRLRYSTRLAELPQLESPLPSQGSQAASAVVDGEEDNADSSRRPGGGGGAAAATTDWRAFDKF
VASQLSPREEQHTCRATDDDDMAALLLLDGGGQEDDAGRWLGSAGLLSAVAADATDCGLGTSCVPGDI
N

SEQ ID NO: 5 - NM_187584.1| *Oryza sativa* (japonica cultivar-group)

ATGGAATCATGCGTCCCTCCTGGGTTTCAGGTTCCACCCACCGACGAGGAGCTCGTCGGCTACTACCT
CCGCAAGAAGGTGCGCTCCAGAAAGATCGACCTCGACGTCATCCGCGACATCGATCTCTACCGCATCG
AACCCTGGGATCTCCAAGAACATTGTGGGATCGGGTACGATGAGCAAAGCGAGTGGTACTTCTTCAGC
TACAAGGACAGGAAGTACCCGACGGGGACGAGGACGAACAGGGCGACAATGGCGGGTTCTGGAAGGC
GACGGGGAGGGACAAGGCGGTGCACGACAAGAGCAGGCTCATCGGCATGAGGAAGACACTCGTCTTCT
ATAAGGGCAGGGCGCCTAATGGCCAGAAGACCGACTGGATCATGCACGAGTACCGCCTCGAGACCGAC
GAGAACGCGCCGCCACAGGAAGAAGG

FIGURE 26 (continued)

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ATGGGTGGTGTGCCGAGCATTCAAGAAGAGGACGGCGTATCCGGCGAGGAGCATGGTGGAGACGTGGG
ACTACTCCTTGACGAGCGCAACATCATGAGCGCCGCGGCGGCGGCGGCGTTCGCCGATCCGAGCGCG
GCGTACGCGCAGATGAGGCGGCAGCACAGGAGCGGGCGGTTCAAGCAGGAGGCGGAGCTGGACGGCGC
CGCCACAGCCCTCCTCCACTACTCCAGCCACCTCGCCGAGCTGCCGCAGCTCGAGAGCCCCCTCCGCGG
CTGCGGCGCCGCTCCAGCCCAACCCGAGCCAGCTGGCCACCGCCGCGGCGAGGACGACGACTGCAAGGGC
GATAATGGCGGTAGGAGGGCCAAGAAAGCCCCGCGCCGCGGCGACAAGGTGGCGACGACCACGGACTG
GAGAGCGCTCGACAAGTTCGTCGCGTCGCAGCTTAGCCCCGGGGAGTGTGGCAGCATGGAGGCAACGG
CGGAAGCCGCGGCGGCGGCAGTCGCCGGTGTGAGCTCGCCGCTGGACCACGGCGATGACGACATGGCA
GCATTGCTGTTTCTCAACAGCGACGAGAGAGACGAGGTGACAGGTGGACGGGGTTGCTCGGCTCCGG
CGCCGGCGCGAGCGGCGTTCGACGGCGACCTCGGAATCTGTGTGTTTGACAAATGA

SEQ ID NO: 6 - 11973.m05887 protein no apical meristem, NM_187584

MESCVPPGFRFHPTDEELVGYYLRKKVASQKIDLDVIRIDIDLYRIEPWDLQEHCGIGYDEQSEWYFFS
YKDRKYPTGTRTNRATMAGFWKATGRDKAVHDKSRLIGMRKTLVFYKGRAPNGQKTDWIMHEYRLETD
ENAPPQEEGWVVCRAFKKRTAYPARSMVETWDYSLHERNIMSAAAAAFADPSAAYAQMRRQHRSGRF
KQEAELDGAATALLHYSSHLAELPQLESPSAAAAPLQPNPSQLATAGEDDDCKGDNNGRRRAKKARAAG
DKVATTTDWRALDKFVASQLSPGECGSMEATAEAAAAAVAGVSSPLDHGDDDMAALLFLNSDERDEV
RWTGLLGSGAGASGVDGDLGICVFDK

SEQ ID NO: 7 - XM_467007.1| *Oryza sativa* (japonica cultivar-group), mRNA

ATGGACACTTTCTCCCATGTGCCACCTGGTTTCCGCTTTCACCCTACTGACGAGGAGCTCGTCGATTA
CTACCTGAGGAAGAAGGTGGCATCGAAGAAAATCGACCTCGACGTTATAAAAGACGTCGACCTGTACA
AAATCGAGCCCTGGGATCTCCAAGAGAAGTGCAAGATTGGCATGGAAGAACAGAATGACTGGTACTTC
TTCAGCCACAAAGACAAAAAGTACCCGACGGGCACCCGCACCAACCGGGCCACGGGCGCCGGCTTCTG
GAAGGCGACGGGGAGGGACAAGCCCATCTACGCCCGCAGCTGCCTCGTCGGGATGAGGAAGACACTCG
TCTTCTACAAGGGCCGTGCCCCAATGGCCAGAAGTCGGACTGGATCATGCACGAGTACCGCCTCGAG
ACCAACGAAAACGGCACACACCTGAGGAAGGATGGGTGGTCTGCCGGGTGTTCAAGAAGCGGGTGGC
GACGGTGCGGAGAATGGCCGACGGATCACCGTGCTGGTTTCGATGACCACGGCGCCGTCCGGTGC GTTCA
TGCCGGACCTCAGCTCGCCGAGGCAGCTACTGCCGCACCACCACCACCACCACCCGGGCTCGTCGGCG
GCGCTGTACCACGGCCACCACCACCAGCAGCTGCAGCAGATGTACGGTCACTGCAAGCCGGAGCTGGA
GTACCACCACCTCCTGCCGCAGGAGGCCTTCCTGCAGCATCTTCCTCAGCTGGAGAGCCCCAAGCCGC
CGCCGCCGCCTCCTGCGGCGGCGGCCTACATTGGCGGCCACCTCGGATCGTCGTCGTCCACCGCCCTT
ACTACTCACGACGACGAAGCCTCCGGCTCCGCCGCGCAGCAGCAGCCGCGTTCGTTGGAGGCTGTTTA
CATGGCCGGCGCCGGCGTTCGGCATCGGCGTCGACGCGTCGGTGACGGACTGGAGGCTACTGGACAAGT
TCGTCGCGTCTCAGCTGCTCAGCAAGGAGTCCATGTCCAGCTACGGATCCCATCCGGCTCAGGTGTTT
CAGGCTGCAGACGGTGGCAAGCATGAAGAGGCTTTGGACTACGCTTCGACGTCCGCCGGCTCCGGCGG
CGGCGAGGCTGATCTGTGGAATAG

FIGURE 26 (continued)

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SEQ ID NO: 8 - 11972.m09332 protein No apical meristem protein XM_467007

MDTFSHVPPGFRFHPTDEELVDYYLRKKVASKKIDLDVIKDVDLYKIEPVDLQEKCKIGMEEQNDWYF
FSHKDKKYPTGTRTNRATGAGFWKATGRDKPIYARSLVGMKRTL VFYKGRAPNGQKSDWIMHEYRLE
TNENGTTP EEGWVVC RVFKRVATVRRMADGSPCWFDHGA VGFMPDLSSPRQLLPHHHHHHPGSSA
ALYHGH HHQQLQ QMYGHCKPELEYHHLLPQEAF LQHLPQLES PKPPPPPPAAAA YIGGHLGSSSSSTAL
TTHDDEASGSAAQQQPPSLEAVYMAGAGVGIGVDASVTDWRLLDKFVASQLLSKESMSSYGSHPAQVF
QAADGGKHEEALDYASTSAGSGGGEADLWK

SEQ ID NO: 9 - XM_473322.1 Oryza sativa (japonica cultivar-group), predicted mRNA

ATGGAAGTGAAGCAAGGATACACCTCCTGTTGATCAAGCTAGTCTTCTATAGGAGTGCAGAAGAGCG
AGAATCAGCCTCTGTTTCATATTA ACTTGCTACCAGTTCGGGAGCTATACTTTGATCCGCGGAAGAAGA
TGGACGCATTCTCCCATGTCCCGCCAGGTTTTTCGTTTCCACCCTACTGACGAGGAACTCGTGATTAC
TACCTTAGGAAGAAGGTAGCACTGAAGAAGATAGACTTGGACGTCATAAAAGATATTGATCTGTACAA
AATTGAGCCTTGGGACCTACAAGAACAATGCAAGATTGGAACGAGGAGCAGAACGAGTGGTACTTCT
TCAGCCACAAGGACAAGAAGTACCCGACGGGCACACGCACCAACAGGGCGACCACTGCCGGCTTTTGG
AAGGCCACCGGGAGGGACAAGCCGATCTATGTCAAGAACTGCCTTGTGGGATGAGGAAGACGTTGGT
TTTCTACAGGGGCCGGGCTCCCAACGGACAGAAGTCGGACTGGATCATGCACGAGTATCGCTTGGAGA
CCAACGAATACGGAGCTCCCCAAGAGGAAGGATGGGTGGTCTGCAGGGTGTTC AAGAAGCGAGTCGCG
GCGGTGCAAAGGGCGGCCGGCGACGGCGGCGACTCACCTTTCTGGTTCAACGAGCACGTCGCGTTCAT
GGCGCCGGCGCCAGGCCTCGACTCGCCGTACCATGGCCACCGCCAGAGCCACCCTTGCAAGCTGGAGG
TAGAGTATCACCACCACCTCCTTCCTCAGGAGGCGGCGCCGTTTCATGCACCTCCCAAGGCTGGAGAGC
CCCAAGCTACCGGCCGCCGACATCATTGTCGCCACCGCAGCGTCGTCCGCTCTCCAGCCGTGCGGCCA
CACGACGGCGCAGCAGCTGCAGCTGCAGATCGAGCCGGTCTACGTGACGGCCGATGCGTTCGGCAGCAG
ATTGGAGGGATCTTGACAAGCTGGTGGCGTCTCAGTTCGGCCACGGCGACTCGACTGCGAAGGAGCCC
AGTTACTGCAATCCGGTGCAGGTGTTTCAGGTTCGAGGGGAAGCAGGAGGATAGCTTGGATTACGTGTC
CACGTCTGCCTCCTGCGGAGGGGAGGAGGATTTGTGGAAATAG

SEQ ID NO: 10 - OSJNBb0020O11.1protein_id="XP_473322.1"

MEVEARIHLLLIKLVFYRSAEERESASVHINLLPVRELYFDPRKKMDAFSHVPPGFRFHPTDEELVDY
YLRKKVALKKIDLDVIKDIDLYKIEPVDLQEQCKIGNEEQNEWYFFSHKDKKYPTGTRTNRATTAGFW
KATGRDKPIYVKNCLVGMKRTL VFYRGRAPNGQKSDWIMHEYRLETNEYGAPQEEGWVVC RVFKRVA
AVQRAAGDGGDSPFWFNEHVAFMAPAPGLDSPYHGHRQSHPCLEVEYHHHLLPQEAAPFMHLPRLES
PKLPAADIIVATAASSALQPCGHTTAQQLQLQIEPVYVTADASAADWRDLDKLVASQFGHGDSTAKEP
SYCNPVQVFQVEGKQEDSLDYVSTSASCGGEEDLWK

FIGURE 26 (continued)

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SEQ ID NO: 11 – *Medicago truncatula* ABE89364.1 clone mth2-70o13

ATGATGGAGTCATGTGTCCACCTGGATTTCGGTTCCACCCAACGGATGGAGAGCTTGTGGTTATTA
TCTAAGAAAGAAAGTAGCTTCTCACAAGATTGATCTTGATGTTATCAAAGAGATCGATCTATATCGTA
TTGAACCCTGGGATCTCCAAGAGAGATGTAGAATTGGGAATGAGGAGCAACATGAGTGGTATTTTTTT
AGTCACAAAGATAAGAAATATCCAACAGGGACGAGAACGAATAGAGCTACAATGGCAGGGTTCTGGAA
AGCAACCGGAAGAGATAAGTCGGTGTATGAACGAACAAAACCTGATTGGAATGAGGAAGACACTCGTTT
TCTACAAAGGAAGAGCACCTAATGGACAGAAAACCTGATTGGATCATGCATGAATATAGGCTTGAAACA
GTTGAAAATGCACCTCCACAGGCAAGTGAAGAAGGTTGGGTTGTGTGCAAAGCATTCAAGAAAAAAC
AAGTGTCCAAGCAAAAACAAATGAAAGATGGGATCCAAGCCACTTACATGATGAACAAACAAGTAGCA
TCATCTCAAGGGTGGACCCTATTGACCTCATCTTAAGACAACCACAGAGGATTTCAAGTCAAAATTTT
ATGTACAAACAAGAGATAGAAGCAGAAGCAGATACCTTATTAAGGTTTCATGCATTCAGAACAAATTGGT
ACCTCTTCTCAACTACAAAGTCCCTCTTTAACAAAGAGGCAAACTCAATGCCAATAATATCAGAGA
AAGTGACTGATTGGAGGGATCTTGACAAGTTTGTGGCTTCTCAGTTGAGTCAAGAAGATCATAGGCAT
GAAACAAGCTCAGACATGTCATTGTTCTACTTCAGAGTAGTAAGGATGATGAAGAGAACAAGTTAAG
CTCATTTTTTAACACAAGGTCAGATTGTGACATTGGAATATGTGTATTTGAAAATTAA

SEQ ID NO: 12 - *medicago* ABE89364.1| No apical meristem (NAM) protein [*Medicago truncatula*]

MMESCVPPGFRFHPTDGELVGYLRLKKVASHKIDLDVIKEIDLYRIEPWDLQERCRIGNEEQHEWYFF
SHKDKKYPTGTRTNRATMAGFWKATGRDKSVYERTKLIGMRKTLVFYKGRAPNGQKTDWIMHEYRLET
VENAPPQASEEGWVVCFAFKKTSVQAKTNERWDPSHLHDEQTSSIIISRVDPIDLILRQPQRISAQNF
MYKQEIIEAEDTLLRFMHSEQLVPLPQLQSPSLTKRQNSMPIISEKVTDWDRDLDKFVASQLSQEDHRH
ETSSDMSLFLQLQSSKDDEENKLSSFLTRSDCDIGICVFEN

SEQ ID NO: 13 - NM_101098.2 *Arabidopsis thaliana* ANAC007/EMB2749; (ANAC007/EMB2749)

ATGAATTCATTTTCCCACGTCCCTCCGGGTTTTAGATTTACCCGACAGATGAAGAAGCTTGTAGACTA
CTACCTGAGGAAAAAGTCGCATCGAAGAGAATAGAAATTGATTTATAAAGGACATTGATCTTTACA
AGATTGAGCCATGGGACCTTCAAGAGTTGTGCAAAATTGGGCATGAAGAGCAGAGTGATTGGTACTTC
TTTAGCCATAAAGACAAGAAGTATCCACAGGGACTCGAACCAATAGAGCAACAAAAGCAGGGTTTTG
GAAAGCCACCGGAAGAGATAAGGCTATCTATTTGAGGCATAGTCTAATTGGCATGAGGAAAACACTTG
TGTTTTACAAGGGAAGAGCCCCAAATGGACAAAAGTCTGATTGGATCATGCACGAATACCGCTTAGAA
ACCGATGAAAACGGAAGTCCCTCAGGAAGAAGGATGGGTTGTGTGTAGGGTTTTCAAGAAGAGATTGGC
TGCAGTTAGACGAATGGGAGATTACGACTCATCCCCTTCACATTGGTACGATGATCAACTTTCTTTTA
TGGCCTCCGAGCTCGAGACAAACGGTCAACGACGGATTCTCCCAATCATCATCAGCAGCAGCAGCAC
GAGCACCAACAACATATGCCATATGGCCTCAATGCATCTGCTTACGCTCTCAACAACCCTAACTTGCA
ATGCAAGCAAGAGCTAGAACTACACTACAACCACCTGGTACAACGAAATCATCTTCTTGATGAATCTC
ATTTATCGTTCCTCCAACCTCCTCAACTAGAAAGCCCTAAGATTCAACAAGATAACAGTAATTGCAAC
TCTCTTCCTTATGGAACAAGCAACATCGATAATAACTCGAGCCATAATGCTA

FIGURE 26 (continued)

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ACTTGCAGCAATCAAATATCGCGCATGAGGAACAATTGAATCAAGGAAATCAGAACTTCAGCTCTCTA
TACATGAACAGCGGCAACGAGCAAGTGATGGACCAAGTCACAGACTGGAGAGTTCTCGATAAATTTGT
TGCTTCTCAGCTAAGCAACGAGGAGGCTGCCACAGCTTCTGCATCTATACAGAATAATGCCAAGGACA
CAAGCAATGCTGAGTACCAAGTTGATGAAGAAAAAGATCCGAAAAGGGCTTCAGACATGGGAGAAGAA
TATACTGCTTCTACTTCTTCGAGTTGTCAGATTGATCTATGGAAGTGAGCTGAAAGAGAAGACATATA
AATGCATATATACATATATATATATACGTACACACGAACACTAATCAAGTGTAGATGATGATGATGGT
ACAGATTTATATTTGCTTTGATTGATTCTTACTACATTATTGAACTTATGTCATATGCATATATACAT
TGCGTATCTATGCATATTTATACTTGTACTCAATATGATTAACCATATATAAACTCTAATCTAAATGT
AA

SEQ ID NO: 14 - ANAC007/EMB2749" ="AT1G12260"NP_172690.1"

MNSFSHVPPGFRFHPTDEELVDYYLRKKVASKRIEIDFIKDIDLYKIEPVDLQELCKIGHEEQSDWYF
FSHKDKKYPTGTRTNRATKAGFWKATGRDKAIYLRHSLIGMRKTLVIFYKGRAPNGQKSDWIMHEYRL
TDENGTPQEEGWVVCVFKKRLAAVRRMGDYDSSPSHWYDDQLSFMASELETNGQRRILPNHHQQQHH
EHQQHMPYGLNASAYALNNPNLQCKQELELHYNHLVQRNHLDESLSFLQLPQLESPIQQDNSNCN
SLPYGTSNIDNNSHNANLQQSNIAHEEQNLQGNQNFSSLYMNSGNEQVMDQVTDWRVLDKFKVASQLS
NEEAATASASIQNNAKDT SNAEYQVDEEKDPKRASDMGEEYTASTSSSCQIDLWK

SEQ ID NO: 15 - NM_104947.1| Arabidopsis thaliana ANAC026; transcription factor (ANAC026)

ATGAATTCGTTTTTCAAGTACCTCCTGGCTTCAGATTTTCATCCTACTGATGAAGAAGTTGTAGACTA
CTACTTGAGGAAAAAGTTGCATCAAAGAGAATAGAAATCGATATCATCAAGGATGTTGATCTTTACA
AGATTGAGCCATGTGATCTTCAAGAGTTATGCAAGATAGGAAACGAAGAGCAGAGCGAATGGTACTTC
TTTAGTCATAAAGACAAGAAGTATCCACGGGAACTCGAACCAATAGAGCCACGAAAGCAGGATTTTG
GAAAGCCACTGGAAGAGACAAGGCTATATATATAAGACATAGTCTTATCGGTATGAGGAAAACACTTG
TGTTTTACAAAGGAAGAGCCCCAAATGGTCAGAAATCCGATTGGATCATGCACGAATATCGCTTAGAA
ACAAGTGAAATGGAACCCCTCAGGAAGAAGGATGGGTAGTATGTAGGGTATTCAAGAAGAAATTGGC
AGCGACAGTGAGGAAAATGGGAGATTACCATTTCATCACCATCGCAGCATTGGTACGATGATCAGCTCT
CTTTTATGGCCTCCGAGATCATTTCTAGTTCTCCACGACAGTTTCTTCCCAATCATCATTATAACCGC
CACCATCACCAGCAGACATTGCCTTGTCGCTCAATGCATTCAACAACAACAACTCCTAAGTTGCAATG
CAAGCAAGAGCTCGAGTTACATTACAATCAAATGGTACAACATCAACAACAAACCATCATCTTCGTG
AATCTATGTTTCTCCAGCTTCCTCAGCTCGAAAGCCCTACCAGTAATTGCAATTCTGACAACAACAAT
AACACAAGAAATATTAGTAACTTGCAAGAAATCATCAAATATATCTCATGAGGAACAATTGCAACAAGG
GAATCAAAGTTTCAGCTCTCTGTATTACGATCAAGGAGTAGAGCAAATGACTACTGACTGGAGAGTTC
TCGATAAATTTGTTGCTTCACAGCTTAGCAATGATGAAGAGGCTGCAGCCGTGGTTTCTTCTTCTTCT
CATCAAAACAACGTCAAGATTGACACGAGAAACACGGGTATCATGTGATAGATGAGGGAATAAATTT
GCCGGAGAATGATTCTGAAAGGGTTGTTGAAATGGGAGAAGAGTATTCAAATGCTCATGCTGCTTCTA
CTTCTTCAAGTTGTCAGATTGATCTCTAG

FIGURE 26 (continued)

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SEQ ID NO: 16 - ANAC026"AT1G62700" ="NP_176457.1"

MNSFSQVPPGFRFHPTDEELVDYYLRKKVASKRIEIDI IKDVDLYKIEPCDLQELCKIGNEEQSEWYF
 FSHKDKKYPTGTRTNRATKAGFWKATGRDKAIYIRHSLIGMRKTLVIFYKGRAPNGQKSDWIMHEYRL
 TSENGTPQEEGWVVCRVFKKKLAATVRKMGDYHSSPSQHWYDDQLSFMASEIISSSPRQFLPNHHYNR
 HHHQQTLPCLNFAFNNNNPNLQCKQELELHYNQMVQHQQQNHHLRESMFLQLPQLESPTSNCNSDNNN
 NTRNISNLQKSSNISHEEQLOQGNQSFSSLYDQGVEMTTDWRVLDKFVASQLSNDEEAAAVVSSSS
 HQNNVKIDTRNTGYHVIDEGINLPENDSERVEMGEEYSNAHAASTSSSCQIDL

SEQ ID NO: 17 - XM_476289.1| *Oryza sativa* (japonica cultivar-group)

ATGGATGGATCTAGTATGAGCAGCAGCAGCACGCAGCAGCAGGCGCAGGTTCTCTCTGGATTTCGTTT
 CCACCCGACGGACGAAGAGCTGGTGGATTACTACCTTCGGAAGAAGGTGGCCGCAAGAAGGATTGATC
 TCAATGTCAATCAAGGACGTCGATCTCTACAAGATTGAGCCATGGGATCTGCAAGAGCGTTGCCGGATC
 AATGGCGGGTCGGCGGCGGAGGAGCAGAACGAATGGTACTTCTTCAGCCACAAGGACAAGAAGTACCC
 GACGGGGACGAGGACCAACCGTGCGACGGCGGCGGGGTTCTGGAAGGCGACGGGGCGAGACAAGCCCA
 TCTACGCCACCAAGCAGCACAGCCTCCTCGTGGGCATGAGGAAGACGCTCGTCTACTACCGCGGCCGC
 GCCCCCAACGGCCACAAGTCCGACTGGATCATGCACGAGTACCGCCTCGAGACCACCGAGACGGCCCC
 GCCGCAGGAAGAAGGGTGGGTGGTATGCCGGGTGTTCAAGAAGAGATTACCCACAACAAGAAGAGATT
 CAGACCATGACGCACCTTGCGGCAGCTGGTACGTTGATGAAGATGCACCGGGCGCCTTCATGTCTCCG
 ATGATGATCACCAGATCATCAATATTGCGCCACACCAACACCACGCCGGCATCACGCTGCAAGAGCA
 ACACCTCCACACCACTTACAAGCACAGAGACCTCACTACTAAGATTACAGCAGCTCCAAGTCCCTGCGG
 CAGGCCATCATCTCCTCAACACCATGCCCCATGACCTGGAGAGTTCTACTTCTCTCTTCCATTCTCTT
 TTGGTCTCACCTGATCACCACCAATCAACATGCACCATGCTCAGGCTGATCCCTTCTTTGACGACAT
 GCATGCAGTCGATCAAGCCACTACCACTGACTGGAGAGTTCTTGACAAGTTTGTTGCCTCTCAGCTTA
 GCAATGATGCTACAAACAAGCCTGCGGATCATTATACTGATGAAGGAGACATTCTTCAGGTCAGTGAC
 AAGCAGCAAGAGGTGGCAGCCGCCGATTATGCGTCCACATCAACGTCAAGCAGCCAAATTGATCCATG
 GAAGTGA

SEQ ID NO: 18 - OSJNBa0075G19.15"NAM-like protein"="XP_476289.1"

MDGSSMSSSSTQQQAQVPPGFRFHPTDEELVDYYLRKKVAARRIDLNVIKDVDLYKIEPWDLQERCRI
 NGGSAAEEQNEWYFFSHKDKKYPTGTRTNRATAAGFWKATGRDKPIYATKQHSLLVGMKRLVYYRGR
 APNGHKSDWIMHEYRLTETETAPPQEEGWVVCRVFKRLPTTRRSDHDAPCGSWYVDEDAPGAFMSP
 MMITRSSILRPHQHAGITLQEQHLHTTYKHRDLTKIQQLQVPAAGHLLNTMPHDLESSTSSFHSL
 LVSPDHHQINMHHAQADPFFDDMHAVDQATTTDWRVLDKFVASQLSNDATNKPADHYTDEGDILQVSD
 KQQEVAAADYASTSTSSSQIDPWK

FIGURE 26 (continued)

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SEQ ID NO: 19 - NM_127362.1| Arabidopsis thaliana ANAC037; transcription factor (ANAC037)

ATGGAGCCAATGGAATCTTGTAGCGTTCCTCCAGGATTTAGGTTCCATCCGACGGACGAAGAGCTTGT
CGGGTACTATCTAAGGAAGAAAATCGCATCGCAAAGATTGATCTCGACGTCATCAGAGACATCGATC
TCTACAGAATAGAACCATGGGATCTACAAGAACAATGTCGAATCGGTTATGAGGAACAAAATGAATGG
TATTTTTTTTAGTCACAAGGACAAGAAATATCCAACGGGGACAAGAACTAATAGAGCGACCATGGCTGG
ATTTTGGAAAGCCACGGGAAGAGACAAAGCTGTTTACGACAAAACAAAATAATTGGTATGAGGAAAA
CACTTGTGTTCTACAAAGGACGTGCACCTAATGGCAAGAAATCCGATTGGATCATGCATGAGTACCGG
CTCGAGTCAGATGAGAATGCACCGCCCCAGGAAGAAGGATGGGTGGTTTGTAGAGCATTCAAAAAAG
AGCTACAGGGCAAGCCAAGAACACGGAACTTGGAGCTCAAGTTACTTTTACGATGAAGTTGCACCGA
ATGGAGTTAACTCGGTTATGGACCCCATGATTACATATCTAAGCAGCAACATAACATTTTTGGGAAA
GGTTTGATGTGTAAGCAAGAACTAGAAGGAATGGTTGATGGTATAAACTATATACAATCGAATCAATT
CATTCAGCTCCCACAACCTCCAAAGCCCTTCTCTCCCGCTGATGAAAAGACCTTCAAGCTCGATGTCCA
TAACATCAATGGATAACAATTACAATAAACTCCCATTAGCGGATGAAGAAAGCTTCGAGTCATTC
ATAAGAGGAGAGGATAGAAGGAAGAAGAAAAAGCAAGTAATGATGACGGGAAATTGGAGAGAGTTAGA
CAAGTTTGTGCTTCACAACCTTATGAGCCAAGAAGACAATGGAACCTTCAAGTTTCGCAGGTCATCATA
TAGTTAATGAAGATAAAAACAACAATGATGTGGAGATGGATTCGTCAATGTTTTTGGAGCGAAAGAGAA
GAAGAAAACAGGTTCTGTCAGTGAATTCTTGAGTACAACTCGGATTATGATATTGGGATTTGCGTATT
TGATAATTGA

SEQ ID NO: 20 - ANAC037"AT2G18060"NP_179397.1"

MEPMESCSVPPGFRFHPTDEELVGYYLRKKIASQKIDLDVIRDIDLYRIEPWDLQEQCRIQYEEQNEW
YFFSHKDKKYPTGTRTNRATMAGFWKATGRDKAVYDKTKLIGMRKTLVFYKGRAPNGKKS DWIMHEYR
LES DENAPPQEEGWVVCRAFKKRATGQAKNTETWSSSYFYDEVAPNGVNSVMDPIDYISKQQHNI FGK
GLMCKQELEG MVDGINYIQSNQFIQLPQLQSPSLPLMKRPSSSMSITSMNNYNYKLPLADEESFESF
IRGEDRRKKKKQVM MTGNWRELDKFVASQLMSQEDNGTSSFAGHHIVNEDKNNNDVEMDSSMFLSERE
EENRFVSEFLSTNSDYDIGICVFDN

SEQ ID NO: 21 - NM_119783.2| Arabidopsis thaliana ANAC076; transcription factor (ANAC076)

CTTTCTCTTCACATTCACCGAACTTATAACCAAGATCAATATCAGTTCTCTCTCTCGATGAACATCA
TCTTCTACACAGCCATCTTTCTTTGACTTCTTCTTCTTCTTCTTAATATAACGGCTCGTTTCTTTTGT
TTCCAAACGAGTAAATAGTGTCTTATACACATATCTATAATTCCACAGGTTGAAGAAAAGAAATAATG
GAATCGGTGGATCAATCATGTAGTGTTCCTCCGGGATTCAGATTCCATCCAACAGATGAAGAGCTCGT
TGGTTACTATTTAAGGAAAAAAGTTGCATCGCAAAGATCGATCTTGATGTCATAAGAGATATTGATC
TCTACAGAATCGAACCATGGGATTTACAAGAGAGCTGCCGAATCGGATATGAGGAAAGAAATGAATGG
TATTTCTTCAGCCACAAAGATAAGAAATATCCAACAGGAACAAGAACAACAGAGCGACCATGGCTGG
GTTTTGGAAAGCCACGGGCCGAGACAAGGCTGTTTACGACAAGTCAAACTGATTGGTATGAGAAAAA
CACTTGTGTTCTACAAAGGAAGAGCCCCCTAATGGCCAAAAAACCGATTGGATCATGCATGAATACCGG
CTAGAGTCAGATGAGAATGCACCTCCTCAGGAAGAAGGGTGGGTGGTTTGTAGAGCGTTCAAGAAAAA
GCCAATGACCGGGCAAGCCAAGAACACAGAACTTGGAGCTCAAGTTACTTTTACGACGAATTA

FIGURE 26 (continued)

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CCGAGTGGAGTACGCTCAGTTACGGAGCCTCTTAACCTACGTATCTAAGCAGAAACAAAACGTTTTTGC
ACAAGATTTAATGTTCAAGCAAGAACTAGAAGGATCAGATATCGGTTTAACTTCATCCACTGCGATC
AATTCATTCAACTTCCGCAGCTTGAAAGCCCTTCACTCCCTCTTACCAAAAGACCAGTGAGCTTGACG
TCAATTACATCATTGGAGAAGAATAAAAAATATCTACAAAAGACATTTAATAGAAGAGGATGTGAGCTT
CAATGCGCTAATAAGTAGTGGAATAAAGATAAGAAGAAGAAAACATCAGTGATGACGACGGATT
GGAGAGCACTCGATAAATTTGTTGCTTCTCAACTTATGAGCCAAGAAGATGGAGTTTCGGGTTTTGGA
GGTCATCATGAAGAAGATAACAATAAAATCGGTCATTACAATAACGAAGAGAGCAATAACAAGGGATC
AGTAGAGACTGCTTCTTCCACGTTATTGAGTGATAGAGAAGAAGAGAACAGATTCATCAGTGGATTAT
TGTGTTCCAACCTGGACTATGACTTATATAGGGATTTACATGTTTGATAAAAGATAACACTATAATAT
GGTGCGTAACGTTTGCTATATAGGTACGTAGAATTTATTGATACAGTATAACATATATAAAGATGTGT
GAAAGATTTGTTTTCTTCTACTATATATACTTTTTTCGTGAA

SEQ ID NO: 22 - ANAC076"AT4G36160"NP_195339.1"

MESVDQSCSVPPGFRFHPTDEELVGYLRRKKVASQKIDLDVIRIDLYRIE PWDLQESCRIGYEEERNE
WYFFSHKDKKYPTGTRTNRATMAGFWKATGRDKAVYDKSKLIGMRKTLVIFYKGRAPNGQKTDWIMHEY
RLESDENAPPQEEGWVVCRAFKKKPMTGQAKNTETWSSSYFYDELPSGVRVSVTEPLNYVSKQKQNVFA
QDLMFKQELEGS D I G L N F I H C D Q F I Q L P Q L E S P S L P L T K R P V S L T S I T S L E K N K N I Y K R H L I E E D V S F
N A L I S S G N K D K K K K K T S V M T T D W R A L D K F V A S Q L M S Q E D G V S G F G G H H E E D N N K I G H Y N N E E S N N K G S
V E T A S S T L L S D R E E E N R F I S G L L C S N L D Y D L Y R D L H V

SEQ ID NO: 23 - NM_187584.1| Oryza sativa (japonica cultivar-group)

ATGGAATCATGCGTCCCTCCTGGGTTTCAGGTTCCACCCACCGACGAGGAGCTCGTCGGCTACTACCT
CCGCAAGAAGGTCGCTCCCAGAAGATCGACCTCGACGTCATCCGCGACATCGATCTCTACCGCATCG
AACCCTGGGATCTCCAAGAACATTGTGGGATCGGGTACGATGAGCAAAGCGAGTGGTACTTCTTCAGC
TACAAGGACAGGAAGTACCCGACGGGGACGAGGACGAACAGGGCGACAATGGCGGGGTTCTGGAAGGC
GACGGGGAGGGACAAGGCGGTGCACGACAAGAGCAGGCTCATCGGCATGAGGAAGACACTCGTCTTCT
ATAAGGGCAGGGCGCCTAATGGCCAGAAGACCGACTGGATCATGCACGAGTACCGCCTCGAGACCGAC
GAGAACGCGCCGCCACAGGAAGAAGGATGGGTGGTGTGCCGAGCATTCAGAAGAGGACGGCGTATCC
GGCGAGGAGCATGGTGGAGACGTGGGACTACTCCTTGACGAGCGCAACATCATGAGCGCCGCGGCGG
CGGCGGCGTTCGCCGATCCGAGCGCGGCGTACGCGCAGATGAGGCGGCAGCACAGGAGCGGGCGGTTT
AAGCAGGAGGCGGAGCTGGACGGCGCCGCCACAGCCCTCCTCCACTACTCCAGCCACCTCGCCGAGCT
GCCGCAGCTCGAGAGCCCCTCCGCGGCTGCGGCGCCGCTCCAGCCCAACCCGAGCCAGCTGGCCACCG
CCGGCGAGGACGACGACTGCAAGGGCGATAATGGCGGTAGGAGGGCCAAGAAAGCCCGCGCCGCCGGC
GACAAGGTGGCGACGACCACGGACTGGAGAGCGCTCGACAAGTTCGTCGCGTCGCAGCTTAGCCCCGG
GGAGTGTGGCAGCATGGAGGCAACGGCGGAAGCCGCGGCGGCGGCAGTCGCCGGTGTGAGCTCGCCGC
TGGACCACGGCGATGACGACATGGCAGCATTGCTGTTTCTCAACAGCGACGAGAGAGACGAGGTCGAC
AGGTGGACGGGGTTGCTCGGCTCCGGCGCCGGCGCGAGCGGCGTCGACGGCGACCTCGGAATCTGTGT
GTTTGACAAATGA

FIGURE 26 (continued)

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SEQ ID NO: 24 - OJ1015F07.11" ="NP_912473.1" NM_187584.1

MESCVPPGFRFHPTDEELVGYYLRKKVASQKIDLDVIRIDIDLYRIEPWDLQEHCGIGYDEQSEWYFFS
YKDRKYPTGTRTNRATMAGFWKATGRDKAVHDKSRLIGMRKTLVIFYKGRAPNGQKTDWIMHEYRLET
ENAPPQEEGWVVCRAFKKRTAYPARSMVETWDYSLHERNIMSAAAAAFADPSAAYAQMRRQHRSGRF
KQEAELDGAATALLHYSSHLAELPQLESFSAAPLQPNPSQLATAGEDDDCKGDNGGRRRAKKARAAG
DKVATTTDWRALDKFVASQLSPGECGSMEATAEAAAAAVAGVSSPLDHGDDDMAALLFLNSDERDEV
RWTGLLGSGAGASGVDGDLGICVFDK

SEQ ID NO: 25 - NM_125632.1| Arabidopsis thaliana ANAC101; transcription factor (ANAC101)

ATGGAAAGTCTCGCACACATTCCTCCCGGTTATCGATTCCATCCGACCGATGAAGAACTCGTTGACTA
TTATCTCAAGAACAAAGTTGCATTCCTCCGGGAATGCAAGTTGATGTTATCAAAGATGTTGATCTCTACA
AAATCGAGCCATGGGACATCCAAGAGTTATGTGGAAGAGGGACAGGAGAAGAGAGGGAATGGTATTTT
TTAGCCACAAGGACAAGAAATATCCAAGTGGGACACGAACCAATAGAGCAACGGGCTCCGGATTTT
GAAAGCAACGGGTGAGACAAGGCCATTTACTCAAAGCAAGAGCTTGTGTTGGGATGAGGAAGACTCTTG
TCTTTTACAAAGGTAGGGCCCCAAATGGTCAGAAATCTGATTGGATAATGCACGAATACCGTCTTGAG
ACCGATGAAAATGGACCGCCTCATGAGGAAGGATGGGTGGTTTGTGCGGCTTTCAAGAAGAAGCTAAC
CACGATGAAGTACAACAATCCAAGAACAATGATGGGATCATCATCAGGCCAAGAATCTAACTGGTTCA
CGCAGCAAATGGATGTGGGGAATGGTAATTACTATCATCTTCCTGATCTAGAGAGTCCGAGAATGTTT
CAAGGCTCATCATCATCACTATCATCATTACATCAGAATGATCAAGACCCTTATGGTGTCGTACT
CAGCACTATTAACGCAACCCCAACTACAATAATGCAACGAGATGATGGTCATGTGATTACCAATGATG
ATGATCATATGATCATGATGAACACAAGTACTGGTGATCATCATCAATCAGGATTACTAGTCAATGAT
GATCATAATGATCAAGTAATGGATTGGCAAACGCTTGACAAGTTTGTGCTTCTCAGCTAATCATGAG
CCAAGAAGAGGAAGAAGTTAACAAAGATCCATCAGATAATTCTTCGAATGAAACATTTTCATCATCTCT
CTGAAGAGCAAGCTGCAACAATGGTTTCGATGAATGCTTCTCCTCTTCTTCTCCATGTTTCTTCTAC
TCTTGGGCTCAAAATACACACACGTAA

SEQ ID NO: 26 - ANAC101"AT5G62380" id="NP_201044.1"

MESLAHIIPPGYRFHPTDEELVDYYLKNKVAFPQMVDVIKDVLDLYKIEPWDIQELCGRGTGEEREWYF
FSHKDKKYPTGTRTNRATGSGFWKATGRDKAIYSKQELVGMKTLVIFYKGRAPNGQKSDWIMHEYRLE
TDENGPPHEEGWVVCRAFKKKLTMMNYPNPTMMGSSSGQESNWFQQMDVGNNGNYHLPDLESPRMF
QGSSSSSLSLHQNDQDPYGVVLSTINATPTTIMQRDDGHVITNDDDHMMIMNTSTGDHHQSGLLVND
DHNDQVMDWQTLDFVASQLIMSQEEEEVNKDPSSNETFHHLSEEQAATMVSMNASSSSSPCSFY
SWAQNTHT

FIGURE 26 (continued)

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SEQ ID NO: 27 - NM_126028.1| Arabidopsis thaliana ANAC105; transcription factor (ANAC105)

ATGATGAAGGTTGATCAAGATTATTTCGTGTAGTATACCGCCTGGATTTAGGTTTCATCCGACAGATGA
AGAAGTTGTCGGATATTATCTCAAGAAGAAAATCGCCTCCCAGAGGATTGATCTCGACGTTATCAGAG
AAATTGATCTTTACAAGATCGAACCATGGGATCTACAAGAGAGATGTAGGATAGGGTACGAGGAGCAA
ACGGAGTGGTATTTCTTCAGCCATAGAGACAAGAAGTATCCGACTGGGACTAGGACAAACCGAGCCAC
CGTGGCCGGTTTTCTGGAAAGCAACGGGCCGGGACAAGGCGGTTTACCTCAACTCCAACTTATCGGTA
TGAGAAAAACGCTTGTCTTTTACCGAGGTCGAGCGCCTAATGGCCAAAAGTCCGATTGGATCATTCAC
GAATACTACAGCCTCGAGTCACACCAGAACTCTCTCCACAGGAAGAAGGATGGGTAGTGTGTAGAGC
ATTTAAGAAACGAACGACCATCCCAACAAAAAGGAGGCAACTTTGGGATCCGAACTGCTTATTCTACG
ACGACGCCACTCTCTTGGAACCTCTCGACAAGCGAGCCAGACATAATCCTGATTTTACCGCCACACCG
TTCAAGCAAGAACTACTCTCCGAGGCCAGTCACGTCCAGGATGGAGATTTTCGGATCTATGTACCTTCA
ATGCATCGATGATGATCAATTCTCCCAGCTTCTCAGCTCGAGAGCCCCCTCTCTCCGTCGGAAATAA
CTCCCCATAGTACTACTTTTTTCTGAGAACAGTAGCCGGAAAGATGACATGAGCTCCGAGAAGAGGATC
ACTGACTGGAGATATCTAGATAAGTTCGTGGCGTCTCAATTTTTGATGAGTGGAGAAGACTAA

SEQ ID NO: 28 - ANAC105"At5g66300"AAU94387.1"

MMKVDQDYSCSIPPGFRFHPTDEELVGYYLKKKIASQRIDLVDVIREIDLYKIEPVDLQERCRIGYEEQ
TEWYFFSHRDKKYPTGTRTNRATVAGFWKATGRDKAVYLNLSKLIGMRKTLVFYRGRAPNGQKSDWIIH
EYYSLESHQNSPPQEEGWVVCRAFKKRTTIPTKRRQLWDPNCLFYDDATLLEPLDKRARHNPDTATP
FKQELLSEASHVQDGFSGMYLQCIDDDQFSQLPQLESPLPSEITPHSTTFSENSSRKDDMSSEKRI
TDWRYLDKFVASQFLMSGED

SEQ ID NO: 29 - AK071064.1|:c927-1 Oryza sativa (japonica cultivar-group) cDNA clone

CCATCTTAATTTTTTACTTCTTTACTTAATTATCTGTCCTACTATATATGTTAATTCATGGATATTAA
TATGGAATATGGATGCAGGAGGAAGGTTGGGTGGTTTGCCGCGCGTTTCAGAAGCCGATGCCCCAACCA
GCAGCAGCACAGGCTGTCCTACGGCTGCATCCCCGGCAGCTACGGCGCCGGAGCCTACGCCGCCGTCC
CCGACAACTACAGCTTGCTGCTGCACCACGACAACCCTAGCTTCGCCGGGCGGCCATTGATGAGCGCC
GCTGCCTCAGCTCTCTTCGCCAACAACAATAACAGCGTCGTCGACCACAGCAACATTCTGAGTTC
AGAGTCCAAGCTTCACTTCTCCGACATGATGCCGCCTCTGGAGAGCCCCACCATCGTCGACGGCGAGG
GCTACGTCTCGCAGGCTAGCAGCTGCGTCGACGTCGATCAGCAAGCCGGCATCGTCGACTGGAACCTG
CTCACCAGCTTGCTGCCGCCGCCGGCGCATCAGCTCTTCCACCACCTGCCTTCCGCTTCGGGAGTTAT
TACAAGTAGAGTGAGAGGAGACGGCGCGGCGGCGGCGGCGGCGGCGGATGGAGAGGGAGAACCGGGT
GGAGACCATCTCCCGGCTGGCCAGTGGCGCATCGACACCTTCGGCCCCCTCCTCCTACCGCCGCTCCG
ATTCCTTCAAGATCGGCATCTGGAAGTGGTTCCCTTCCCAATCCCAATCCCCCACTACTCAGAGATCA
CCGATTTGCCCTATCAAATCAAATCATCCGCCAATTCGATCCGAATCCGTGCAGGTACCTATCGGTGG
AGAAGGCTCGATATGTATACGTGGGGCTGTTCCCGGAGCCCGGCGGGTGGCCAAGGAACGGCCCCCG
CTCGCCCCGTTTCTTCTCCGAGCTTGCTGGTCCGGCCCCAATG

FIGURE 26 (continued)

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SEQ ID NO: 30 – translation AK071064 sense

MQEEGWVVCRAFQKMPNPQQQHRLSYGCI PGSYGAGAYA AVPDNYSLLLHHDNPSFAGRPLMSAAASA
LFANNNNNNSVVDHSNILSSESKLHFSDMMPPLESPTIVDGE GYVSQASSCVDVDQQAGIVDWNLLTSL
LPPPAHQLFHHLPSASGVITSRVRGDGAAAAAAGWRGRTGWRPSPGWPSGASTPSAPPPTAAPIPSR
SASGTGSLPNPNPFLLRDHRFALSNQII RQFDPNPCRYLSVEKARYVYVGLFPEPGRVAKERPPLARF
LLRACWSGPN

**SEQ ID NO: 31 - gi|18409948|ref|NM_105851.1| Arabidopsis thaliana ANAC030;
transcription factor (ANAC030) mRNA, complete cds**

ATCTTGTTTCTTACTCATTTCTCTAACAATTTTCCAAATTAAATACGTTTATAGGATCATCGTGGATG
GATAATATAATGCAATCGTCAATGCCACCGGGATTCCGATTTTCATCCGACAGAGGAAGAGCTTGTGGG
TTATTACCTAGATAGGAAGATCAATTCAATGAAGAGTGCTTTAGATGTCATTGTAGAGATTGATCTCT
ACAAAATGGAGCCATGGGATATACAAGCGAGGTGTAACTAGGGTATGAAGAGCAAAACGAGTGGTAC
TTCTTTAGTCATAAGGACAGGAAGTACCCTACCGGGACTAGGACCAACCGAGCCACTGCGGCTGGGTT
CTGGAAAGCCACGGGTAGAGACAAGGCGGTACTATCAAAAAACAGTGTCTATCGGAATGCGGAAGACAC
TTGTCTACTACAAGGGTCGAGCTCCTAATGGAAGAAAGTCCGATTGGATCATGCACGAATACCGTCTC
CAAACTCCGAGCTTGCCCCGGTTCAGGAGGAAGGCTGGGTGGTGTGTCGAGCATTTAGGAAGCCAAT
TCCAAACCAGAGGCCATTAGGGTACGAGCCATGGCAGAACCAGCTCTACCACGTCGAAAGTAGTAACA
ACTACTCATCTTCAGTGACAATGAACACGAGTCATCATATCGGTGCATCTTCATCAAGTCATAACCTT
AATCAATGCTCATGAGCAATAACCACTACAATCCTAATAATACATCCTCATCGATGCATCAATATGG
CAACATTGAGCTCCCGCAGTTGGACAGCCCGAGCTTGTGCGCTAGTTTAGGGACGAATAAAGATCAGA
ACGAGAGTTTCGAGCAAGAAGAAGAGAAGAGCTTTAACTGTGTGGATTGGAGAACTAGATACCTTG
CTTGAGACACAAGTCATACATCCGCATAACCCTAATATTCTTATGTTTCGAAACGCAGTCGTATAATCC
GGCGCCAAGCTTCCCTTCCATGCATCAAAGCTATAATGAGGTCGAAGCTAATATTCATCATTTCTCTTG
GATGCTTCCCTGACTCGTAATTAACAAAAAACAACACTTCTATATATTGATTTGTATTCTATGATTTAA
TTGTTCCATCTGGAAAATAACATTTATAACTGTCTATTTGTAAAAGAAGTTTGTGTTTATTACGTAGA
AATTTGTTGTTG

SEQ ID NO: 32 - ANAC030"AT1G71930" ="NP_177338.1"

MDNIMQSSMPPGFRFHPTEEEELVGYLDRKINSMSKALDVIVEIDLYKMEPWDIQARCKLGYEEQNEW
YFFSHKDRKYPTGTRTNRATAAGFWKATGRDKAVLSKNSVIGMRKTLVYYKGRAPNGRKS DWIMHEYR
LQNSE LAPVQEEGWVVCRAFRKPIPNQRPLGYEPWQNQLYHVESSNNYSSSVTMNTSHHIGASSSSHN
LNQMLMSNNHYNPNNTSSSMHQYGNIELPQLDSPSLSPSLGTNKDQNESFEQEEEEKSFNCVDWRTLDT
LLETQVIHPHNPNILMFETQSYNPAPSFPSMHQSYNEVEANIHHSLGCFPDS

FIGURE 26 (continued)

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SEQ ID NO: 33 - NM_197511.1| Oryza sativa hypothetical protein OSJNBa0053C23.15

ATGCAGCCGCCGCGGAGCTCCATCGGAGCATGGGAGGCGAGCTACTCCTACCACGACCCCGCCGTCTT
CGTCGGCGGCGGGGAACACTTCAAGCAAGAGGCCGCGGCCGAGCTGGACGGCGTCGCCGCCGCCGCCG
GAGCTAACGCCTTCCTGCGGTACTCCACCCGCCTGGCCGAGCTCCCGCAGCTGGAGAGCCCGCCGCTG
CCAAGCCAGGGGAGCCAGGCGGCCTCGGCCGTCGTCGACGGCGAGGAAGATAACGCCGATTCTAGCAG
GCGCCCTGGCGGCGGCGGCGGCCGCCGCCGCGGTGACCACGGACTGGAGGGCGTTCGACAAGTTTCG
TCGCGTCCCAGCTCAGCCCCGAGGAGCAGCACACCTGCCGGGCCACCGACGACGACGACATGGCAGCG
CTGCTGCTCCTCGACGGCGGCGGGCAGGAGGACGACGCCGGGAGGTGGCTGGGCTCCGCCGGGTTGCT
GAGCGCCGTGGCGGCCGACGCGACGACGGACTGCGGCCTCGGCACCAGCTGCGTGCCTGGCGACATCA
ACTGA

SEQ ID NO: 34 - OSJNBa0053C23.15"NP_922493.1"NM_197511

MQPPRSSIGAWESYSYHDPVAVFVGGEHFKQEAAAEELDGVAAGANAFRLRYSTRLAELPQLESPPL
PSQGSQAASAVVDGEEDNADSSRRPGGGGAAAAVTTDWRAFDFKQVSQLSPEEQHTCRATDDDDMAA
LLLLDGGGQEDDAGRWLGSAGLLSAVAADATTDCLGTSCVPGDIN

SEQ ID NO: 35 - AB217775.1 Zinnia elegans Ze567 mRNA for NAC-domain protein Ze567

ATGGACACAATGAATCAATCATCATGTACTGTCCCTCCAGGTTTTTCGTTTTTCATCCTACCGATGAAGA
ACTTGTGTGTTACTATCTCAGAAAGAAGGTTGCATCTCAAAAGATTGATCTTGATGTCATTAAAGACA
TCGATCTTTATCGAATCGAACCATGGGATCTTATAGAGAGATGTCGGATCGGATACGAGGAGCAAAAT
GAGTGGTATTTCTTCAGTCACAAGGATAAAAAGTATCCAACAGGGACAAGGACAAATAGGGCAACTAT
GGCAGGTTTTTGAAGGCAACGGGTAGAGACAAAGCTGTTTACGAAAACTAAGGCTCATAGGAATGA
GAAAAACCCTAGTTTTCTACAAAGGAAGGGCACCAAATGGCCAGAAAACCGATTGGATCATGCACGAG
TACAGGCTCGAATCTGAAGAAAATGGACCTCCTCAGGAAGAAGGATGGGTAGTATGTCGAGCATTCAA
GAAACGTGCAACCGGACAAACAAGAACAACACCAGCATGGGAATCAAATTACTTCTTAGATGAATCAA
GCCTCCTTACATCCACAATGGATGATTACACCACAATTC AACCTTCAAATATTCCTTTGACATCAAGT
TTCATGTGCAAGCAAGAGTTGGAAGCATCAGAAAATTTGAACTTTATTCATTGTGATCAGTTTATTCA
ACTTCCACACCTCGAAAGCCCATCCCTCCAATCGATAAAACGGCCTATAAGCTCCATACTATATGAAC
ATGATCAACAAGAAGACGATCAAATCACAAAAGAATCACAAACAACGTTAGGAGTAAAGATGAAGTG
AGGGATTGGAGGGATCTTGATAAGTTTGTAGCTTCTCAATTGAGCCAAGAGGAAGAGATTGATGTGT
CGAAGAAGGGTTTTCAACGAATTTCCAAGAGAACATTGATCATTCTACTAGTTTGAATCATATGTTTA
ATTATCAAGATGGTATTGAAGAATACAGTGGTTGTGACAAAGGGGGCAAGTTAAATGGATTCTTGAGT
TCAACAAGCTCAGATCATTTTGATGTTGGAATTTGCATATTTGATAAATTATGA

FIGURE 26 (continued)

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SEQ ID NO: 36 - Ze567"NAC-domain protein Ze567"BAE20090.1"

MDTMNQSSCTVPPGFRFHPTDEELVGYYLRKKVASQKIDLDVIKDIDLYRIEPWDLIERCRIGYEEQN
 EWYFFSHKDKKYPTGTRTNRATMAGFWKATGRDKAVYEKLRLIGMRKTLVIFYKGRAPNGQKTDWIMHE
 YRLESEENGPPQEEGWVVCRAFKKRATGQTRTTPAWESNYFLDESSLTSTMDDYTTIQPSNIPLTSS
 FMCKQELEASENLNFIHCDQFIQLPHLESPSLQSIKRPISSILYEHDQQEDDQITKRITNNVRSKDEV
 RDWRDLDFVASQLSQEEEIRCVEEGFSTNFQENIDHSTSLSHMFNYQDGIEEYSGCDKGGKLNGLS
 STSSDHFVDVGICIFDKL

SEQ ID NO: 37 - AJ833965.1 Zea mays partial mRNA for hypothetical(nac6 gene)

ATGCATCCAGGTGTTGGACCATTTGTCGGTGCCACCAGGCTTCCGCTTCCATCCGACTGATGAGGAGCT
 CCTCTACTACTACCTGAGGAAAAAGGTTGCTTATGAGCCCATAGATCTTGATGTCATAAGGGAGATTG
 ATCTCAATAAGCTTGAGCCCTGGGATCTCAAAGAAAGATGCAAAATAGGCACTGGGCCTCAAAACGAG
 TGGTACTTCTTCAGCCACAAGGACAAGAAGTACTCAACGGGAACGAGAACGAACCGTGCCACGACGGC
 GGGATTCTGGAAGGCGACTGGCCGAGACAAGGCCATCTTCCTTGGCAGCGCCAGGAGGATCGGCTTGA
 GAAAGACCTGGTGTCTATATCGGCAGGGCGCCGCACGGGAAGAAGACTGAGTGGATCATGCACGAG
 TACCGCCTTGATGAAGAGAACGTTGAAATTCAGGAAGATGGATGGGTGGTATGTAGGGTTTTCAAGAA
 GAAGAACTATGAGCAGAGAGGCCACAACATGGCTGAGATGGCGGCACTGGACGACGATGAGCTCCAGC
 CTTTCACGGTTCCTGTCGTCCTGCTGGCACTAGCTCCCTGCCAACAACAGACCACAAGAACAACCTT
 CACCTCATGCAATATGACTTCCCTTCTTTCGACCTTCCATGCAGCTCCCACAGCTGATGAGCGCCGA
 CCAGCCCCGTGCCAACCTTATCCCCAGCCATCCTGGCGTCGCCACGGCCATGAGCTCATCAATCGACG
 TTGAGTGCTCGCAGAACCTGCTGACGATGCTGACATCCAACGGCAGCGACGGGATGCTCCACGTCCGC
 GCTGGTGGTGGTGGAGCTGGTGTGACCGCTTCGCTGGCAGCAGAGATTGGTTCGATCCTAGACAAGCT
 CCTCGCCTCGCACCAGAACCTCGGACAGCTCTTCCACGGCAAGGTCACCGCAGCATCTGCCTCCCCAA
 TGGCTCCATACCATCAGCAGCTCATGGAACTCGGGTGGCTCGTCGTCGTCGTCGTCCTTGAGAGGCT
 TCCACTGCAGTACCTCAGCGGCGAGACGACCGATCTCCTCAGGTTCCCCAAGTAATTATTGGATCGAC
 CTCAAGTTTAGCTACCTTGTTGAGCAGTGACCATATCAGGATTTTGGTTGACTACTAGGCTGCTTAAT
 TCGGCCTACTTCGTATGGAGTTTAGTGCTTTTAAATGTATATATGGTGCAACTGTTTGGGGCATGCAG
 GCATGGAATGCCATCGATCTACCATGGTTGCTTGCTTGGCCAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 38 – Maize nac6CAH56056.1

MHPGVGPLSVPPGFRFHPTDEELLYYYLRKKVAYEPIDLDVIREIDLNKLEPWDLKERCKIGTGPNQNE
 WYFFSHKDKKYSTGTRTNRATTAGFWKATGRDKAIFLGSARRIGLRKTLVFIYIGRAPHGKKTEWIMHE
 YRLDEENVEIQEDGWVVCRVFKKKNYEQRGHNMAEMAALDDDELQPFTVPVVPAGTSSLPTTDHKNNP
 HLMQYDFPSFDPMSQLPQLMSADQPVPTLFPSHPGVATAMSSSIDVECSQNLLTMLTSNGSDGMLHVR
 AGGAGAGVDRFAGTTDWSILDKLLASHQNLGQLFHGKVTAASASPMAPYHQQLMELGWLVVVVVLAEA
 STAVPQRRDDRSPQVPQVIIGSTSSLATLLSSDHIRILVDY

FIGURE 26 (continued)

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SEQ ID NO: 39 – gos2 promoter

AATCCGAAAAGTTTCTGCACCGTTTTTCACCCCCTAACTAACAATATAGGGAACGTGTGCTAAATATAA
AATGAGACCTTATATATGTAGCGCTGATAACTAGAACTATGCAAGAAAACTCATCCACCTACTTTAG
TGGCAATCGGGCTAAATAAAAAAGAGTCGCTACACTAGTTTCGTTTTCTTAGTAATTAAGTGGGAAA
ATGAAATCATTATTGCTTAGAATATACGTTACATCTCTGTCATGAAGTTAAATTATTTCGAGGTAGCC
ATAATTGTCATCAAACCTCTTCTTGAATAAAAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGAGAG
ATTTTTTTTTAAAAAATAGAATGAAGATATTCTGAACGTATTGGCAAAGATTTAAACATATAATTATA
TAATTTTATAGTTTGTGCATTCTGTCATATCGCACATCATTAAGGACATGTCTTACTCCATCCCAATTT
TTATTTAGTAATTAAGACAATTGACTTATTTTTTATTATTTATCTTTTTTCGATTAGATGCAAGGTAC
TTACGCACACACTTTGTGCTCATGTGCATGTGTGAGTGCACCTCCTCAATACACGTTCAACTAGCAAC
ACATCTCTAATATCACTCGCCTATTTAATACATTTAGGTAGCAATATCTGAATTCAGCACTCCACCA
TCACCAGACCACTTTTAATAATATCTAAAATACAAAAAATAATTTTACAGAATAGCATGAAAAGTATG
AAACGAACTATTTAGGTTTTTCACATACAAAAAAGAAATTTTGCTCGTGCGGAGCGCCAATCT
CCCATATTGGGCACACAGGCAACAACAGAGTGGCTGCCCACAGAACAACCCACAAAAAACGATGATCT
AACGGAGGACAGCAAGTCCGCAACAACCTTTTAACAGCAGGCTTTGCGGCCAGGAGAGAGGAGGAGAG
GCAAAGAAAACCAAGCATCCTCCTCCTCCCATCTATAAATTCCTCCCCCTTTTCCCCTCTCTATATA
GGAGGCATCCAAGCCAAGAAGAGGGAGAGCACCAGGACACGCGACTAGCAGAAGCCGAGCGACCGCC
TTCTTCGATCCATATCTTCCGGTCGAGTTCTTGGTCGATCTCTTCCCTCCTCCACCTCCTCACAG
GGTATGTGCCCTTCGGTTGTTCTTGGATTTATTGTTCTAGGTTGTGTAGTACGGGCGTTGATGTTAGG
AAAGGGGATCTGTATCTGTGATGATTCTGTTCTTGGATTTGGGATAGAGGGGTTCTTGATGTTGCAT
GTTATCGGTTTCGGTTTGATTAGTAGTATGGTTTTCAATCGTCTGGAGAGCTCTATGGAAATGAAATGG
TTTAGGGTACGGAATCTTGCGATTTTGTGAGTACCTTTTGTGTTGAGGTAAAATCAGAGCACCGGTGAT
TTTGCTTGGTGTATAAAAGTACGGTTGTTTGGTCCTCGATTCTGGTAGTGATGCTTCTCGATTTGAC
GAAGCTATCCTTTGTTTATTCCCTATTGAACAAAAATAATCCAACCTTTGAAGACGGTCCCGTTGATGA
GATTGAATGATTGATTCTTAAGCCTGTCCAAAATTTTCGCAGCTGGCTTGTTTAGATACAGTAGTCCCC
ATCACGAAATTCATGGAAACAGTTATAATCCTCAGGAACAGGGGATTCCCTGTTCTTCCGATTTGCTT
TAGTCCCAGAATTTTTTTTCCCAAATATCTTAAAAAGTCACTTTCTGGTTCAGTTCAATGAATTGATT
GCTACAAATAATGCTTTTATAGCGTTATCCTAGCTGTAGTTTCAAGTTAATAGGTAATACCCCTATAGTT
TAGTCAGGAGAAGAACTTATCCGATTTCTGATCTCCATTTTTAATTATATGAAATGAACTGTAGCATA
AGCAGTATTCAATTTGGATTATTTTTTTTTTATTAGCTCTCACCCCTTCATTATTCTGAGCTGAAAGTCTG
GCATGAACTGTCCTCAATTTTGTGTTTCAAATTCACATCGATTATCTATGCATTATCCTCTTGATCTA
CCTGTAGAAGTTTCTTTTTGGTTATTCTTGGACTGCTTGATTACAGAAAGAAATTTATGAAGCTGTAA
TCGGGATAGTTATACTGCTTGTCTTATGATTCAATTCCTTTGTGCAGTTCTTGGTGTAGCTTGCCAC
TTTACCAGCAAAGTTC

SEQ ID NO: 40 – protochlorophyllide reductase promoter

TTGCAGTTGTGACCAAGTAAGCTGAGCATGCCCTTAACCTCACCTAGAAAAAGTATACTTGGCTTAA
CTGCTAGTAAGACATTTTCAGAACTGAGACTGGTGTACGCATTTTCATGCAAGCCATTACCACTTTACCT
GACATTTTGGACAGAGATTAGAAATAGTTTCGTACTACCTGCAAGTTGCAACTTGAAAAGTGAAATTT
GTTCCCTTGCTAATATATTGGCGTGTAATCTTTTATGCGTTAGCGTAAAAAGTTGAAATTTGGGTCAA
GTTACTGGTCAGATTAACCAGTAAGTGGTTAAAGTTGA

FIGURE 26 (continued)

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AAGATGGTCTTTTAGTAATGGAGGGAGTACTACACTATCCTCAGCTGATTTAAATCTTATTCCGTCGG
 TGGTGATTTTCGTCAATCTCCCAACTTAGTTTTTCAATATATTCATAGGATAGAGTGTGCATATGTGTG
 TTTATAGGGATGAGTCTACGCGCCTTATGAACACCTACTTTTGTACTGTATTTGTCAATGAAAAGAAA
 ATCTTACCAATGCTGCGATGCTGACACCAAGAAGAGGGCGATGAAAAGTGCAACGGATATCGTGCCACG
 TCGGTTGCCAAGTCAGCACAGACCCAATGGGCCTTTCCTACGTGTCTCGGCCACAGCCAGTCGTTTAC
 CGCACGTTTACATGGGCACGAACTCGCGTCATCTTCCCACGCAAAACGACAGATCTGCCCTATCTGGT
 CCCACCCATCAGTGGCCACACCTCCCATGCTGCATTATTTGCGACTCCCATCCCGTCCTCCACGCCC
 AAACACCGCACACGGGTCGCGATAGCCACGACCCAATCACACAACGCCACGTACCATATGTTACGGG
 CAGCCATGCGCAGAAGATCCCGCGACGTGCTGTCCCCCGTGTGCGTTACGAAAAAATATCCCACCAC
 GTGTCGCTTTCACAGGACAATATCTCGAAGGAAAAAATCGTAGCGGAAAATCCGAGGCACGAGCTGC
 GATTGGCTGGGAGGCGTCCAGCGTGGTGGGGGGCCACCCCTTATCCTTAGCCCGTGGCGCTCCTCG
 CTCCTCGGGTCCGTGTATAAATACCCTCCGGAACCTCACTCTTGCTGGTCACCAACACGAAGCAAAAGG
 ACACCAGAAACATAGTACACTTGAGCTCACTCCAAACTCAAACACTCACACCA

SEQ ID NO: 41 – Motif I

K/P/R/G I/S/M D/A/E/Q L/I/V D I/V/F I Q/V/R/K E/D L/I/V D.

SEQ ID NO: 42 – Motif II

C K/R Y/L/I G XXX G/Y/N D/E E Q/R T/N/S EW

where 'X' is any amino acid or a gap.

SEQ ID NO: 43 – Motif III

GWVVCRA/V F X¹ K X²

where 'X¹' and 'X²' may be any amino acid, preferably X¹
 is Q/R/K, preferably X² is P/R/K.

SEQ ID NO: 44 – adapter primer

AAGCAGTGGTATCAACGCAGAGTACGCGGG

SEQ ID NO: 45 – primer: OsNAM2-2

CTCTCCAGAGGCGGCATCATGTCGGA

SEQ ID NO: 46 – primer: OsNAM2-1

TGATCGGGATGAGGAAGA

FIGURE 26 (continued)

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SEQ ID NO: 47 – primer: OsNAM2-3

GATCAGTCTCGGTCATCGATG

SEQ ID NO: 48 – primer: prm08733

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGGATCGGCATGAGGAG

SEQ ID NO: 49 – primer: prm08734

GGGGACCACTTTGTACAAGAAAGCTGGGTTCGATCGATCAGTCTCGGT

FIGURE 26 (continued)

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SEQ ID NO: 50 - CDS4035 - XM_470088.1 - Oryza sativa

TCACAACCCACAACATTTTCAAACAACGCAAAGCAGTAGCAGCAGCGAGAAGCAAGCAAGAAGCGATG
GGGATGGGGATGAGGAGGGAGAGGGACGCGGAGGCGGAGCTGAACCTGCCGCCGGGGTTCAGGTTCCA
CCCCACGGACGACGAGCTGGTGGAGCACTACCTGTGCAGGAAGGCGGCGGGGCAGCGCCTGCCGGTGC
CGATCATCGCCGAGGTGGATCTCTACAAGTTCGACCCGTGGGATCTGCCCGAGCGCGCGCTGTTCCGGC
GCCAGGGAGTGGTACTTCTTCACCCCGCGGGATCGCAAGTATCCTAATGGGTACAGCCCCAACCGCGC
CGCCGGCAACGGGTACTGGAAGGCCACCGGCGCCGACAAGCCCGTCGCGCCGCGGGGGCGCACGCTTG
GGATCAAGAAGGCGCTCGTGTTCTACGCCGGCAAGGCGCCGCGAGGGGTCAAGACTGATTGGATCATG
CATGAGTACCGGCTCGCCGATGCTGGCCGCGCCGCGCGGGCGCCAAGAAGGGATCTCTCAGGTTGGA
TGATTGGGTGCTGTGTGCGGCTGTACAACAAGAAGAACGAGTGGGAGAAGATGCAGCAGGGGAAGGAGG
TGAAGGAGGAGGCGTCCGACATGGTTACGTCGCAGTCGCACTCGCACACCCACTCGTGGGGCGAGACG
CGCACGCCGGAGTCGGAGATCGTGGACAACGACCCCTTCCCGGAGCTGGACTCGTTCCCGGCGTTCCA
GCCTGCGCCGCCGCCGGCGACGGCGATGATGGTGCCCAAGAAAGAATCGATGGACGACGCCACCGCGG
CCGCCGCCGCCGCCGCCACCATCCCCAGGAACAACAGCAGCCTGTTTCGTGGACCTGAGCTACGACGAT
ATCCAGGGCATGTACAGCGGCCTCGACATGCTGCCGCCGGGCGACGACTTCTACTCGTCGCTCTTCGC
GTCGCCGCGGGTGAAGGGGACGACGCCACGCGCCGCGCGCCGGCATGGGCATGGTCCCGTTCTGA

SEQ ID NO: 51 - CDS4035 - XP_470088.1 - Oryza sativa

MGMGMRRERDAEAEELNLPFGFRFHPTDDELVEHYLCRKAAGQRLPVPPIAEVDLYKFDPWDLPERALF
GAREWYFFTPRDRKYPNGSRPNRAAGNGYWKATGADKPVAAPRGRTLGIKKALVFYAGKAPRGVKTDWI
MHEYRLADAGRAAAGAKKGSRLRDDWVLCRLYNKKNEWKMQQKKEVKEEASDMVTSQSHSHTHSWGE
TRTPESEIVDNDPFPELDSFPAFQPAPPPATAMMVPKKE SMDDATAAAAAAATIPRNNSSLFVDLSYD
DIQGMYSGLDMLPPGDDFYSSLFASPRVKGTTPRAGAGMGMVPF

SEQ ID NO: 52 - AB028185.1 - Oryza sativa

TCGACCCACGCGTCCGCTCTTCCCAACACTAGTAGGATAAAGCCACAGAGAGAGCAGTAGTAGTAGCG
AGCTCGCCGGAGAACGGACGATCACCGGAGAAGGGGGAGAGAGATGAGCGGCGGTCAGGACCTGCAGC
TGCCGCCGGGGTTCCGGTTCCACCCGACGACGAGGAGCTGGTGATGCACTACCTCTGCCGCCGCTGC
GCCGGCCTCCCCATCGCCGTCCCACATCATCGCCGAGATCGACCTCTACAAGTTTCGATCCATGGCAGCT
TCCCCGGATGGCGCTGTACGGAGAGAAGGAGTGGTACTTCTTCTCCCCGCGAGACCGCAAGTACCCGA
ACGGGTGCGCGCCGAACCGCGCCCGCGGGTGGGGTACTGGAAGGCGACCGGCGCCGACAAGCCGGTG
GGCTCGCCGAAGCCGGTGGCGATCAAGAAGGCCCTCGTCTTCTACGCCGGCAAGGCGCCCAAGGGCGA
GAAGACCAACTGGATCATGCACGAGTACCGCCTCGCCGACGTCGACCGCTCCGCCCCGAAGAAGAACA
GCCTCAGGTTGGATGATTGGGTGCTGTGCCGATTTACAACAAGAAGGGCGGGCTGGAGAAGCCGCCG
GCCGCGGCGGTGGCGGCGGCGGGGATGGTGAGCAGCGGCGGCGGCGTCCAGAGGAAGCCGATGGTGGG
GGTGAACGCGGCGGTGAGCTCCCCGCCGAGCAGAAGCCGGTGGTGGCGGGCGGCGTTCCCGGACC
TGCGCGGCTACTACGACCGGCGGTGCGACTCGATGCCGCGGCTGCACGCCGACTCGAGCTGCTCGGAG
CAGGTGCTGTCGCCGGAGTTCGCGTGCGAGGTGCAGAGCCAGCCCAAGATCA

FIGURE 27

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GCGAGTGGGAGCGCACCTTCGCCACCGTCGGGCCCATCAACCCCGCCGCCTCCATCCTCGAC
CCCGCCGGCTCCGGCGGCCTCGGCGGCCTCGGCGGCGGCGGCAGCGACCCCTCCTCCAGGACATCCT
CATGTACTGGGGCAAGCCATTCTAGACGACCAAAAAAAAAAAAAAAAAACAACCGCATTGGCAGCAATGGT
GTCAGTGAACACCGTGCAGGCTAGCTAGCTTCATGGCCGGTGAACCTTGACTCAGGCGAGCCGCCGGA
GTTGACTCAAAGATAATTAAAAGAAGTGTTTAAGTGGATTGGATTGGATTAGACAGAGGAGATGAGG
ACTCGAGAAAGGCGGCGATGAGACCGTGGTTGGGGGGACCCTGGCCTGGACTGAACGACGACGAGGCA
GCAGCAGAAAGATGGTGAATTGCATCGGGTGGCATGTCAGTGTGTGTGTATAGTGGCATGTACATAG
TACATGGTGATTGATTCGGTATACAGGGGGCTAGCTTTCCTGTTTCTGTTTAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

SEQ ID NO: 53 - BAA89800.1 - Oryza sativa

MSGGQDLQLPPGFRFHPTDEELVMHYLCRRRCAGLPIAVPIIAEIDLYKFDPWQLPRMALYGEKEWYFF
SPRDRKYPNGSRPNRAAGSGYWKATGADKPVGSPKPVAIKKALVFYAGKAPKGEKTNWIMHEYRLADV
DRSARKKNSLRLLDDWVLCRIYNKKGGLEKPPAAAVAAAGMVSSGGGVQRKPMVGVNAAVSSPPEQKPV
VAGPAFPDLAAYYDRPSDSMPRLHADSSCSEQVLSPEFACEVQSQPKISEWERTFATVGPINPAASIL
DPAGSGGLGGLGGGSDPLLQDILMYWGKPF

SEQ ID NO: 54 - AB028184.1 - Oryza sativa

CCCCTCGAGGTCGACCCACGCGTCCGCTTCCATTAGCGACTAATCCAGCCTTCGTAAAGGGTGATTAG
AATTTGATTAATTTCAAGGCCTCAGATCGGAGATTGAATGGAGTGCGGTGGTGCGCTGCAGCTGCCGC
CGGGGTTTCAAGTTCCACCCGACGGACGACGAGCTGGTGATGTACTACCTGTGCCGCAAGTGCGGCGGC
CTCCCCCTCGCCGCCCCGGTGATCGCCGAGGTGGACCTCTACAAGTTCAACCCATGGGATCTCCCCGA
GAGGGCGATGGGAGGGGAGAAGGAGTGGTACTTCTTCTCGCCGCGGGACCGGAAGTACCCGAACGGGC
AGCGGCCGAACAGGGCGGCGGGGACGGGGTACTGGAAGGCGACGGGGGCGGACAAGCCGGTGGGGTCG
CCGCGGGCGGTGGCGATCAAGAAGGCGCTCGTCTTCTACGCCGGAAGCCGCCCAAGGGCGTCAAGAC
CAACTGGATCATGCACGAGTACCGCCTCGCCGACGTCGACCGCTCCGCCGCCGCCGCAAGCTCTCCA
AGTCCTCCCACAACGCCCTCAGGTTGGATGATTGGGTGTTGTGCCGAATCTACAACAAGAAGGGAGTG
ATCGAGAGGTACGACACGGTGGACGCCGGCGAGGACGTGAAGCCGGCGGCGGCGGCGGCGGCGGCGAA
GGGTGGTTCGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGAA
ACGACCAGGAGCCGGAGTCCGAGATGCTGTGCTTCGACCGGTCCGGGGTCGGCGGACCGCGACTCGATG
CCGCGGCTGCACACCGACTCCAGCGGGTCCGAGCACGTGCTGTGCGCGTCCCGTCCCGGACGACTT
CCCCGGCGGCGGCGACACGACTACGCCGAGAGCCAGCCAGCGGCGGATGCGGCGGGTGGCCCGGCG
TCGACTGGGCCGCCGTCGGCGACGATGGCTTCGTTCATCGACAGCTCCCTCTTCGAGCTGCCCTCGCCG
GCGGCGTTCTCCCGCGCCGCCGCGGCGACGGCGCCGCCTTCGGCGACATGTTACGTACCTGCAGAAGCC
GTTCTAATTAACGGAACGTGACGCCTCTGCAAACGCTAATTAGCTCACTAACCCTGTGAGGTCGATC
GTGTAATTCTTTTACCAGTCTAGGGTACAGCCAAAAACCAAAATTAACCGTGTGTCGATCGATCGAT
CGATCCATGGATCGATGATCGCCTCCACCGGCAGATCAAAATCGAAGCAAAAAATCAGGGAGAATTCT
TGGTACTTCCAGTACCTCTCGTCGACACCAGTGTGCGGGTTTCTGCACCGCGGATCCTCGCTGGCCG
CATCGTAACGGCGAGCGAGGTTAAAAATAGTGGAGAATTCAAGAACACATCCCTGATTTTGTGTTCTG
CCGATGGGGAGTACCGTGAGCATGGTAGAAATGACTGGTAAATTTTCGTTGATGATAG

FIGURE 27 (continued)

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GTAGCCAGAGTCGATGTAACCAGTCGATTTTTTTTTTTTTTTGGTTTTAGTTGACATGCCTTCCTGATA
GATTTCAGAACAAACAATAGAGAAGAGAGGAGAAAAAACACAGAGGAGAAATTCAGAGACCAAAGTTC
AAAGTTTTGGAATTTTCAGGGGCGCCAGCAGCTGATGGTATTGTCAGTCGTGTCTAGGTTTCGTAGAGG
AAATTAATAATGTAGAAGAACGGGTACTTCAGTTCACTTCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 55 - BAA89799.1 - *Oryza sativa*

MECGGALQLPPGFRFHPTDDELVMYYLCRKCGGLPLAAPVIAEVDLYKFNPWDLPERAMGGEKEWYFF
SPRDRKYPNGQRPNRAAGTGYWKATGADKPVGSPRAVAIKKALVFYAGKPPKGVKTNWIMHEYRLADV
DRSAAARKLSKSSHNLRLDDWVLCRIYNKKGVIERDYDVEDGDKPAAAAAAAAAKGGRIGGGGGAAA
MKVELSDYGFYDQEPESMLCFDRSGSADRDSMPRLHTDSSGSEHVLSPSPSPDDFPGGGDHDAESQ
PSGGCGGWPGVDWAAVGDDGFVIDSSLFELPSPAAFSRAAGDGAAFGDMFTYLQKPF

SEQ ID NO: 56 - AK107330.1 - *Oryza sativa*

ATCCTCCACAAGAGAACTAGGATCTTCAAGTATAGCTAGCATTGCGCCCTCATTTTCATCCATGGCAA
TGCAGCTGTCCTTGCTGTCTTGCCAACGGGTTTTCGTTTCCATCCAACCGATGAGGAAGTAGTCATC
AACTACCTCCAGAGGCGTGCTACCGGGCTATCGTGCCCATCCCCATAATCGCGGATGTCGAAATATA
CAACTTCAACCCGTGGGAGCTTCCATCCATGGCTCTATTTGGGGAACATGAGTGGTACTTTTTTACAC
TACGCGACCACAGGTACCCCAATAGTGTGCGCCCTAGTCGCTCAGCGGCGTCAGGCTTTTGGAAGGCC
ACCGGCACTGACAAGCCCGTCCAAGTTGCTAACATGCAAAGCACTCCTGTAGCTATGAAGAAGGCACT
TGTATTCTATGTTGGCCGCCCGCCCATGGAAACCAAGACTACATGGATCATGCATGAGTACCGTCTCA
CAAACACGGGAGGGTCCACTGCCTCCACCCATCCTTGTCTTCATCCACCGCACACCCTTCTGTGAAG
CTAGACGAGTGGGTGCTATGCAAGATCTTCAACAAGTCCCCAGAGCCGGACAACACCGCACACCACATC
AAACGTCGTCTCACGGTTACAGTGCTCGCCGCCGCTGCCGCCGCCGGCGGCACCGCCCGGCAACTACC
CGCCGCTGCCGGTGGGTGCGACGAACGACGGCGGCGTGTTGCTGCGCCGGCGACATGCTCTTCACC
ATCCAAGAGCACCAGGAGGGAACACCATCGATGCTGCCGCCGATCCCTAACCTTGAGCCACCGGCGGC
ACAATTGGGAATTCCTCTCTCAATGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGATGGCCATGGCCGCC
TTGAGGAAGAGGACACCAGCGCTACACCTTACCGACCAGGAAATGGAGCAGATGCTCATGGACCTG
ATGGACCAGGATTTCTTTGGCAATGATCAACCCAGGAGTGAATTTAGTATCTATTGTACCAGATAGAATAAAACCA
GAAAAGAAATAAAAGAAGGCCAAAGAAAAAAGCAAAAAGAAAATTGTATAATTACTAGGTTTGGATGC
CGTCTGTAGAACCTTGTGTGCTATGTAACCTTTTTTCTTTGTATTTTGGCATTTTTCATCATATTGTGTC
ATAAATAAAGCAGGGCTTTCTTTTGTAGTTTGCCATCTCAATCTTGCACCGTGATGTTATAAAAAAAC
AAAATTAATTATTGTGCTACACTGTACTTTTGGCTGTGTTCCGC

SEQ ID NO: 57 - AK107330.1 - *Oryza sativa*

MAMQLSLPVLPTGFRFHPTDEELVINYLQRRATGLSCPIPIIADVEIYNFNPWELPSMALFGEHEWYF
FTLRDHRYPNVSRPSRSAASGFWKATGTDKPVQVANMQSTPVAMKKALVFYVGRPPMETKTTWIMHEY
RLTNTGGSTASHPSLSSSTAHPVSVKLDEWVLCKIFNKSPEPDNTAPPSNVVSRLQCSPLPPPAAPPG
NYPPLPVGATNDGGVFACAGDMLFTIQEHQEGTSPMLPPIPNLEPPAATIGNSSLNGTAAAAAADGH
GRLEEDTSAYTFTDQEMEQLMDLMDQDFFGNDQPQE

FIGURE 27 (continued)

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SEQ ID NO: 58 - AK069257.1 – *Oryza sativa*

atgccgagcagcggcgcccatgcctgcccttccaccaggcttccgcttccacccaccgacgagga
gctcatcggttcaactacatgaaccaggccgcctccgtcaagtgcccggtgccaatcatcgccgagg
tcaacatctacaagtgaacccatgggaccttccctggtaaggctttgttcggcgagaaacgaatggtac
ttcttcagcccgagggaaccgcaagtaacccaacggcgctcgccccaacggcgccggtcggggta
ctggaaggccaccggcaccgacaagtccatcctctccactccgaccagcgacaacatcggcgtcaaga
aggccctcgcttcttacaagggaagcctcccaaggcggtcaagaccgactggatcatgcacgagtac
cgtctcaccggcacatcagctaacagcaccaccaccacaaagcagcgtagagcgatccatgaccat
gaggctggacgactgggtgctgtgcagaatccacaagaagagcaacgacttcaattcctctgaccaac
acgaccaagaacccgaggaatcaaccgctcgaacagcttgaagacatccatgacaacaactcctctgaa
caacctccagctccagctgacatgaacaaccaacagtcagatttccagcccatgacggcgatgagcat
gagcaagtcatgctccctcaccgatctcctcaacaccatcgactgcgcccgcgtctcgcagtttctcc
tcgacggctcatccgacgccatcgctgagcctcctgctcctcccagccccctaatacacacaacact
catccaaattaccaaactaaactataacattaacagcaacagcagcatgccacacgccttcgagtc
acgcctagatcatcacgatgggttacgttaacaattataatgttaatggcctgaggaggaagagaatga
tggcggtgtagtgcaacttcccttgatgatggcagcagcagcaatgactttgtgcatgccgttgtcaag
aaaccgcagctgctgccagtgattcgaggggtagtggttttgaggagggttactgcaaccagcagct
ttcagagactgcgactggctttcagtttcagaacggcaatctgctgagccatccatttctctgaaca
atcatctgcagatgcagtag

SEQ ID NO: 59 - AK069257.1 – *Oryza sativa*

MPSSGGAMPALPPGFRFHPTDEELIVHYLMNQAASVKCPVPIIAEVNIYKCNPWDLP GKALFGENEWY
FFSPRDRKYPNGARPNRAAGSGYWKATGTDKSI LSTPTSDNIGVKKALVFYK GKPKGVKTDWIMHEY
RLTGTSANSTTTTKQRRASSMTMRLLDDWVLCRIHKKSNDNFSSDQHDQPEESTVEQLEDIHDNNSSE
QPPAPADMNNQQSDFQPM TAMSMSKSCSLTDLLNTIDCAALSQFLLDGSSDAIAEPPAPPSPLIYTTP
HPNYQTLNYNINSNSSMPHAFESRLDHDG YVNNYNVNGLRKRMMAC SATSFDDGSSSND FVHAVVK
KPQLLP SDRSGSGFGGYCNQQLSETATGFQFQNGNLLSHPFPLNNHLQMQ

SEQ ID NO: 60 - AY625683.1 - *Triticum aestivum*

ACGAGGCACTCGCCCCAATCTCGAACAACGGCCGTCGGATCCATCATCATCGGCAGCGGAGCGATTCC
ATCGACCAGCTTTCTACAGACGGACATGGGGATGCCGGCCGTGAGGAGGAGGGAGAGGGACGCGGAGG
CGGAGCTCAACCTGCCCCCGGCTTCCGCTTCCACCCACCGACGACGAGCTCGTCGAGCACTACCTC
TGCCGCAAGGCGGCGGGGAGCGCCTCCCGGTCCCCATCATCGCCGAGGTCGACCTCTACCGCTTCGA
CCCCTGGGCGCTCCCTGACCGCGCCCTCTTCGGCACCCGCGAGTGTTACTTCTTACCCCCCGCGACC
GCAAGTACCCCAACGGCTCCCGACCCAACCGCGCCGCGGCAACGGCTACTGGAAGGCCACCGGCGCC
GACAAGCCCGTCGCGCCCCGCGGCGGGCGGACCATGGGGATCAAGAAGGCCCTCGTGTTTTACGCGGG
CAAGGCGCCTAAGGGGGTCAAGACCGACTGGATCATGCATGAGTATCGCCTCGCCGACGCGGCGCG
CCGCCGCCAGCAAGAAGGGCTCGCTCAGGCTGGACGACTGGGTGCTCTGCCGGCTCTACAACAAGAAG
AACGAGTGGGAGAAGATGCAGCTGCAGCAGCAAGGGGAAGAGGAGACGATGATGGAGCCCAAGGCGGA
GA

FIGURE 27 (continued)

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ACACGGCCTCCGACATGGTGGTCACCTCGCACTCCCACTCGCAGTCCCAGTCCGACTCGCACTCGTGG
GGCGAGGCGCGCACGCCGGAGTCGGAGATCGTCGACAACGACCCGTCGCTGTTCCAGCAGGCGACGGC
GGCGGCGTTCAGGCCAGAGCCCCGCGGCCCGCGCGGCACACAGGAGATGATGGCCACGCTGATGG
TGCCCAAGAAGGAGGCGGCGGACGAGGCCGGCAGGAACGACCTCTTCGTCGACCTCAGCTACGACGAC
ATCCAGAGCATGTACAACGGCCTCGACATGATGCCGCCCGGGGACGACCTGCTCTACTCCTCCCTCTT
CGCCTCCCCCGTGTCCGCGGGAGCCAGCCCGGCGCCGCGGCATGCCGGCCCCGTTCTAAGCAGAGC
AAAGACAGAGACCGTCAGAGACCCCGAGATCGACAGAAGTGGAATGGACGACTTCTTGGCCGCGAGCG
AGCGAGACCGCGGTGCAGTGTAATACAGCATAGGAAACGGGAGGGAGGGAGGTGGCGTCGTGTCGAG
AGAAGCCGGCGTCGTGCCGGGGCGTGCCGTTGTACATGGAGAGCCCGCGCCGGGGCCTGGCCGGCTG
GGTTGATTCTTTTGTCTTACTACCTTGACTCTCAATGCGGATGTAGCTCTTTCTTCTCACTCCTCA
CTAGTAGAATCGACCGACCGAATACATATGTAGCTCTGTTCTTTCCTTCTTTCAGTAGAAATCAACC
AAATTTTGCTGTTATGCTGC

SEQ ID NO: 61 - AAU08786.1 - Triticum aestivum

MGMPAVRRRRERDAEAEELNLPFGFRFHPTDDELVEHYLCRKAAGQRLPVPPIAEVDLYRFDPPWALPDRA
LFGTREWYFFTFRDRKYPNGSRPNRAAGNGYWKATGADKPVAPRGGRMGIIKKALVFYAGKAPKGVKT
DWIMHEYRLADAGRAAASKKGSRLDDWVLCRLYNKKNEWKMQLOQQGEEETMMEPKAENTASDMVV
TSHSHSQSQSHSHSWGEARTPESEIVDNDPSLFQQATAAAFAQSPAAAAAHQEMMATLMVPKKEAAD
EAGRNDLFVDLSYDDIQSMYNGLDMMPPGDDLLYSSLFASPRVRGSQPGAGGMPAPF

SEQ ID NO: 62 - AY103772.1 - Zea mays

GCACGAGGAACCCGCCCACAGGACAGGACACACAGAGCCGAGCCACCCACCCACCATCGGCGACCAG
CAGCCAGCCGCGGGAGCGAGCTGTTTAAAGACACCGAGTCGGAGTCGGACGGAGGACTGGCAGGCACA
ACCGAAGCCACCGCTTCTAGTTCTCGGGTTCATCGCCAGCAATCCAGACCACATAATGGGACAGCCGG
TGACGAGGAGGAGGGAGAGGGACGCGGAGGCGGAGCTGGACCTGCCGCGGGGGTTCGGGTTCCACCCC
ACAGACGACGAGCTGGTGGAGCACTACCTGTGCCGCAAGGCGGCGGGGAGCGCCTCCCCGTGCCCAT
CATCGCCGAGGTGGACCTGTACAGGTTTCGACCCGTGGGACCTGCCGGAGCGCGCGCTCTTCGGGGCCC
GGGAGTGGTACTTCTTCACGCCCAGGGACCGCAAGTACCCCAACGGCTCCCGCCCCAACCGCGCCGCC
GGCGACGGGTACTGGAAGGCCACCGGCGCCGACAAGCCCGTCGCGCCGCGCGCCCGCCGCGGACGC
CCGCACGCTCGGGATCAAGAAGGCGCTCGTCTTCTACGCCGCAAGGCGCCGCGCGGGGTCAAGACAG
ACTGGATCATGCACGAGTACAGGCTCGCTGACGCCGCGGACGCGCCAAGAAGGGGTGCTCAGGTTG
GATGACTGGGTGCTGTGCCGGCTGTACAACAAGAAGACGAGTGGGAGAAGATGCGGCTGGGGAAGGG
GGCAGCCGCGGCGCAGTCAAAGAGGAGGAGGCCATGGACATGAGCACCTCCCACTCGCAGATCACCC
ACTCGTGGGGCGAGACGCGCACGCGGAGTCGGAGATCGTGGACAACGACCTGCCGTTCCCGGATCCG
GCGATGATGGTGCCCAAGAAGGAGCGGGTGGACGACGGCGGCAGCGCCAGGACCAGCGACCTGTTTCGT
GGATCTCAGCTACGACGACATCCAAGGCATGTACAGCGGCCTCGACATGCTGCCGCGGCGCGGAGG
ACTTGTAATCCTCGCTCTTCGCGTCGCCCAGGGTCAGGGGGAACCAGCCACCGGACCCGCGGNGTTG
GGCCCCCTTCTGAGTGAGCTCAGGCGAAGATGGAGGCATGGAGATCAGGAGAGA

FIGURE 27 (continued)

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SEQ ID NO: 63 - AY103772.1 - Zea mays - translation

MGQPVTRRRERDAEAE LDLPPGFRFHPTDDELVEHYLCRKAAGQRLPVPIIAEVDLYRFD PWDLPERA
LFGAREWYFFT PRDRKYPNGSRPNRAAGDGYWKATGADKPVAPRAAADARTLG IKKALVFYAGKAPR
GVKTDWIMHEYRLADAGGRAKKGSLRLDDWVLCRLYNKKNEW EKMR LGKGAAGAVKEEEAMD MSTSH
SQITHSWGETRTPESEIVDNDLPFPDPAMMVPKKERVDDGGSARTSDLFVDLSYDDIQGMYSGLDMLP
PAGEDLYSSLFASPRVRGNQPTGPAXLGPF

SEQ ID NO: 64 - AJ010829.1 - Triticum aestivum

AATTCGGCAGGACAGTCCACCACGCACGTGCAGCAGCACCAGCGCCCGAGAATCCCATTCCCATCG
ACGGAGAAGAAGAAGTGAAGAAACAATGGTGATGGCAGCGGCGGAGCGGCGGGACGCGGAGGCGGAGC
TGAACCTGCCGCCGGGGTTCCGGTTCCACCCGACGGACGAGGAGCTGGTGGCGGACTACCTCTGCGCG
CGCGCGGCGGCGCGCGCGCGCGGTGCCCATCATCGCCGAGCTCGACCTCTACCGGTTGACCCGTG
GGAGCTCCCGGAGCGGGCGCTCTTCGGGGCGCGGGAGTGGTACTTCTTCACGCCGCGGGACCGCAAGT
ACCCCAACGGCTCCCGCCCCAACC GGCGCGCGGGGGCGGCTACTGGAAGGCCACCGGCGCGGACAGG
CCCGTGGCGCGCGCGGGCAGGACCGTCGGGATCAAGAAGGCGCTCGTCTTCTACCACGGCAGGCCGTC
GGCGGGGGTCAAGACGGACTGGATCATGCACGAGTACCGCCTCGCCGGCGCCGACGGACGCGCCGCCA
AGAACGGCGGCACGCTCAGGCTTGACGAATGGGTGCTCTGCCGCCTATACAACAAGAAGAACAGTGG
GAGAAGATGCAGCGGCAGCGGCAGGAGGAGGAGGCGGCGGCCAAGGCTGCGGCGTCACAGTCGGTCTC
CTGGGGTGAGACGCGGACGCCGGAGTCCGACGTCGACAACGATCCGTTCCCGGAGCTGGACTCGCTGC
CGGAGTTCCAGACGGCAAACCGCTCAATACTGCCCAAGGAGGAGGTGCAGGAGCTGGGCAACGACGAC
TGGCTCATGGGGATCAGCCTCGACGACCTGCAGGGCCCCGGCTCCCTGATGCTGCCCTGGGACGACTC
CTACGCCGCCTCGTTCCTGTCGCCGGTGCCACGATGAAGATGGAGCAGGACGTCAGCCATTCTTCT
TCTGAGCTCTCAATACTCTCACGGTCGCACTGTTGTGTGCGGCGTAACTGTAGATAGTTACATTTGT
TCAGGATTTATTTGTAACGTTGCTTCTTTTATACGATACTCTCTTCTTCTAAAAA AAAAAAAAAA
AA

SEQ ID NO: 65 - CAA09371.1 - Triticum aestivum

MVMAAAERRDAEAE LNLPPGFRFHPTDEELVADYLCARAAGRAPPVPIIAELDLYRFD PWELPERALF
GAREWYFFT PRDRKYPNGSRPNRAAGGGYWKATGADRPVARAGRTVGIKKALVFYHGRPSAGVKTDWI
MHEYRLAGADGRAAKNGGTLRLDEWVLCRLYNKKNQWEKMRQRQEEEEAAKAAASQSVSWGETRTPE
SDVDNDPFP ELDLPEFQTANASILPKEEVQELGNDDWLMGISLDDLQPGSLMLPWDDSYAASFLSP
VATMKMEQDVSPFFF

SEQ ID NO: 66 - NM_186659.2 - Oryza sativa

CATCCAACAACCCACCACCCTCATTCCTCAAGTCCCAAGATCGAACACCTCGTGTCCATGGCGGCGG
CGAAGCGGCGAGTGC GCGACGCGGAGGCGGACCTGAACCTCCCGCCGGGCTTCCGCTTCCACCCCACC
GACGAGGAGCTGGTGGCGCACTACCTCTGCCC GCGCGCCGCGGGCCGCGCCGCCCGCCCGGTCCCCATCAT
CGCCGAGCTCGACCTCTACCGCCACGACCCATGGGACCTCCCCACCGCGCCCTCTTCGGCCGCGCG
AGTGGTACTTCTTACCCCGCGCGACCGCAAGTACCCCAACGGCTCCCGCCCCAACC GCGCGCGCGCC
TCGGGCTACTGGAAGGCCACCGGCGCCGACAA

FIGURE 27 (continued)

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GCCCGTGCTGCACAACGGCAGGACGGCCGGGATCAAGAAGGCGCTCGTGTTCTACCACGGCAAGCCCC
CCCGCGGGCGTCAAGACGGAGTGGATCATGCACGAGTACCGCCTCGCCAAGAAGGGCGGGCGCCGCCGCC
GCCGCGGGCGCGGGCGCGCTCAGGCTGGATGACTGGGTGCTGTGCCGGCTGTACAACAAGAAGAACGA
GTGGGAGAAGATGCAGAGCAGGAAGGAGGAGGAGGAGGCCATGGCGGCGGCGCAGTCGTGGGGGGAGA
CGCGGACGCCGGAGTCGGAGGTCTGTCGACAGCGACGCGTTCCCGGAGATGGACTACTCGCTGCCGGCG
GCGTCGTTTCGACGACGCCCTGCTGCCCCAAGGAGGAGGCGCGCGACGACGACTGGCTCATGGGGATGAG
CCTCGACGACCTCCAGGGCCTCGGCTCGCTGCTGCAGGCCGACGACCTCTCCATGCTCGCGCCGCCGC
CGGCGGCGAAGACGGAGCCGCTCGGCGCGCCATTCTTCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTGTGACTGCACCACTGTATATAAATTCAGAGTTTTTCAGACATGTTTCAGTATTCAGAGTTCTCA
GGCAAGTTTCAGAATTCAGAGATGGTTAAGGATTAGTGGCTTATGAGCAGTATGATATGCAGGTTAGTT
TCTAGTTTACAGTGTACTCCAGATTGGAGATTTGATTAATGATTTGATTCTAATTAATGTAGTATA
CTGAGTGTACTCATCATCACAGATTCATCAGAGCTGTGTCAAGTGACAATCTTTTTTTTTTTATTT
CCTGGATCAAGTTCACCATGTTGTGCTCAAGATTTGTGGATAAATGCACATCCATCCTTGAATTGGC

SEQ ID NO: 67 - NP_911548.1 - *Oryza sativa*

MAAAKRRVRDAEADLNLPFGFRFHPTDEELVAHYLCPRAGRAAPVPIIAELDLYRHDPWDLPHRALF
GRREWYFFTPRDRKYPNGSRPNRAAASGYWKATGADKPVLHNGRTAGIKKALVFYHGKPPRGVKTEWI
MHEYRLAKKGGAAAAAGAGALRLDDWVLCRLYNKKNEWEKMQSRKEEEEAMAAAQSWGETRTPESVV
DSDAFPEMDYSLPAASFDDALLPKEEARDDDLWLMGMSLDDLQGLGSLQADDLSMLAPPPAAKTEPLG
APFF

SEQ ID NO: 68 - DQ267442.1 - *Elaeis guineensis*

AGGCAGAAATCTCACCGCCGCCTCAGCCATTTCTAAAGCTTGGTACAAGGAACGGTAATCCTCCAGGC
AATCGAGTTGCGAGGACGCTGACAATGGGGAGCAGGAGAAGAGATGCTGAGGCGGAGCTCAACCTGCC
GCCGGGATTCCGGTTCACCCGACCGACGAGGAGCTCGTCGTTTACCTCTGCAAGAAGGTGGCCT
GCCAGCGCTGCCCGTGCCCATCATCGCCGAGGTGATCTCTACAAATATGACCCATGGGATCTGCCA
GAGAAGGCGTTGTTCTGGGCTAAAAGAGTGGTATTTCTTCAACCCCTCGTGATCGAAAAGTACCCGAATGG
CTCGAGGCCTAACAGGGGCCGCCGGGAGGGGGTACTGGAAGGCGACCGGTGCTGATAAACCCGTGACCC
CGAAGGGGAGCAGTAGGCCTCTCGGGATCAAGAAAGCCTTGGTGTTTTACTCTGGGAAGGCACCAAGA
GGAGTGAAGACTGATTGGATCATGCATGAGTACAGGCTTGCCGACACGAACCGAGCAGCCAACAAGAA
GGGAAGCCTAAGGCTTGATGACTGGGTCTTTGCCGTTGTACAACAAGAAGAACACCTGGGAGAAGA
TGCAGCAACAAAAGGAGGCAGCATCGTTTGGAGAGACGATGGATTCTGTGGATGACACAGGATCGGAC
AGCTTCAGAACACCCGAATCGGACATAGATAACGATGTCATGTTCCCGGACTTTGACGATATGGCTCA
GGTTGGAGCTCACCCACCTCAAGCTTTCAATGGAATGCAAGGAGTACGAGTCAACAATATAACTGGGT
ATCAGCCAGCAATAGAGCAGCGTCCAAAAGAGGAGAATGACTGGTTCACGGACCTGAATCTGGATGAC
TTCCACAGTACATGCATGGCTTTTGGATCAACACCTGCTCTCGATATGTCGGACCATGATTACTACTA
CTCAAACCTTCCACAACCTGAGATCAAACCAGAGTGACCTGCTACCCTTCTAAAGCTACGAATCCCAGC
TGTATATAAGTGAAAATAGGCAGGAGGTGACAATCTAGTGGTAGAACTCTGTAGGATTCTTTTGTTC
CACCAATTTTATATAGGTAAATCCATTACATAAGCAAGGGACAGTCGCTGATGTACATATGATAATATT
ATTTTGTGGTAGACCTTCTGTT

FIGURE 27 (continued)

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TGAATTAGTTTTACAAATTTTGAGCATTGTCTAGTGGTAGAATATCTTCGTTTCGATTACAGAACTT
GCCTCAGCAACAGGAAACATATTCACACACACACACACACAAAAAAGAAAAGCAGCAGCAGGAATC
AGAATAAGTTATAGATGGTGGGATAATCTTAAGTGACAGTATATAACACTGCGCACAAAAAGGTGGAC
AGTGAGAACTCAAAGGAGAATCAGCCGTGGCATGCGGTCATAGTTATTCGTTTCAGAGAGACAGTTTAT
AGCATCTGCTTGGGATCTTTGTTTAGTGCGACACAACCAACAGTAGGAACAAAGAATATCTGTGGACA
TCCACAAGTCCAGGGTAGTATCGAGGAAACAAGCAACGTTGTGTGCGATTGACAAGAGTGACCCTCCA
AATGTTAAGTTTTCTGGAAGAGGGGAAAGAAGTGGAAGCATAAGCGCATGCATAAGCAAGCACATCAC
CAGCGAAAGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 69 - ABB72844.1 - *Elaeis guineensis*

MGSRRRDAEAEELNLPFGFRFHPTDEELVVHYLCKKVACQRLPVPIIAEVDLYKYDPWDLPEKALFGLK
EWYFFTFRDRKYPNGSRPNRAAGRGYWKATGADKPVTPKGSSRPLGIKKALVFYSGKAPRGVKTDWIM
HEYRLADTNRAANKKGSRLDDWVLCRLYNKKNTWEKMQQKEAASFGETMDSVDDTGSDSFRTPESD
IDNDVMFPDFDDMAQVGAHPQAFNGMQGVRVNNITGYQPAIEQRPKEENDWFTDLNLDHSTCMF
GSTPALDMSDHDYYSNLPQLRSNQSDLLPF

SEQ ID NO: 70 - AB028183.1 - *Oryza sativa*

GCAGCATCAACAAAGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCGTTGGTGGTGGTGGTGTGTCATCA
CCAACATTTTCACGAGAGGAGAAGGATGGAAATGGCGGCGGCGGTTGGGGGCAGCGGGAGGAGGGACG
CGGAGGCGGAGCTGAACCTGCCGCCGGGCTTCCGTTTCCACCCGACCGACGAGGAGCTCGTGGTGCAC
TACCTCTGCCGAAGGTTGCCCGGCAGCCGCTCCCCGTCCCAATCATCGCCGAGGTGCACCTCTACAA
GCTCGACCCCTGGGATCTCCCTGAGAAGGCGTTGTTTCGGGAGGAAAGAGTGGTACTTCTTCACGCCGA
GGGACCGGAAGTACCCGAACGGGTTCGAGGCCGAACCGCGCAGCGGGGAGAGGGTACTGGAAGGCGACG
GGAGCCGACAAGCCGGTGGCGCCCAAGGGGAGCGCGAGGACGGTGGGGATCAAGAAGGCGCTCGTGTT
CTACTCCGGGAAGGCGCCGAGGGGGGTCAAGACGGACTGGATCATGCACGAGTACCGCCTCGCCGACG
CCGACCGCGCCCCGGGCGGCAAGAAGGGCTCACAGAAGCTGGACGAGTGGGTGCTGTGCCGGCTGTAC
AACAAGAAGAACAACCTGGGAGAAGGTGAAGCTGGAGCAGCAGGACGTGGCCTCCGTGGCGGCGGGCGG
GCCGCGCAACCACCACCATCAGAACGGCGAGGTCATGGACGCGGCGGGCGGCTGACACCATGTCCGACA
GCTTCCAGACGCACGACTCCGACATCGACAACGCCTCCGCCGGCCTGCGGCACGGTGGGTGCGGCGGC
GGCGGCTTCGGCGACGTGGCGCCGCCGAGGAATGGGTTTCGTGACGGTGAAGGAGGACAACGACTGGTT
CACCGGCCTCAACTTCGACGAGCTGCAGCCGCCGTACATGATGAACCTGCAGCACATGCAGATGCAGA
TGGTGAATCCGGCGGCGCCAGGGCACGACGGCGGCTACTTGAGTCCATCAGCTCGCCGCAGATGAAG
ATGTGGCAGACAATCCTGCCACCATTCTGAGATGGATGGAGCAAGAAAAAGGTTGCTGTAGATAAAGG
GCGGAAATAGGAGTGATGGCTAGAAAATTATTAGATTTACTAGAACGAAAATGATTAGAAATCTGGCA
AGCATGATTCTGCAAATGTGGTGGTAGATGCTTGAGTATGTAATTCATTTGTTTCAGTATATGCATTT
GGTAATCTGCAAAACAAAAAAAAAAAAAAAAAAAAA

FIGURE 27 (continued)

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SEQ ID NO: 71 - BAA89798.1 - *Oryza sativa*

MAAAVGGSGRRDAEAEELNLPFGFRFHPTDEELVVHYLCRKVARQPLPVPIIAEVDLYKLDPWDLPEKA
LFGRKEWYFFTFRDRKYPNGSRPNRAAGRGYWKATGADKPVAPKGSARTVGIKKALVFYSGKAPRGVK
TDWIMHEYRLADADRAPGGKKGSQKLDEWVLCRLYNKNNWEKVKLEQQDVASVAAAAPRNHHHQNGE
VMDAAAADTMSDSFQTHSDIDNASAGLRHGGCGGGGFGDVAPPRNGFVTVKEDNDWFTGLNFDELQP
PYMMNLQHMQMOMVNPAAPGHGGYLSISSPQMKMWQTILPPF

SEQ ID NO: 72 - DQ028770.1 - *Glycine max*

TTCCAGAGTTGGTGTTAGTCTTGGTGTAGTGTAGCTAGGGAGGGATATATATCTGAGTAAGATGGCAT
CAGAGCTTGAATTGCCCCCAGGCTTCAGATTCCATCCAACGGACGAGGAGCTGGTGTTGCACTATCTC
TGCCGCAAATGCGCGTCGCAGCCAATCGCCGTTCCCATCATCGCCGAAATCGACCTCTACAAATACGA
CCCCTGGGACTTACCCGATTGGCTACTTATGGAGAGAAAGAGTGGTACTTCTTTTACCACGGGACC
GGAAATACCCAAACGGTTCGAGGCCGAACCGGGCGGCTGGCACCGGTTACTGGAAGGCAACCGGGGCG
GATAAGCCCATTGGTCAGCCCAAACCGGTTGGGATTAAAAAAGCTTTGGTGTTTTACGCAGGGAAAGC
TCCTAAAGGGGACAAAAGCAATTGGATCATGCACGAGTATCGTCTCGCAGACGTAGATCGCTCCGTTT
GCAAAAAGAACACCCTAAGGTTGGATGATTGGGTGCTTTGCCGTATTTACAACAAGAAGGGCACGATC
GAGAACTGCAACCAAGCAGCGATGTTGCTCATAGCCGAAATATCGAATCCTCGGAGATCGAAGACAG
GAAGCCGGAGATTCTGAAAAGCGGAGGAGGTTGTCTTCCGCCGCTGCGCCGGTGCCTGCGCCGCCGC
AAGCGACGGCGAAGACGGATTACATGTACTTCGACCCGTCGGATTCAATCCCGAAGCTGCACACGGAC
TCGAGCTGTTGCGAGCAGGTGGTATCGCCGGGATTGCGCAGCGAGGTGCAAAGCGAGCCCAAGTGGAA
CGAGTGGGAGAAAAGCCTCGAATTTCCATTTAATTACGTGGATGCCACTCTCAACAACAGCTTCATGG
CCCAATTCCAGGGCAATAATCAGATGTTGTGCGCGCTGCAGGACATGTTTATGTACTGGCCCAACAAG
TCCTTTTGAGCACATCATGATGGTTTTAAATTACGATCCACAATTGCTCTTAAGATTTTCTGACTCAC
CATGCGACCACAATCGTAATTTAAAACCATGTACATAAAATCCACGCGCGCCGCCATTTCGATTTG
CACGGTAGCACGAGACTCAAGGTCCATGAGTGTGCCTGTAA

SEQ ID NO: 73 - AAY46122.1 - *Glycine max*

MASELELPPGFRFHPTDEELVLHYLCRKCASQPIAVPIIAEIDLYKYDPWDLPLGLATYGEKEWYFFSP
RDRKYPNGSRPNRAAGTGYWKATGADKPIGQPKPVGIKKALVFYAGKAPKGDKSNWIMHEYRLADVDR
SVRKKNTLRLLDDWVLCRIYNKKGTIEKLQSSDVAHSRNIESSEIEDRKPEILKSGGGCLPPPAPVPA
PPQATAKTDMYFDPSDSIPKLHTDSSCSEQVVSPPGFASEVQSEPKWNEWEKSLEFPFNVDATLNNS
FMAQFQGNQMLSPQLQDMFMYWPNKSF

SEQ ID NO: 74 - AY498713.1 - *Lycopersicon esculentum*

GGCACGAGCAAAGCAGGAGCAGGAGCAGCAACAAACAGAGAGAAGAAAACAGAGGAAGATAAGAGGAA
AATTTATCGAATTGGAATCGAGAGAAAAGGGGAAGTGAAGTTGCCAAGAGTGAGAATTTCAAAGGAAA
TGAACAAAGGAGCAAACGGAAATCAGCAATTGGAGTTACCGGCGGGATTGAGATTCATCCGACAGAC
GACGAATTGGTGAGCACTATCTCTGCAGGAAATGCGCCGGACA

FIGURE 27 (continued)

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GTCGATTGCTGTATCAATTATAGCTGAAATTGATCTTTACAAGTTTGATCCATGGCAGTTGCCTGAGA
AGGCTTTGTACGGTGAAAAAGAGTGGTATTTTTCTCACCAAGGGATAGAAAATATCCGAACGGTTCA
CGGCCGAACCGAGCAGCAGGAACCGGTTATTGGAAGGCAACCGGAGCTGATAAACCGGTGGGAAAACC
CAAAACCTTAGGGATAAAGAAGGCACTTGTGTTCTATGCCGAAAAGCACCCAGAGGTATAAAAACAA
ATTGGATTATGCACGAGTACCGCCTCGCCAACGTGGACCGCTCTGCTGGCAAGAACAATAACTTGAGG
CTTGATGATTGGGTATTGTGTCTGAATATACAACAAGAAAGGCACACTTGAGAAGCATTACAATGTGGA
CAACAAGGAAACTACAAGCTTTGGAGAATTTGATGAAGAAATAAAACCAAAAATATTGCCACACAAT
TAGCACCGATGCCACCACGGCCTCGATCGACACCAGCAAACGACTACTTTTATTTCGAGTCATCAGAG
TCGATGACTAGAATGCACACGACAAACTCGAGCTCTGGCTCAGAGCATGTCTTGTCTGCCATGTGACAA
GGAGGTTTCAGAGCGCGCCCAAATGGGACGAAGACCACAGAAACACCCCTTGATTTTCAGCTAACTATT
TGGATGGTTTACTAAATGAACCATTTGAAACCCAAATGCAGCAGCAAATTTGCAACTTTGACCAGTTC
AACAAATTTCCAAGACATGTTCTTATACATGCAAAAACCTTACTAAAATTTGTATAAATTCATTGGATCT
AAATTGAGTGTGATCCATGACATTTTCTTTGTTCTTTGGTGGTGTAGGTCAACTTTTTATTAAGTAGT
TTAGAGAAGTACAAAATGCTAGTCAAATTTGGTGGGCTACAGCACAAATGAGCCTTGATAAGCATAGC
CAAAGAGTCGTATAGAAGGGCTTATTATTATTGTAAGGTATGTAAAAACAAATGAAAATTTGTTAATA
TCAAGTTATCATTTCTTCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 75 - AY498713.1 - *Lycopersicon esculentum*

MNKGANGNQLELPAGFRFHPTDDELVQHYLCRKACAGQSIASVSIIEIDLYKFDPWQLPEKALYGEKE
WYFFSPRDRKYPNGSRPNRAAGTGYWKATGADKPVGKPKTLGIKKALVYAGKAPRGIKTNWIMHEYR
LANVDRSAGKNNNLRLDDWVLCRIYNKKGTLKHYNVNDKETTSFGEFDEEIKPKILPTQLAPMPRP
RSTPANDYFYFESSESMTRMHTTNSSSGSEHVLSPCDKEVQSAPKWDEDHRNTLDFQLNYLDGLLNEP
FETQMQQQICNFDQFNNFQDMFLYMQKPY

SEQ ID NO: 76 - AY245883.1 - *Brassica napus*

CGAAGAAAAGAGAAGACTTTTGAAAAAAAAAATGAAAGCAGGGCTAAACTTACCAGCAGGATTCCGAT
TCCACCCAACGGACGAAGAGCTTGTGCAATTCTACCTTTGCCGGAATGCGCATCGGAGGAGATCTCA
GCTCCGGTCATCGCCGAAATCGATCTCTACAAGTTCAACCCCTGGGAGCTTCTTGAGATGTCTCTGTA
CGGAGAGAAAGAGTGGTACTTCTTCTCGCCACGAGACCGGAAATACCCAAACGGTTCGCGTCCTAACCC
GGGCGGCGGGAACCGGTTATTGGAAGCCACCGGAGCTGATAAACCGATCGGTAAACCGAAGACGCTG
GGTATTAAGAAAGCGCTCGTGTTCTACGCAGGGAAAGCTCCCAAAGGGATTAAGACGAATTGGATTAT
GCACGAGTATCGCCTCGCTAATGTGGACAGATCAGCTTCTGTTAACAAAAAGAACAACCTTCGACTTG
ATGATTGGGTGTTATGTGCAATCTACAACAAGAAAGGGACCATGGAGAAGTACTACCCTGCTGATGAG
AAACCGATGACCGTGACGGCGGCTTCATCGCCTTTCGATGCGTCGGACTCGACTTACCCGACGTTGCA
AGAGGATGACTCGAGCAGCTCGGGGGGTCGCGTGGTGTGCGCGGATGCGCGGGAGGTGCAGAGCGAGC
CTAAATGGGGGGAGTTTGAGAATGCTTTTGATGCTTCCATGTTTCGGTGGTGGCTCCATGGACTTGCTG
CAGAGTGAAGATTTTGTGCCTCAGTTCTTGTACCAGCCTTCTTATGATTTCAACTCCT

FIGURE 27 (continued)

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GGCAGGAGGATCCGCCGGAGCAGAAACCGTTCTTGAATTGGAGTTTTGCTCCACAGGGGTGAAAAAGG
AAGAGAGTGAAAGGTTTTTGGTCTGTGTTGTGATATGTGTTAGAGAGAAGTTCTCAATCATCTTTTG
TTTCTTAGTAGTGAGAGAAAGATTGTAGAGTGTTGATAGTTTCTTAGCATCTTCAATGTTTCATTGGC
AGGTGAATTCTTGTTATTTTCATCAGAAATTTATATGAAAAATTATACCTT

SEQ ID NO: 77 - AAP35052.1 - Brassica napus

MKAGLNLPA GFRFHPTDEELVQFYLCRKCASEEISAPVIAEIDLYKFNPWELPEMSLYGEKEWYFFSP
RDRKYPNGSRPNRAAGTGYWKATGADKPIGKPKTLGIKKALV FYAGKAPKGIKTNWIMHEYRLANVDR
SASVNKKNNLRLDDWVLCRIYNKKGTMKEYYPADKPMPTVTAASSPFDASDSTYPTLQEDDSSSSGGR
VVSPDAREVQSEPKWGEFENAFDASMFGGGSMDLLQSEDFVPQFLYQPSYDFNSWQEDPPEQKPFLNW
SFAPQG

SEQ ID NO: 78 - XM_475238.1 - Oryza sativa

ATGAGCGGCGGCGGCGAAGGGGCGGCGGCGGCGGAGAGGCAGGAGCTGCAGCTGCCGCCGGGGTTTCAG
GTTCCACCCGACGGACGAGGAGCTGGTGATGCACTACCTCTGCCGGCGGTGCGCCGGCCCTCCCCATCG
CCGTCCCCATCATCGCCGAGGTCGACCTCTACAAGTTCGATCCATGGCATCTCCCAAGAATGGCGCTG
TACGGCGAGAAGGAGTGGTACTTCTTCTCCCCTCGGGACCGCAAGTACCCGAACGGGTGCGGGCCGAA
CCGCGCCGCGGGGTCCGGGTACTGGAAGGCCACCGGCGCCGACAAGCCGGTGCGGACGCGGAGGCGG
TGGCCATCAAGAAGGCGCTCGTCTTCTACGCCGGCAAGGCGCCCAAGGGCGACAAGACCAACTGGATC
ATGCACGAGTACCGCCTCGCCGACGTCGACCGCTCCGCCCGCAAGAAGAACACCCTCCGGCTAGATGA
TTGGGTCTGTGCCGAATCTACAACAAGAAAGGCGGCGTGAGAAAGCCGAGCGGCGGCGGCGGCGGCG
AACGTTTCAATATGATGAGCCACGGGGAGACCGCGTCGGCGGGGCTCGCCGCCGGAGCAGAAGCCGGCC
GTGCTGCCGCCGCCGCCACCGCCGTACGCGGCGGCGGCGGCGGCGTTCTCGGAGCTGGCGGCGTTCTACGA
CGTGCGGCGGTCGGACTCGGTGCCGCGGGCGCACGGCGCGGACTCGAGCTGCTCGGAGCACGTGCTGA
CGACGTCGGCGTCTGTCGGCGGCGGTCGTCGAGCGGCGGAGGTGCAGAGCCAGCCCAAGATCGCCGAG
TGGGAGCGCACGTTCCGCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG
CCAGCTCGACCCCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
GGGCAAGCCGTTCTGA

SEQ ID NO: 79 - XP_475238.1 - Oryza sativa

MSGGGEAAAAERQELQLPPGFRFHPTDEELVMHYLCRRRCAGLPIAVPIIAEVDLYKFDPWHLPRMAL
YGEKEWYFFSPRDRKYPNGSRPNRAAGSGYWKATGADKPVGTTPRPVAIKKALV FYAGKAPKGDKTNWI
MHEYRLADVDRSARKNTLRLDDWVLCRIYNKKGVEKPSGGGGGERSNMMSHGETASAGSPPEQKPA
VLPPPPPPYAAAAPFSELAIFYDVRPSDSVPRAHGADSSCSEHVLTTSSASSGGVVERPEVQSQPKIAE
WERTFAGAAAPAGAVSTAGPILGQLDPAAAVAGGGDPLLQDILMYWGKPF

FIGURE 27 (continued)

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SEQ ID NO: 80 - AJ401151.1 - *Solanum tuberosum*

GGTCAAACAACCTGAACTAACAAAGCAGCAGCAGCAGCAACAAACAGAGAAGACAACAGAGGAAGATA
AACAAAGGAAATTAAGAGGGAGATTTATCGAATCGAAAGGGAAAGGGAAGTTACGAAGAGTGAGAATT
TGAAGGAAATGAACAAAGGAGCAACCGGAAATCAGCAATTGGAGTTACCGGCGGGATTTCAGATTCCAT
CCGACAGACGACGAATTGGTGCAGCATTATCTCTGCAGGAAATGTGCCGGACAGCCAATTGCAGTATC
AATTATAACTGAAATTGATCTTTACAAGTTTGATCCATGGCAGTTGCCTGAAAAGGCTTTGTACGGTG
AAAAGGAGTGGTATTTTTCTCACCAAGGGATAGAAAATATCCTAACGGTTCACGGCCGAACCGAGCA
GCAGGAACCGGTTATTGGAAGGCAACCGGAGCAGATAAACCGGTGGGAAAACCCAAAACATTAGGGAT
AAAGAAGGCACCTTGTGTTTTATGCTGGAAAAGCACCTAGAGGAATAAAAACCAATTGGATTATGCATG
AGTACCGGCTCGCCAATGTGGACCGGTCTGCTGGCAAGAACAATAACTTGAGGCTTGATGATTGGGTA
TTGTGTGCAATTTACAACAAGAAAGGCACACTTGAGAAGCATTACAATGTGGACAACAAGGAACTGC
AAGCTTTGGAGAATTTGATGAAGAAATAAAAACCAAAAATATTGCCACACAATTAGCACAGATGCCAC
CACGGCCCCGATCGACACCGACAAACGACTACTTCCATTTTGAATCATCGGAGTCGATGACTAGAATG
CACACCACAACTCGAGCTCTGGCTCAGAGCATGTCTTGTCGCCATGTGACAAGGAGGTTTCAGAGCGC
GCCCAAATGGGACGAAGACCACAGAAACACCCTTGATTTTCAGCTAAATTATCTGGATGGTTTACTAA
ATGAACCATTTGAAACCCAAATGCAGCAGCAAAGTTGCAACTTTGACCAGTTCAACAATTTCCAAGAC
ATGTTCTTTTACATGCAAAAGCCTTACTAAAATTGTATAAATTCATTGGATCTAAATTGATTGTGATC
CATGACATTTTCTTTGTTCTTTGGTGGTGTAGGTCAACTTTTATTAATTAGTTTAAAAAGTACAAAA
TGCAAGTCAAATTTGGTGGGCTGTAATGAGCCTTTGATAAGCATAGCCAAAGAGTCATATAGAAGGGC
TTATTAATGTTATTATTGTAAGGTACATGTAAAACAAATGAAAATTTGTTAATATCAAGTTATCATTC
TTC

SEQ ID NO: 81 - CAC42087.1 - *Solanum tuberosum*

MNKGATGNQQLELPAGFRFHPTDDELVQHYLCRKCAGQPIAVSIITEIDLYKFDPWQLPEKALYGEKE
WYFFSPRDRKYPNGSRPNRAAGTGYWKATGADKPVGKPKTLGIKKALVFYAGKAPRGIKTNWIMHEYR
LANVDRSAGKNNNLRLDDWVLCRIYNKKGTTLEKHYNVDNKETASFGFEDEEIKPKILPTQLAQMPPRP
RSTPTNDYFHFESSESMTRMHTTNSSSGSEHVLSPCDKEVQSAPKWDEDHRNTLDFQLNYLDGLLNEP
FETQMQQQSCNFDQFNNFQDMFFYMQKPY

SEQ ID NO: 82 - NM_147856.2 - *Arabidopsis thaliana*

CGATTACAATCTTGAGCAGACGAAGAAAACCCAAAAAATCCAGATCCAGCTGAAATTGAATTTTCA
ACCAACGAAGAAGAGATTTTCCAAGAGCAACAGACAAGAAGAAGAGAATGAAGTCGGAGCTAAATTT
ACCAGCTGGGTTCCGATTCCATCCAACGGACGAGGAGCTTGTGAAATTCTACTTGTGCCGGAAATGTG
CTTCCGAGCAGATCTCGGCTCCGTTATCGCCGAGATTGATCTCTACAAGTTCAATCCTTGGGAGCTT
CCAGAGATGTCTCTGTACGGAGAGAAAGAGTGGTACTTCTCTCACCTAGAGATCGGAAATACCCAAA
CGGTTTCGCGTCCTAACCGGGCAGCAGGAACCGGTTATTGGAAAGCTACCGGAGCAGATAAACCGATTG
GTAAACCGAAGACGTTGGGTATCAAGAAAGCACTCGTCTTCTACGCAGGGAAAGCTCCAAAAGGGATT
AAGACCAATTGGATAATGCATGAGTATCGTCTCGCTAATGTTGATAGATCAGCTTCTGTTAACAAAA
GAACAACCTACGAC

FIGURE 27 (continued)

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TTGATGATTGGGTTTTATGTCTGAATATACAACAAGAAAGGAACCATGGAGAAGTATTTCCCCGCGGAT
GAGAAGCCGAGGACCACGACAATGGCTGAACAGTCATCATCACCTTTTGATACATCAGACTCGACTTA
CCCGACATTGCAAGAGGATGATTCCAGCAGCTCAGGTGGTCACGGTCACGTGGTGTACCGGATGTTT
TGGAGGTTTCAGAGCGAGCCTAAATGGGGAGAGCTTGAGGATGCTTTGGAAGCTTTTGATACTTCAATG
TTTGGTAGTTCCATGGAGTTGTTGCAGCCTGACGCTTTTGTCCCTCAGTTCCTGTATCAGTCTGATTA
TTTCACTTCCTTCCAGGATCCGCCTGAGCAGAAACCATTCTTGAATTGGAGTTTTGCTCCACAGGGGT
AAAAACGGAAGAGACCAAAAAAGGTGTTGCTAGTAGTACTGTGATGTGCCAGAGAGAAGAGTCTCAT
CTCAACTCATCCCTGGCTCTTAGTAGTAAAAGAAGATTGTAGAATGTTAATAGCTTTTAGCATCAATG
TCTCATTAGCAGGCACATTCTTGTTCTTTCATGAGAAGTTTATATGAAAACATAAAAATTTATATTCAA
ATTCTTCAAGATGTTGCACTTATGTAGATACTGATATTAAATAACAACCTAACCTTTATGAGATATCA
TGCTCTCCGGAAGCATTTTTTGTATGAGTATCATCAGCTGAATCGAGGCGATTTCTCAGAGCTGTTAT
TCCTATGTCTCTGAGACTTTTGATTCTCGTTTTCTTGACCTGAGGTTTCTTTTTGGAAGACTTCTCTC
TTTCCTTCTGTTCAAGCTGTGTGGAGGGTTTTTCAGATCCATTATTCCCACGAGGAGTCTTCATTTTG
GGATC

SEQ ID NO: 83 - NP_680161.1 - Arabidopsis thaliana

MKSELNLPAGFRFHPTDEELVKFYLCRKCASEQISAPVIAEIDLYKFNPWELPEMSLYGEKEWYFFSP
RDRKYPNGSRPNRAAGTGYWKATGADKPIGPKTLGIKKALVFYAGKAPKGIKTNWIMHEYRLANVDR
SASVNKKNNLRLDDWVLCRIYNKKGTMKEYFPADEKPRTTTMAEQSSSPFDTSDSTYPTLQEDDSSSS
GGHGHVVSVDVLEVQSEPKWGELEDALEAFDTSMFGSSMELLQPDAFVPQFLYQSDYFTSFQDPPEQK
PFLNWSFAPQG

SEQ ID NO: 84 - AF509873.1 - Petunia x hybrida

CCCATTCTCAGTATCTAGACACCCAAAAATAAAAAATAAAAAGATTTATTATTTTTTCATCAAGAAATT
CGTTAGAAAAATCAAAAAATGACAACAGCAGAATTGCAATTACCTCCAGGGTTTAGATTTACCCAAC
TGATGAAGAACTTGTGATGCACTATTTATGTAGAAAAATGTGCTTACACAACCAATTGCTGTACCAATTA
TTGCTGAAATTGATCTCTACAAATATGACCCATGGGATCTTCCTGATTTGGCATTGTATGGGGAGAAA
GAATGGTATTTCTTTTACCTAGGGACCGAAAGTATCCGAACGGTTCACGACCAATCGAGCAGCTGG
AACAGGTTATTGGAAAGCCACTGGAGCTGATAAACCAATTGGACATCCTAAGGCAGTTGGAATTAATA
AGGCATTGGTGTTTTACGCTGGCAAGGCTCCGAAAGGCGAGAAAACAAATTGGATTATGCACGAATAC
AGACTTGCTGATGTTGATCGATCTGCTCGTAAGAATAACAATAGCTTAAGGCTAGATGATTGGGTTTT
GTGCCGAATCTACAACAAAAAGGGCTCAATTGAAAAGAATCAACTCAATAACAAGAAAATAATGAATA
CTAGCTATATGGATATGACAGTATCAAGTGAAGAAGACCGAAAGCCAGAGATTCTACCACCGCTACCA
CCTCAGCCTGCGCCGCAACAGCAACAAGTTTATAACGATTTTTTCTACCTGGATCCATCAGATTCAGT
ACCAAAAAATCCACTCAGATTCAAGCTGCTCGGAACATGTGGTTTTACCAGAGTTCACTTGTGAGAGAG
AAGTTCAGAGCGAAGCCAAGTTAAGTGAGTGGGAAAAAGCTGCCCTTGATCTTCATTTAATTACATG
GATGCCACTACTGGAGCTACCACACTGGATAATAGCCTTTTAGGTTTACAGTTTCAGAGCAGTTATCA
GATGTCGCCATTGCAGGATATGTTTCATGCACCTGCACAAACCTTTTTAAGGTCNAAAGTGAAGGAATC
AATCATTTTACGGCCGCATGTTTGTTAAAATGAGACTAAGTTAAAGTTCCCGTGACTTGCGCACGTTG
CGGGCTGTTTATAGGAATTAGTTACCATCCTTTTGGGTTTCCNCATTGGGCAATTGTTTAAAACNAC
NTTTTTGTGTTATATAGTTTTTAATAATGTTNCCCCCTNAATTNATTTAAAAAAA

FIGURE 27 (continued)

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SEQ ID NO: 85 - AAM34773.1 - *Petunia x hybrida*

MTTAE LQLPPGFRFHPTDEELVMHYLCRK CASQPIAVPIIAEIDLKYDPWDL PDLALYGEKEWYFFS
PRDRKYPNGSRPNRAAGTGYWKATGADKPIGHPKAVGIKKALVFYAGKAPKGEKTNWIMHEYRLADVD
RSARKNNNSLRLDDWVLCRIYNKKGSIEKNQLNNKKIMNTSYMDMTVSSEEDRKPEILPPLPPQPAPQ
QQQVYNDFFYLDPSDSVPKIHSDSSCSEHVVSPEFTCEREVQSEAKLSEWEKAALDLPFN YMDATTGA
TTLDNSLLGSQFQSSYQMSPLQDMFMHLHKPF

SEQ ID NO: 86 - AB218789.1 - *Prunus mume*

ACACACAGCACAGTCGAATCAAACGACGCCGTT CAGAATGTCCTCCTCCGATTTACAGCTGCCGCCCG
GCTTCAGGTTCCACCCGACGGACGAAGAGCTCGTGAAGCACTACCTCTGCCGCAAATGCCAGTCGCAG
CCGATTTCCGGTCCCGATAATCGCCGAAATCGATCTCTACAAATACAACCCCTGGGACCTCCCTGGTTT
GGCGTTGTACGGTGAGAAAGAGTGGTATTTCTTTTCGCCGAGGGACCGGAAGTATCCGAATGGTTTCGA
GGCCGAACCGGGCGGCCGGGAGCGGCTATTGGAAGGCGACCGGAGCGGATAAGCCGATCGGGAGCCCG
AAGCCAGTCGGGATTAAGAAGGCCCTGGTTTTCTACGCCGAAAAGCTCCGAGAGGAGAGAAGACCAA
TTGGATTATGCACGAGTATCGCCTCGCCGACGTCGACCGCTCGCCTCGCAAAAAGAGCAGCAGCCTAA
GGTTGGACGATTGGGTTCTGTGTGCGCATATACAACAAAAGGGCACCGTCGAGAAACAGCAGCAGCAG
CAACAACAGCAACAACAGCAAACGACGAGTCGTATGAGTAGCGGCTCGGAATTTCGAGGACAGGAAGCC
GGAGAATCTGGCGTGTCTCCGCCGCCGGCTGCGGTAGCCCCACTCGCCCGAACGACTACGTGTACT
TCGACACGTCGGACTCTGTGCCGAGGCTGCACACGGACTCAAGCTGCTCGGAGCACGTGGTGTGCCCG
GAGTTCACTTGCGAGGTGCAGAGCGAGCCCAAGTGGAAGGAGTGGGAGAAGGCCCTCGATTTTAACTA
CAATTACATGGACACCAGTGTAGAGAACGGGTTCCGGGCCGAGTTCAGAGCGCTAATCAGATGTGCG
CGCTGCAGGATATTTTCATGTACCTACAGAAGCCGTATTGATTTTGATGAAGCGGGGCCTACAATTGC
ATTGCTATGAGTCGCCGCATCGGACGGCAACGGGAGACCCAGGTCGATGAGAGTGC GTTTTCGATGCT
GTGACAAGGGAAGGGAAGGGGATTTGCGTCGCGGGGTCCACCATTTGGGCCCAAGGCTGGGTGATT
TGGGAGCGTTGATATAAAGATGATATATATAGATGGAAAAAAGATGATGGGGCTGGTTTTGGAAGATA
GAAATATGAAGAAGTTTGGTTTTTAATGTGTACAGCATGTATGTATAGATATAAATAGGTAATGTTGT
TCACATGATGATTTTGAAGGGCCGTCTAAATCGTAATATTTGTTCTTTGTGAAAAAAAAAAAAAAAAAA
AAA

SEQ ID NO: 87 - BAE48667.1 - *Prunus mume*

MSSSDLQLPPGFRFHPTDEELVKHYLCRKCSQPISVPPIIAEIDLKYNPWDL PGLALYGEKEWYFFS
PRDRKYPNGSRPNRAAGSGYWKATGADKPIGSPKPVGIKKALVFYAGKAPRGEKTNWIMHEYRLADVD
RSPRKSSSLRLDDWVLCRIYNKKGTVEKQQQQQQQQQQQTTSRMSSGSEFEDRKPENLACPPPPAAV
APTRPNDYVYFDTSDSVPRLHTDSSCSEHVVSPEFTCEVQSEPKWKEWEKALDFN YNYMDTSVENFG
PQFQSANQMSPLQDIFMYLQKPY

FIGURE 27 (continued)

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SEQ ID NO: 88 - AY245885.1 - Brassica napus

ATTTTCATTAGGATTATATTACTAGAGACAGATCCTCGAATAGAAAAGAAAATGTCAGAACTACAGCTG
CCTCCAGGATTCCGATTTACCCAACCGACGAAGAGCTGGTGATGCACTATCTCTGCCGCAAATGCGC
CTCTCAGTCCATCGCCGTCCCCATCATCGCTGAGATCGATCTCTACAAATATGATCCTTGGGAGCTTC
CCGGTTTAGCCTTGTACGGTGAGAAGGAATGGTATTTCTTCTCT
CCAAGAGACAGAAAATATCCGAATGGTTCTCGGCCGAACCGGTCAGCTGGTTCTGGGTTACTGGAAAGC
TACTGGAGCTGATAAACCGATCGGACTTCCTAAACCGGTTGGGATTAAGAAGGCTCTGGTTTTCTACG
CCGGGAAAGCTCCAAAGGGTGAGAAAACCAATTGGATCATGCATGAGTACCGTCTTGCCGACGTTGAC
CGATCATCGGCTGCTCGCAAGAAGAAGAATAGTCTCAGGCTGGATGATTGGGTTCTTTGTGCGATTTA
CAACAAAAAAGGAGCCATCGAGAAGCGAGGACCACCACCAACTCCGGTTGTTTACGGCGACGAGGTG
TGGAGGAGAAGCCGAGGCTGTGCGAGATGGGCATGCCTCCTCCGCCGGTGATGCCGAATGATTTCTGTG
TACTTTGACACGTCGGACTCGGTGCCAAAGCTGCATACGACGGAGTCGAGCTGCTCGGAGCAGGTGGT
GTCGCCGGAGTTACGAGCGAGGTTTACGAGCGAGCCCAAGTGGAAGGATTGGTCTGGGTGAGAAAAGTA
GCCTTGATTTTGGGTTTAATTACATAGATGCCACCGCGTTCCGGGGAGGAGGAGGGAGCAATCAGCTG
TTTCCGCTACAGGACATGTTTCATGTACAACATGCCCAAGCCTTATTAGGTGAAGGCAAACGCTCGTCT
ATGGGTATCACGAGATCGGTTACGTTACGGTTCGGTCAATGAGTGTGCCGCCATTAGATATTTATTAC
CATGATGTTTGTGTTTCACTGTTACTTTTATTTTCTAAGCGGTCAGATTACGGGAAATCTCTAATCGG
ATGGCGGTCGATGTGTCATTGTACTAGTGTGTTTGGTAGAAGAATCCACATGTCTTTTCTTTTTTGG
GCTTTAGTGGGCGATAAAAGTCAAAGCTAAGGATATTTGTTATTATCTCCTTCGTAATAATCAATTA
AATATTTCTTG

SEQ ID NO: 89 - AAP35054.1 - Brassica napus

MSELQLPPGFRFHPTDEELVMHYLCRKCASQSIAPVPIIAEIDLYKYDPWELPGLALYGEKEWYFFSPR
DRKYPNGSRPNRSAGSGYWKATGADKPIGLPKPVGIIKKALVFYAGKAPKGEKTNWIMHEYRLADVDRS
SAARKKKNSLRLLDDWVLCRIYNKKGAIEKRGPPPTPVVYGDEVVEEKPRLSEMGMPPPPMPNDFVYF
DTSDSVPLKHTTESSCSEQVVSPEFTSEVQSEPKWKDWSGEKSSLDGFGFNYIDATAFGGGGGGNSQLFP
LQDMFMYNMPKPY

SEQ ID NO: 90 - NM_125774.3 - Arabidopsis thaliana

ATGGACTTTGCTCTCTTCTCCTCGATTTCAATCTTTGAGATAAACCACAAAGATCCTCCGATTCGAAG
GTTTATAAAAACTCAAATCGAATCTTATCCACAAGAAAACAACAAGGTACTTTTCCAAAAATGAAGG
CGGAGTTGAATTTGCCGGCGGGATTCCGATTTTCATCCGACGGACGAAGAGCTTGTCAGTTCTATCTT
TGCCGGAGATGTGCGTCAGAACCGATTAACGTTCCGGTTATCGCAGAGATTGACTTGTACAAATTCAA
TCCATGGGAGCTTCCAGAAATGGCGTTGTACGGTGAGAAAGAATGGTACTTCTTCTCGCATAGAGACC
GGAAATACCCAAACGGGTCGAGACCAAACCGGGCAGCTGGAACCGGTTATTGGAAAGCGACTGGAGCT
GATAAACCGATCGGAAAACCGAAGACGTTAGGGATTAAGAAAGCACTCGTCTTCTACGCAGGAAAAGC
TCCGAAAGGGATTAAAACGAATTGGATTATGCACGAGTATCGTCTCGCTAATGTCGATCGATCTGCTT
CTACCAACAAGAACAACACTTAAGACTTGATGATTGGGTTTTGTGTGCGGATATACAATAAGAAAGGA
ACAATGGAGAAGTATTTACCGGCGGCGGCTGAGAAACCGACGGAAAAGATGAGTACGTCGGACTCAAG
ATGCTCAAGTCACGTGATTTACCGGACGTCACGTGTTCTGATAACTGGGAGGTTGAGAGTGAG

FIGURE 27 (continued)

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CCCAAATGGATTAATCTGGAAGACGCGTTAGAGGCATTTAATGATGACACGTCCATGTTTAGTTCCAT
TGGTTTGTGCAAAATGACGCCTTTGTTCTCAGTTTCAGTACCAGTCCTCCGATTTTCGTCGATTTCGT
TTCAGGACCCGTTTCGAGCAGAAACCGTTCTTGAATTGGAATTTTGCTCCTCAAGGGTAAAAATAATCG
GCAAAAAGTTGAAGCTTTTCAGAGTCTTCGATCACCGGCATTGTGTGCGATCCTGACCCGGAGACCAA
GTCGGGTCATACGATTACATAATCGGGTTATTGAGATTTCCACATTTGGATTTCCGAGACTAACCAAC
TTAACGGATTCTGGGGTAATTGGGGGGTTTTGCACAGGTGAATCACACTGAGTCAGCAAGTTTCGATT
TTTTGGTTTTGTTTTGTAATGATTGATTAAATGTCTAAAGATATCACGAAGTAGATACAGAAGAACTG
TAAAGCAATTGTGACCAACCATTATGAATCATATATATATTCAATGAAGCATGAGCTTATTTCTTCT
TTAATGAAGCAATGTACATTTTTCTCCAA

SEQ ID NO: 91 - NP_201184.2 - Arabidopsis thaliana

MDFALFSSISIFEINHKDPPIRRFIKTQNRILSTRKQQTGTFPKMKAELNLPAGFRFHPTDEELVKFYL
CRRCASEPINVPVIAEIDLYKFNPWELPEMALYGEKEWYFFSHRDRKYPNGSRPNRAAGTGYWKATGA
DKPIGKPKTLGIKKALVFYAGKAPKGIKTNWIMHEYRLANVDRSASTNKKNNLRLLDDWVLCRIYNKKG
TMEKYLPAAAEKPTKMSSTSDSRSSHVISPDVTCSDNWEVESEPKWINLEDALEAFNDDTSMFSSIG
LLQNDAFVPPQFQYQSSDFVDSFQDPFEQKPFNLWNFAPQG

SEQ ID NO: 92 - AY714222.1 - Capsicum annuum

GCAGGCAAACACACAAAGCAACAGCTGCAAACAGCAAAGAAACACAACGGAGATTTATTTCAGACGCC
TTTGATCTTCAGATAAGAAACAGGCAAGTTACCAAGAGTGATATTTATTGAGACGTCCTTGATTTTAG
CTGGGAAACAGGCAAGTTTTACAAAGAGAATGATCAAAGGAATCGTTGGAAATCAGCAATTGGGGTTA
CCTGCAGGATTTTCGATTTACCCCTACTGATGAAGAGTTGGTGCAGCATTATTTGTGCAGGAAATGTGC
AGGACAGAGTATTTCTGTTTCGATTATAGCTGAAATTGATCTTTACAAGTTTGATCCTTGGCAGTTGC
CTGAAAAGGCATTATACGGTGAAAAGAGTGGTATTTTTCTCCCAAGAGGATAGAAAATACCCGAAC
GGTTCAAGGCCGAACCGGGCAGCAGGAACCGTTATTGGAAAGCGACCGGAGCAGATAAACCGGTGGG
AAAACCGAAACATTAGGGATAAAAAAGGCACTTGTATTTTATGCTGGAAAAGCACCAAGAGGTATAA
AGACTAATTGGATTATGCATGAGTATCGACTTGCTAATGTGGACAGATCTGCTGGAAAGAGTAATAAC
TTGAGGCTTGATGATTGGGTATTGTGTGCAATATACAACAAGAAGGGGCACACTTTGAGAAGTATTAC
AATGTGGGCCAGCAAGAGAGGTGAGAGTTTTGGGGAATTTGAGGATGAAATAAAACCAAAAATATTTTC
CAACACAAGTAGCACCGGCTCCGGGGCAGTGGCCCCACGACCCCAATCAACCCCGCAAGCGACTAC
TTCAACTTTGAAACATCCGAGTCGATGACTACTACTAGGATGCACACGACAACTCGAGCTCTGGCTC
AGAGCATGTCTTGTGTCATGTGACAAGGAGGTTTCAGAGTGCACCTAAATGGGACGACCTTGAACCG
CCGCCCTTGATTTCCAGATAAATTATTTGGATGGTTTGCTGAACGACCCTTTTGAAATCCAAATGCAG
CAGCAAAATTGCAACATTGACCAGTTCAACACTTTCCAGGACATGTTCTTATACATGCAAAAACCTTA
GTAGAATTGTATAAATCATGTGATTCAAATTGATTTTGATCCATGACATTTTGTTGGTTCTTTGGTGG
TGTAGGTCAACTTTTTATTGATTAGATTAGAAAAGTAGAAATGCTATTCAAATTTGGTGGGCTATAGC
TCAAATGAGCCTTCGCTAGATAGCCAAAGGATTATGTAGAAGGCTTATTGTAAGGTACAGGTAAACA
AATGAAAATTTGTTAATATCAATTTATCATTCTTCAAAAAAAAAAAAA

FIGURE 27 (continued)

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SEQ ID NO: 93 - AAW48094.1 - *Capsicum annuum*

MIKGIVGNQQLGLPAGFRFHPTDEELVQHYLCRKACAGQSSISVSIIAEIDLYKFDPWQLPEKALYGEKE
WYFFSQEDRKYPNGSRPNRAAGTGYWKATGADKPVGKPKTLGIKKALVIFYAGKAPRGIKTNWIMHEYR
LANVDRSAGKSNLRLDDWVLCRIYNKKGHTLRSITMWASKRGESFGEFEDEIKPKIFPTQLAPAPGQ
WPPRPQSTPASDYFNFETSESMTTTRMHTTNSSSGSEHVLSSCDKEVQSAPKWDDLGTAAALDFQINYL
DGLLNDPFEIQMQQQNCNIDQFNTFQDMFLYMQKP

SEQ ID NO: 94 - NM_100054.2 - *Arabidopsis thaliana*

AAGTTTCAAAAACGCCAAGTTTCAGAGGTAGAGAGAGAGATACTACAATTGATTAGGATAGGATCAGG
ATCATCCTCAACAACCTCCTCCTAATTCCCTCCTCCATTCATAGTAACAATAATATTAAGAAAGAGGGT
AAACTATGTCAGAATTATTACAGTTGCCTCCAGGTTCCGATTTACCCCTACCGATGAAGAGCTTGTC
ATGCACTATCTCTGCCGCAAATGTGCCTCTCAGTCCATCGCCGTTCCGATCATCGCTGAGATCGATCT
CTACAAATACGATCCATGGGAGCTTCCTGGTTTAGCCTTGATGGTGAGAAGGAATGGTACTTCTTCT
CTCCCAGGGACAGAAAATATCCCAACGGTTCGCGTCCTAACCGGTCCGCTGGTTCTGGTTACTGGAAA
GCTACCGGAGCTGATAAACCGATCGGACTACCTAAACCGGTCCGAATTAAGAAAGCTCTTGTTTTCTA
CGCCGGCAAAGCTCCAAAGGGAGAGAAAACCAATTGGATCATGCACGAGTACCGTCTCGCCGACGTTG
ACCGGTCCGTTTCGAAGAAGAAGATAGTCTCAGGCTGGATGATTGGGTTCTCTGCCGGATTTACAAC
AAAAAAGGAGCTACCGAGAGGCGGGGACCACCGCTCCGGTTGTTTACGGCGACGAAATCATGGAGGA
GAAGCCGAAGGTGACGGAGATGGTTATGCCTCCGCCGCCGCAACAGACAAGTGAGTTCGCGTATTTTCG
ACACGTCGGATTCCGGTGCCGAAGCTGCATACTACGGATTTCGAGTTGCTCGGAGCAGGTGGTGTGCGCG
GAGTTCACGAGCGAGGTTTCAGAGCGAGCCCAAGTGGAAGATTGGTCCGGCCGTAAGTAATGACAATAA
CAATACCCTTGATTTTGGGTTTAATTACATTGATGCCACCGTGGATAACGCGTTTGGAGGAGGAGGGA
GTAGTAATCAGATGTTTCCGCTACAGGATATGTTTCATGTACATGCAGAAGCCTTACTAGAAGGGAATT
CCTTTCTCTGCCGCCGAAACGCAACGCAAAACGACCCTCGTTTTTGCCTTTATGGCAACACGAGACCGT
TTTATATGGTCAATGAGTGTGCCGATTTCGGCCATTAGATTTCTGTTTCAGTCTTCGTTTATTCTATAGA
CCGTCCGATTTTCAGATCATCCCTAATCGGACGGTGGTTCGTTGGATGTATCAGTAGTGTATTACTGTGT
TAGGTAGAAGAAAATCCACTTGTTCTTAAATTGGCATAAAAGTCAGAAGCTAATATTTATATGTGCCG
CAATCAATTTAATATTTTCTGTCT

SEQ ID NO: 95 - NP_171677.1 - *Arabidopsis thaliana*

MSELLQLPPGFRFHPTDEELVMHYLCRKCASQSIAPVPIIAEIDLYKYDPWELPGLALYGEKEWYFFSP
RDRKYPNGSRPNRSAGSGYWKATGADKPIGLPKPVGIKKALVIFYAGKAPKGEKTNWIMHEYRLADVDR
SVRKKKNSLRLDDWVLCRIYNKKGATERRGPPPPVVGDEIMEEKPKVTEMVMPPPPQQTSEFAYFDT
SDSVPKLHTTSSCSEQVVSPEFTSEVQSEPKWKDWSAVSNDNNNTLDFGFNYIDATVDNAFGGGGSS
NQMFPLQDMFMYMQKP

FIGURE 27 (continued)

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SEQ ID NO: 96 - AY573802.1 - *Lycopersicon esculentum*

CTAAATTCCTTCTTGTTTATCATTTTTCTCTCTTCCCAAAAAAAAAAATCCCAAAATTTAATCATAATAC
AATTTCGAATTTATCAACCTCGTACTACGTACATATTTTTGTTGGTACGTAAAATACTGAATTCAGGTC
AACTCAAACATCGTAAATTGTGATTTCTTTATGGAAAGTACGGATTCATCAACCGGGACACGTCATCA
GCCTCAACTCCCACCGGGGTTTCGATTCCACCCGACGGACGAAGAACTCATCGTCCACTACCTCAAAA
AACGAGTCGCCGGCGCTCCGATTCCGGTGGATATTATTGGTGAAATTGATCTTTATAAGTTTGATCCA
TGGGAACCTCCTGCTAAGGCAATATTCGGAGAGCAAGAATGGTTCTTTTTTAGTCCAAGAGATAGAAA
ATATCCTAACGGGGCGAGGCCAAATCGGGCTGCAACATCGGGTTATTGGAAGGCTACCGGAACCGACA
AGCCGGTTTTTTACTTCCGGTGGAACACAAAAGGTTGGGGTAAAAAAGGCGCTCGTTTTTTACGGCGGT
AAACCACCAAAAGGGGTAAAAACTAATTGGATCATGCATGAATACAGAGTTGTAGAAAATAAAACAAA
TAACAAGCCACTTGGTTGTGATAATATTGTTGCCAACAAAAAAGGATCTTTGAGGCTAGATGATTGGG
TTTTATGTCGAATTTACAAGAAGAATAACACACAAAGGTCCATAGATGATTTGCATGATATGTTGGGA
TCGATACCACAAAATGTACCAAATTCAATATTACAAGGAATAAAGCCTTCAAACATGTTGATCAATATT
GCTCGAAAAATGAATCGAATATGTACGATGGAATTATGAATAACACGAACGATATTATCAACAATAATA
ATAGATCCATTCCACAAATATCGTCAAAGAGAACGATGCATGGAGGTTTGTATTGGAATAACGACGAA
GCAACAACAACAACAACAATATTGATAGGAACCATTTCTCAAATACAAAAGGTTCTTTGTTGAGAA
CAACGAGGACGATGGACTTAACATGAATAATATTTTCGCGAATTACAAATCATGAACAAAGTAGCTCCA
TTGCCAATTTCTTGAGCCAGTTTCTCCTCAAATCCTTCGATTCAACAACAACAACAACAAGAAGAA
GTATTGGGATCTCTTAATGATGGGGTCGTCTTTCGACAACCTTATAATCAAGTTACTGGCATGAATTG
GTACTCTTAAAGATATAAAAAGGCAAAAAATAGTTAGCCCTGTAAAATCAATCGATCAATCAATCATA
GATATATTATATATGGATTTTCGTTATATTTTACTTTTAGTTAGAAATTAATATATAGAATATCTTCTAT
CTCACATTAACAAATAAGAACATTTATAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 97 - AAU43922.1 - *Lycopersicon esculentum*

MESTDSSTGTRHQPQLPPGFRFHPTDEELIVHYLKKRVAGAPIPVDIIGEIDLYKFDPWELPAKAI FG
EQEWWFFSPRDRKYPNGARPNRAATSGYWKATGTDKPVFTSGGTQKVGVKKALVFYGGKPPKGVKTNW
IMHEYRVVENKTNNKPLGCDNI VANKKGSRLDDWVLCRIYKKNNTQRSIDDLHDMLGSI PQNPVNSI
LQGIKPSNYGTILLENESNMYDGIMNNTNDI INNNNRSIPQISSKRTMHGGLYWNNDEATTTTTTTIDR
NHSPNTRKFLVENNEDDGLNMNNISRITNHEQSSSIANFLSQFPQNPSIQQQQQQQEEVLGSLNDGVV
FRQPYNQVTGMNWYS

SEQ ID NO: 98 - NM_118875.2 - *Arabidopsis thaliana*

AAAAGATCGACGAACATAAAAAACAAAACATATAATTTGGGTTTTTAGAGTTCGAAACTTGAAATCTT
TTTTTTTTTTGGTTGCTGAGGAATCGAAGTAGAAGAGTATAAATGGGTGTTAGAGAGAAAGATCCGTTA
GCCCAGTTGAGTTTGCCACCAGGTTTTAGATTTTATCCGACAGATGAAGAGCTTCTTGTTCAGTATCT
ATGTCGGAAAGTTGCAGGCTATCATTTCTCTCTCCAGGTCATCGGAGACATCGATCTCTACAAGTTTCG
ATCCTTGGGATTTGCCAAGTAAGGCTTTGTTTGGAGAGAAGGAATGGTATTTCTTTAGCCCAAGAGAT
CGGAAATATCCGAACGGGTCAAGACCCAATAGAGTAGCCGGGTCGGGTATTGGAAAGCAACGGGTAC
TGACAAAATTATCACGGCGGATGGTC

FIGURE 27 (continued)

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GTCGTGTCGGGATTAAAAAGCTCTGGTCTTTTACGCCGAAAAGCTCCCAAAGGCACTAAAACCAAC
TGGATTATGCACGAGTATCGCTTAATAGAACATTCTCGTAGCCATGGAAGCTCCAAGTTGGATGATTG
GGTGTGTGTCGAATTTACAAGAAAACATCTGGATCTCAGAGACAAGCTGTTACTCCTGTTCAAGCTT
GTCGTGAAGAGCATAGCACGAATGGGTCGTCATCGTCTTCTTCATCACAGCTTGACGACGTTCTTGAT
TCGTTCCCGGAGATAAAAGACCAGTCTTTTAATCTTCCTCGGATGAATTCGCTCAGGACGATTCTTAA
CGGGAACCTTGATTGGGCTAGCTTGGCAGGTCTTAATCCAATTCAGAGCTAGCTCCGACCAATGGAT
TACCGAGTTACGGTGGTTACGATGCGTTTCGAGCGGCGGAAGGTGAGGCGGAGAGTGGGCATGTGAAT
CGGCAGCAGAACTCGAGCGGGTGAAGTCTCAGAGTTTCGGGTACAGCTCGAGTGGGTTTGGTGTTCGGG
TCAAACATTCGAGTTTAGGCAATGAGAGAGATGTGAAGTTACTGATGGGTGAAAAAAGTAAAAA
ACTTGAGATAGTAGAGTGGAATGATGTAAATAATAGGGATTTATATGGGGCTTTTACCGATTTCGG
TGAGGCTTAGGATTCCACAAAGGAAAAAGGCTCGACTGGGGACTAGTTTGATCCAATTGACGGCCCA
CAAATGTGTAATGTTTCTCAACGGAGAGAAAAATAAATGGTTACCAATATTTTTACACCGGTTATGTG
TTGATACCATTTGCACAAAACGGTTTAAAGTCTGAATTGAATAACTTAACACCCAAAATTTGGTAAAA
AGCTTAATACAAAAGTTCAAAGGCATTTTCGCTTACTGCGACACTCGGAGTTGCAGAGTACTCTACG
TAACAGACTCTGTTTCATAGAGTTTGCGGCACCGGTGGTGGGACATTCTTGCGGACACAGTATGTACTT
TTGGAAGCATCGTTCCTAAGGGTTGCTGCAGTAACTCCTTGTGACTTGGCTCGCAAGAAACATAACA
TGGCCGCAAGAAAAACAGCATTAAACGAAGAGGTGTTTGAGATCTTCATGTCTAGTTTATTCTTCCTG
TTTTATTATGTGTCGACTGGTGTCAAAGAAACGTGTTGATTGTGAATTTGTAGACGCCACTCTGTAA
ATTTATTTAAATAAACTATTTTACTTCACGTT

SEQ ID NO: 99 - NP_567773.1 - Arabidopsis thaliana

MGVREKDEPLAQLSLPPGFRFYPTDEELLVQYLCKRVAGYHFSLQVIGDIDLYKFDPWDLPSKALFGEK
EWYFFSPDRKYPNGSRPNRVAGSGYWKATGTDKIITADGRRVGIKKALVYAGKAPKGTCTKNWIMHE
YRLIEHSRSHGSSKLLDDWVLCRIYKKTSGSQRQAVTPVQACREEHSTNGSSSSSSSQLDDVLDSPFEI
KDQSFNLPRMNSLRITLNGNFDWASLAGLNPIPELAPTNGLP SYGGYDAFRAAEGEAESGHVNRQNS
SGLTQSFYSSSGFGVSGQTFEFRQ

SEQ ID NO: 100 - DQ022843.1 - Triticum aestivum

ATTGATTCCGTTCCACCTGCTCACCGTCGCCATGCCAATGGGCAGCAGCAGCGCCGCCATGCCCGCC
CTCCCTCCCGGCTTCCGGTTCCACCCACCGACGAGGAGCTCATCGTCCACTACCTCGGCAGGCAGGC
CGCGTCCATGCCAGCCCCGTGCCCATCATCGCCGAGGTCAACATCTACAAGTGCAACCCATGGGACC
TCCCCGGCAAGGCCTTGTTCCGGGAGAATGAGTGGTACTTCTTCAGCCCCCGGGATCGCAAGTACCCC
AACGGCGCGCGCCCCAACCGCGCGCGCGGGTCCGGCTACTGGAAGGCCACCGGCACCGACAAGGCCAT
CCTGTCCACGCGCGGCAACGAGAGCATCGGCGTCAAGAAGGCGCTCGTCTTCTACCGGGGCAAGCCGC
CCAAGGGCGTCAAGACCGACTGGATCATGCACGAGTACCGCCTCACCGCGCGCGACAACCGGACCACC
AAGCGCAGAGGATCCTCCATGAGGCTGGATGACTGGGTGCTGTGTAGGATCCACAAGAAGTGCAACAA
CTTGCACAACTTCTCCTCCTCTGACCAGGAACAGGAGCACGAGCAGGAGAGCTCCACCACCGTGGAGG
ACTCGCACAACAACCACACCGTGTGTCGCGCCAAAGTCGGAGGCCTTCGACGGCGACGGCGACGACCAG
CTGCAGCTGCAGCAGTTCCGCCCCATGGCGATCGCCAAGTCGTGCTCCCTCACCGACCTGCTCAACAC
CGTCGACTACGCGCGCTCTCGCACCTCCTCCTCGACGGCGCGCGCGCGCGCGCTCG

FIGURE 27 (continued)

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TCGTCCGACGCCGGAGCAGACTACCAGCTGCCGCCGAAAACCCGCTCATCTACTCGCAGCCTCCATG
 GCAACAAACGCTACACTATAATAACAATAACAATGGCTACGTGAACATCGACACCATCGACGTGCCTC
 AGATACCCGAGGCCCGTGTAGATGACTACGGCATGAATGGCGATAGGTACAACGGCATGAAGAGGAAG
 AGGTCCAGCGGCAGTTTGTACTGCAGCCAGCTGCAGCTCCCGGCGGATCAGTACAGCGGCATGCTGAT
 CCATCCGTTCCCTCAGCCAGCAGCTGCACATGTGAAGAACCAGAGAGCTTGGATCGAAGAGATCATCAT
 TGTTCCATTTGAACTTGCTGTAGATCGAGGGGATCCCCCGCTGTGGCAGATAGGCAGGGATCTAGCTT
 GCTTGCTGTGTCGTGACCGACCGACCGATAAGAACGGACAAATTTCAGAATTCTTGGTGTAGCACAAA
 AGCTGTAAATTACGGGGGTTTATTGTGAAATAAATAAATCCAGTATTATTAAG

SEQ ID NO: 101 - AAY44098.1 - *Triticum aestivum*

MPMGSSSAAMPALPPGFRFHPTDEELIVHYLGRQAASMPSPVPIIAEVNIYKCNPWDLP GKALFGENE
 WYFFSPRDRKYPNGARPNRAAGSGYWKATGTDKAILSTPANESIGVKKALVFYRGKPPKGVKTDWIMH
 EYRLTAADNRRTTKRRGSSMRLDDWVLCRIHKKCNNLHNFESSDQEQEHEQESSTTVEDSHNNHTVSSP
 KSEAFDGDGDDQLQLQQFRPMAIAKSCSLTDLNLTVDYAAALSHLLLDGAGAGASSSDAGADYQLPPEN
 PLIYSQPPWQQTLHYNNNNNGYVNIDTIDVPQIPEARVDDYGMNGDRYNGMKRKRSSGSLYCSQLQLP
 ADQYSGMLIH PFLSQQLHM

SEQ ID NO: 102 - AY625682.1 - *Triticum aestivum*

GCAGCATTTTTATGCAGTAGCCATCTTCTCCTCCTCCTCCCCCGCCTTCCAGCTAGCCACCTAGCTC
 ACTATCACATCATCCAGCAGCCACACCAACTCATATTGATTCCGTTCCCACCTGCTCGCCATCGCCA
 GCCATGCCAATGGGCAGCAGCGCCGCCATGCCGCCCTCCCTCCCGGCTTCCGGTTCCACCCACCGA
 CGAGGAGCTCATCGTCCACTACCTCCGCAGGCAGGCGCGTCCATGCCAGCCCCGTGCCCATCATCG
 CCGAGGTCAACATCTACAAGTGCAACCCATGGGACCTCCCCGGCAAAGCTTTGTTCCGGGGAGAATGAG
 TGGTACTTCTTCAGCCCCCGGGATCGCAAGTACCCCAACGGCGCGCGCCGAACCGCGCCGCGGGTC
 CGGCTACTGGAAGGCCACCGGCACCGACAAGGCCATCCTGTCCACGCCGGCCAACGAGAGCATCGGGG
 TCAAGAAGGCGCTCGTGTCTACAGGGGCAAGCCGCCAAGGGCGTCAAGACCGACTGGATCATGCAC
 GAGTACCGCCTCACCGCAGCCGACAACCGGACCACCAAGCGCAGAGGATCCTCCATGAGGCTGGATGA
 CTGGGTGCTGTGTAGGATCCACAAGAAGTGCGGCAACTTGCCCAACTTCTCCTCCTCTGACCAGGAAC
 AGGAGCATGAGCAGGAGAGCTCCACCGTGAGGAGCTCGCAGAACAACCACACCGTGTCGTCGCCAAG
 TCCGAGGCCTTCGACGGCGACGGCGACGACCACCTCCAGTTGCAGCAGTTCCGCCCCATGGCGATCGC
 CAAGTCGTGCTCCCTCACCGACCTGCTCAACACCGTCGACTACGCCGCGCTCTCGCACCTCCTCCTCG
 ACGGCGCCGGCGCCTCGTCGTCGGACGCCGGAGCAGACTACCAGCTGCCTCCCGAAAACCCACTCATC
 TACTCGCAGCCTCCATGGCAACAAACGCTACACTATAATAACAACAACGGCTACGTGAACAACGAGAC
 CATCGACGTGCCTCAGCTACCCGAGGCGCGCGTAGATGACTACGGCATGAATGGCGATAAGTATAACG
 GCATGAAGAGGAAGAGATCCAGCGGCAGCTTGTACTGCAGCCAGCTGCAGCTCCCAGCGGATCAGTAC
 AGCGGCATGCTGATCCATCCGTTCCCTCAGCCAGCAGCTGCACATGTGAAGAACCAGAGAGCTTGGGTC
 GAAGAGATCATCATTGTTCCATTTGAACTTGCTGTAGATCGAGAGGATCCCCCGCTGTGGCAGATAGG
 CAGGGATCTAGCTAGCTTGCTGTGTGTCGTGAACGACCGACCGATAAGAACGGACAAATTTCAGAATTCT
 TGGTGTAGCACAAAGCTGTAAATTACGGGGGTTTATTGTGAAATAAATTAATCCAGTATTATC

FIGURE 27 (continued)

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SEQ ID NO: 103 - AAU08785.1 - *Triticum aestivum*

MPMGSSAAMPALPPGFRFHPTDEELIVHYLRRQAASMPSPVPIIAEVNIYKCNPWDLPGKALFGENEW
YFFSPDRKYPNGARPNRAAGSGYWKATGTDKAILSTPANESIGVKKALVFYRGKPPKGVKTDWIMHE
YRLTAADNRTTKRRGSSMRLLDDWVLCRIHKKCGNLPNFSSSDQEQEHEQESSTVEDSQNNHTVSSPKS
EAFDGDGDDHLQLQQFRPMAIAKSCSLTDLLNTVDYAALSHLLLDGAGASSSDAGADYQLPPENPLIY
SQPPWQOTLHYNNNNGYVNNETIDVPQLPEARVDDYGMNGDKYNGMKRKRSSGSLYCSQLQLPADQYS
GMLIHPFLSQQLHM

SEQ ID NO: 104 - AY742218.1 - *Saccharum officinarum*

ATGAGCGGCGGCGGTCTCAGGATCTGCAGCTGCCGCCGGGGTTCCGGTTCACCCGACGGACGAGGAGCT
GGTGATGCACTACCTCTGCCGCCGCTGCGCCAGCCTGCCCATCGCCGTCCTCATCGCCGAGATCG
ACCTCTACAAGTTCGATCCATGGCAGCTCCCCAGGATGGCGCTGTACGGCGAGAAGGAGTGGTACTTC
TTCTCCCCGCGGGACCGCAAGTACCCGAACGGGTCCAGGCCCAACCGCGCCGCGGGTCCGGCTACTG
GAAGGCCACCGGCGCCGACAAGCCCGTGGGCACGCCCAAGCCGCTCGCCATCAAGAAGGCGCTCGTCT
TCTACGCCGGCAAGGCGCCCAAGGGCGAGAAGACCAACTGGATCATGCACGAGTACCGCCTCGCCGAC
GTCGACCGCTCCGCCCGCAAGAAGAAGCAGCCTCAGGTTGGATGACTGGGTCCTGTGCCGCATCTACAA
CAAGAAGGGAGGGCTGGAGAAGCCGGCGGCGGCGTCTCCGGCGACCACAAGCCGATGGTGTTCGCCG
CGGGCGCGGTGAGCTCCCCGCCGGAGCAGAAGCCGTTCTGTGGCGACGCCGGGCGGGCTGCCCCCGCC
GCGTTCACGGCGGACCTGGCGGCGTACTACGACCGGCGTCCGGACTCGATGCCGCGGCTGCACGCGGA
CTCCAGCTGCTCGGAGCAGGTGCTGTGCGCCGGAGCAGCTGGCGTGCAGCCGGGAGGTGCAGAGCCAGC
CCAAGATCAGCGAGTGGGAGCGCACCTTCGCCTCCGACCCCGTCAACCCCGCTGGCTCCATGCTCGTC
GACCCCGTCTGCGGTGGCCACGCCGGCGACCCGCTGCTGCAGGACATCCTCATGTACTGGGGCAAGCC
GTTCTAG

SEQ ID NO: 105 - AAW62955.1 - *Saccharum officinarum*

MSGGGQDLQLPPGFRFHPTDEELVMHYLCRRCASLPPIAIVPIIAEIDLKFDPWQLPRMALYGEKEWYF
FSPDRKYPNGSRPNRAAGSGYWKATGADKPVGTPKPLAIKKALVFYAGKAPKGEKTNWIMHEYRLAD
VDRSARKKNSLRLDDWVLCRIYNKKGLEKPAAASSGDHKPMVFAAGAVSSPPEQKPFVATPGGLPPA
AFTADLAAYYDRPSDSMPRLHADSSCSEQVLSPEQLACDREVQSQPKISEWERTFASDPVNPAGSMLV
DPVVGGHAGDPLLQDILMYWGKPF

SEQ ID NO: 106 - AK063406.1 - *Oryza sativa*

AACTAGCTTAGCTAGACAGCGTGTGTTGGTGGTGGTGGTGGTGTGTGTGTGTGTGAGGAGGGTGATCG
ATCGATCGAGCGATGGAGAGCCCGGACTCGTCGTCCGGCTCGGCGCCACCGCGAGTACTACGGCGGCA
ACAGCAGCAGCCGGGCTCGGCGCCGGAGCTGCCGCCGGGGTTCCGGTTCACCCGACGGACGAGGAGC
TGGTGGTGCCTACCTCAAGAAGAAGGCCGCTCCGTTCCGCTCCCCGTACCATCATCGCCGAGGTC
GATCTCTACAAGTTCGATCCCTGGGATCTCCCCGAGAAGGCGAACTTCGGGGAGCAGGAGTGGTATTT
CTTCAGCCCCGAGGGACCACAAGTACCCGAACGGGGCGCGGCCGAACCGGGCGGCGACGTCGGGGTACT
GGAAGGCCACCGGCACCGACAAGCCCATCATGTGCTCGGGGAGCACCCGCGAGAAGGTGGCGTGAAG
AAGCGCTCGTGTCTACCG

FIGURE 27 (continued)

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GGGCAAGCCACCCAAGGGCGTCAAGACTAACTGGATCATGCACGAGTACCGTCTCACGGACACGTCTA
GCTCCGCGCCGCCGCTCGCTACGACCAGGCGGCCGCCGCCCATCACCGGCGGTAGCAAGGGCGCC
GTCTCTCTCAGGCTGGATGACTGGGTGCTGTGCCGCATATACAAGAAGACGAACAAGGCCGGTGCGGG
GCAGAGGAGCATGGAGTGCGAGGACTCCGTGGAGGACGCGGTGGCCGCGTACGCGCCGCTCGTCGCAGC
AGCATGCCACGGCTGCTGCTGGCATGGCCGGTTCGGACGGCGCCGGAGGAGTTGCTGCAGCGCACGGC
GGCGACTACAGTTCACTGCTCCATCACGACAGCCACGAGGACACCTTCCTCGTAAACGGCCTGCTCAC
CGCGGAGGACGCCGCCGGCCTCTCGACCGGCGCCAGCTCTCTCAGCCAGCTCGCCGCGGCGGCGAGGG
CGGCGGCGACACCGTGCGACGCCACCAAGCAGCTTCTTGCTCCGTCTCCAACCCATTCAACTGGTTC
GAGGCATTCTTCCACGGGCCAAGGAGTTTCCTAGTGGGCTAAGCAGGAGTAGCAGAGACATCGGCGA
CATGTGCTGTATCGACGGTGGACAGGAGCCTGTCTGAGGCTGGCGCCGTGGCCATTGACACCGGCG
ACGCCGCCAATGGCGCAAACACTATGCCTGCATTTATCAATCCTCTCGGCGTGCCAGGGTGCAACCTAC
CAACAACACCAAGCCATCATGGGTGCCTCGTTGCCATCGGAGTCAGCAGCAGCAGCAGCCGCCTGCAA
TTTCCAGCATCCGTTCCAACCTCTCCAGGGTGAATTGGGATTCTGAATAAAAGGTGCCGGCATTATGC
ATACACATATATGCACATGCATACATGCATGGCTTTTCAAGTAGTAGCACAACATTACTAGTAATTAA
TCACACTAATGTGTGTGGCAGTCGCATTCAGTGAGCACTGATCGAGTAGTTGCATGAACACAACACTA
ATGCATGCACTACATATATATGGCCGCATTGCTCCTAGGGCACGTACCTGTACGAACTAGGTAAGTGA
CCTAACCAGCTAGATCATGTTTCAAGATAAGGAGAAGAAGCCGCATGCAAACACGTAGATCATATGGCT
TTGCCTTCACATGCGTTTGCATCATATATATCGCATTCAGAAAGTAGTGCTGCAGCTAACACATAGAT
ATGGTGTTAGCTTCATGCGTTTGTACCATATATAGCGGATGCAGAAAGTAGCTAGTTGCACTGTTTCAT
CATTATCCCATGAGATATGAACTTTATAT

SEQ ID NO: 107 - AK063406.1 - *Oryza sativa*

MESPDSSSSGSAPPRVLRRQQQPGSAPELPPGFRFHPTDEELVVHYLKKKAASVPLPVTIIAEVDLYK
FDPWDLPEKANFGEQEWFYFFSPRDHKYPNGARPNRAATSGYWKATGTDKPIMSSGSTREKVGVKALV
FYRGKPPKGVKTNWIMHEYRLTDTSSSAAVATTRPPPPITGGSKGAVSLRLDDWVLCRIYKKTNKA
GAGQRSMECEDSVEDAVAAYAPSSQQHATAAAGMAGSDGAGGVAAAHGGDYSSLLHDSHEDTFLVNG
LLTAEDAAGLSTGASSLSQLAAAARAAATPCDATKQLLAPSPTPFNWFEAFLPRAKEFPSGLSRSSRD
IGDMSLSSTVDRSLSEAGAVAITDGAANGANTMPAFINPLGVQGATYQQHQAIMGASLPSESAAAAA
ACNFQHPFQLSRVNWDS

SEQ ID NO: 108 - AC145753.1 – *Medicago truncatula*

ATGGGAACCCACAGACCAATTTGCCACCAGGTTTTAGGTTCCACCCTACTGATGCAGAACTCATTCT
TCACTACCTTAGGAAAAAAATTGCCTCCATTCCCTTGCTGTTCATCATTGCTGAAGTTGATATTT
ATAAGTTGGATCCTTGGGATTTACCAGCTAAGGCTTCATTTGGTGAGAAAGAATGGTACTTTTTTAGT
CCTAGAGATAGAAAGTACCCAAACGGTGCAAGGCCAAACAGGGCAGCTGCTTCAGGGTATTGGAAAGC
CACTGGCACTGATAAGACCATAGTGGCATCATTGCCATGTGGAGGAGGAAGATCACAAGAGAACATTA
TTGGTGTCAAAAAGGCTCTTGTTTTTTACAAAGGAAAACCCCAAGGGTATTAAGACTAATTGGATC
ATGCATGAATATCGTCTTGTTGACAACAATAAACCTATTAAGCTCAAAGATTCTTCCATGAGGTTGGA
TGATTGGGTGCTATGCCGAATTTACAAGAAATCAAAATGTGCACTAACTTCAACAGAATCATCAGAAA
CTATGGTAGGTGAAGTGGAACATGCAGAAGAGACACAATTCAGAAACCCCTATTTCCAATCACCAAA
AACACAAC

FIGURE 27 (continued)

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CTCACCTCTTCAAAACACACTCATGTCTCAAAAATCAGTGTCCTTTTCAAACCTATTAGATGCTATGG
ACTACTCCATGTTAAGCAGCTTCTTATCTGAAAATTCCAACAACCCATCAGGAATTGGAACAAGTTCA
GGTTTCAACACTGAAAATTTTAACCAACAACAATCTTCCCATATCAACACTTGCAACAATTACATGTC
TCAGAAGAATCCTCAATCCAACACTTTAAAGCACCAGCTTTCAAACGTAGATGAAGACATGTTATACC
CATCAAAGAAGTACTTGAGTTCCTCTTGCAATTTTCCTAACATCAATTCTCAGTATGAAAACCTACCTT
ATGAAGCAATCTTTGATGAATCAACAATTGCTTTTAGGTCCTCATCATCAATATCAAGGCTAATCCAA
AATACCACAAAAATTAAGTGGTACCAAAAAAAAAAAGATTATGAAATAGAAAAGTTAAGTAAGATTTTC
TAGAAGTTGGGCCCACCAAATTACACCAATGTCATCATTAAGTAAGGATTGCTAATTTAATAGTAGTG
CACAAAATATAGTGTGTTCTATTTTGTCCATTTTAATTTTTTTTCTAGGAATTG

SEQ ID NO: 109 - AC145753.1 – *Medicago truncatula*

MGTPQTNLPFGFRFHPTDAELILHYLRKKIASIPLVSIIEVVDIYKLDPWDLPAKASFGEKEWYFFS
PRDRKYPNGARPNRAAASGYWKATGTDKTIVASLPCGGGRSQENIIGVKKALVFYKGKPPKGIKTNWI
MHEYRLVDNNKPIKLDSSMRLDDWVLCRIYKKSCKALTSTESSETMVGEVEHAEETQFQETLFPITK
NTTSPLQNTLMSQKSVSFSNLLDAMDYSMLSSFLSENSNNPSGIGTSSGFNTENFNQQQSSHINTCNN
YMSQKNPQSNTLKHQLSNVDEDMLYPSKKYLSSSCNFPNINSQYENYLMKQSLMNQQLLLGPHHQYQG

FIGURE 27 (continued)

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SEQ ID NO: 110 – *Oryza sativa* – rcc3 promoter

TCGACGCTACTCAAGTGGTGGGAGGCCACCGCATGTTCCAACGAAGCGCCAAAGAAAGCCTTGCAGAC
TCTAATGCTATTAGTCGCCTAGGATATTTGGAATGAAAGGAACCGCAGAGTTTTTCAGCACCAAGAGC
TTCCGGTGGCTAGTCTGATAGCCAAAATTAAGGAGGATGCCAAAACATGGGTCTTGGCGGGCGCGAAA
CACCTTGATAGGTGGCTTACCTTTTAACATGTTTCGGGCCAAAGGCCTTGAGACGGTAAAGTTTTCTAT
TTGCGCTTGGCGATGTACAATTTTATTCTCTATTCAATGAAATTGGTGGCTCACTGGTTCATTAAAA
AAAAAAGAATCTAGCCTGTTTCGGGAAGAAGAGGATTTTGTTCGTGAGAGAGAGAGAGAGAGAGAGA
GAGAGAGAGAGAGAAGGAGGAGGAGGATTTTCAGGCTTCGCATTGCCCAACCTCTGCTTCTGTTGGCC
CAAGAAGAAATCCCAGGCGCCCATGGGCTGGCAGTTTACCACGGACCTACCTAGCCTACCTTAGCTATC
TAAGCGGGCCGACCTAGTAGCCACGTGCCTAGTGTAGATTAAAGTTGCCGGGCCAGCAGGAAGCCACG
CTGCAATGGCATCTTCCCCTGTCCTTCGCGTACGTGAAAACAAACCCAGGTAAGCTTAGAATCTTCTT
GCCCCGTTGGACTGGGACACCCACCAATCCCACCATGCCCCGATATTCTCCGGTCTCGGTTTCATGTGA
TGTCCTCTCTTGTGTGATCACGGAGCAAGCATTTCTTAAACGGCAAAGAAAATCACCAACTTGCTCAC
GCAGTCACGCTGCACCGCGCGAAGCGACGCCCCGATAGGCCAAGATCGCGAGATAAAATAACAACCAAT
GATCATAAGGAAACAAGCCCCGCGATGTGTCGTGTGCAGCAATCTTGGTCATTTGCGGGATCGAGTGCT
TCACAGCTAACCAAATATTCGGCCGATGATTTAACACATTATCAGCGTAGATGTACGTACGATTTGTT
AATTAATCTACGAGCCTTGCTAGGGCAGGTGTTCTGCCAGCCAATCCAGATCGCCCTCGTATGCACGC
TCACATGATGGCAGGGCAGGGTTCACATGAGCTCTAACGGTCGATTAATTAATCCCGGGGCTCGACTA
TAAATACCTCCCTAATCCCATGATCAAAACCATCTCAAGCAGCCTAATCATCTCCAGCTGATCAAGAG
CTCTTAATTAGCTAGCTAGTAGTATTAGCTGCGCTTGTGATC

SEQ ID NO: 111 - Motif I

A/P/S/N V/L/I/A P/S/D/V/Q V/I I A/T/G

SEQ ID NO: 112 - Motif II

N G/S S/Q/A/V RP N/S

FIGURE 27 (continued)

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SEQ ID NO: 113 - Motif VI

C/Y R/K L/I Y/H/F N/K K K/N/C/S/T

SEQ ID NO: 114 - Motif VII

N E/Q/T WEK M/V Q/R/K

SEQ ID NO: 115 - Motif VIII

WGE T/A RTPES E/D

SEQ ID NO: 116 - Motif IX

V/L PK K/E E S/R/A/V M/V/A/Q/R D/E D/E/L A/G/D

SEQ ID NO: 117 - Motif X

S L/Y DD L/I Q G/S L/M/P G/Y S/N

SEQ ID NO: 118 - Motif XI

DS M/V/I P R/K L/I/A H T/A/S D/E SS C/G SE

SEQ ID NO: 119 – forward primer

CCAACACTAGTAGGATAAAG

SEQ ID NO: 120 – reverse primer

ACCACTGGGCTAATTAATTA

SEQ ID NO: 121 – forward primer

GGTCGACCCACGCGTCCGCT

SEQ ID NO: 122 – reverse primer

AACTGAAGTACCCGTTCTTA

SEQ ID NO: 123 – forward primer

ATCCTCCACAAGAGAACTA

FIGURE 27 (continued)

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SEQ ID NO: 124 – reverse primer

AGTACAGTGTAGCACAATAA

SEQ ID NO: 125 – primer

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGGGGATGGGGATGAG

SEQ ID NO: 126 – primer

GGGGACCACTTTGTACAAGAAAGCTGGGTTCGATCACCACCTGTTCCG

SEQ ID NO: 127 – primer

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGGAGTGCGGTGGTG

SEQ ID NO: 128 – primer

GGGGACCACTTTGTACAAGAAAGCTGGGTGTCACGTTCCGTTAATTAGAA

SEQ ID NO: 129 – primer

GGGGACAAGTTTGTACAAAAAAGCAGGCTTAAACAATGCCGAGCAGCG

SEQ ID NO: 130 – primer

GGGGACCACTTTGTACAAGAAAGCTGGGTCTACTGCATCTGCAGATGA

FIGURE 27 (continued)

95/173**SEQ ID NO: 131, OsAP2-2 encoding sequence (AP2-EREBP)**

CATGTGCGGCGGGCGCCATCCTCTCCGACCTCATCCCGCCGCGCGGGTACCGCCGGCGACCTCT
 GGCTGGAGAAGACCAAGAAGCAGCAGCAGCAGAAGAAGAACAAGGGCGCGAGGAGGCTGCCACTG
 CGCCAAGAGGAGGAGGATGATTTTCGAGGCCGACTTCGAGGAGTTCGAGGTGGATTCCGGCGAGTGGGA
 GGTGGAGTCCGACGCCGACGAGGCCAAGCCGCTCGCCGCGCCCCGGAGCGGCTTCGCTAAAGGTGGAT
 TGAAAAACACTACTGTTGCTGGTGCTGATGGGCCTGCAGCAAGGTCTGCTAAAAGGAAGAGAAAGAAC
 CAATTCAGGGGTATCCGCCAGCGGCCATGGGGCAAATGGGCTGCGGAAATCAGAGATCCTCGCAAAGG
 TGTCGCGCTCTGGCTTGGCACCTTCAACTCTCCTGAGGAAGCTGCCAGAGCTTATGATGCTGAAGCAC
 GAAGGATTCGAGGCAAGAAGGCCAAGGTCAATTTCCAGATGGGGCTCCAGTGGCTTCTCAGAGGAGT
 CATGCTGAGCCCTCCTCCATGAACATGCCTGCTTTCAGCATCGAAGAGAAGCCGGCCGTCATGTCAGC
 AGGCAACAAAACCATGTACAACACAAATGCTTATGCCTACCCTGCTGTTGAGTACACCTTACAGGAGC
 CATTTGTGCAGATTGAGAATGTCTCATTTGTTCTGCAATGAACGCGATTGAGGATACTTTCTGTGAAC
 CTGTCCTCTGATCAAGGGAGCAACTCCTTGGTTGCTCGGACTTTAGCCAGGAGAATGATATCAAGAC
 CCCTGACATAACTTCCATGCTTGACCGACCATGACAGGTGTTGATGACTCCGCATTCCTCCAGAACA
 ATGCCAGTGATGCAATGGTACCTCCTGTGATGGGGAATGCTAGCATTGATCTTGCTGACCTGGAGCCG
 TACATGAAATTTCTGATCGATGGTGGTTCGGATGAGTCGATTGACACCTTCTGAGCTCTGATGGATC
 TCAGGATGTGGCCAGTAGCATGGACCTTTGGAGCTTCGATGACATGCCCCTGTGCGCCGAGTTCTACT
 GAGGGGTTTGGG

SEQ ID NO: 132, OsAP2-2, deduced protein sequence, (AP2-EREBP)

MCGGAILSDLIPPPRRVTAGDLWLEKTKKQQQKKKNKGARRLPLRQEEEDDFEADFEEFEVDSGEWE
 VESDADEAKPLAAPRSGFAKGLKNTTVAGADGPAARSARKRKNQFRGIRQRPWGKWAAEIRDPRKG
 VRVWLGTENSPEEAARAYDAEARRIRGKKAKVNFPDGPVASSQRSHAEPSSMNMPAFSIEEKPAVMSA
 GNKTMYNNTNAYAYPAVEYTLQEPFVQIQNVSFVPAMNAIEDTFVNLSSDQGSNSFGCSDFSQENDIKT
 PDITSMLAPTMTGVDDSAFLQNNASDAMVPPVMGNASIDLADLEPYMKFLIDGGSDESIDTLLSSDGS
 QDVASSMDLWSFDDMPVSAEFY

SEQ ID NO: 133, Motif XII

(R/I/V/L/K) (R/K/Q/D/E/A) (I/L) (R/Y/H) G(A/S/R/K/T/D/G/H/L/N) (K/T/R/N/G)
)A(K/R/E) (V/L/P/T) NF(P/V)

SEQ ID NO: 134, Motif XIII

MCGG(A/S) (I/V/L) (I/L) (S/H/A/Y/G/P/E) (D/G/H/Y/E/Q/N)

SEQ ID NO: 135, Motif XIV

(K/N/R/S/H/M/Q/P/A/E) (R/K/H/A/G/E/V/P/M) (E/K/A/R/S/Q/T/V/G/H/P) (R/K/
 Q/S/G) (K/G/P/S/R/T/A/N) (T/N/R/S/A/Y/H/G) (L/Q/H/V/R/K/A/P/G) (Y/F) (R/W
 /K/L/M)G(I/V) (R/Q/H) (R/Q/W/K)R(P/K/T)

SEQ ID NO: 136, Motif XV

SD(Q/T/E/V) (G/S) SNSF(G/D/E/S/N) (C/S)S(D/E) (F/Y/L) (G/S) (W/Q/L) (E/G/S)
 (N/E/D)

FIGURE 28

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SEQ ID NO: 137, Motif XVI

(L/I/F/M)W(S/T/N/M) (F/Y/L/I) (D/E/Q/G) (N/D/H/E) (I/Y/F/S/M/L/V/D/H/N/E/G)

SEQ ID NO: 138, Motif XVII

(D/E/S) (F/A/W/D) (E/A) (A/D/L) (D/A/G/E) (F/G/L) (N/E/R/G/Q/W) (E/G/V/D/R) F(E/K/V/Y/G/D/L/I) (V/R/D/S/N/A/E) (D/G/T/E/R/A/Y/L/F)

SEQ ID NO: 139, NM_001067153.1| Oryza sativa (japonica cultivar-group) Os07g0674800 (Os07g0674800) mRNA, complete cds

GACTCGTCAGCTTAGAGCACCGCAAGCGCGCAGCAGCAGCAAAGATGTGTGGCGGCGCGATCATTTCC
GACTTCATCCCGCAGCGGGAAGCCACCGCGCGGCCACCGGCAGCAAGCGTGCCCTCTGCGCCTCCGA
CTTCTGGCCGTCGGCGTCGCAGGAAGCCGCCGACTTCGACCACCTCACCGCCCCCTGCACCTTCACCC
CCGACCAAGCGGCAGAGGAGCCGACCAAGAAGCGGGAGCGGAAGACGCTGTACCGTGGCATCAGGCGG
CGGCCGTGGGGGAAGTGGGCGGCGGAGATCCGCGACCCGGCGAAGGGCGCGCGCGTCTGGCTCGGCAC
CTTCGCCACCGCCGAGGCGGCGGCCCGCGCCTACGACCGCGCCGCCCGCCGCATCCGCGGGGCCAAGG
CCAAGGTCAACTTCCCCAACGAGGACCCGCCACTCGACGACCCGGCCGCCGACGGCCACAGCCACGGC
GGCGCCGCCATCCCGTGCAGGGAGTTTCATGGACTACGACGCCGTCATGGCGGGCTTCTTCCACCAGCC
CTACGTCGTCGCCGACGGCGTGCCGGCCGTGCCGGCGGAGGAGGCGCCACGGTGGCGTACGTGCACC
ACCACCTGCCGCCGCGAGCCGCGAGGACGCGGGGCTGGAGCTCTGGAGCTTTGATAACATCCACACG
GCCGTGCCGATGTGAGATCGATCTGATGATCATTTCAGATCGATGCTAGCTCATGTGTTTTTAATTATA
TCTTCACAGCAGAAACAAAAAAGTTCAATTTCAGTTTATTTTGTGTTATACGTTTTAAATGTTTC
ATTAGGTTTTTCATGTTATAGGAGTGATTATCGGATTGAACTCTCAAGTGACCGACTTCTGAGTTCTT

SEQ ID NO: 140, LOC_Os07g47790.1|11977.m08994|protein|AP2-EREBP

MCGGAIISDFIPQREAHRAATGSKRALCASDFWPSASQEAADFHLTAPCTFTPDQAAEEPTKKRERK
TLYRGIRRRPVGKWAAEIRDPAK GARVWLGT FATAEAAARAYDRAARRIRGAKAKVNFNPEDPPLDDP
AADGSHHGGAAPCREFM DYDAVMAGFFHQPYVVADGVPAPVPAEEAPT VAYVHHHLPPQPQQDAGLEL
WSFDNIHTAVPM

SEQ ID NO: 141, AY781352.1| Triticum aestivum ethylene-responsive element binding protein 1 (EREB1) mRNA, complete cds

CTCTCCACCCGCGGCCCCACGTGCTCCCAGCCATGTGCGGCGGCGCCATCCTCTCCGACATCATCCCG
CCGCCGCGCCGGGCCACCGGCGGCAACGTCTGGCGGGCGGACAAGAAGAGGAGGGCCAGGCCCGACGC
CGCCGCGGGGAGGCCCCGCCGCGTGCCCGAGGAGGAGTTCCAGGAGGAGGAGGGCGACGCGGAGTTTCG
AGGCCGACTTCGAGGGGTTTCGTGGAGGCGGAGGAGGAGTCCGACGCGGAGGCCAAGCCCTTCCCCGTC
CGCAGGACCGGCTTCTCCGGAGATGGACTGAAGGCAACTGCTGCTGGTGATGATGACTGTGCCTCAGG
GTCTGCTAAAAGGAAGAGAAAGAGCCAGTTCAGGGGCATCCGCCGCCGCCCTTGGGGTAAATGGGCTG
CTGAAATAAGAGATCCTCGCAAGGGTGTCGCTGTCTGGCTTGGCACTTACA ACTCTGCTGAGGAAGCT
GCCAGAGCCTATGATGTTGAAGCCCGCAGAATTCGTGGCAAGAAGGCAAAGG

FIGURE 28 (continued)

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TCAATTTCCCAGAAGAAGCTCCCATGGATCCTCAGCAACGCTGCGCTACCTCTGTGAAGGTGCCCCGAGT
TCAACACCGAACAGAAGCCAGTACTCAACACCATGGGCAACACAGATGTGTATTCCTGCCCTGCTGTTG
ACTACACCTTAAATCAGCAATTTGTGTCAGCCTCAGAACATGTCGTTTGTGCCTACAGTGAATGCAGTTG
AGGCTCCTTTTCATGAATTTTCTCTGACCAGGGGAGCAACTCCTTTAGTTGCTCAGACTTCAGCTGGG
AGAATGATATCAAGACCCCTGACATAACTTCTGTGCTTGCATCCATTCCCACCTCAACTGAGGTCAATG
AATCTGCATTTCTCCAGAACAATGGCATTAATTCAACGGTACCTCCTGTGATGGGTGATGCTAATGTTG
ATCTTGCCGACTTGGAGCCATACATGAAGTTCCTGATGGACGATGGTTCAGATGAGTCAATTGACAGCA
TTCTAAGCTGTGATGTACCGCAGGACGTTGTGCGCAACATGGGCCTTTGGACCTTTGATGACATGCCCT
TGTCTGCTGGTTTCTACTGAGGGAATCGAGGTCGCTGGGTGCCTGTATATATAGACAAAGGAATAAGTA
TTCTGGACATCAACAAGTGCTTGTGTCTGGTGCCTCTAGAATCGAGCAGTAGCGACGTCAGTCTATGGT
TATGTCTAGCTTAAATGGTCAGGAGACCTAAGTCTTTTGAATAGACCTCTGTCTTGTGCCCCAGACT
ATATTATATCTATATATGAAACCAGTATGTGATGGGAACTGCTTATTTGTATTCTGTTTCTACCTTA
TTGTAATTGCTACAAGTGGCTGTAAACCTTTTAACTTTGAAAAAAA

SEQ ID NO: 142, AAX13280.1| ethylene-responsive element binding protein 1 [Triticum aestivum]

MCGGAILSDIIPPPRRATGGNVWRADKRRARPDAAGRPRRVPEEEFQEEEGDAEFADFEFGFVEAE
EESDGEAKPFPVRRRTGFSGDGLKATAAGDDDCASGSARKRKRSQFRGIRRRPWGKWAEEIRDPRKGVR
VWLGTYNSEEAARAYDVEARRIRGKKAKVNFPEEAPMDPQQRCATSVKVPEFNTEQKPVLTMTGNTD
VYSCPAVDYTLNQFVQPNMSFVPTVNAVEAPFMNFSSDQGSNSFSCSDFSWENDIKTPDITSVLAS
IPTSTEVNESAFLLQNNGINSTVPPVMGDANVDLADLEPYMKFLMDDGSDESIDSILSCDVPQDVVGNM
GLWTFDDMPLSAGFY

SEQ ID NO: 143, NM_001049403.1| Oryza sativa (japonica cultivar-group) Os01g0313300 (Os01g0313300) mRNA, complete cds

ATCCAAATCCAACGTCCGCCTAAAGAAAAACACGCACACACTTCTTCTGCTTCCCTCCCCTTGTTTCC
GCTCCACTTCCCTTCCAAGCAAGAAAACCGAGGCTTCAGCTTAGCTAGGACCGACCGATCCGATGTGC
GGCGGTGCAATCATCTACGACTACATCCCGGCGCGCCGCGGTTGTGCGCCTCCGACTTCTGGCCCCGA
CGCCGACGACTCCGACCCCCACACCCCGCTCCCGAGAAACCGCCGCGCGGAAGAGGGAGCGGAAGA
ACAGTACCGCGGGATCAGGCAGCGGCCGTGGGGGAAGTGGGCGGCGGAGATCCGCGACCCGGTGAAG
GGGGTGC GCGTCTGGCTCGGCACCTACCCGACCGCCGAGGCCGCGCGCGGGCCTACGACCGCGCCGC
GCGCCGCATCAGGGGCGCCAAGGCGAAGGTCAACTTCCCCAACGACTTCGGCGCCGCCCCCGCGCCGG
CCGCGGCGGCGGCGAAGGCCGTCCCTCGCGTCCGCGCCACGCCGGCCGTGCTCCCGCCGCCAAGATG
GAGGCGGTGTCCGAGGGCGCCGCGCCTGCTCCTCCGACGAGGTCAAGGAGCTGTCCGAGGAGCTGCT
CGCGTACGAGAACTACATGAGCTTCTCGGCATCCCCTACATGGAGGGCGGCGCCGCTCCGCGCCG
GCGCCGAGGAAGCCGCGGCGCCCGCGGGCTCTGGACCTTCGAAGACTACGAGCTGCCGTGCTAGCG
CTCTAGTAAAAATGTCACAATAAAAATGACATGTATGTGAAAAAATTTTCCCTACCCGTAGTAAGTA
ACAGTGTCTTTTTTTACCGTACTCTATGCGTTATTTTTGTTGAAATTAATCCATTGTTGAAGTTGTA
ACTGTGCATGGTCCGCGCCAGTCT

SEQ ID NO: 144, LOC_Os01g21120.1|11971.m08596|protein|AP2-EREBP

MCGGAIIDYDIPARRRLCASDFWPDADDSDPHTPAPEKPPRAKRRERKNQYRGIRQRPWGKWAEEIRD
VKGVRVWLGTYPTEAAARAYDRAARRIRGAKAKVNFNDFGAAPAPAAAAAKAVPRVAPTPAVLPPP
KMEAVSEGAGACSSDEVKELSELLAYENYMSFLGIPYMEGGAASAAGAEAAAPAGLWTFEDYELPS
LAL

FIGURE 28 (continued)

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SEQ ID NO: 145, NM_001055712.1| *Oryza sativa* (japonica cultivar-group) Os03g0183000 (Os03g0183000) mRNA, complete cds

AAAGGCATTTCGCAACACACACTTGAAGAAAAAAACACGACGAACACGTTAAAAAAGGTCGAAGAGA
AGTGGGAGACCCAAACCGCGAACAATGTGTGGAGGCGCCATCCTCGCCGAGTTCATCCCGGCGCCGTC
GCGCGCCGCGGCGGCGACCAAGCGGGTGACCGCCAGCCACCTGTGGCCGGCCGGCTCCAAGAACGCCG
CCCGCGGCAAGAGCAAGAGCAAGAGGCAGCAGAGGAGCTTCGCCGACGTCGACGACTTCGAGGCCGCC
TTCGAGCAGTTCGACGATGACTCCGACTTCGACGACGCGGAGGAAGAAGACGAAGGACACTTCGTGTT
CGCGTCCAAATCTCGTGTCTCGCCGGGCACGACGGGCGCGCGGCGGCGAGGGCGGCGAGCAAGAAGA
AGCGGGGGCGGCACTTCCGAGGCATCCGGCAGCGGCCATGGGGGAAGTGGGCGGCGGAGATCCGCGAC
CCGCACAAGGGCACGCGCGTCTGGCTCGGCACGTTCAACACCCCGGAGGAGGCCGCACGCGCCTACGA
CGTCGAGGCGCGCCGCTCCGCGGCAGCAAGGCCAAGGTCAACTTCCCCGCCACGCCCGCCGCCGCGC
GCCACGCCGCGGCAACACGAGAGCCACCGCCGTGCCACCGCCGGCGACAGCACCCGCCGCCGCCCG
CCGCGCGGACTGAAGCGAGAATTCTCGCCGCCTGCTGAGACCGCGCTACCTTTCTTCACCAACGGCTT
CGTCGACCTGACGACCGCCGCGGCGCCGCCACCGGCCATGATGATGACGAGCTCCTTCACCGACAGCG
TCGCCACGTCGGAGTCCGGCGGGAGCCCCGCCAAGAAGGCGAGGTCCGACGACGTCGACTCGTCCGAG
GGCAGCGTCGGCGGCGGCGAGCAGCAGCTGGGTTTACCGACGAGCTGGAGTTCGACCCGTTTCATGCT
GTTCCAGCTCCCCTACTCCGACGGCTACGAGTCCATCGACAGCCTCTTCGCCGCGGCGGCGACGCCAACA
GCGCGAACACCGACATGAACGCCGCGGTCAACCTGTGGAGCTTCGACGACTTCCCAATCGACGGCGCC
CTTTTCTGATGTACTCCTCCATTGATGCAGTTTGTGCACTCAATTGTTAATCACGTCGTCGTTGATGA
ATGTTTAAACGGAGGATGATGGGGTGCAGCTGATATCATGGCTTGCTTGATTACCGAATTATATTGCG
GTGTTTGTGTTTGTCAATTAGATTCTGAATCTGTACTACTGCCGATCTTATGATCAAACTATATATT
AAGTTTATGTACTCTTAATTTGTGGGCTACTTTTACGGGGTCTTCGTAAGTCTGCTGAAATAGTCCTA
TGAAATCGATCATGTGCGCAATATCGTCGTCAATTATCGTGGTTCGTGGTTGTTAATGATGTCAAATAA
GTCTATGAAAACCTGGTCTCTTGGTGTGTTATGTACCACTGATCGATCCATCATTGATCTCTGTCTAT
GTTGAGATGGATCGTGTAAGAATATCATAATTTGCTGGATTGAGTCCAGTCCGTAATGTATTTGGTTT
GTACAACTGC

SEQ ID NO: 146, LOC_Os03g08470.1|11973.m06355|protein|AP2-EREBP

MCGGAILAEFIPAPSRAAAATKRVTASHLWPAGSKNAARGKSKSKRQQRSFADVDDFEAAFEQFDDDS
DFDDAEEEDEGHFVFASKSRVVAGHDGRAARAASKKKRGRHFRGIRQRPWGKWAAEIRDPHKGTRVW
LGTENTPEEAARAYDVEARLRGSKAKVNFATPAAARPRRGNTRATAVPPPATAPAAAPPRGLKREF
SPPAETALPFFTNGFVDLTAAAPPPAMMMTSSFTDSVATSESGGSPAKKARSDDVDSSEGSVGGGSD
TLGFTDELEFDPFMLFQLPYSDGYESIDSLFAAGDANSANTDMNAGVNLWSFDDFPIDGALF

SEQ ID NO: 147, AJ515477.2| *Triticum aestivum* erebp gene for ethylene response element binding protein

CTTTCCTTTCGCTTAGCTCTCCACCCGCGGCCCCACGTGCTCCCAGCCATGTGCGGCGGCGCCATCCT
CTCCGACATCATCCCGCCGCGCGCCGGCCCGCGGCGGCGCCCTCTGGCAGGCGGACAGGAAGAAGA
GGAGGGCCGGGCCCCGCGCGTGGCCGAGGAGGAGCCCGAGGAGGAGGCGGAGGAGGGCGACGAGGAC
TTCGAGGCCGACTTCGAGGGGTTCTGTGACGAGGAGTCCGACGGCGAGGTCAAGCCCTTCCCCGCCCCG
CAGGAGCGGCTTCTCCGAGATGGATTGAAGGCAACTGCTGCTGGTGAATATGACTGTGCCTCAGGGT
CTGCTAAAAGGAAGAGAAAGAACCAGTTCAGGGGCATCCGCCGCCGCCCTTGGGGTAAATGGGCTGCT
GAAATAAGAGATCCTCGCAAGGGTGTCCGTGTCTGGCTTGGTACTTACAACCTCC

FIGURE 28 (continued)

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GCTGAGGAAGCTGCCAGAGCCTATGATGTTGAAGCCCGCAGAATTCGTGGCAAGAAGGCAAAGGTC
AATTTCCAGAGAAGCTCCTATGGCTCCTCAGCAACGCTGCGCTACTGCTGTGAAGGTGCCCCGAGTT
CAACACCGAACAGAAGCCGGTACTCAACACCATGGGCAACGCAGATGTGTATTCTGCTCTGCTGTTG
ACTACACCTTAAATCAGCAATTTGTGCAGCCTCAGAACATGTCGTTTGTGCCTACAGTGAATGCAGTT
GAGGCCCTTTTCATGAATTTTCTCTGACCAGGGTAGCAACTCCTTTAGTTGCTCAGACTTCAGCTG
GGAGAATGATATCAAGACCCCTGACATAACTTCTGTGCTTGCATCCATTCCCACCTCAACAGAGGTCA
ATGAATCTGCATTTCTCCAGAACAATGGCATCAATTCACGGTACCTCCTGTGATGGGTGATGCTAAT
GTTGATCTTGCCGACTTGGAGCCATACATGAAGTTCCTGATGGACGATGGTTCAGATGAGTCAATTGA
CAGCATTCTAAGCTGTGATGTACCCAGGATGTGGTCGGCAACATGGGCCTTTGGACCTTTGATGACA
TGCCCTTGTCTGCTGGTTTCTACTGAGGGAATCGAGGTCGCTGGGTGCCTGTATATATAGACAAAGGG
AATAAGTATTCAGGACATCAACAAGTGCTTGTGTCTGGTGCCTCTAGAATTGAGCAGTAGCGATGTCA
GTCTATGGTTATGTCTAGCTTAAATGGTCAGGTGACTGAGGTCTTTTGAATAGACCTCTGTCTTGTG
CCCCCAGACTATACTTATATCTATATATGAGACCAGTATGTGATGGGGAAGTCTTATTTTGTATTCA
TGTTTCTACCTTATTGTAAGTGTACAAGAGGCTGTAAACCTTTTAAATTTGAAGCCAGTGTGTGTTG
TGTGTGCTTAAAAAAAAAAAAAAAAAAGTATCTGC

SEQ ID NO: 148, CAD56466.1| ethylene response element binding protein [Triticum aestivum]

MCGGAILSDIIPPPRRPAGGRLWQADRKKRRAGPRRVPEEEPEEEAEEGDEDFEADFEGFVDEESDGE
VKPFPARRSGFSGDGLKATAAGEYDCASGSAKRKRKNQFRGIRRRPWGKWAAEIRDPRKGVVRVWLGT
NSAEAAARAYDVEARRIRGKKAKVNFPEEAPMAPQQRCAVAVKVPFNTQKPVLTNMGNAADVYSCSA
VDYTLNQFVQPNMSFVPTVNAVEAPFMNFSSDQGSNSFSCSDFSWENDIKTPDITSVLASIPTSTE
VNESAFLQNNGINSTVPPVMGDANVDLADLEPYMKFLMDDGSDESIDSILSCDVPQDVVGNMGLWTFD
DMPLSAGFY

SEQ ID NO: 149, NM_130320.2| Arabidopsis thaliana DNA binding / transcription factor (AT2G47520) mRNA, complete cds

GTTCTAGTTTGGAGTTGGAAGCGTAAAAACAAAAACAAAAATGTGTGGGGGAGCTATCATTCTCTGA
TTTCATCTGGTCGAAATCTGAGTCAGAACCGAGTCAACTCGGCTCTGTTAGCAGCAGGAAGAAGCGTA
AACCCGTCTCAGTGAGTGAAGAAAGAGATGGGAAACGAGAGAGGAAGAATCTGTACAGAGGGATAAGG
CAGAGGCCATGGGGCAAATGGGCAGCGGAGATTCTGTGACCCGAGCAAAGGTGTACGTGTCTGGCTTGG
CACATTCAAACCGCCGACGAAGCTGCTCGAGCCTACGACGTTGCTGCCATCAAATCCGTGGCCGGA
AAGCCAACTGAATTTCCCAAACACTCAAGTAGAAGAAGAAGCCGATACTAAACCAGGGGGGAATCAA
AATGAGCTGATTTCCGAAAACCAAGTAGAGAGCTTATCGGAGGACCTGATGGCATTGGAGGATTACAT
GAGATTCTATCAGATTCCGGTTGCCGACGACCAATCGGCGACCGATATTGAAATTTATGGAGCTATC
AAGACTCCAATTAAATCTCTTATTTCCCGCCGGTTTGCTCACTCATTAAATATGCTGC

SEQ ID NO: 150, AT2G47520

MCGGAIISDFIWSKSESEPSQLGSVSSRKKRKPVSVSEERD GKREKKNLYRGIRQRPWGKWAAEIRDP
SKGVRVWLGTFTKTADEAARAYDVAAIKIRGRKAKLNFNTQVEEADTKPGGNQNELISENQVESLSE
DLMALEDYMRFYQIPVADDQSATDIGNLWSYQDSN

FIGURE 28 (continued)

SEQ ID NO: 151, NM_001054854.1| *Oryza sativa* (japonica cultivar-group)
Os02g0782700 (Os02g0782700) mRNA, complete cds

SEQ ID NO: 152, LOC_Os02g54160.1|11972.m10445|protein|AP2-EREBP

SEQ ID NO: 153, AY831392.1| *Oryza sativa* (indica cultivar-group) BTH-induced ERF transcriptional factor 1 (BIERF1) mRNA, complete cds

FIGURE 28 (continued)

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GGCCAAGGCGGCGCCCCCAACTGCAGATGGGATGTTGACTACAAAGCTTGTCCAACATGATGGACCTA
CTGCTAGATCGGCAAAGCGCAAGAGGAAGAATCAGTACAGGGGGATCCGCCAGCGTCCCTGGGGCAA
TGGGCAGCTGAAATCCGAGACCCAGCAAGGGTGTCCGTGTTTGGCTTGGAACATATAACACTGCTGA
GGAGGCAGCTAGGGCATATGACGCTGAAGCCCGCAAGATCCGTGGCAAGAAAGCCAAGGTCAACTTTC
CTGATGAACCAGCTGTTGCTCAGAAGCTCTCCCTGAAGCAAAACGCTGCCAAGCAAGAGAACTAGCT
CCACCTCTGAAGTCTGTGGCGATGATGCTTTCTTTCAGCTAAACAGTTCAGACAATGATTTGTTTGC
AATGCTTGCAAAGGTGCCTGCAAAGCCGGCAGAGCCTGTTGATCTCATGCCTCCAGTCAAACCTCTTG
CTTCCACTGAGACATTCGAGATGAACATGCTCTCTGATACGAGCAGCAACTCATTGGCTCTTCAGAC
TTTGGTTGGGAGGATGACACCCTGACCCAGACTACACTTCAGTCTTTGTTTCTAATGCTGCCATGCC
AGCATATGGTGAACCTGCTTACCTGACAGGTGGAGCGCCAAAGAGAATGAGGAACAACATATGGTATCG
CCGTGCCCCAGGGAAATGGCATGCCTAATCTCGCACAACATGCCACCTTCGATCCCGAGATGAAG
TATTTGCCATTACCTTATGTTGAGAGCAGCTCAGATGAATCAATGGACAACCTTCTGCAAAATGATGC
TACACAAGACGGGGCAAGCAACGAGGGCATCTGGAGCCTTGATGAGCTGCTCATGGCAGCTGGTGCCT
ACTGAGGAGACGAAATGTTCTGGTCAGTGTGGTCTGTCACTAGCAAACCATGTAAGGCACTCCACACT
ACCTACTATTTTGATTTCTTGTAGATACATTTTCATGTTTGAATGTGTATGGCCAAGATGAAGAGCTG
GTGATGTCTGCTATGTTTTGTAGAGGGATGCTACCAAAGTAATGCTAGAATATTACAAGCTGCTATCA
GCTGTACTCTCTATGACAATGTTTATACTATGTTTGCTGTATGGTGTGGTCTATGATTTGAAGTATGT
CGGAGACTAATTCAAATAATGCCCTTGGGCCATGGTGTGTGCCTTGGTAAATGGTGCCTTTATTTAAG
GGTTATATTAGGTTGGTGCCTCAGTAATTGCCGTTTCTACCAAAAAAAAAAAAAAAAAA

SEQ ID NO: 154, LOC_Os09g26420.1|11979.m05794|protein|AP2-EREBP

MCGGAIISGFIPPSAAAAAAAAVAKKQQGRRVTADVLWPGMLRKGKAAAAEEDFEADFREFERGMSDD
EAEGGGGEEEEDDDDVVVVVPPPAARFVVRAAKAAPPTADGMLTTKLQHDGPTARSAXHKRKNQY
RGIRQRPWGKWAAEIRDPSKGVVWLGTYNTEEAARAYDAEARKIRGKKAKVNFPEPAVAQKLSLK
QNAAKQEKLAPPLKTCGDDAFFQLNSSDNDLFAMLAKVPAKPAEPVDLMPPVKPLASTETFEMNMLSD
TSSNSFGSSDFGWEDDTLTPDYTSVFVPNAAMPAYGEPAYLTGGAPKMRMNNYGIAPVQNGMPNLAQ
NMPTFDPEMKYLPLPYVESSSDSDMDNLLQNDATQDGASNEGIWSLDELMAAGAY

SEQ ID NO: 155, AY271985.1| Triticum aestivum ethylene-responsive element binding protein (TaERF2) mRNA, complete cds

ATGTGCGGCGGCGCCATCCTCTCCGACATCATCCCGCCGCCGCGCGGGCCACCGGCGGCAACGTCTG
GCGGGCGGACAAGAAGAGGAGGGCCAGGCCCGACGCCGCGCGGGGAGGCCCCGCCGCGTCCCCGAGG
AGGAGTTCCAGGAGGAGGAGAGCGACGCGGAGTTTCGAGGCCGACTTCGAGGGGTTCTGAGAGCGGAG
GAGGAGTCCGACGGCGAGGCCAAGCCCTTCCCCGTCCGAGGAGCGGCTTCTCCGAGATGGATTGAA
GGCAACTGCTGCTGGTGTATGATGACTGTGCTTCAGGGTCTGCTAAAAGGAAGAGAAAGAACCAGTTCA
GGGGCATCCGCCGCCGCCCTTGGGGTAAATGGGCTGCTGAAATAAGAGATCCTCGCAAGGGTGTCCGT
GCCTGGCTTGGCACTTACAACTCTGCTGAGGAAGCTGTCAGAGCCTATGATGTTGAAGCCCGCAGAAT
TCGTGGCAAGAAGGCAAAGTCAATTTCCAGAAGAAGCTCCCATGGCTCCTCAGCAAACGCTGCGCTA
CCTCTGTGAAGGTGCCCGAGTTCAACACCGAACAGAAGCCAGTACTCAACACCATGGGCAACGCAGAT
GTGTATTCTGCCCCTGCTGTTGACTACACCTTAAATCAGCAATTTGTGCAGCCTCAGAACATGTCGTT
TGTGCCTACAGTGAATGCAGTTGAGGCTCCTTTTCATGAATTTTCTCTGACCAGGGGAGCAACTCCT
TTAGTTGCTCAGACTTCAGCTGGGAGAATGATATCAAGACCCCTGACATAACTTCTGTGCTTGCATCC
ATTCACCTCAACTGAGGTCAATGAATCTGCATTTCTCCAGAACAATGGCATTAATTCAACGGTACC
TCCTGTGATGGGTGATGCTAATGTTGATCTTGCCTACTTG

FIGURE 28 (continued)

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GAGCCGTACATGAAGTTCCTGATGGACGATGGTTCAGATGAGTCAATTGACAGCATTTCTAAGCTGTGA
TGTACCGCAGGACGTTGTCTGGCAACATGGGCCTTTGGACCTTTGATGACATGCCCTTGTCTGCTGGTT
TCTACTGA

SEQ ID NO: 156, AAP32468.1| ethylene-responsive element binding protein [*Triticum aestivum*]

MCGGAILSDIIPPPRRATGGNVWRADKKRRARPDAAGRP RRVP EEEFQEEESDAEF EADFEGFVEAE
EESDGEAKPFPVRRSGFSGDGLKATAAGDDDCASGSAKRKRKNQFRGIRRRP WGKWAAEI RDP RKGVR
AWLGTYN SAE EAVRAYDVEARRIRGKKAKSISQKKLPWLLSKRCATSVKVPEFNTEQKPVLNTMG NAD
VYSCPAVDYTLNQQFVQPQNMSFVPTVNAVEAPFMNFSSDQGSNSFSCSDFSWENDIKTPDITSVLAS
IPTSTEVNES AFLQNNGINSTVPPVMGDANVDLAYLEPYMKFLMDDGSDESIDSILSCDVPQDVVGNM
GLWTFDDMPLSAGFY

SEQ ID NO: 157, AY271984.1| *Triticum aestivum* ethylene-responsive element binding protein (TaERF1) mRNA, complete cds

ATGTGCGGCGGGCGCCATCCTCTCCGACATCATCCCGCCGCGGGGAGGCCCTGCCGTGCGCCTGAGGA
GGAGTTCCAGGAGGAGGAGGGCGACGCGGAGTTCGAGGCCGACTTCGAGGGGTTCTGGAGGCGGAGG
AGGAGTCCGACGCGGAGGCCAAGCCCTTCCCCGTCGCGAGGAGCGGCTTCTCCGGAGATGGATTGAAG
GCAACTGCTGCTGGTGATGATGACTGTGCCTCAGGGTCTGCTAAAAGGAAGAGAAAAGAACAGTTCAG
GGGCGTCCGCGCGCCGCTTGGGGTAAATGGGCTGCTGAAATAAGAGATCCTCGCAAGGGTGTCCGTG
TCTGGCTTGGTACTTACAACCTCCGCTGAGGAAGCTGCCAGAGCCTATGGTGTTGAGGCCCGCAGAATT
CGTGGCAAGAAGGCAAAGGTCAATTTCCAGAGAAGCTCCTATGGCTCCTCAGCAACGCTGCGCTAC
TGCTGTGAAGGTGCCCCAGTTCAACACCGAACAGAAGCCGGTACTCAACACCATGGGCAACGCAGATG
TGATTTCCTGCTCTGCTGTTGACTACACCTTAAATCAGCAATTTGTGCAGCCTCAGAACATGTCGTTT
GTGCCTACAGTGAATGCAGTTGAGGCCCTTTTCATGAATTTTCTCCTGACCAGGGTAGCAACTCCTT
TAGTTGCTCAGACCTCAGCTGGGAGAATGATATCAAGACCCCTGACATAACTTCTGTGCTTGCATCCA
TTCCCACCTCAACAGAGGTCAATGAATCTGCATTTCTCCAGAACAAATGGCATCAATTCAACGGTACCT
CCTGTGATGGGTGATGCTAATGTTGATCTTGCCGACTTGGAGCCATACATGAAGTTCCTGATGGACGA
TGGTTCAGATGAGTCAATTGACAGCATTCTAAGCTGTGATGTACCCAGGATGTGGTCGGCAACATGG
GCCTTTGGACCTTTGATGACATGCCCTTGTCTGCTGGTTTCTACTGA

SEQ ID NO: 158, AAP32467.1| ethylene-responsive element binding protein [*Triticum aestivum*]

MCGGRHPLRHHPAAGRPCR APEEEFQEEEGDAEF EADFEGFVEAE EESDGEAKPFPVRRSGFSGDGLK
ATAAGDDDCASGSAKRKRKNQFRGVRRRP WGWAAEI RDP RKGVRVWLGTYN SAE EAA RAYGVEARRI
RGKKAKVNFPEEAPMAPQQRCAVAVKVPEFNTEQKPVLNTMG NADV YSCSAVDYTLNQQFVQPQNMSF
VPTVNAVEAPFMNFSSDQGSNSFSCS DLSWENDIKTPDITSVLASIPTSTEVNES AFLQNNGINSTVP
PVMGDANVDLADLEPYMKFLMDDGSDESIDSILSCDVPQDVVGNMGLWTFDDMPLSAGFY

FIGURE 28 (continued)

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SEQ ID NO: 159, NM_001036108.1| Arabidopsis thaliana RAP2.12; DNA binding / transcription factor (RAP2.12) mRNA, complete cds

AAAACAACAAAGCAAAGCGTTGAAGAGAGAAGAAGAAGCAAAGATATAACCCCCAAAAGTATCAATTA
GTTTCCATTTTCGCCGCTAAGATTCTGTTTTCGAACATTTACACCCTCAAGAATCGCCGCCATGTGTG
GAGGAGCTATAATATCCGATTTTCATTCCACCGCCGAGGTCTCGCCGTGTTACTAGCGAGTTTATTTGG
CCGGATCTGAAGAAGAATTTGAAAGGATCGAAGAAAAGCTCGAAGAATCGTTCGAATTTCTTCGATTT
TGACGCTGAGTTCGAAGCTGATTTCCAAGTTTTCAAAGATGATTCGTCTATCGATTGCGATGATGATT
TCGACGTCGGTGATGTTTTCGCCGATGTGAAACCATTCGTTTTCACTTCGACTCCAAAACCCGCCGTC
TCCGCCGCTGCGGAAGGTTTCAGTTTTTGGTAAGAAAGTTACTGGCTTGGATGGGGACGCTGAGAAATC
TGCAAATAGGAAGAGGAAGAATCAGTACCGAGGGATTAGGCAACGTCCTTGGGGAAAATGGGCTGCTG
AGATACGTGATCCAAGGGAAGGTGCTAGAATCTGGCTTGGAAACGTTCAAGACAGCTGAGGAAGCTGCT
AGAGCTTACGATGCTGCAGCGCGGAGAATCCGTGGATCTAAAGCTAAGGTGAATTTCCCTGAAGAAAA
CATGAAGGCTAATTTCTCAGAAACGCTCTGTGAAGGCTAATCTTCAGAAACAGTGGCTAAACCTAACC
CTAACCCAAGTCCAGCTTTGGTTCAGAACTCGAACATCTCCTTTGAAAATATGTGTTTCATGGAGGAG
AAACACCAAGTGAGCAACAACAACAACCAGTTTGGGATGACAACTCCGTTGATGCTGGATGTAA
TGGGTATCAGTATTTTCAGCTCTGACCAGGGTAGTAATCTTTTCGATTGTTCCGGAGTTTGGTTGGAGCG
ATCAAGCTCCGATAACTCCCGACATCTCTTCTGCGGTTATCAACAACAACAACCTCAGCTCTGTTCTTT
GAGGAAGCCAATCCAGCTAAGAAGCTCAAGTCTATGGATTTTCGAGACACCTTACAACAACACTGAATG
GGACGCTTCACTGGATTTCTCAACGAAGATGCTGTAACGACTCAGGACAATGGTGCAAACCTATGG
ACCTATGGAGTATTGATGAAATTCATTCCATGATTGGAGGAGTCTTCTGAAGAGATCCAGTTTCATGA
GTTCTCTGTTTGCATTGCGAGAAGCCATGAGCCTCTATCTTGAGGGTAGTTGTGATGAAGTTAAGTAGA
GGCTTATTTTTAGGGGTTGTGGTAGTTTTTGTTTTAGTGAATCTTTTGAATTCGTTTGTGTTTGT
TTGTTACTTTATGCCCCAAAACCTTTAACATTTGTCATAATGTGTTTGAACCTCTCATCTGTTTAA
TCAAATAAATCTTCTTTGTATGCT

SEQ ID NO: 160, AT1G53910.1 Arabidopsis AP2-EREBP family transcription factor, protein sequence 358AA

MCGGAIISDFIPPPRSRRVTSEFIWPD LKKNLKGSKSSKNRSNFFDFDAEF EADFQGFKDDSSIDCD
DDFDVGDV FADV KPFVFTSTPKPAVSAAAEGSVFGKKVTGLDGD AEKSANRKRKNQYRGIRQRPWGKW
AAEIRD PREGARIWLGTAE EAARAYDAAARRIRGSKAKVNFPEENMKANSQKRSVKANLQKPVAK
PNPNPSPALVQNSNISFENMCFMEEKHQVSNNNNNQFGMTNSVDAGCNGYQYFSSDQGSNSFDCSEFG
WSDQAPITPDISSAVINNNNSALFFEEANPAKKLKSMDFETPYNNTEWDASLDFLNEDAVTTQDNGAN
PMDLWSIDEIHSMIGGVF

SEQ ID NO: 161, AY088204.1| Arabidopsis thaliana clone 42960 mRNA, complete sequence

AAAAACAACAAAGCAAAGCGTTGAAGAGAGAAGAAGAAGCAAAGATATAACCCCCAAAAGTATCAATT
AGTTTCCATTTTCGCCGCTAAGATTCTGTTTTCGAACATTTACACCCTCAAGAATCGCCGCCATGTGT
GGAGGAGCTATAATATCCGATTTTCATTCCACCGCCGAGGTCTCGCCGTGTTACTAGCGAGTTTATTTG
GCCGGATCTGAAGAAGAATTTGAAAGGATCGAAGAAAAGCTCGAAGAATCGTTCGAATTTCTTCGATT
TTGACGCTGAGTTCGAAGCTGATTTCCAAGTTTTCAAAGATGATTCGTCTATCGATTGCGATGATGAT
TTCGACGTCGGTGATGTTTTCGCCGATGTGAAACCATTCGTTTTCACTTCGACTCCAAAACCCGCCGT
CTCCGCCGCTGCGGAAGGTTTCAGTTTTTGGTAAGAAAGTTACTGGCTTGGATGGGGAAAGCTGAGAAAT
CTGCAAATAGGAAGAGGAAGAATCAGTACCGAGGGATTAGGCAACGTCCTTG

FIGURE 28 (continued)

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GGGAAAATGGGCTGCTGAGATACGTGATCCAAGGGAAGGTGCTAGAATCTGGCTTGGAACGTTCAAGA
 CAGCTGAGGAAGCTGCTAGAGCTTACGATGCTGCAGCGCGGAGAATCCGTGGATCTAAAGCTAAGGTG
 AATTTCCCTGAAGAAAACCTGAAGGCTAATTCTCAGAAACGCTCTGTGAAGGCTAATCTTCAGAAACC
 AGTGGCTAAACCTAACCCTAACCCAAGTCCAGCTTTGGTTTCAGAACTCGAACATCTCCTTTGAAAATA
 TGTGTTTCATGGAGGAGAAACACCAAGTGAGCAACAACAACAACCAAGTTTGGGATGACAACTCC
 GTTGATGCTGGATGTAATGGGTATCAGTATTTTCAGCTCTGACCAGGGTAGTAATCTTTTCGATTGTTT
 GGAGTTTGGTTGGAGCGATCAAGCTCCGATAACTCCCGACATCTCTTCTGCGGTTATCAACAACAACA
 ACTCAGCTCTGTTCTTTGAGGAAGCCAATCCAGCTAAGAAGCTCAAGTCTATGGATTTTCGAGACACCT
 TACAACAACACTGAATGGGACGCTTCACTGGATTTCTCAACGAAGATGCTGTAACGACTCAGGACAA
 TGGTGCAAACCCTATGGACCTATGGAGTATTGATGAAATTCATTCCATGATTGGAGGAGTCTTCTGAA
 GAGATCCAGTTTCATGTAAATAAGGCTGCATGTTTGTGAGTTTCCCGCATCGTTCTGTTTATCAACCTC
 CAAAACCTTCTAATGTCTGTTACTTGCATCTTCTTCTGCTGTCTCTGTCTCTCTCAGGAGTTCC
 TGTTTGCATTGCGAGAAGCCATGAGCCTCTATCTTGAGGGTAGTTGTGATGAAGTTAAGTAGAGGCTT
 ATTTTTAGGGGTTGTGGTAGTTTTTGTGTTTAGTGAATCTTTTGAATTCGTTTGTGTTTTGTTTTGTT
 ACTTTATGCCCCAAACTCCTTTAACATTTGTCATAATGTGTTTGAACCTCCTCATCTGTTTAATCAA
 ATAAATCTTCTTTGTATGCT

SEQ ID NO: 162, AAM65746.1| AP2 domain containing protein, putative [Arabidopsis thaliana] RAP2;12

MCGGAIISDFIPPPRRRVTSSEFIWPDLLKKNLKGSKSSKNRSNFFDFDAEFEADFQGFKDDSSIDCD
 DDFDVGDVDFADVVPFVFTSTPKPAVSAAAEAGSVFGKKVTGLDGEAEKSANRKRKNQYRGIRQRPWGKW
 AAEIRDPREGARIWLGTAEAAARAYDAAARRIRGSKAKVNFPEENLKANSQKRSVKANLQKPVAK
 PNPNSPALVQNSNISFENMCFMEEKHQVSNNNNNQFGMTNSVDAGCNGYQYFSSDQGSNSFDCSEFG
 WSDQAPITPDISSAVINNNNSALFFEEANPAKKLKSMDFETPYNNTEWDASLDFLNEDAVTTQDNGAN
 PMDLWSIDEIHSMIGGVF

SEQ ID NO: 163, NM_112281.2| Arabidopsis thaliana RAP2.2; DNA binding / transcription factor (RAP2.2) mRNA, complete cds

GGAGAGTAACATCGAGACAAAGAAGAAAACTAAAAAAGAGAACCCCAAAGAATCGAATATTTATTAT
 TTCGCCCCGAAGATTCTATTTCTGATCATTTACACCCCTAAAAAGAGTAGAGCTTTCGTGAAGCCACC
 ATGTGTGGAGGAGCTATAATCTCCGATTTTCATACCTCCGCCGAGGTCCCTCCGCGTCACTAACGAGTT
 TATCTGGCCGGATCTGAAAAACAAAGTGAAAGCTTCAAAGAAGAGATCGAATAAGCGATCCGATTTCT
 TCGATCTTGACGATGATTTTGAAGCTGATTTCCAAGGGTTTAAGGATGACTCGGCTTTTGAAGTGCAGAA
 GACGATGATGATGTCTTCGTCAATGTTAAGCCTTTCGTCTTCACCGCAACTACTAAGCCCGTAGCTTC
 CGCTTTCGTCTCCACTGGTATATATTTGGTAGGTTTACGATATGCCAAGAAAACCTGTAGAGTCCGCTG
 AGCAAGCTGAGAAATCTTCTAAGAGGAAGAGGAAGAATCAATACCGAGGGATTAGGCAGCGTCCTTGG
 GGAAATGGGCTGCGGAGATCCGTGATCCGAGAAAAGGCTCCCGAGAATGGCTTGGAACATTCGACAC
 TGCTGAGGAAGCAGCAAGAGCTTATGATGCTGCAGCACGCAGAATCCGTGGCACGAAAGCTAAGGTGA
 ATTTTCCCGAGGAGAAGAACCCTAGCGTCGTATCCCAGAAACGTCCTAGTGCTAAGACTAATAATCTT
 CAGAAATCAGTGGCTAAACCAACAAAAGCGTAACCTTGGTTTCAGCAGCCAACACATCTGAGTCAGCA
 GTACTGCAACAACCTCCTTTGACAACCTCTTTGGTGATATGAGTTTCATGGAAGAGAAGCCTCAGATGT
 ACAACAATCAGTTTGGGTAAACAACCTCGTTTCGATGCTGGAGGTAACAATGGATACCAGTATTTTCAGT
 TCCGATCAGGGCAGTAACCTCCTTCGACTGTTCTGAGTTTCGGGTGGAGTGATCACGGCCCTAAAACACC
 CGAGATCTCTTCAATGCTTGTCAATAACAACGAAGCATCATTTGTTGAAGAAACCAATGCAGCCAAGA
 AGCTCAAACCAAACTCTGATGAGTCAGACGATCT

FIGURE 28 (continued)

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GATGGCATACTTGACAACGCCTTGTGGGACACCCCACTAGAAAGTGGAAGCCATGCTTGGCGCAGATG
 CTGGTGTCTGACTCAGGAAGAGGAAAACCCAGTGGAGCTATGGAGCTTAGATGAGATCAATTTTCATG
 CTGGAAGGAGACTTTTGAAGTGATCGATGGTTCCTTAGTTTGTAATAAAGCTGTGTTGGATTTTGCT
 GTTGGGGGATGGTACAAGTCACACCTCAAGCTCTATGCATTGGTATCTCATGAGCCTCTCTCCATAG
 AGAGTTTCTCTTTTAATTTTGTGCGAAATAAAAAAGGTGTGATGAAGTAAATAGAGGTATAATAATATC
 TATCTATTAAGTCTTGTGTTTGTCTTTTCATTTTGTATTTCTTTTCTATTTAAAAGACAGTTTATTAG
 TCTTCTGAGCTCTCTTTTGTATCTTTGTTATAGCGTATCATCACCCCTCGAAAGTGAATGTTTTGTAC
 CCCCAACTTGTTTTAGCATTATAATAAAGTCTCTTTGGAACCTTCTC

SEQ ID NO: 164, AT3G14230.1 Arabidopsis AP2-EREBP family transcription factor, protein sequence 379AA

MCGGAIISDFIPPPRSLRVTNEFIWPD LKNKVKASKKRSNKRSDFFDLDDDFEADFQGFKDDSAFDCE
 DDDDVFEVNVKPFVFTATTKPVASAFVSTGIYLVGSAYAKKTVESAEQAEKSSKRKRKNQYRGIRQRPW
 GKWAAEIRDPRKGSREWLGTFTAEAAARAYDAAARRIRGTAKVNFPEEKNPSSVVSQKRPSAKTNL
 QKSVAKPNKSVTLVQQPHTLSQQYCNNSFDNSFGDMSFMEEKPQMYNNQFGLTNSFDAGGNNGYQYFS
 SDQGSNSFDCSEFGWSDHGPKTPEISSMLVNNNEASFVEETNAKKLKPNSESDDL MAYLDNALWDT
 PLEVEAMLGADAGAVTQEEENPVELWSLDEINFMLEGDF

SEQ ID NO: 165, NM_180251.1| Arabidopsis thaliana RAP2.2; DNA binding / transcription factor (RAP2.2) mRNA, complete cds

GGAGAGTAACATCGAGACAAAGAAGAAAACTAAAAAGAGAACCCCAAAGAATCGAATATTTATTAT
 TTCGCCCCGAAGATTCTATTTCTGATCATTTACACCCCTAAAAAGAGTAGAGCTTTCGTGAAGCCACC
 ATGTGTGGAGGAGCTATAATCTCCGATTTTCATACCTCCGCCGAGGTCCCTCCGCGTCACTAACGAGTT
 TATCTGGCCGGATCTGAAAAACAAAGTGAAAGCTTCAAAGAAGAGATCGAATAAGCGATCCGATTTCT
 TCGATCTTGACGATGATTTTCGAAGCTGATTTCCAAGGGTTTAAGGATGACTCGGCTTTTGACTGCGAA
 GACGATGATGATGTCTTCGTCAATGTTAAGCCTTTCGTCTTCACCGCAACTACTAAGCCCGTAGCTTC
 CGCTTTCGTCTCCACTGTAGGTTTCAGCATATGCCAAGAAAACCTGTAGAGTCCGCTGAGCAAGCTGAGA
 AATCTTCTAAGAGGAAGAGGAAGAATCAATACCGAGGGATTAGGCAGCGTCCCTGGGGAAAATGGGCT
 GCGGAGATCCGTGATCCGAGAAAAGGCTCCCGAGAATGGCTTGGAACATTCGACACTGCTGAGGAAGC
 AGCAAGAGCTTATGATGCTGCAGCACGCAGAATCCGTGGCAGCAAAGCTAAGGTGAATTTTCCCGAGG
 AGAAGAACCCTAGCGTCGTATCCCAGAAACGTCCTAGTGCTAAGACTAATAATCTTCAGAAATCAGTG
 GCTAAACCAACAAAAGCGTAACTTTGGTTTCAGCAGCCAACACATCTGAGTCAGCAGTACTGCAACAA
 CTCCTTTGACAACTCTTTTGGTGATATGAGTTTCATGGAAGAGAAGCCTCAGATGTACAACAATCAGT
 TTGGGTTAACAACCTCGTTTCGATGCTGGAGGTAACAATGGATACCAGTATTTTCAGTTCCGATCAGGGC
 AGTAACTCCTTCGACTGTTCTGAGTTCGGGTGGAGTGATCACGGCCCTAAACACCCGAGATCTCTTC
 AATGCTTGTCAATAACAACGAAGCATCATTTGTTGAAGAAACCAATGCAGCCAAGAAGCTCAAACCAA
 ACTCTGATGAGTCAGACGATCTGATGGCATACTTGACAACGCCTTGTGGGACACCCCACTAGAAAGTG
 GAAGCCATGCTTGGCGCAGATGCTGGTGCTGTGACTCAGGAAGAGGAAAACCCAGTGGAGCTATGGAG
 CTTAGATGAGATCAATTTTCATGCTGGAAGGAGACTTTTGAAGTGATCGATGGTTCCTTAGTTTGTA
 TAAAGCTGTGTTGGATTTTGTGTTGGGGGATGGTACAAGTCACACCTCAAGCTCTATGCATTGGTAT
 CTCATGAGCCTCTCTTCCATAGAGAGTTTCTCTTTTAATTTTGTGCGAAATAAAAAAGGTGTGATGAAG
 TAAATAGAGGTATAATAATATCTATCTATTAAGTCTTGTGTTTGTCTTTTCATTTTGTATTTCTTTTC
 TATTTAAAAGACAGTTTATTAGTCTTCTGAGCTCTCTTTTGTATCTTTGTTATAGCGTATCATCACCC
 TCGAAAGTGAATGTTTTGTACCCCAACTTGTTTAGCATTATAATAAAGTCTCTTTGGAACCTTCTC

FIGURE 28 (continued)

106/173**SEQ ID NO: 166, AT3G14230.2 Arabidopsis AP2-EREBP family transcription factor, protein sequence 375AA**

MCGGAIISDFIPPPRSLRVTNEFIWPD LKNKVKASKKRSNKRSDFFDLDDDFEADFQGFKDDSAFDCE
 DDDDV FVNVKPFVFTATT KPVASAFVSTVGSAYAKKTVESAEQAEKSSKRKRKNQYRGIRQRPWGKWA
 AEIRDPRKGSREWLGTFTAE EEARAYDAAARRIRG TKAKVNFPEEKNP SVVSQKRPSAKTNNLQKSV
 AKPNKSVTLVQQPT HLSQQYCNNSFDNSFGDMSFMEEKPQMYNNQFGLTNSFDAGGNNGYQYFSSDQG
 SNSFDCSEFGWSDHGPKTPEISSMLVNNNEASFVEETNA AKKLKPNSDESDDL MAYLDNALWDTPLEV
 EAMLGADAGAVTQEEENPV ELWSLDEINFMLEGDF

SEQ ID NO: 167, NM_180252.1| Arabidopsis thaliana RAP2.2; DNA binding / transcription factor (RAP2.2) mRNA, complete cds

GGAGAGTAACATCGAGACAAAGAAGAAAACTAAAAAAGAGAACCCCAAAGAATCGAATATTTATTAT
 TTCGCCCCGAAGATTCTATTTCTGATCATTTACACCCCTAAAAAGAGTAGAGCTTTCGTGAAGCCACC
 ATGTGTGGAGGAGCTATAATCTCCGATTTTCATACCTCCGCCGAGGTCCCTCCGCGTCACTAACGAGTT
 TATCTGGCCGGATCTGAAAAACAAAGTGAAAGCTTCAAAGAAGAGATCGAATAAGCGATCCGATTTCT
 TCGATCTTGACGATGATTTTGAAGCTGATTTCCAAGGGTTTAAGGATGACTCGGCTTTTGACTGCGAA
 GACGATGATGATGTCTTCGTCAATGTTAAGCCTTTTCGTCTTCACCGCAACTACTAAGCCCGTAGCTTC
 CGCTTTTCGTCTCCACTGGTTTCAGCATATGCCAAGAAAAGTGTAGAGTCCGCTGAGCAAGCTGAGAAAT
 CTTCTAAGAGGAAGAGGAAGAATCAATACCGAGGGATTAGGCAGCGTCCCTGGGGAAAATGGGCTGCG
 GAGATCCGTGATCCGAGAAAAGGCTCCCGAGAATGGCTTGGAACATTCGACACTGCTGAGGAAGCAGC
 AAGAGCTTATGATGCTGCAGCACGCAGAATCCGTGGCACGAAAGCTAAGGTGAATTTTCCCGAGGAGA
 AGAACCTAGCGTCGTATCCCAGAAACGTCCTAGTGCTAAGACTAATAATCTTCAGAAATCAGTGGCT
 AAACCAAACAAAAGCGTAACCTTGGTTTCAGCAGCCAACACATCTGAGTCAGCAGTACTGCAACAACCTC
 CTTTGACAACCTCTTTTGGTGATATGAGTTTCATGGAAGAGAAGCCTCAGATGTACAACAATCAGTTTG
 GGTTAACAACTCGTTCGATGCTGGAGGTAACAATGGATACCAGTATTTAGTTCCGATCAGGGCAGT
 AACTCCTTCGACTGTTCTGAGTTCGGGTGGAGTGATCACGGCCCTAAACACCCGAGATCTCTTCAAT
 GCTTGTCATAACAACGAAGCATCATTTGTTGAAGAAACCAATGCAGCCAAGAAGCTCAAACCAAACCT
 CTGATGAGTCAGACGATCTGATGGCATACTTGACAACGCCTTGTGGGACACCCCACTAGAAAGTGGAA
 GCCATGCTTGGCGCAGATGCTGGTGCTGTGACTCAGGAAGAGGAAAACCCAGTGAGCTATGGAGCTT
 AGATGAGATCAATTTTCATGCTGGAAGGAGACTTTTGAAGTGATCGATGGTTCCTTAGTTTGTAATAA
 AGCTGTGTTGGATTTTGCTGTTGGGGGATGGTACAAGTCACACCTCAAGCTCTATGCATTGGTATCTC
 ATGAGCCTCTCTCCATAGAGAGTTTCTCTTTTAATTTTGTGGAATAAAAAAGGTGTGATGAAGTAA
 ATAGAGGTATAATAATATCTATCTATTAAGTCTTGTGTTTGTCTTTTCATTTTGTATTTCTTTCTAT
 TTAAAAGACAGTTTATTAGTCTTCTGAGCTCTCTTTTGTATCTTGTATAGCGTATCATCACCCCTCG
 AAAGTGTAATGTTTTGTACCCCCAACTTGTTTAGCATTATAATAAAGTCTCTTTGGAACCTTCTC

SEQ ID NO: 168, AT3G14230.3 Arabidopsis AP2-EREBP family transcription factor, protein sequence 374AA

MCGGAIISDFIPPPRSLRVTNEFIWPD LKNKVKASKKRSNKRSDFFDLDDDFEADFQGFKDDSAFDCE
 DDDDV FVNVKPFVFTATT KPVASAFVSTVGSAYAKKTVESAEQAEKSSKRKRKNQYRGIRQRPWGKWAA
 EIRDPRKGSREWLGTFTAE EEARAYDAAARRIRG TKAKVNFPEEKNP SVVSQKRPSAKTNNLQKSV
 KPNKSVTLVQQPT HLSQQYCNNSFDNSFGDMSFMEEKPQMYNNQFGLTNSFDAGGNNGYQYFSSDQGS
 NSFDCSEFGWSDHGPKTPEISSMLVNNNEASFVEETNA AKKLKPNSDESDDL MAYLDNALWDTPLEVE
 AMLGADAGAVTQEEENPV ELWSLDEINFMLEGDF

FIGURE 28 (continued)

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SEQ ID NO: 169, NM_112550.3| Arabidopsis thaliana ATEBP/RAP2.3; DNA binding / transcription factor (ATEBP/RAP2.3) mRNA, complete cds

ATAAAGGCATTTTCAGCTCCACCGTAGGAACTTTCTCTTGAAAGAAACCCACAGCAACAAACAGAGAA
AATGTGTGGCGGTGCTATTATTTCGATTATGCCCCCTCTCGTCACCAAGGCCAAGGGCCGTAAACTCA
CGGCTGAGGAACTCTGGTCAGAGCTCGATGCTTCCGCCGCCGACGACTTCTGGGGTTTCTATTCCACC
TCCAAACTCCATCCCACCAACCAAGTTAACGTGAAAGAGGAGGCAGTGAAGAAGGAGCAGGCAACAGA
GCCGGGGAAACGGAGGAAGAGGAAGAATGTTTATAGAGGGATACGTAAGCGTCCATGGGGAAAATGGG
CGGCTGAGATTTCGAGATCCACGAAAAGGTGTTAGAGTTTGGCTTGGTACGTTCAACACGGCGGAGGAA
GCTGCCATGGCTTATGATGTTGCGGCCAAGCAGATCCGTGGTGATAAAGCCAAGCTCAACTTCCCAGA
TCTGCACCATCCTCCTCCTCCTAATTATACTCCTCCGCCGTATCGCCACGATCAACCGATCAGCCTC
CGGCGAAGAAGGTCTGCGTTGTCTCTCAGAGTGAGAGCGAGTTAAGTCAGCCGAGTTTCCCGGTGGAG
TGTATAGGATTTGGAAATGGGGACGAGTTTCAGAACCTGAGTTACGGATTTGAGCCGGATTATGATCT
GAAACAGCAGATATCGAGCTTGAATCGTTCCTTGAGCTGGACGGTAACACGGCGGAGCAACCGAGTC
AGCTTGATGAGTCCGTTTCCGAGGTGGATATGTGGATGCTTGATGATGTCATTGCGTCGTATGAGTAA
AAGAAAAAAATAAGTTTAAAAAAAGTTAAATAAAGTCTGTAATATATATGTAACCGCCGTTACTTTT
AAAAGGTTTTTACCGTCGCATTGGACTGCTGATGATGTCTGTTGTGTAATGTGTAGAATGTGACCAA
TGGACGTTATATTACGGTTTGTGGTATTATTAGTTTCTTAGATGGAAAACTTACATGTGTAAATAAG
ATTTGTAATGTAAGACGAAGTACTTATAACTTCTTAAGTGTGTTGTGGTAG

SEQ ID NO: 170, AT3G16770.1 Arabidopsis AP2-EREBP family transcription factor, protein sequence 248AA

MCGGAIISDYAPLVTKAKGRKLTAEELWSELDAASAADDFWGFYSTSKLHPTNQVNVKEEA
VKKEQATEPGKRRKRKNVYRGIRKRPWGKWAAEIRDPRKGVVRVWLGTFTAEAAAMAYDV
AAKQIRGDKAKLNFDPDLHHPPPPNYTPPPSSPRSTDQPPAKKVCVVSQSESELSQPSFPV
ECIGFGNGDEFQNLISYGFEPDYDLKQQISSLESFLELDGNTAEQPSQLDESSEVSEVDMWML
DDVIASYE

SEQ ID NO: 171, NM_001066815.1| Oryza sativa (japonica cultivar-group) Os07g0617000 (Os07g0617000) mRNA, complete cds

AGACTACAAGCCATTAAACAGAGACGACCAACGACTTAACCACACTTCTTCTTTGTGCTGTCCAACCT
CCATTGTTGGGTGTGAAAGCTTTGGCTCATCTGCCATGTGTGGAGGATCCATTCTCGGCGACCTTCAC
TTGCCGGTGCGGCGGACAGTGAACGCCGGTGACCTGTGGGGAGACGCCGGCAAGGGTAGAGATGGTGG
CGACGGCTTGAAGAAGAGGAAGGGGAGTTCTTGGGATTTTCGATGTTGATTGCGATGATGATGATGATG
ATGACTTTGAGGCTGATTTTGAGGAGTTTGAGGATGACTATGGCGATGATGATGATGTGGGTTTCGGG
GACGACGACCAAGAATCCGACATGAACGGTCTCAAGCTCGCCGGATTTCAGCACCACGAAGCTCGGCCT
CGGCGGCAGCAGGAAGAGGAAGACGCGATACCGAGGGATCCGGCAGCGGCCATGGGGGAAATGGGCGG
CGGAGATCAGGGACCCCGCAAGGGCGTCCGCGTCTGGCTCGGCACGTTCCGGCACCGCCGAGGAGGCC
GCCATGGCGTACGACGTCGAGGCACGCCGATCCGCGGCAAGAAAGCCAAGGTCAACTTCCCCGACGC
CGCCGCCGCCGCCCGAAGCGGCCACGGCGTTCTTCGGCGAAGCATTCGCCGAGCAGCAGAAGGCCA
GGTCGTCGTCGTCGTCGCCGGCGAGCCTGAACGCCAGCGACGCCGTGTCCAAGTCCAACAACAACCGC
GTCAGCTCGGCTGGGAGCAGCACCGACGCCACCGCCGCCGATCGCCATCGACGACGGCGTCAAGCT
CGAGCTGCTCTCGGAGACGGATCCTTCTCCGCCCATGGCCGCCGCCGCCGCGCGTGGCTCGACGCGT
TCGAGCTGAACGATCTTGACGGATCAAGATGCAAGGACAACGCATTTCGATCACCAGATTCACAAGGTA
GAAGCGGCTGTCGCTGATGAATTCGCGTTCTACGACGATCCGAGCTACATGCAGCTGGGTACCAGCT
CGATCAGGGCAACTCGTACGAGAACATCGACGCGCTCTTCGGCGGCGAGGCCGTCAACATTGGTGGAC
TCTGGAGCTTCGACGACATGCCAATGGAGTTCAG

FIGURE 28 (continued)

AGCTTATTGAGCATTTGATTCTATTTAGGAGGGAGTGAATTATTTGGGAGGAAGAATCGATGTTGTAA
CTTGTA AAAATCTCTGATGATGATCTCTGCATCATATGATCAATTTGAGTGCAGTTTTGTTTTGTAAA
TACGAATTC TTTATTATGATGTTAGGTTCTTAATTTGCCCTTCTTCATCAGGGATTTGTT CAGGCTTT
TGTTGTGATGACTGATTGGACGAGGGAAAGATTGCGTTTTTTTGTTGTCATGTTGGGTACTCTACTCTT
CTGTTCTTAAAGTTGATAAGTGCCAAAATTTGTGAGAGG

MCGGSILGDLHLPLVRRRTVNAGDLWGDAGKGRDGGDGLKKRKGSSWDFDVCDDDDDDDFEADFEED
 DYGDVVGFQESDMNGLKLAFSTTKLGLGSRKRKTRYRGIRQRPWGKWAEEIRDPRKGV
 WLGTFGTAEAAAYDVEARRIRGKKAKVNFDAAAAAPKRPRRSSAKHSPQQQKARSSSSSPASLNA
 SDAVSKSNNNRVSSAGSSTATAAAIAIDDGVKLELLSETDPSPMAAAAAAWLDAFELNDLDGSRCK
 DNAFDHQIHKVEAAVADEFAFYDDPSYMLGYQLDQNSYENIDALFGGEAVNIGGLWSFDDMPMEFR
 AY

CTCGCGCCATCCAAGCGCCCGCCTCTATATATGCGCGCCGCCACCATGTCCAGCTCCGGCAACTAGCT
ACTGCGAAGTGCGAACTGATCAGATCGTCGAGAGGAAACCCAAGATCCAACGACGACATGTGTGGCGG
CGCGATTCTGGCTAACATCATAACGGGCCACCCACGCCCCGCAAGTGCCGCCCCACCACCGCCACCG
CCACCCCCAAGGCGACGACACCGAACGTCTGTCGTCTGTCGTC AACCTCGTCGACAAAGAGGCCGAGGTC
AGCGAGAGCTCCGGTGCCAGCAGCAGCGCGCTGCCGGACTTCTCGTGGCAGGGCATGTCTGGCGTCTGTC
CGACGACGACGCCGCGGCGCAGCAGGCACTCCTCGACGCCGCCGGCGGCGCCAAAGAAGCGTCCCCGGA
GCGAGCCCCACGTACCTCCGACGACGAAGTGCTCCCGGCGTCATTTCGACAGTGACAACAACACCGCC
GCCGCCGGCCTGCTCCCGCTCGACGATCCTTTCTTGTTTCGGCGACCAGTTCGGCGACCTCAACGGCGG
CGCGTTTCGCCTCGCTCATGGACGGGCTGTTTCGCCGCCGGTGAAGCGAACGTCTGCCGCGAGAGCGTGG
GGCTCTGGAGCTTCGGCGACGACTTTCTCAACGCGTCTACTATTAGCTAGGGCTTCCATAGTTCTTG
TACTTTACTTGTACTGTACTGTATTGTACTGATTGTTAACGTTGCCATAAAGCAATCTTGCTAGTTTG
T

MCGGAILANIIIPATPPRPATAAHVWPGGDGEKRRKVGGGGCDDDFEAAFERFGREDSEMEEEVEEVV
 VGKKA AVR RR RAT PAAGRRARPSKYWGVRRRPWGKWA AE IRDPVEGV RVWLGT FATAEAAA HAYDAAA
 RDLRGATAKLNFPSSSSSTAATPRPRKCRPTTATATPKATT PNVVVVVNLVDKEAEVSESSGASSAL
 PDFSWQGSASSDDDAQAALLDAAGGAKKRPRSEPHVTSDDDEVLPA SFDSDNNTAAAGLLPLDDPF
 LFGDOFGDLNGGAFASLMDGLFAAGEANVAGESVGLWSFGDDFLNASYY

TCATCACAAAGCTCACAAGTTTACAACCCAACACCCAAAAGCAAAGAAAAGCAGCAACCAAAGATGTG
CGGCGGAGCGATCCTTGCGGAGCTCATACCGAGCGCGCCGGCGGCGAGGCGCGTCACGGCGGGCCACG
TCTGGCCGGGCGACGCCAACAAGGCCAAGAAGAAGGGCGCGCGCGCCGACGACTTCGAGGCGCGGTTT
CGCGACTTCGACAACGACTCCGATGACGAGGAGATGATGGTGGAGGAGGCGGAGGAGGAGGAGGCGAC
CTCCGAGCACAAAGCCGTTTCGTCTTCCGCGCCAAGAAGGCGGCGGCGGCGGCGGTTCGAGC

FIGURE 28 (continued)

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AGGCGCAGGAAGCCGGCGCAGTACAGGGGCGTGC GGCGCCGGCCGTGGGGGAAGTGGGCGGCGGAGAT
 CCGCGACCCCGTCAAGGGCATCCGCGTCTGGCTCGGCACCTTCACCAACGCCGAGGCCGCGCGCTCG
 CCTACGACGACGCCGCGCGGCCATCCGCGGGGACAGGGCCAAGCTCAACTTCCCTTCCGCTACCACC
 CCTGACACCCGCAAGCGCGGCCGCCACCGCCGCCGCCGCCCGCCCGTCAAGGCGACCCCGGTTCAT
 CAACCTCGTTCGAGGAGGAGGACGAGGAGGAGGTGCGCGCCGCCATGGCGTCCATCAAGTACGAGCCCG
 AGACCAGCGAGAGCTCCGAGTCGAACGCCCTCCCGGACTTCTCCTGGCAGGGCATGTTCGGCCTCCGAC
 GAGTTCGCGCTCGCCGCGGCGGCGCTGTCTGCTCGACAGCGACGACGACCTCGCCAAGAAGCGTCCGAG
 GACCGAGCCGGAGGACACCACCGACTCCGGCTCCGGCGACGACACCGACGCGCTGTTCGACGCGCTGC
 TGTTGCGCGACCAGTACAACCACTTCAACGGCGGCGCCTACGAGTCCCTGGACAGCCTGTTCAGCGCC
 GACGCCGTGCAGACCACCGCCGCCGCCGCCGCCGCCGACCAGGGCATGGGGCTCTGGAGCTTCGACGA
 CGGCTGCTGCCTCGTCGACGTCGAGGCCAGCTTGTCCTTCTAGGCTCTAGCCGTCGTCTCCGGCGACC
 CTGTGACTCGATCTTGTACCATGTCATGTACATAGAAGAGTGGTTTTGCCAAGCAAGCATGTGTTTCGT
 CCTGGTTCCTTTTCGGTAATGAAAAATTATGTGAGGCTTCTCGTTCT

SEQ ID NO: 176, LOC_Os03g08500.1|11973.m06358|protein|AP2-EREBP

MCGGAILAELIPSAARRVTAGHVWPGDANKAKKKGARADDFEAAFRDFDNDSDDEEMMVEEAE
 ATSEHKPFVFRAKKAAAAASSRRRKPAQYRGVRRRPWGKWAAEIRDVPKIRVWLGTFTNAEAAALAY
 DDAARAI RGDRAKLNFP SATTPDTRKRGRATAAAAPAVKATPVINLVEEEDEEVEAAAMASI KYEPET
 SESSESNALPDFSWQMSASDEF AVAAAAALSLDSDDDLAKKRPRTEPEDT TDSGSGDDTDALFDALLF
 ADQYNHFNGGAYESLDSLFSADAVQTAAAAAADQGMGLWSFDDGCCLVDVEASLSF

**SEQ ID NO: 177, Arabidopsis thaliana DNA binding / transcription factor (AT1G72360)
 (gi|12325262:c71325-71139, c71053-70452) Arabidopsis thaliana chromosome 1 BAC
 T10D10 genomic sequence, complete sequence**

ATGTGCGGAGGAGCTGTAATTTCCGATTACATAGCGCCGAGAAGATTGCGAGATCATCTGGAAAGTC
 TTCCTGGAGAAGTAATGGCGTCTTTGACTGCTCAATCTACGATTTTCGATGGAAATTTTCGATGAATTAG
 AGTCCGATGAGCCATTTGTCTTCTCCTCTACTCACAAACATCATGCTTCAGGCTCAGCATCAGATGGG
 AAGAAGAAACAGAGCAGTCGGTACAAAGGAATCAGAAGAAGGCCTTGGGGGAAGATGGGCGGCTGAGAT
 ACGTGATCCAATCAAAGGAGTTTCGAGTTTGGCTCGGGACTTTCAACACAGCTGAAGAAGCTGCAAGAG
 CTTATGATCTTGAAGCTAAGAGAATCCGTGGAGCCAAAGCTAAGCTCAATTTCCCTAACGAATCCTCT
 GGAAAGAGGAAAGCCAAGGCTAAGACTGTGCAACAGGTAGAGGAGAATCATGAGGCTGATCTTGATGT
 GGCGGTGGTAAGCTCAGCGCCTAGTAGTAGCTGTCTTGATTTCTTGTGGGAGGAGAATAATCCGGACA
 CGCTTCTGATTGATACACAATGGCTCGAAGATATCATCATGGGCGATGCGAATAAGAAACATGAACCT
 AATGATAGTGAAGAAGCCAACAACGTTGATGCTTCTCTGCTTTCTGAAGAGCTTCTTGCTTTTGAGAA
 CCAGACCGAATATTTCTCGCAGATGCCTTTTACGGAGGGAAACTGTGATTCCTCAACGTCTCTGAGTA
 GTCTCTTTGATGGAGGCAATGACATGGGTCTATGGTCCTGA

**SEQ ID NO: 178, AT1G72360, AAG52589.1|AC016529_20 putative AP2 domain
 transcription factor; 71325-70452 [Arabidopsis thaliana]**

MCGGAVISDYIAPEKIARSSGKSSWRSNGVFDCSIYDFDGNFDELESDEPFVFSSTHKHHASGSASDG
 KKKQSSRYKGIRRRPWGRWAAEIRDPIKGVVRVWLGTFTNAEEAARAYDLEAKRIRGAKAKLNFPNESS
 GKRKAKAKTVQQVEENHEADLDVAVVSSAPSSSCLDFLWEENNPD TLLIDTQWLEDIIMGDANKKHEP
 NDSEEANNVDASLLSEELLA FENQTEYFSQMPFTEGNCDSS TSLSSLFDGGNDMGLWS

FIGURE 28 (continued)

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**SEQ ID NO: 179, NM_001055711.1| *Oryza sativa* (japonica cultivar-group)
Os03g0182800 (Os03g0182800) mRNA, complete cds**

CCCGCGTCGCGCCATAGCGACGTCTCTCCCGGAGAAAGAAGAGCGCGCCGCGCCATGTGCGGCGGTGC
AATCCTCGCCGATTTACCCCCGGCGAGGGTGCCCCGGCGGCTGACCGCCGCGGAGCTCCTGCCGGTGA
CCCCGACTCCCCCGCGCGCGAGAGGAGAACCACCCGGAAGCGCAAGTCCGACGTCGACTTCGAGGCG
GAGTTCGAGCTTTTCGAGGACGACGACGACGATGAGTTCGAGCTTCCGACGATGGCGACGAGAG
TTTGGCCGTGTCATGTGTGTCGTCCCCCAAGTCGAAGGCAGTACCTTCGTTTTCTTTTTCTGTCGGATG
TCTCCTCGAGCTCCAGGCCGCGGCGGCGGTGGCGGCGGCGGCGGCGGCGGTCGTGCGAAGGCGAGCAAG
AAGAGCAAGTACAGGGGCGTCCGGCGCCGCGCTCGGGGAGGTTTCGCGGCGGAGATCAGGGACCCCAA
GAAGGGGCGGCGGTGTGGCTCGGCACGTACGGCAGCGCCGAGGAGGCCGCCATGGCCTACGACCGCG
AGGCCCCGCGCATCCGCGGCAAGGGCGCGAGGGCTCAACTTCCCCCGCGACGGCGATGGCTCCCCTCGC
CGGAGTAACGACCGGCCCTGCTGGACCATCGACCTCAACCTCCCCGCGGCGGCGCGTCTCCGGTGACGA
CGACGACGCCATGGCCGTGACGCGCGCAGACGCAGACGCAGGCAGTGCTGGCCGTGCAGCAGCCTATG
CAGATCAAGAAGCACTGAGCGCGGCAAAGTGCAAGATCAAGCAGTGTCCTCGCGACGAACAGATGGCG
AGCGCCACACCTGAGCTCATGGAGGAGGACGCGAGCAGCAGCAGAAACATGGTGCCCTGTCCATGGC
GCTGCAGCTGCAGTATGCGGCGATGATCGCCGAATGCGACCGCGAGATGGAGGAGATCGCCGCCGTGG
AGAGGGACCTCGAGAGGCGCAGGAGGCAGGTGTTTCGAGCGCAGAGGCCACCTGGTCAGGCAGGCCTCT
CTTCTGCTCGACTGACGATCTTGCTGAACTGAACTCTGAATGTTTGAGCTTGTCTGAAGTCTGAACTC
TGCACTATGCCATATGGTGTTCACCTTCACTGTGAGGCTGACATGTGGGCCAGACGTCCGTTTGCCT
TGCTTGCTTTTGAGCTGCAACTGGGCGTTGTGCTGCAAGCCTGCAAAGTGCTGTGTAAAGTTTGTGG
GATTGTGTGTGTGGATCTTGATCCTTGCTGACTTTGCAAGCTTTAATTTTGTGAGGAACAATAGTATT
TTAGATTGGTGTGTAAATATAGAAATAAATAATAGTAGCAACTAAATTTTGGTTTTTCAGCTCTTCAT
CAGATGGTTTGTGATGGGAACAAAATTTCAAACATGAGCAAATTAAGGTCATGTTATTATCAATTGTG
AT

SEQ ID NO: 180, LOC_Os03g08460.1|11973.m06354|protein|AP2-EREBP

MCGGAILADFTPARVPRRLTAAELLPVTPTPPAAERRTTRKRKSDVDFEAEFELFEDDDDDDEFELSD
DGDESLAVSCVSSPKSKAVPSFSFSSDVSSSSRPRRRVAAAAAGRRKASKKSKYRGVRRRPSGRFAAE
IRDPKKGRRVWLGTYGSAEEAAMAYDREARRIRGKGARLNFPRDGDGSPRRSNDRPCWTIDLNLPA
VSGDDDDAMAVDAADADAGSAGRAAAYADQEALSAKCKIKQCPRDEQMASATPELMEEDASSSRNMV
PLSMALQLQYAAMIAECDREMEIEIAVERDLERRRRQVFERRGHLVRQASLLLD

**SEQ ID NO: 181, NM_001061846.1| *Oryza sativa* (japonica cultivar-group)
Os05g0361700 (Os05g0361700) mRNA, complete cds**

AGAAGAAAAGCCTTGTGAGTTGGTAATTGATAGTAGCAAGACAATGTGTGGGGGAGCGATCATCGCCG
ACTTCGTCCCGCCCGCGGCGCCGCGCGCGCTGCCTCCGACATCTCCGACAACGCCGTCTCTCC
GCTGCCGGTGCCGGTGACGAGTCGTTTCGCGGCGGCCAAGGCGCCGCGCGCGGGGAGGAAGACGGCGTA
CCGCGGCATCCGGCGCCGCGCGTGGGGACGCTGGGCGGCGGAGATCCGCGACCCGAGGAAGGGCGCCC
GCGTCTGGCTCGGCACCTACGCCACCGCCGAGGAGGCCGCGCGCTACGACGTCGCGGCGCGCGAC
ATCCGCGGCGCCAAGGCCAAGCTCAACTTCCCCCGACCATCGGCGCCGCGCGCGCCACCGCCGCC
CAAGAAGCGACGCAAAGCCGCGCGCGGCGGAACCACCACCACCACCACCAGCAGGAGAGCTCAG
GCTCCTCGTCGGCGTCGTCGCTGCCTCCACCCCGCGCGCGCGCGAGCACCAGCTCCGCGAGTGC
ATGTCCGGGCTGGAGGCGTTCTTGGGCCTCGAGGAGGAGGAGGACGCGGCGCGCGCGGTGAGCCATG
GGACGCCGTGACATGATGCTCGAGTAGGCTCGCCGGAATGGCAGCG

FIGURE 28 (continued)

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TTGCCATGCTCATGCATCCAAGCTTATTCATGCATGCAGCAGCAAGATATACAACCTTTAGTACTACTA
CTATGTTAATTACTACTTACTGCGTAGGTAAATGAAATAAAATGGGGTTGGTTAATTAGGGTGTTCTT
CTGGGAATCCTTGGCTTTGCTAATTGCTAGTACTACTATGTACTTTGGCGTTAAGCATTGCATTGCCA
GGTGATGCATGTCATGTAATCGTGGTAATTATATGGCCGTCCTCCTAGAGCTAGCTAGCAGATTAGAT
TTACTATATAAAGTGGTAGTAGAAATATATGTCCTCCTAGAGCTAACTAGTGTCTTGTAATGATTTCA
GACTTCTTGGGCAACATGAGCAATGCATTTGCACTTCCACTTTACATCT

SEQ ID NO: 182, LOC_Os05g29810.1|11975.m07218|protein|AP2-EREBP

MCGGAI IADVFPPAGARRAAASDISDNAVL SAAGAGDESFAAAKAPAPGRKTAYRGIRRRPWGRWAAE
IRDPRKGARVWLGT YATAEEAARAYDVAARDIRGAKAKLNFPTIGAAAAPPPPKRRKAAAAANHHH
HHHQESSGSSSASSLPPTPPPAEHQLRECMGSL EAFGLGLEEEEDDGGAGEPWD A V D M M L E

SEQ ID NO: 183, NM_001056603.1| Oryza sativa (japonica cultivar-group) Os03g0341000 (Os03g0341000) mRNA, complete cds

ACCTCGCTCTCCTCGTCACCGCGATCGATCGATCGCCGCCGGTTTAGATTTCTTCTACGCGGACCG
CACCCACGCGCTAGGTTTAGCTAGCTAGTTTGCTTGCGCGCAAGCGTCGATCGAGCTAGCTAGTGAAG
ATAGATATGTGCGGCGGCGCCATCCCGCTGATCAGCAGCCGCGGCCCGGCGGCAAGAGGAGCCTCTC
CGCCGCCGATGAGCTCTGGCCGCCGCCGCGCAGCACGCCAGCGACGCCGCGGAGCAAGCGGCGG
CGGATGAGGAGGAGCAGGAGCAGCAGCCGCGCGGAGGAGGAGCGGCGAGGGGAGCGGAGGACGCTG
TACCGGGGCATCCGGCGCAGGCCGTGGGGGAAATGGGCGGCGGAGATCCGCGACCCGGCCAAGGGCGC
CCGCGTCTGGCTCGGCACCTTCGCCACCGCCGAGGCTGCCGCGCGGGCTACGACCGCGCCGCCCGC
GCATCCGCGGCACCAAGGCCAAGGTCAACTTCCCCAACGAGGACAACGCCTTCGCCGCCGCGCCGCCG
CCGTACCACCTCGCCGCCTACTACGGCGACGCCTCCTCCACCTCCTACCTCTACCCGATGGCCATGAC
GCCCCGCCGCCCGGACTGAGGGAGCAGCAGCTGATGACGACGACGGCGGTGGAGTACAGCGTTAATG
ACGCCGTCGACGTGGCCAGCGTTTACTTCCAGCCGCCGCCGCCGCGGCTTGCTTACGAGTTCAGCGCC
GTCGGCGGTGGCGCCGTCTGTCGTGCCGGTGTCGGCGGTGGCGCCGGCGATGACGTACGGACAGAGCCA
AGAGGTGGCGGCTCCGCTCATGTGGAATTTTCATGACATCACGGCCATGCCAATGTGATTGTCTTACC
GTGGAGATTAAGGCATTTAAAGGCTTATAGATAACATAAATTTGCCATGTATGATCAATGGTTAATTC
CTATTGCTCAAGGGCTTATATTAAGGGTTACCTACACGGCATGGCTAGCTTAGCCTACAATTTATGTT
TCTTGCAATTTCTTTCTTTTTTTTGGAGATGAGCTAGTGTGTTATACTATTTGTTTCATCTTTCTGGTA
GTGGTGGATACATTTTCGCCGGCTAGGGTTGGAATTTGTAAATAGAAGATGGTCAATAATAAGATTGT
TTCTGGCT

SEQ ID NO: 184, LOC_Os03g22170.1|11973.m07620|protein|AP2-EREBP

MCGGAIPLISSRGPGGKRSLSAADELWPPPPQHASDDPAEQAAADEEEQEQQPAARRQRRGERRTLYR
GIRRRPWGKWA AEIRDPAKGARVWLGT FATAEAAARAYDRAARRIRG TKAKVNFPNEDNAFAAAPPPY
HLAAYYG DASSTSYLYPMAMTPAAAGLREQQLMTT TAVEYSVND A V D V A S V Y F Q P P P P A V A Y E F S A V G
GGAVVVPVSAVAPAMTYGQSQEVAAPLMWNFDDITAMPM

SEQ ID NO: 185, NM_001071041.1| Oryza sativa (japonica cultivar-group) Os10g0390800 (Os10g0390800) mRNA, complete cds

GTCTCAAACCCAATCAAACCTCCAACCAAACCTCACCTACCTACCCCCAACCCATCCAGAGCTAGAGCTA
TGTGCGGCGGCGCGATCCTCGCCGACCTCATACCGTCGCCGCGCTCCGGCGGCCACACCAAAAAGAAC
AAGCGGCGGCGGATCAGCGACGACGAGGACTTCGAGGCCGCCTTCGAGGAGTTCGACGCCG

FIGURE 28 (continued)

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CGACGACGACTCCGACTCCGACTCCGAGTCCGAGGAGGTAGACGAGTACGACGTCGTCGTCGACGACG
ACGACAGCGAGGACGGCGTGGTGGTTCTTCCGCCGCCGCCGCCGCCGCCGCCGCGTATTCCACATGAG
CGCCATGGCGCGAGGCGGTTCGCGGGCGTGAGGAAGCGGCCGTGGGGGAAGTGGGCGGCGGAGATCCG
CGACCCCGTGCGCGGCGTGCGCGTCTGGCTCGGTACCTTCCCCACCGCCGAGTCCGCCGCGCGCGCCT
ACGACGCCGCCGCCGCCGCCCTCCGCGGCGCCAAGGCCAAGCCCAACTTCCCCTCCGCGCCGCCGCC
TCGGCTGCTGCTCACCGCCGCAAGAAGCGCGCGCCACGCCGCCACGCGCTCGCCGTCGTCCTCCGCC
CGCCACCAGCGAGGTCACGGCGGCGTCCGCGTCCGCGTCCAGCGATGTCCCCGCGCGGCGGCTTCGCTT
CCTTCGTCGGCGAGCCCGGGCACGGCGGCGCCAAGTCGATGCCGACGACGAGCCACACCTCGCAGCCA
GCCCCGCCGGCGACGGTGGCGTCCGAGAAGTCGACGACCCGGAGGTGTTGACCCGTACGACGTCCA
CGGCGGCCTCGCCTCCTACTTCGCCGGCGGCGCGTACGAGTCCCTGGAGAGCCTGTTTCGCGCACGGCG
GCGACAGCGCCCGCGTCGACCAAGCGGCGAGCGACCACTGGCCGGCGGCGCTATGGAGCTTCGACAG
GACGGCTCGTTCTGCTTCTGATGCTGTCAAATCACATCGCCATTGGCGGCCATTGCAAGCCATGGCAT
GGCACCTGATGATGCTGATCCAGTGAAGTGGTCACTCGTTCTTGATGCGTTTTTTCAGTTTCTTGACAG
TGTTTTTCCCCAGCAACAGTGAAGTAGTATTTCAGTTATTCACTGTTTCAGTCATGAGTTCATCGCAAAA
TATGATGTAAGTATGTGTCTTGAGATTGTTTTAGCAGTGGCTTTTGTGTGTATAATGTATTTCTCTGT
AATTAATTAATAGCTGTTTTTCAGTGATAAACTAAATTTTCTG

SEQ ID NO: 186, LOC_Os10g25170.1|11980.m05467|protein|AP2-EREBP

MSQTQSNSNQTHLPTPNPSRARAMCGGAILADLIPSPRSGGHTKKNKRRRISDDDEFEAAFEEDDAGD
DDSDSDSESEEVDEYDVVDDDDSEDGVVVLPPPPPPPPVIPHERHGARRFRGVRKRPWGKWAAEIRD
PVRGVRVWLGTFTAESARAYDAAARRLRGAKAKPNFPSAPPPSAAHRRKKRRAHAATRSPSSPPA
TSEVTAASASASSDVPAPAFASVGEPPGHGAKSMPTTSHTSQPAPPATVASENVDDPEVDFPYDVHG
GLASYFAGGAYESLESLEFAHGGDSAAMDQAASDHWPALWSFADDGSFCF

**SEQ ID NO: 187, gi|46093789:c67744-67046 Oryza sativa (japonica cultivar-group)
genomic DNA, chromosome 9, PAC clone:P0663H05**

ATGCGCCGCCGCGTCTCCTCCTCCTCCTCCTCCTCCTCGTCCTCGTCGCCGGCGAGGCATCACAAGGC
GCGGCGCAGCAGGAGGAAGCTCGCCGTCGACGAGGACTGGGAGGCCGCTTCCGCGAGTTCTCTCCC
GCGACCACGACGACGACGACGACGACGACGACGAGTACGATGTCGTTGTTGCGCCGTTGATCCGTGGT
AGTGACAAGTGCCTCCACGGCCACGAGGTGGTGGCGTCGACGGTCGGCGGTGGCGCAAGCGGCGGACG
ACGACGAGCCGACGACGACGACGAGCGGCGGCGGCGGCGGCGGAGGAGAGCAAGCGGAGCTACCCGT
ACCGCGGCATCCGGCAGCGGCCGTGGGGGAGGTGGGCGTCGGAGATCCGCGACCCCGTCAAGGGCATC
CGCGTCTGGCTCGGCACCTTCGACACCGCCGAGGGCGCCGCGCGCGCTACGACGACGAGGTTGCGCG
CATCTACGGCGGCAACGCCAAGACCAACTTCCCCCATCGCCGCCACGCCGCCGCCGCCGAGAGCAAGC
CAGCGGCGGAGAGGAGCCCTCGACGACGCCGACGACGACGACGAGGACTCCGGCGACTCGCGCATA
CTCATCGAGTGCTGCTCCGACGACCTGATGGACAGCCTCCTCGCCGCCTTCGACATGACCACGGCGA
CATGCGCTTCTGGAGCTAA

SEQ ID NO: 188, LOC_Os09g11460.1|11979.m04408|protein|AP2-EREBP

MRRRVSSSSSSSSSSSPARHHKARRSRRLAVDEDWEAAFREFLSRDHDDDDDDHDGQHVVVAPLIRG
SDKCVHGHEVVASTVGGGASGRRRRADDDDGERRRRRRREKRSYPYRGIRQRPWGRWASEIRDPVKGI
RVWLGTFTDAEGAARAYDDEVRIYGGNAKTNFPSPPTPPPPEKPAERSPSTTPTTTTETDSGDSRI
LIECCSDDLMDSLLAFFDMTTGDMRFS

FIGURE 28 (continued)

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SEQ ID NO: 189, AY044235.1| *Lycopersicon esculentum* transcription factor JERF1 (JERF1) mRNA, complete cds

TTCAAATTGAGCTTTTTCTCCATTAAAATTCTCTCTGCAAATTTATAGTTTTTCTTTTTTCACTTTTT
 GAGAAGAAATCAAAAGCTATGTGTGGTGGTGCAATTATCTCCGATTTGGTACCTCCTAGCCGGATTTC
 TCGCCGGTTAACCGCTGATTTTCTATGGGGTACATCCGATCTGAACAAGAAGAAGAAGAACCTAGTA
 ATTACCACTCAAAGCCCTTGAGGTCTAAGTTTATTGACCTTGAAGATGAATTTGAAGCTGACTTTTCA
 CACTTCAAGGATAATTCTGATGATGATGATGATGTGAAGGCATTTGGCCCCAAATCCGTGAGATCTGG
 TGATTCAAAGCTGCGAAGCTGACAGATCCTCCAAGAGAAAGAGGAAGAATCAGTACCGGGGGATCAGAC
 AGCGTCCTTGGGGTAAGTGGGCAGCTGAAATACGTGATCCAAGGAAAGGTATTCGAGTCTGGCTTGGT
 ACTTTCAATTCAGCCGAAGAGGCAGCCAGAGCTTATGATGCTGAGGCGCGAAGGATCAGAGGCAAGAA
 AGCTAAGGTGAACCTTCTGATGAAGCTCCAGTGTCTGTTTCAAGACGTGCTATTAAGCAAAATCCCC
 AAAAGGCACTTCGTGAGGAAACCCTGAACACAGTTCAGCCCAACATGACTTATATTAGTAACTTGGAT
 GGTGGATCTGATGATTCGTTTCAAGTTTTTTCGAAGAGAAACCAGCAACCAAGCAGTACGGCTTCGAGAA
 TGTGTCTTTTACTGCTGTAGATATGGGACTGGGCTCAGTTTCCCCTTCAGCTGGTACAAATGTTTACT
 TCAGCTCTGATGAAGCAAGTAACACTTTTGACTGCTCTGATTTTCGGTTGGGCTGAACCGTGTGCAAGG
 ACTCCAGAGATCTCATCTGTTCTGTTCGGAAGTCTTGAAACCAATGAGACTCATTTTGATGATGATTC
 CAGACCAGAGAAAAAACTGAAGTCCTGTTCCAGCACTTCATTGACAGTTGACGGTAACACTGTGAACA
 CGCTATCTGAAGAGCTATCGGCTTTTGAATCCCAGATGAAGTCTTGCAGATCCCATATCTCGAGGGA
 AATTGGGATGCATCGGTTGATGCCTTCTCAATACAAGTGCAATTCAGGATGGTGGAAACGCCATGGA
 CCTTTGGTCCTTCGATGATGTACCTTCTTTAATGGGAGGTGCCTACTAAGCTGCATACACATCTTCCC
 CTGCTAAGTTTTGTAAATAACGCTTCATTTGAGTGAAGTTTGCCTGCTGCTTTACGTTTATCACCAA
 CTAAAAGACTATATATGTGTTGTATTAATTTATTCAAATTTACTCGTTTGATATATGTAAGTATGTA
 TCCTTGTTTTTCATAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 190, AAK95687.1| transcription factor JERF1 [*Lycopersicon esculentum*]

MCGGAIISDLVPPSRISRRLTADFLWGTSDLNKKKKNPSNYHSKPLRSKFIDLEDEFEADEFQHFKNDS
 DDDDDVKAFGPKSVRSGDSNCEADRSSKRKRKNQYRGIRQRPWGKWAAEIRDPRKGIRVWLGTFNSE
 EAARAYDAEARRIRGKKAKVNFPEAPVSVSRAIKQNPQKALREETLNTVQPNMTYISNLDGGSDDS
 FSFEEKPATKQYGFENVSTAVDMGLGSVSPSAGTNVYFSSDEASNTFDCSDFGWAEPCARTPEISS
 VLSEVLETNETHFDDDSRPEKKLKSCSSTSLTVDGNTVNTLSEELSAFESQMKFLQIPYLEGNWDASV
 DAFLNTSAIQDGGNAMDLWSFDDVPSLMGGAY

SEQ ID NO: 191, NM_001069317.1| *Oryza sativa* (japonica cultivar-group) Os09g0287000 (Os09g0287000) mRNA, complete cds

AGATATTCAGACACACACCTTCAATAACTTGCAAGGATAACTCAAACACTTGAATCAGATCAGACAA
 AAACATCATAAGAATATCACGATGTGTGGAGGAGCACTGATCCCGAACGACTATGGCGACAAGCCGCC
 GCCGCCGCCGTCGGAGTCGTTCGGAGTGGGACGCCACAACGAAGATGAAGAAGAAGAAGAAGCGTGGTG
 GCGGCGGCGACGACGACTGGGAGGCCGCCTTCCGGGAGTTCATCGCTGGCGACGACGACGACGACGAC
 GGCGGCGTTCATGTTCCCTTCTGGTGCAGGGACGATGGAGACGACCACAGAGGTGGCGCCGGCGGC
 GGCGGTGGTGGAGAGGCCGCGCGCGCGCGCAAGGGTGAGGCGGAGCTACCCGTACCGCGCGCGTCCGGC
 AGCGGCCCGTGGGGGCGGTGGGCGTCGGAGATCCGCGACCCCGTCAAGGGCGCCCCGCGTCTGGCTCGGC
 ACCTTCGACACCGCGCTCGAGGCCGCGCGCGCCTACGACGCCGAGGCGCGCC

FIGURE 28 (continued)

GCATCCACGGCCACAAGGCAAGGACCAACTTCCCGCCCGACGAGCCTCCGCTGCCGGCGCCATCGCAG
GCGCCGTTCTGCTTCCCTGCTCGACGACGACGACGACGACGGCGTGGCCCGTGGAACAGCCCGGC
GTCGTCGTCGGCGCCGGACAGAGCCTCCGCTTGACGACGTCGTCGACGGTGGCGTCCGGCGAGCGAG
GCGATGAGCTCATACTGCTGGAGTGCTGCTCCGACGACGTGATGGACAGCCTCCTCGCCGGCTTCGAC
GTGTCCAGCGAACCACGCAGTGTTTTGGGAATGGTTAATTAGCAGCGCGCACGCCTGATTAGATCGGT
ACATGTGAAGTACAAGAGAAGTAGTTACTACTAGCTAGGAGCAAATTAAGTTGGAGTGCAAGAATAAA
ATATGCATGTCTCTGCACTACTACTGTAGTGTTAGCAAGTTTGCTCATTTGTTCTGTTGTATCCTTTCA
TGTCCATTTAGACTTCCCAATGCTACATAAGGATGTACATATGTATGATGTTGTGTGCCTTGTTAAT
CAATGAATGTAAATATCTTTATATTGCTTTTGTAC

MCGGALIPNDYGDKPPPPPSSESEWDATTKMKKKKKRGGGGDDDDWEAAFREFIAGDDDDDDGGVSMFP
 SGAGTMETTTEVAPAAAVVERPRRRRRVRRSYPYRGVRQRPWGRWASEIRDPVKGARVWLGTFTAVE
 AARAYDAEARRIHGHKARTNFPPDEPPLPAPSQAPFCFLDDDDDDDGVARGNSPASSAPDRASACT
 TSSTVASGERGDELILLECCSDDVMDSLLAGFDVSSEPRSVLGMVN

GACAATTATACATTTCCTCGTCAAAACATAAATCATGTGTGGTGGTTCTATAAATCTCCGATTACATAGA
CCCTAGCCGGACTTCTCGCCGGCTCACCGCCGAGTTTCTATGGGGTCGTTTTCGATCTCGGTAAGAAGC
AAAAAAATCCCAACAATTATCACTCTAAAGCTAAGCATTTGCGATCTGAAGTTGTTGACGACTTTGAA
GCCGATTTTCAGGACTTCAAAGAGTTATCCGATGATGAGGATGTTCAAGTCGATGTCAAGCCATTTGC
CTTCTCTGCTTCCAAACACTCTACTGGTTCCAAATCTTTGAAAACCTGTTGATTCAGACAAGGATGCTG
CTGCTGATAAATCCTCTAAGAGAAAGAGGAAGAATCAATATAGAGGGATCAGACAGAGACCTTGGGGT
AAGTGGGCAGCTGAAATACGTGACCCAAGGAAAGGGGTTCTGGGTCTGGCTGGGAACCTTCAATACTGC
AGAAGAAGCTGCCAAAGCTTATGATATTGAGGCGAGGAGGATCAGAGGCAAGAAGGCTAAGGTAACT
TTCCTGATGAAGCTCCCGCCCCCTGCATCAAGACACACTGTAAAGGTGAATCCTCAGAAGGTCTTCCCT
GAGGAGAGCCTGTATTCACTTCAGTCCGACTCAGCAATCATGAACAGCGTGGAGGATGACCATTATGA
TTCTTTTGGATTTTTTGAAGAGAAACCCATGACAAAACAGTATGGATATGAGAATGGGAGCAGTGCTT
CTGCAGATACGGGATTTGGTTCTGTTCCCTTCAGCTGGCGGTGATATCTACTTCAACTCTGATGTA
GGAAGCAACTCTTTTGAATGCTCTGATTTTGGTTGGGGAGAGCCATGCTCCAGGACTCCAGAGATATC
ATCTGTTCTGTGAGCTGCTATTGAATGTAATGAAGCTCAATTTGTTGAAGATGCCAATTCTCAGAAAA
AGTTGAAATCATGCACCAACAACCCCGTAGCTGATGATGGAACCCCGTTACTATGGTACCTGAAGA
GCTTCCAGCTTTTGAACCTCAGATGAATTTCTTTCATCTCCCATATATGGAGGGAAATTGGGATGCAT
CAGGTGGTAACTTCCTCAACACAAGTGCAACTCAAATGGTGGTGAAAATGCTATGGACCTGTGGTCC
TTTGATGATGTTCCCTCTTTAATGGGAGGTATCTTTTAAGTCAACATGCCTTGAGTTTTGTAAATAAG
GCTTCATGTGAGTGATTTTTTGTGCTTTGTATAATGTACTTAGTGCAAATATTTGATATGTTAATTTGA
TCTCCGTAACTTGTCTTTTAGGTGTGTCTGGTGGTGGAAGAAGAATGATCCACAGAGAACCATGAT
TAAGCCATGGATAATGCACTAAGTAGAGCAGTGCATAGGTAATTAGGTTTAAATTACTACTAGTAGAG
ATGTTAAATTTCGAGTTTTACTTAAAAACAATTGGGCTGTATGGATTATGAGAATTGATGAGACCTCGA
TGCTTGCTATAACGTTACCTTTTTTAGTGTTGCTTTCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 28 (continued)

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SEQ ID NO: 194, AAQ91334.1| JERF3 [*Lycopersicon esculentum*]

MCGGSIIISDYIDPSRTSRRLTAEFLWGRFDLGKKQKNPNNYHSKAKHLRSEVVDDFEADFQDFKELSD
DEDVQVDVKPFAFSASKHSTGSKSLKTVDSKDAAADKSSKRKRKNQYRGIRQRPWGKWAAEIRDPRK
GVRVWLGTFTAEAAKAYDIEARRIRGKKAKVNFPEAPAPASRHTVKVNPQKVLPEESLYSLQSDS
AIMNSVEDDHYSFGFFEEKPMTKQYGYENGSSASADTGFGSFVPSAGGDIYFNSDVGSNSFECSDFG
WGPECSRTPEISSVLSAAIECNEAQFVEDANSQKKLKSCTNNPVADDGNPRYYGT

SEQ ID NO: 195, AY496704.1| *Lycopersicon esculentum* ethylene-binding protein mRNA, complete cds

TCATTTCTGTATCAATCAATATTCTTTGTTTCTGCTGTTTTGATGAAATCACACTAAGATGTGTGGTG
GTGCAATTCTTGCTGATATCATTCCTCCTCGTGACCGCCGTTTGTTCATCCACCGACCTATGGCCGACT
GATTTCTGGCCAATTTCCACCCAAAATGTTCTCTCAACCCCAAACGAGCTCGACCCTCTACAGGTGG
TGAGCAGATGAAGAAGAGGCAAAGGAAGAATCTTTACAGAGGGATAAGACAACGTCCATGGGGTAAAT
GGGCTGCTGAAATTCGTGACCCGAGAAAAGGGGTTAGGGTTTGGTTAGGTACTTTCAACACTGCTGAA
GAAGCTGCAAGAGCTTATGATAGAGAAGCTCGTAAATCAGGGGTAAGAAAGCTAAAGTTAATTTCCC
CAATGAAGATGACGACCATTACTGCTACAGTCATCCAGAGCCCCCTCCCTTGAACATTGCTTGTGATA
CTACTGTTACTTACAATCAAGAATCAAATAACTGTTACCCCTTTTACTCAATCGAGAACGTTGAACCT
GTTATGGAATTTGCAAGTTATAATGGAATTGAAGATGGAGGAGAGGAGATGGTGAAAAATTTGAATAA
CAGGGTTGTAGAGGAAGAGGAGAAAACAGAGGATGAAGTGCAGATACTTTCTGATGAGCTGATGGCTT
ATGAGTCATTGATGAAGTTCTATGAAATACCGTATGTTGACGGGCAATCAGTGGCGGCGACGGTGAAT
CCAGCGGCGGAGACCGCCGTGGGCGGTGGCTCGATGGAGCTTTGGAGTTTGTATGATGTTAGTCGTCT
ACAACCAAGTTATAATGTAGTTTAATTATGTTTTGTTTAACTTTTCATAATTTTATTTTATCGAAT
TAGGAAGAATTGAGTTTTTATAATTTAATCAATTGTGTAAACTATGTTTCTAATTCATTAATATTAT
ATTGGATATGTTGTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 196, AAR87866.1| ethylene-binding protein [*Lycopersicon esculentum*]

MCGGAILADIIPPRDRRLSSTDWLWPTDFWPISTQNVPLNPKRARPSTGGEQMKKRQRKNLYRGIRQRP
WGKWAAEIRDPRKGVRVWLGTFTAEAAARAYDREARKIRGKKAKVNFPEDEDDHICYSHPEPPPLNI
ACDTTVTYNQESNNCYPFYSIENVEPVMFASYNGIEDGGEEMVKNLNNRVVEEEEKTEDEVQILSDE
LMAYESLMKFYEIPYVDGQSVAAATVNPAETAAGGGSMELWSFDDVSRLQPSYNVV

SEQ ID NO: 197, NM_106706.1| *Arabidopsis thaliana* DNA binding / transcription factor (AT1G80580) mRNA, complete cds

ATGGAAAACAGCTACACCGTTGATGGTCACCGTCTTCAATATTCGGTTCCGTTAAGCTCCATGCATGA
AACCAGTCAAACTCCGAACTTACGGATTATCCAAAGAGTCGCCGTTGGTCTGCATGCCCTTGTTTCG
AAACCAACACTACTTCATTTCGATATCTCTTCTCTTTTCTCGTTTAAACCCAAAACCGAAGCCGAAAAC
ACGCATCGTGTTCATGGACGATTCCATCGCCGCCGTCGTGGGCGAAAACGTTCTTTTCCGGTGATAAAA
CAAAGTCTCTGATCACTTGACCAAAGAAGGTGGTGTGAAGCGGGGCGGAAGATGCCGCAGAAGACCG
GAGGATTCATGGGAGTGAGAAAACGGCCGTGGGGGAGATGGTCGGCGGAGATAAGAGACAGGATAGGG
CGGTGCAGACACTGGTTAGGAACGTTTCGACACGGCGGAAGAGGCAGCGCGTGCG

FIGURE 28 (continued)

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TATGACGCGGCGGCGAGGAGGCTTAGAGGGACCAAAGCCAAGACCAATTCGTGATTCCTCCGCTTTT
 TCCCAAGGAAATAGCTCAGGCTCAGGAGGATAATAGGATGAGGCAGAAGCAGAAGAAGAAGAAGA
 AAAAAGTGAGTGTGAGGAAGTGTGTTAAAGTCACATCGGTTGCACAGTTGTTTCGATGATGCCAATTTT
 ATAAATTCTTCTAGTATTAAAGGAAATGTGATTAGTTCTATTGATAATCTTGAAAAAATGGGTCTAGA
 GCTTGATTTGAGTTTAGGGTTGTTGTCTAGGAAGTGA

SEQ ID NO: 198, AT1G80580.1 Arabidopsis AP2-EREBP family transcription factor, protein sequence 256AA

MENSYTVDGHRQLQYSVPLSSMHETSQNSETYGLSKESPLVCMPLFETNTTSFDISSLFSFNPKEPEN
 THRVMDDSI AAVVGENVLFGDKNKVS DHLTKEGGVKRGRKMPQKTGGFMGVRKRPWGRWSAEIRDRI
 RCRHWLGTFTAE EAA RAYDAAARRLRG TKAKTNFVIPPLFPKEIAQAQEDNRMRQKQKKKKKKKVS
 RKCVKVTSAQLFDDANFINSSSIKGNVISSIDNLEKMGLELDLSLGLLSRK

SEQ ID NO: 199, AY286010.1| Nicotiana tabacum callus-expressing factor (CEF1) mRNA, complete cds

GAATTCGGCACGAGAAAAAAGAAAGAAGTTTACTCCGTCAAAAACGAAACTGATTTCTGCATAAACT
 TTTCTGCTGAGAGAAAAACAAAAAGCATGTGTGGTGGTGCTATAATCTCCGATTACATTGCCCGAGCC
 GAAC TTCTCGCCGGCTCACC GCCGAGTTGCTATGGGGCCGGTCCGATCTGAGTAATAAGCAAAAAAAT
 CCTAACAATTATCACTCCAAGCCGTTGAGATCCCAAGTAGTTGACCTAGACGATGACTTCGAGGCTGA
 TTTTCAGGACTTTAAAGATTTCTCCGATGACGAGGATGTTCAAGTCGATGTCAAGCCATTTGCCTTCT
 CTGCTTCGAAAACTCTAATGTTGAAGGCTCCAAATCTGTGAAAACGATGATTCAGACAAGGATGCT
 GATAGATCCTCTAAGAGAAAGAGGAAGAATCAGTATAGGGGGATCAGACAGCGACCTTGGGGTAAGTG
 GGCAGCTGAAATACGTGACCCAAGAAAAGGGGTTCGGGTGTGGCTGGGAAC TTTCAATACTGCAGAAG
 AAGCTGCCAGAGCTTATGATGTTGAGGCTAGGAGGATCAGAGGCAATAAAGCTAAGGTAAACTTTCCC
 GATGAAGCTCCAGTGCCTGCCTCGAGACGTACTGTTAAGGTGAATCCTCAAAGGTCTTCTTAAGGA
 GATCCTGGACTCGGTT CAGCCGACTCGACTATCATAACAACATGGAGGATTGCTGTTATGATTCTT
 TGGGATTTCTTGAAGAGAAACCCATGACGAAGCAGTTTGGATGTGAGGATGGGAGCAGTGCTTCTGGA
 GATACGGGATTTGGCTCATTTGCCCTTCAGCTGGTACCGATATCTACTTCAACTCTGATGTTGGAAG
 TAACTCTTTTGACTGCTCTGATTTTGGTTGGGGAGAGCCATGTGCCAGGACTCCAGAGATATCATCCG
 TTCTGTCAGCTGTTATTGAAAGCAATGAATCTCAACTTGTGGAAGATGATACCAGTCCAATGAAAAA
 CTGAAATCAAGCCCCATTAATCCAGTAGCTGATGATGGAAATACCGCAAACAAGCTATCTGAAGAGCT
 TTCAGCTTTTGAAACCCAGATGAAGTTCCTTCAGATCCCCTATCTGGAGGGAAATTGGGATGCATCAG
 TTGATACTTTCCTCAACTCAAGTGCAACTCAGGATGGTGATAATGCTATGGACTTATGGTCCTTTGAT
 GATGTTCTTCTTTATTGGGAGGTGTCTTTTAAGTCAGCATGCCTTGTCTAGTTTTTGTAATAAGGC
 TTCATGTGAGTGAAC TTTGCTATTGTTTTGCCTCAAAGAAAGGCTCTTTATTATGTACAGAAGCTTTT
 TGAAATGGTAAATAGTTTAATCTCTGTTTAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 200, AAP40022.1| callus-expressing factor [Nicotiana tabacum]

MCGGAIISDYIAPSRTSRRLTAELLWGRSDLSNKQKNPNNYHSKPLRSQVVDLDDDFEADFQDFKDFS
 DDEDVQVDVKPFAFSASKNSNVEGSKSVKTDSDSKDADRSSKRKRKNQYRGIRQRPWGKWAAEIRDPR
 KGV RVWLGT FNTAE EAA RAYDVEARRIRGNKAKVNFPEAPVPASRRTVKVNPQKVLPKEILDVQPD
 STI INMEDCCYDSLGFLEEKPMTKQFGCEDGSSASGDTGFGSFAPSAGTDIYFNSDVGSNSFDCSDF
 GWGEPCARTPEISSVLSAVIESNESQLVEDDTS PMKKLKSSPINPVADDGNTANKLSEELSAFETQMK
 FLQIPYLEGNWDASVDTFLNSSATQDGDNAMDLWSFDDVPSLLGGVF

FIGURE 28 (continued)

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SEQ ID NO: 201, AJ606475.1| *Fagus sylvatica* mRNA for ethylene transcription factor (erf1 gene)

CAAACACACTGAAGAATTAAGTCATTTGGGAATCAGGTTTCTTGGAAAAACCCCTGCCAAAGCCCCTT
 CAAGGCTCTCAGCTTTGAGTCCCCAGATGTGTGGAGGAGCTATAATCTCCGACTTTATAGCGCCAACC
 GGGTCGCGGCGGTTGACGGCGGATTATCTCTGGGGCGATCGGAAAAAACCCATTTTCAGGAAAGCGATT
 CTCGAAGCCTGTAGTCGATTTGGACGACGAATTCGAGCTCGATTTTCAGGGCTTTAAGGACGAGGAGG
 AGTCTGATATCGACGAGGAAGAGGTCCTTGTGCAAGATGTCAAGCCCTTCACTTTTTCTGCTCCTCCT
 AGCTCTGGATCTAAGCCTGTAAAATCCGTGGAATTCAATGGGCAAGCTGAGAAATCTGCAAAGAGAAA
 GAGGAAGAATCAGTATCGGGGGATCCGGCAGCGCCCATGGGGTAAGTGGGCTGCTGAGATTCGAGACC
 CAAGGAAAGGGGTCCGTGTCTGGCTTGGAACTTTTAACACTGCAGAAAAAGCTGCAAGAGCTTATGAT
 GCAGAGGCACGGAGAATTTCGTGGCAAGAAGGCTAAGGTGAATTTTCCCGATGAGACTCCCCGTGCTTC
 TCCAAAGCGTTCAGTTAAGGCAAATCTGCAGAAGCCACTTGCCAAGGCAAACCTGAACTCTGTCCAGC
 CCAACCTGAACCAAAAATTTCAATTTTATGAACAACTCTGATCAGGACTATACCATGGGTTTGATGGAA
 GAGAAACCTTTACAAACCAGTATGGGTATATGGATTCCATCCCTGCCAATGCAGATGTTGGACTAAA
 ACCCTTTGCTTCCAATAATACTACCCCGTACTTTAACTCAGATCAGGGGAGTAACTCGTTTGATTGTT
 CTGACTATGGATGGGGAGAACAGGGCTCTAAGACTCCAGAAATCTCATCTGTTCTTTTCAGCTACTTTA
 GAAGGGGATGAATCTCAGTTTGTGGAGGATGCTATGCCACGAAGAAATGAAGTCAGACTCTGGGAA
 TGCAGTGTTCAATTGAAAATAACACTGCAAAGACACTGTCAGAGGAGCTCTCAGCTTTTGAGTCCCAGA
 TGAACCTTTCAGATGCCATTTCTTGAGGGAAGCTGGGAATCCAACATGGAGGCACTGTTTCAGTGGGGAC
 ACAACTCAGGATGGTAACTCGATGGATCTTTGGAGCTTCGATGACCTCCCCGTTATGGCTGGGGGAGT
 TCTGTGACCGCAAACTATTTTCCGCATGCTTGCTGTTCTAGTTTATGTATAAATAAGGCTAAATACA
 TGTTAGAATGGTTTGTCTATTCTGTGGAGATGGACATGCCTGTGGTTTCAAACAAGCTGAACACTGAAT
 GCTTAAGACTCTATGAAGGGATGTACTGAAGTAGTGTGTTCTACTGTTGTATGAGGGAGTACATAGG
 TCCCTATTTAGGATCCCTTTGAGAGACTACCTTGAAGACATTGAATTTTGGGATTTTGAATTTGATGT
 TTTTGTATTGATGATTATGTGTGATGAAACCTCTGTCATAAAAATACTAACTAAAAACCTGATGTAT
 GTCAACTGTGTTTAGTGTGTTGTTTCAAAAAAAAAAAAAAAAAA

SEQ ID NO: 202, CAE54591.1| ethylene transcription factor [*Fagus sylvatica*]

MCGGAIISDFIAPTGSRRLTADYLGDRKKPISGKRFSKPVVDLDDEFELDFQGFKDEEESDIDEEEV
 LVQDVKPFTEFAPPSSGSKPVKSVEFNGQAEKSAKRKRKNQYRGIRQRPWGKWAAEIRDPRKGVRVWL
 GTFNTAEKAARAYDAEARRIRGKKAKVNFDETPRASPKRSVKANLQKPLAKANLNSVQPNLNQNFNF
 MNNSDQDYTMGLMEEKPFTNQYGYMDSIPANADVGLKPFASNNTPYFNSDQGSNSFDCSDYGWGEQG
 SKTPEISSVLSATLEGDESQFVEDAMPTKKLKS DSGNAVFIE NNTAKTLSEELSAFESQMNFQMPFLE
 GSWESNMEALFSGDTTQDGN SMDLWSFDDL PVMAGGV L

SEQ ID NO: 73, AJ420195.1| *Fagus sylvatica* partial mRNA for ethylene responsive element binding protein (erebp1 gene)

CAACAATATTTTCTCTCACAAAACTAACTCTCTGTATTTCCCAAACTTTCCAAAAAACCATTTTA
 CTTTTACCCATCCGAGCAAAAAAACAAGAGAAAAAAGAAACCCCTCCAAAAAAGCCAAGACCGCC
 ATGTGTGGAGGAGCTATAATCTCCGACTTTATAGCGCCAACCGGGTCGCGGCGGTTGACGGCGGATTA
 TCTCTGGGGCGATCGGAAAAAACCCATTTTCAGGAAAGCGATTCTCGAAGCCTGTAGTCGATTTGGACG
 ACGAATTCGAGCTCGATTTTCAGGGCTTCAAGGACGAGGAGGAGTCTGATATCGACGA

FIGURE 28 (continued)

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GGAAGAGGTCCTTGTGCAAGATGTCAAGCCCTTCACTTTTTCTGCTCCTCCTAGCTCTGGATCTAAGC
CTGTAAAATCCGTGGAATTCATGAGGCAAGCTGAGAAATCTGCAAAGAGAAAGAGGAAGAATCAGTAT
CGGGGGATCCGGCAGCGCCCATGGGGTAAGTGGGCTGCTGAGATTCGAGACCCAAGGAAAGGGGTCCG
TGTCTGGCTCGGAACTTTTAACACTGCAGAAGAAGCTGCAAGAGCTTATGATGCAGAAGCACGGAGAA
TTCGTGGCAAGAAAAGCAAAGGGAATTTCCGATGAGACTTCCCGTGCCAAAGCGTTCAGTTAAGGCA
AATCTGCAGAAGCCACTTGCCAAGGCAAACCTGAACTCTGTCCAGCCCAACCTGAACCAAAATTTCAA
TTTTATGAACTCTGATCAGGACTATACCATGGGTTTGATGGAAGAGAAACCTTTACGAACCAGTATG
GGTATATGGATTCCATCCCTGTCAATGCAGATGTTGGACTAAAATCCTTTGCTTCCAATAATACTGCC
CCATACTTTAACTCAGATCAGGGGAGTAACTCGTTTGATTGTTCTGACTATGGATGGGGAGAACAGGG
CTCTAAGACTCCAGAAATCTCATCTGTTCTTTCAGCCACTTTAGAAGGGGATGAATCTCAGTTTGTGG
AGGATGCTGTGCCCACGAAGAAATTGAAGTCAGACTCTGGGAATGCAGTGTTTCAATTGAAAATAACACT
GCAAAGACACTGTGAGAGGAGCTCTCAGCTTTTGAGTCCCAGATGAACTTTCAGATGCCATTTCTTGA
GGGAAGCTGGGAATCCAACATGGAGGCACTGTTCACTGGGGACACAACCTCAGGATGGTAACTCGATGG
ATCTTTGGAGCTTCGATGACCTCCCCGTTATGGCTGGGGGAGTTCTGTGAGCAAACTATTCCCATGCT
TGCTAGTTTATGTAAATAAGGCTACATGTTAGAATGGTTTGTCTATCTGTGATGGACATGCCGTTTCAA
ACAAGCTGTGAACATGCTTAAGACTCTTATGAAGGATGTACTGAAGTAGTCTACTGTTGTATGAGGAG
TACATAGGTATTTAGGATCCCTTTCTCCCTTGAAGACATTGAATTTGGGATTTTGAATTTGATCTTTG
TATTGATGATTATGTGTGATCTGTCAAAAAATACTAAAAACCTGATGTATGTCAACTTTAGTGTTTG
TTTCTATCTTGGTTCTTTTACAAAAGGGCCTTCAATTTTTGTACTGTTTATTTGTTTTTATGGTTT
TTGATTTTACCTAAAAA

SEQ ID NO: 204, CAD21849.1| ethylene responsive element binding protein [*Fagus sylvatica*]

MCGGAIISDFIAPTGSRRLTADYLWGDRKKPISGKRFSKPVVDLDFELDFQGFKDEEESDIDEEV
LVQDVKPFTEFAPPSSGSKPVKSVEFNGQAEKSAKRKRKNQYRGIRQRPWGKWAAEIRDPRKGVRVWL
GTFNTAEAAARAYDAEARRIRGKSKGNFPMRLPVPKRSVKANLQKPLAKANLNSVQPNLNQNFNFMN
SDQDYTMGLMEEKPFNTQYGYMDSIPVNADVGLKSFASNNAPYFNSDQGSNSFDCSDYGWGEQGSKT
PEISSVLSATLEGDESQFVEDAVPTKKLKS DSGNAVFIENNTAKTLSEELSAFESQMNFMQMPFLEGSW
ESNMEALFSGDTTQDGNMMDLWSFDDLPMAGGVL

SEQ ID NO: 205, DQ412079.1| *Capsicum annuum* putative ethylene-responsive element binding protein (JERF1) mRNA, complete cds

ACGCGGGGAAATTAACCTTTCTCCATTGAAATTCAGTGCAGAAAAAAACCCTTTCCAGTTATAATA
CACTACTTAAATTATTAGAGAAAAGAAAAAGCTATGTGTGGTGGTGCAATTATCTCCGATTTGGTACC
TCCTAGCCGGATTTCCCGCCGGCTAACCGCCGAGTTGCTATGGGGTAACTCTGATCTGAGCAAAAAGA
AGAAAAATCCAGGGAATTATTACTCAAAGCCTTTGAACAGGTCTAAGTTTATTGACCTTGATGAGGAA
TTTGAAGCTGACTTTCAGGACTTCAAGGACTATGCCGATGACGATGTTGATGATGTTAAGCCCTTCGG
TTCCAAATCTGTGAAATCTGGCGATTCAAGCTGCGATACTGAAAAATCTTCCAAGAGAAAGAGGAAGA
ATCAGTACCGGGGGATCAGACAGCGTCTTGGGGTAAAGTGGGCAGCTGAAATTCGTGATCCGAGGAAA
GGGATTCGAGTTTGGCTTGGAACCTTCAATTCTGCGGAAGAAGCAGCTAGAGCTTATGATGTTGAGGC
ACGAAGGATCAGAGGCAAGAAGGCTAAGGTGAACTTTCCTGATGGATCTCCAGCTTCTGCTTCAAGAC
GTGCTGTTAAGCCAAATCCTCAGGAGGCACTTCGCGAGGAAATCTTGAACACAGTTCAGCCGAACACA
ACTTATATCAACAACTTGGACGGCGGATCTGATGATTGCTTTGGCTTTTTCGAAGAGAAACCAGCAGC
AAAGCAGTATGGCTATGAGAATGTTTCTTTTACTGCTGGAGATA

FIGURE 28 (continued)

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TGGGACTGGGTTCAATTTCCCCTTCAACTGGTACAACAAATGTTTACTTCAGTTCTGATGAAGGAAGC
AACACCTTTGACTGCTCTGATTTTCGGTTGGGGTGAACCATGTCCGAGGACTCCAGAGATCTCATCTGT
TCTGTGAGAAGTTCTAGAATGTAATGGTACTCAATCTGATGAAGATGCTAGACCAGAGAAAAAACTGA
AGTCGTGTTCCAACGCTTCCTTGCCAGATGAGGATAACACTGTGCACACGCTATCTGAAGAGCTATCG
GCTTTTGAATCCCAGATGAAGTTCTTGCCAGATCCCATATCTTGAGGGAAATTGGGATGCATCAGTTGA
TGCCTTTGTCAACACAGGCGCAATTCAGGATGGCGGAAATGCGATGGATCTCTGGACCTTCGATGATG
TTCCTTCTTTAATGGGAGGTGTCTACTAAGCCAACACGCACCTTCCCTTACTAAGTTTTGTAAATAAA
GCTTCATTTGAGTGAAGTTTGCAGTTATGTTGTCTCCAAACAAAAAAGACTATATATGTGTTGTATTA
AATTTATTTCATAAATTTACTTGTTTGATACAAAAA

**SEQ ID NO: 206, ABD65407.1| putative ethylene-responsive element binding protein
[Capsicum annuum]**

MCGGAIISDLVPPSRISRRLTAELLWGNSDLKSKKKNPNGNYYSKPLNRSKFIDLDEEFEDFQDFKDY
ADDDVDDVKPFGSKSVKSGDSSCDTEKSSKRKRKNQYRGIRQRPWGKWAEEIRDPRKGIRVWLGTENS
AEEAARAYDVEARRIRGKKAKVNFDPGSPASASRRVKNPNQEALREEILNTVQPNNTTYINNLDGGSD
DSFGFFEEKPAKQYGYENVSF TAGDMGLGISPSTGTTNVYFSSDEGSNTFDCSDFGWGEP CPTPE
ISSVLSEVLECNQTQSD EDARPEKKLKSCSNASLPDEDNTVHTLSEELSAFESQMFLQIPYLEGNWD
ASVDAFVNTGAIQDGGNAMDLWTFDDVP SLMGGVY

SEQ ID NO: 207, AY246274.1| Capsicum annuum PF1 mRNA, complete cds

AGTTATAATACACTACTTAAATTATTAGAGAAAAGAAAAGCTATGTGTGGTGGTGCAATTATCTCCG
ATTTGGTACCTCCTAGCCGGATTTCCCGCCGGCTAACCGCCGAGTTGCTATGGGGTAACTCTGATCTG
AGCAAAAAGAAGAAAATCCAGGGAATTATTACTCAAAGCCTTTGAACAGGTCTAAGTTTATTGACCT
TGATGAGGAATTTGAAGCTGACTTTCAGGACTTCAAGGACTATGCCGATGACGATGTTGATGATGTTA
AGCCCTTCGGTTCCAAATCTGTGAAATCTGGCGATTCAAGCTGCGATACTGAAAAATCTTCCAAGAGA
AAGAGGAAGAATCAGTACCGGGGGATCAGACAGCGTCCTTGGGGTAAAGTGGGCAGCTGAAATTCGTGA
TCCGAGGAAAGGGATTTCGAGTTTGGCTTGGAACCTTCAATTCTGCGGAAGAAGCAGCTAGAGCTTATG
ATGTTGAGGCACGAAGGATCAGAGGCAAGAAGGCTAAGGTGAACCTTCTCTGATGGATCTCCAGCTTCT
GCTTCAAGACGTGCTGTTAAGCCAAATCCTCAGGAGGCACTTCGCGAGGAAATCTTGAACACAGTTCA
GCCGAACACAACCTTATATCAACAACCTTGGACGGCGGATCTGATGATTCGTTTGGCTTTTTTGAAGAGA
AACCAGCAGCAAAGCAGTATGGCTATGAGAATGTTTCTTTTACTGCTGGAGATATGGGACTGGGTTCA
ATTTCCCCTTCAACTGGTACAACAAATGTTTACTTCAGTTCTGATGAAGGAAGCAACACCTTTGACTG
CTCTGATTTTCGGTTGGGGTGAACCATGTCCGAGGACTCCAGAGATCTCATCTGTTCTGTCAGAAGTTC
TAGAATGTAATGGTACTCAATCTGATGAAGATGCTAGACCAGAGAAAAAACTGAAGTCGTGTTCCAAC
GCTTCCTTGCCAGATGAGGATAACACTGTGCACACGCTATCTGAAGAGCTATCGGCTTTTGAATCCCA
GATGAAGTTCTTGCCAGATCCCATATCTTGAGGGAAATTGGGATGCATCAGTTGATGCCTTTGTCAACA
CAGGCGCAATTCAGGATGGCGGAAATGCGATGGATCTCTGGCCTTCGATGATGTTCTTCTTAAATGG
GAGGTGTCTATAAGCCAACACGCACCTTCCCTTATTAAGTTTTGTAAATAAAGCTTCATTTGAGTGAA
GTTTGCAGTTATGTTGTCTCCAAACAAAAAAGACTATATATGTGTTGTATTAAATTTATTTCATAAAT
TTACTTGTTGATGTAAAAA

FIGURE 28 (continued)

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SEQ ID NO: 208, AAP72289.1| PF1; CaPF1 [Capsicum annuum]

MCGGAIISDLVPPSRISRRLTAELLWGNSDLSSKKKKNPGNYYSKPLNRSKFIDLDEEF EADFQDFKDY
ADDDVDDVKPFGSKSVKSGDSSCDTEKSSKRKRKNQYRGIRQRPWGKWAAEIRDPRKGIRVWLGT FNS
AEEAARAYDVEARRIRGKKAKVNFDPGSPASASRRVKNPQEALREEILNTVQPNTTYINNLDGGSD
DSFGFFEEKPAAKQYGYENVSF TAGDMLGSI SPSTGTTNVYFSSDEGSNTFDCSDFGWGEP CPTPE
ISSVLSEVLECNGTQSD EDARPEKKL KSCSNASLPDEDNTVHTLSEELSAFESQM KFLQIPYLEGNWD
ASVDAFVNTGAIQDGGNAMDLWPSMMFLL

SEQ ID NO: 209, AY529642.1| Capsicum annuum ethylene-responsive factor-like protein 1 (ERFLP1) mRNA, complete cds

ATTCTCAAAAATAATTTTTTCATTTCTGATTCAATCTTGTTGTTTCTTTCATTTTGAAAAAAAAGAA
GAAGAAGAAGAGTACTTTAACTACACTGCAAATGTGTGGTGGAGCAATTCCTTGCTGATATCATTCCT
CGTCGTGACCGTCGTCTGTCATCCACAGACTTATGGTCAATTTGTTCTGATGATTTCTGGCCAAATTC
TTCATTTTCCAAGCCATTTTCCACCCAAAATGTTTCCCCTGCAAAGCCCAAACGAACTCAACCCTCTG
CAGGTAATGAGCAAATCCAGAAAGCCAAGAAAAGGCAAAGGAAGAATCTATACAGGGGAATCCGCCAG
CGTCCATGGGGTAAATGGGCAGCTGAAATTCGTGACCCAAGAAAAGGGGTGAGAGTCTGGTTAGGTAC
TTTCAACACTGCTGAAGAAGCTGCTAGAGCTTATGACAAAGAAGCTCGTAAAATCCGGGGAGAGAAAG
CTAAAGTTAATTTCCCAAATGAAGATGATCACTACAGTTATCCAGAGCCTCCTCCTCTCGCTGCTTAC
AATAATACTACTTTTTATAATAATTGCTATGCGTTCGAGAACAAATGAACCCGTTATCGAATATGCAAT
AGCTAACACAATGATCAAAATGGGCTGATTAAAGAGGTGGAAAATATGAATGGAAGGGTCTGGGAGG
AGGAGGAAAAAACAGAGATTCAAGTGCAGAACTCTCTGAGGAACTGATGGCTTATGAGTCATTGATG
AAGTTTTATGAGATCCCTTATGTTGATGGGCAATCAGTGGCGCGGATGGCGAATCCAGCGGCGGAGGC
TGTCTTGGGTGGTGGCTTGATGGAGCTTTGGAGTTTGTATGATGTTAGTCGTCAACAACCTAGTTATA
ATGTAGTTTGATTATTGTTTGTACATTGTTGTATGTTTTTATTTTTTCGGTTTAGGAGAATGGGTTT
CCTTGTAATCTCAATGTTTAAGCAATTGGTAAACTATTGTCTCTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

SEQ ID NO: 210, AAS20427.1| ethylene-responsive factor-like protein 1 [Capsicum annuum]

MCGGAILADIIPRRDRRLSSTDLWSICSDDFWPNSSFSKPFSTQNVSPAKPKRTQPSAGNEQIQKAKK
RQRKNLYRGIRQRPWGKWAAEIRDPRKGVRVWLGT FNTAEEAARAYDKEARKIRGEKAKVNFNEDDH
YSYPEPPPLAAYNNTTFYNNCYAFENNEPVIEYAIANNNDQNGLIKEVENMNGRVVEEEEKTEIQVQK
LSEELMAYESLMKFYEIPYVDGQSVAAMANPAEAVLGGGLMELWSFDDVSRQQPSYNVV

SEQ ID NO: 211, AY781117.2| Gossypium hirsutum ethylene-responsive element binding protein ERF2 mRNA, complete cds

AAAAAACCAACCCATTTATTTCACTACCCAACAACCCAAAAGATAAAAGGAATCGTTTACTTGTTTCGT
AGCAATTTATCGTCATTTCAAGCTCAATTCTCTGAAAATTTTGTGCTGAACCTCTTTTTTCTCTTTG
TACCACCATGTGTGGAGGTGCTATTATCTCCGATTTTCATACCGCCGTCGCGGTGCGGACGATTGACGG
CCGATTTCTTGTGGCCCGATCTGAAAAAATCCGGGTTGAAGAAGGGGTGCGGTAAGAGATACTCGAAG
CCCGTGATCGACTTGGGCGATGATTTGAGACTGACTTTCAGGAGTTCAAAGATGAAGAATCTGATAT
AGATGATTATGATGTTGATGATGTTTTGGCTGATGTAAAGCCCTTTGCTTTTAACGCTACAAAGAAAC
CTGCTTCTGCTGTCTCTCATGGTTCGAACTCTGAAAATCCATGCAATTCAATG

FIGURE 28 (continued)

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GTCAAGCTGAGAAATGTGCGAAAAGAAAGAGGAAGAACCAGTATCGTGGAATCCGGCAGCGCCCATGG
GGTAAATGGGCTGCTGAGATCCGTGACCCAAGGAAAGGGGTAGGGTCTGGTTAGGAACTTTCAATAC
TGCTGAAGAAGCTGCGAGAGCTTATGATGCTGAGGCACGGAGAATTCTGTTAAGAAAGCTAAGGTGA
ACTTCCCTAACGAGACTCCGCGTACCTCTCCAAAGCATGCAGTCAAGACAAATTCTCAGAAACCACTT
TCCAAGTCAAATTCGAGCCCTGTTTCAGCCAAATCTCAACCAGAATTACAATTACTTGAACCAGCCTGA
GCAGGAATACTTTGATACCATGGGTTTCGTAGAAGAGAAGCCATCGGTCAATCAGTTCGCATACGTGG
ACCCTGTTCCCTACGTCTATAGATGCTGGATTTAATCAATCAGATAATGCCCCCTTGTAATTCAATTCA
GACCAGGGAAGTAACCTCGATCAATTGTTCCGACTATGGCTGGGGAGAACAGGGTGCCAAAACCTCCTGA
AATATCATCCATTCTGGAAGCTTCTGTAGAGGGTGATGAGTTTCTTGAGGATGCTAACCTAGCAAGA
AGCTGAAACCAAGTTCCGACAATGTTATGCCTGCCGAAGACAACCTCCGCGAAGACCTTGTCGGACGAG
CTGTTGGCTTTGGACAACCAGATGAAATACTTCCAAATGCCGCCATTTATTGAAGGAAACTGGGACGC
CACTATTGATGCTTTCCTCAATGGAGATGCAACACAGGATGGTGGAACCCGATGGATCTTTGGAACCT
TTGATGATTTCCCTACCATGGCGGAGGGTGTTTTCTGAGCGAACCTTCCATAATAACTAGTGTGTTGTA
AATAAAGCAACATGAATTTGGTCAAAATCTGTTGTGAAGTTGAAGTAAAAACCAAGCTATATGCATGC
TTAAGCCTTGCCCTGCACTGCTTTCAGAGGTTTTTAGTATGTACCCCTTTTTTATGTGTTTTTTTGTAG
ACTTTGGACTAAATTTTAAATTTGAGTGACTGTATAAGTAACTGTGTCTGAATTTGTCTATGTTTGAA
TACTGAAAAACATATGAATGTTTTAAACCCAAAAA

**SEQ ID NO: 212, AAX07458.2| ethylene-responsive element binding protein ERF2
[Gossypium hirsutum]**

MCGGAIISDFIPPSRSRRLTADFLWPDLLKSGGLKKGSGKRYSKPVIDLGDDFETDFQEFKDEESDIDD
YDVEDVLADVLPFAFNATKKPASAVSHGSNSEKSMQFNGQAEKCAKRKRKNQYRGIRQRPWGKWAAEI
RDPRKGVVRVWLGTFTAEAAARAYDAEARRIRGKKAKVNFPNETPRTSPKHAVKTNQKPLSKSNSP
VQPNLNQNYNYLNQPEQEYFDTMGFVEEKPSVNQFAYVDPVPTSIDAGFNQSDNAPLYFNSDQGSNSI
NCSDYGWGEQGAKTPEISSILEASVEGDEFLEDANPSKKLKPSSDNVMPAEDNSAKTLSDELLALDNQ
MKYFQMPPFIEGNWDATIDAFLNGDATQDGGNPMDLWNFDDFPTMAEGVF

**SEQ ID NO: 213, AY572463.1| Gossypium barbadense ethylene response factor 1
mRNA, complete cds**

TTGAGAATCGATGCCCCGATTAATAATTTCTGGGATGTAGTCACTAAAAAGGCCTTCTCATGATTTT
CTTGACAGTTAAAGGTCTTAAATTATATTTCTTGTGACAGTTATGTTGTGATTTGTAGTTTTTCATGG
ATGAGTAATGTTTATTTATGGTTCATGTATCCGTACGATATTAAATTTTCTTTTGTGCTCTATCAT
TGAAGGTTGCAACTCTGAAAAGTCCATGCAGTTCGATGGTCAAGCTGAGAAATGTGCGAAAAGAAAGA
GGAAGAACCAGTATCGTGGAATCCGGCAGCGCCCATGGGGTAAATGGGCTGCTGAGATCCGTGACCCA
AGGAAAGGGGTAGGGTCTGGTTAGGAACTTTCAATACTGCTGAAGAAGCTGCGAGAGCTTATGATGC
TGAGGCACGGAGAATTCGTGGTAAGAAAGCTAAGGTGAACCTCCCTAACGAGACTCCGCGTACCTCTC
CAAAGCATGCAGTCAAGACAAATTCTCAGAAACCACTTCCAAGTCGAATTTGAGCCCTGTTTCAGCTA
AATCTCGACCAGAATTACAATTACTTGAGCCAGCCTGAGCAGGAATACTTCGATACCATGGGTTTCGT
AGAAGAGAAGCCACTGGTCAATCAGTTTGCATATGTGGACCTGTTCCCTACGTCTATAGATGCTGGAT
CTAATCAATCAGATAATGCCCCCTTGTAATTCAATTCGGACCAGGGAAGTAACCTCCATCAATTGTTCC
GACTATGGCTGGGGAGAACAGGGTGCCAGAACCTCTGAAATATCATCCATTCTTGAAAGCTTCTGTAGT
GGGTGAAGAGTTTCTTGAGGATGCTAACCTAGCAAGAAGCTGAAACCAAGTTCTGACAATGTTATGC
CTGCCGAAGACAACCTCCGCGAAGACCTTGTCGGACGAGCTGTTGGCTTTGGACAACCAGATGAAATAC
TTCCAATGCCGCCATTTATTGAAGGAACTGGGACGC

FIGURE 28 (continued)

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CACTATTGATGCTTTCCTCAATGGAGATGCAACACAGGATGGTGGAAACCCGATGGATCTTTGGA
TTGATGATTTCCCTACCATGGCGGAGGGTGTCTTCTGAGCGAACTTTCCATAATACTAGTGTGTA
AATAAAGCAACATGAATTTGGTCAAAATCTGTTGTGAAGTTGAAGTAAAAACCAAGCTATATGCATGC
TTAAGCCTTGCCTGCACTGCTTTCAGAGGTTTTTAGTATGTACCCCTTTTTTATGTGTTTTTTGTAG
ACTTTGGACTAAATTTTAAATTTGAGTGACTGTATAAGTAATTGTGTCTGAATTTGTTTATGTTTGAA
TACTGAAAAACATATGAATGTTTTAACTCTGCTATTGTTTCTCCCAAAAAAAAAAAAAAAAAAAAA
AAAAA

SEQ ID NO: 214, AAT77192.1| ethylene response factor 1 [Gossypium barbadense]

MSNVYLWFMYPYDIKFFFLCSIIEGSNSEKSMQFDGQAEKCAKRKRKNQYRGIRQRPWGKWAAEIRDP
RKGVRVWLGTFTNTAEAAAYDAEARRIRGKKAKVNFNPNETPRTSPKHAVKTNQKPLSKSNLSPVQL
NLDQNYNYLSQPEQEYFDTMGFVEEKPLVNQFAYVDPVPTSIDAGSNQSDNAPLYFNSDQGSNSINCS
DYGWGEQGARTPEISSILEASVVGEEFLEDANPSKKLKPSDDNVMPAEDNSAKTLSDELLALDNQMKY
FQMPFFIEGNWDATIDAFLNQDATQDGGNPMDLWNFDDEFTMAEGVF

SEQ ID NO: 215, AY817134.1| Gossypium hirsutum putative ethylene responsive element binding protein mRNA, complete cds

CGGCACGAGGAGAGAGAGAGAACTAGTCTCGTGCCGGGAAAATTTACAATTAAAAAAATTAATTTTGC
CCTCTAAATTTCTCTAAAAAATCTCCTAAATCCCATACTTTAAATCCAATTCGCCATGTGTGGAGGTG
CGATTATCTCCGATTTTCATTCCGCCTGCGCGGTGCGGACTGGTGACGGCGAATTATTTGTGGCCGGAT
CTGAAAAAATCCGGCTCTAAAAAGCGGTGCGGTAGAAAGCACTCGAAGAAGCCGGCGGTGCGCTTTGA
AGATGACTTCGAGGCTGATTTTTCAGGTGTTTAAGGATGAGGATTCTGATGTCGATGACTTCAACGATG
ATGTTGATGATGTTTTGGCTGATGTTAAGTCCTTTGCTTTTTCTGCTACAAAGAAACCCTCTCCTGCT
GTTTCTCATGGTTCAAACCTCCATAAAATCTGTGGAATTCAGTGGTCAAGCTGAGAAATCTGCAAAAAG
AAAGAGGAAGAACCAGTATCGCGGAATTCGCCAGCGTCCGTGGGGTAAATGGGCTGCTGAGATCCGTG
ATCCTAGGAAAGGGGTAGGGTGTGGCTTGGAACTTTTAATACTGCTGAGGAAGCTGCACGAGCTTAT
GATGCTGAGGCACTGAGAATTCGGGGTAAGAAAGCAAAGGTGAACCTCCCTGATGAGACTCCACGTAC
CACTCCAAAGCATGCTGTTAAATGAATTCTCAGAAACCTCTTCCGGGTCAAATTTGAGTTCTGTTTC
AATCAAGTCTCAACCCAGATTTTCAGTTACTCGAACAACTTGAGCAGGGCTACTATGATACCGTGGGT
TTCATTGAAGAGAAGTCACTAATGGATCAGTTTGCATATGCAGACCCTGTTAGAGCTGCTGTAGATGA
TGGGTTAAAACCCTTTGCTGACCCTGAGAATACCGCTTCGTTTTTTATCTCAGATCCAGGGAGTAACA
ACTTTGACAGTTCCGACCTTGTCTGGGGCGACCAGGGTGCCAAGACTCCTGAAATATCATCCTCTCTT
GAACCTACTCTAGAGGTCAACGAGTTTCTGGACAACGCAAACCCTACGAAGAAGTTGAAACTGAGCTT
GAATAATGTCATGCCTACTGGAGGAGACAATTCGGTAAAGAGTTTATCCGATGAGCTATTAGCTATGG
ACAATCAAGTGAACCTACTTTCAGACACCATTTATTGACGAGAAGTGAATGTTTCGATGGATGACTTC
CTTAATGGAGATGCAACTCAGGTGGCGGAAACGAAATGGGTTTTTGGAGCTTTGATGACTTTCCTTC
CATAGATGGGGTATTTTCTGAACAACTCTCCTTACTTATTATCCGTTCCGTACATAAGGCATCGT
GTTAGCGAGTTTCGACCCTCTGGCAACTGCTTGACTATTGTTTCTATCTTGATATCTCTAACACCGAA
AAATTCAAATTTAAATTTGAGTGACTGTTAGAACTTACAACATTGATTATGTGTGATTTATGATGAA
AATTTGAAACTCCTATGAATGTTTAACCAAAAAAAAAAAAAA

FIGURE 28 (continued)

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SEQ ID NO: 216, AAX20013.1| putative ethylene responsive element binding protein [Gossypium hirsutum]

MCGGAIISDFIIPPARSRLVTANYLWPDLLKSGSKKRSRGRKHSKKPAVGFEDDFEADFQVFKDESDVD
DFNDDVDDVLADVKSFAFSATKKPSPAVSHGSNSIKSVEFSGQAEKSAKRKRKNQYRGIRQRPWGKWA
AEIRDPRKGVVRVWLGTFTAEAAARAYDAEALRIRGKKAKVNFDETPTTPKHAVKMNSQKPLSGSN
LSSVQSSLNPDFSYSNKLEQGYDVTGFIEEKSLMDQFAYADPVRAAVDDGLKPFADPENTASFFISD
PGSNNFDSSDLVWGDQGAKTPEISSSLEPTLEVNEFLDNANPTKKLKLSLNNVMPTGGDNSVKLSLDE
LLAMDNQVNYFQTPFIDENWNVSMDDFLNGDATQVGGNEMGFWSFDDFPSIDGGIF

SEQ ID NO: 217, AY962572.1| Gossypium hirsutum cultivar Xinhai14 putative ethylene responsive element binding protein 3 mRNA, complete cds

ATGTGTGGAGGTGCAATTATTTCCGATTTTCGTGCGCGTGAAACATGACCCGAAATTGACCGGCGATGA
CCTTTGGTCTGAAATTGACATATTCTCCGACCTCCTAGGTTTCGACAACAATGGCAAAGCTTTGTCA
ATCATCAGTTTCATAACAACAACAAGAAGCTGATCAATCCAAAAGACAATCAACTTAACAAAGAGAGA
AGCGAGACGATTGAGAAGACAAGCCGAGTCACTAAAAATGTTGAAAAGACTCAGCGAACTCGGAAAAA
CTTTTACCGAGGAATAAGACAAAGGCCATGGGGCAAATGGGCAGCTGAGATTAGAGACCCTCAAAAAG
GCGTCCGAGTTTGGCTCGGTACCCATAACACAGCCGAAGAAGCGGCTCGAGCCTACGATGAAGCCGCC
AAGCGTATCCGTGGTGATAAAGCCAAGCTCAACTTCCCTCAAACGCCCCACAAAAATCAAGCAGCTTC
ACCAGCTCTTACTCAGCTTCCTCCTGCTAAGAAAAGGTGCATCGTTCCCGAGTTAACTCAACCGAGCT
TCCAGACTGACTCACCACCTTATCCTATGGGTCTTGGGTCTGGAAGAAGTGAAGATTATAAGCCGATT
GAAGTGGTGGAGAGTGAGTTGGAGTTGAAAGAACAATCTGGAGCCTGGAATCATTCTGGGTTTGGGA
GACTAATCATGAGACTATGACTCAACTGAGTGGTAACGGAGGGACTGACTCACTGGAGCTTTGGACAC
TTGATGACCTCGTAACTCAGTATAAGCAACGGCGCTAACATGTTTCATCAGTGGGGGCGAAAATTAAAT
AATAGTTAGCGTTAATAAATGTTTTTTGTGTTAATTAGGGTTTTTTTATTTATACTATCATGCATTAT
ATATATATATAGATGAGAATAAAGGATTAACGCTNTGCTCTTGCATGGATTAGTTAGCGTTAATCAAT
GTTAGTGTGTAATTAGGGTTTTTTATTATGTTAAAAA

SEQ ID NO: 218, AAX68526.1| putative ethylene responsive element binding protein 3 [Gossypium hirsutum]

MCGGAIISDFVAVKHDPKLTGDDLWSEIDIFSDLLGFDNNGKSFVNHQFHNNNKKLINPKDNQLNKER
SETIQKTSRVTKNVEKTQRTKRFYRGIRQRPWGKWA AEIRDPOKGVVRVWLGTHTAEAAARAYDEAA
KRIRGDKAKLNFPQTPTKNQAAASPALTQLPPAKKRCIVPELTQPSFQTDSPPYPMGLSGRSEDYKPI
EVVESELELKEQIWSLESFLGLETNHETMTQLSGNGGTDSELELWTLDDLVTQYKQRR

SEQ ID NO: 219, AY962571.1| Gossypium hirsutum cultivar Xinhai14 putative ethylene responsive element binding protein 2 mRNA, complete cds

ATGTGTGGAGGTGCAATTATTTCCGATTTTCATTGCCGTGAAACGCGGTCGGAAGTTAACCGCCGAGGA
TCTTTGGTCTGAACTTGACACATTCTCCGACCTGTTGGGTCTGGATTACGGAAATGGAAAAGAGTCTT
CTTTCCTCAGTCCGACAACACCAAGCCGGTTCCAAAGCCAAGAACCTTGAAAAAGTGGCAAACGAG
ACGACTCAGAAGACAAGCCGAGGGAGAGAGAAAGAAGGGAAGACTCAGCGAACTCGAAAG

FIGURE 28 (continued)

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AACATTTACAGAGGAATCAGGCAAAGGCCATGGGGGAAATGGGCGGCTGAGATAAGAGATCCTCACAA
 AGGTGTCCGAGTCTGGCTCGGTACATACAACACGGCTGAAGAAGCGGCTCGAGCCTACGATGAAGCCG
 CCAAGCGCATCCGTGGGGAGAAAGCCAAGCTCAACTTCCCTCAAACCTCCACACCTAACTCAGCCTCCT
 GCTAAGAAAAGGTGTATGATGGCTCCTGAGTTGACTCCGCCGAGTTCTGAAACAAAGAGCCCACCAAC
 CCCACAACCTTTTTATGGGTTTTGGTTACGAGAATGGAGTTTACAGACCGAGTGAAGCAATGGAAAGCG
 AGATGGAGCTGAAGGAGCAAATCTCGAGCCTGGAGTCGTTCTGGGTTTGGAGCCTGATGAGACAACA
 ACTGAGTTGAGTGGAAAGTGTGAGCCTGACTCAGTGGACCTTTGGATGCTTGATGACCTTGTGACACA
 TCATCAACAACAGCCTCAGCTCTTTTATTAGAAATTA AAAAGTTTTAATTAGGGTAATGTTATGTTTG
 ATATGATTATGCTTAAGACTTTAATGTTTGTATTAATGAAGGGTAAATAGTTGTGACAATAAAAAGAT
 TGGCCACCCAGTTTTAATTTATATTTATTTCTAATTTGGGTGACATGTAAATTGGTTTCGAGAAACAT
 TGAAGTACCCATAATGTTAGTTCATGTATCAGATATAGTAAACACTTTGGATTAATAAAAAAACCTCC
 TAATATTTTATTTGTAAAAA AAAAAAAAAA

**SEQ ID NO: 220, AAX68525.1| putative ethylene responsive element binding protein 2
 [Gossypium hirsutum]**

MCGGAIISDFIAVKRGRKLTAEDLWSELDTFSDLLGLDYNGKESSFTQSDNTKAGSKAKNLEKVANE
 TTQKTSRGREKEGKTQRTKNIYRGIRQRPWGKWA AEIRDPHKGV RVWLGTYN TAE EAARAYDEAAKR
 IRGEKAKLNFPTPHLTQPPAKKRCMMAPELTPPSSETKSPPTQLFMFGFYENG VYRPSEAMESEME
 LKEQISSLESFLGLEPDETTTELSGSAEPDSVDLWMLDDLVT HHQQQPQLFY

**SEQ ID NO: 221, AY572462.1| Gossypium barbadense ethylene response factor 2
 mRNA, complete cds**

CCATCTGAAAAA A A A A A A A A A CAGGTTTTCTTTAAGATAACACCCAAAAATGTGTGGAGGTGCAATTATTTTC
 CGATTTTCGTCGCCCCCAAATATGACCGGAAATTGACCGGCGATGACCTTTGGTCTGAACTTGACATAT
 TCTCCGACCTCCTAGGTTTCGACAACAATGGCAAAAGCTTTGTCAATCATCAGTTTCATAACAACAAC
 AACAACAAGCTCATTAATCCAAAAGACAATCAACTTAACAAAAGAGAGAAGCGAGACGATT CAGAAGAC
 AAGCCAAGTCACTAAAAAGGTTGAAAAGACTCAGCGAACTCGGAAAAACTTTTACAGAGGAATAAGAC
 AAAGACCATGGGGCAAATGGGCAGCTGAGATTAGAGACCCTCAAAAAGGCGTTTCGAGTTTGGCTCGGT
 ACCTATAACACAGCCGAAGAAGCGACTCGAGCCTACGATGAAGCAGCCAAGCGTATCCGTGGTGATAA
 AGCCAAGCTCAACTTCCCTCAAACGCCCAACAAAAATCAAGCAGCTTCACCAGCTCTTACTCTGCTTC
 CTCCTGCTAAGAAAAGGTGCATCGTTCCCGGAGTTAACTCAACCGAGTTTACCAGACTGGACTCACCA
 CCTATATCCCTATGGGTTCTTGGGGTATGAGAAGAAGTGAAGATTATAAGCCGATTGAAGTGGTGGA
 GAGTGAGTTGGAGTTGAAAGAACAAATCTGGAGCCTTGGAATCATCCCTGGGTTTGGAGACTAACCAT
 GAGACTATGACTCAGCTGAGTGGAACGGTGGGACTGACCCACTGGAGCTTTGGACACTTGATGACCC
 CGTAACCCAGTATAAGCAACGGCGCTAACATGTTTCATTAGTGGGGCGAAAATTAAATAATAGTTAGC
 ATTAATCAATGTTTTTGTGTTACTTAGGGTTTTTTTATTTATGCTATCATGCATTATATATATATATG
 AGAATAAAGGATTAACGCTTTGCTCTTGCATGGATTAGTTAGCGTTAATCAATATTTGTGTTTAGGGT
 TTTTATTATGTTGTTATATATGTATATGCTTATGACTTTCATGTTTGTATCAATGCATTAGTTGCAT
 TATATATATAAGAATAAAGGATTTAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIGURE 28 (continued)

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SEQ ID NO: 222, AAT77191.1| ethylene response factor 2 [Gossypium barbadense]

MCGGAIISDFVAPKYDRKLTGDDLWSELDIFSDLLGFDNNGKSFVNHQFHNNNNNKLINPKDNQLNKE
RSETIQKTSQVTKKVEKTQRTKKNFYRGIRQRPWGKWA AEIRD PQKGV RVWLGT YNTAE EATRAYDEA
AKRIRGDKAKLNFPQTPTKNQAASPALTLPPAKKRCIVPGVNSTEFTRLDSPFISLWVLGV

SEQ ID NO: 223, AY779338.1| Gossypium hirsutum AP2/EREBP transcription factor ERF-2 mRNA, complete cds

GCACGAGGATCTAAGAACCCGAAAAGTAGAGCTTTGGTTCTCTGTCTGCTGCTTCTTTCTTCTCTTGG
TACTTCATTATTTTTCTTTCACTTCCTTTTTGTGAAAAACATTGAAACCCCTTTTCAAGACGCAATA
GAAGATGTGTGGAGGTGCAATCATTTCCGATTTCAATTGCCGTGAAACGCGGTGCGGAAGTTAACCGCCG
AGGATCTTTGGTCTGAACTTGACACATTCTCCGACCTGTTGGGTCTGGATTACGGAAATGGAAAAGAC
CCTTTCACTCAGTTCGACAACACCAAGGCCGGTTCCAAAGCCAAGAACCCTTGAAAAAGTGACAAACGA
GTCGACTCAGAAGACAAGCCGGGGGAGAGAGAAAGAAGGGAAGACTCAGCGAACTCGAAAGAACATTT
ACAGAGGAATCAGGCCAAGGCCATGGGGGAAATGGGCGGCTGAGATAAGAGATCCTCACAAAGGTGTC
CGAATCTGGCTCGGTACATACACACGGCTGAAGAAGCGGCTCGAGCCTACGATGAAGCCGCCAAGCG
CATCCGCGGGGACAAAGCCAAGCTCAACTTCCCTCAAACCTCACGCCTAACTCAGCCTCCTGCTAAGA
AAAGGTGTATGATGGCTCCTGAGTTGACTCCACCGAGTTCTGAAACCAAGAGCCCAACCCACAA
CCTTTTATGGGTTTTGGTTACGAGAATGGAGTTTACAGGCCGAGTGAAGCAATGGAAAGCGAGATGGA
GCTGAAGGAGCAAATCTCGAGTCTGGAGTCCTTCTGGGTTTGGAGCCTGATGAGATGACAACTGAGT
TGAGTGGAAGCGCTGAGCCTGAGTCAGTGAACCTTTGGATGCTTGATCACCTTGTGACACATCATCAA
CAACAGCCTCAGCTCTTTTATTAGAAATTA AAAAGTTTAAATTAGGGTAATGTTATGTTTGATATGAT
TATGCTTAAGACTTTAATGTTTGTATTAAATGAAGGGTAAATAGTTGTGACAATAAAAAGATTGGCCAC
CCAGTTTTAATTTATATTTATTTCTCTAA AATTCTAAAA AAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 224, AAV51937.1| AP2/EREBP transcription factor ERF-2 [Gossypium hirsutum]

MCGGAIISDFIAVKRGRKLTAEDLWSELDTFSDLLGLDYNGKDPFTQFDNTKAGSKAKNLEKVTNES
TQKTSRGREKEGKTQRTKKNFYRGIRRRPWGKWA AEIRD PHKGVRIWLGT YNTAE EAARAYDEAAKRI
RGDKAKLNFPQTPTLTPPAKKRCMMAPELT PPSSETKSPPTPQPFMGFGYENG VYRPSEAMESEME
KEQISSLESFLGLEPDEMTELSGSAEPESVNLWMLDHLVTHHQQQPQLFY

SEQ ID NO: 225, AY827548.1| Gossypium hirsutum EREB1 transcription factor mRNA, complete cds

ATGAGACTATGCGGCCGCTGTTACAAGTCGACGAATCAACTTAACAAAGGGAGAAGCGAGACGATTCA
GAAGACAAGCCGAGTCACTAAAAATGTTGAAAAGACTCAGCGAACTCGGAAAACTTTTACCGAGGAA
TAAGACAAAGGCCATGGGGCAAATGGGCAGCTGAGATTAGAGACCCTCAAAAAGGCGTCCGAGTTTGG
CTCGGTACCCATAACACAGCCGAAGAAGCGGCTCGAGCCTACGATGAAGCCGCCAAGCGTATCCGTGG
TGATAAAGCCAAGCTCAACTTCCCTCAAACGCCCCACCAAAAATCAAGCAGCTTCACCAGCTCTTATTC
AGCTTCCTCCTGCTAAGAAAAGGTGCATCGTTCCCGAGTTAACTCAACCGAGTTTCCAGACTGACTCA
CCACCTTATCCTATGGGTCTTGGGTCTGGAAGAAGTGAAGATTATAAGCCGATTGAAGTGTTGGAGAG
TGAGTTGGAGTTGAAAGAACAAATCTGGAGCCTGGAGTCGTTCTCTGGGTTTG

FIGURE 28 (continued)

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GAGCCTGATGAGACAACAACCTGAGTTGAGTGGAAGTGCTGAGCCTGACTCAGTGGACCTTTGGATGCT
 TGATGACCTTGTGACACATCATCAACAACAGCCTCAGCTCTTTTATTAGAAATTAAAAAGTTTAAATT
 AGGGTAATGTTATGTTTGATATGATTATGCTTAAGACTTTAATGTTTGTATTAATGAAGGGTAAATAG
 TTGTGACAATAAAAAGATTGGCCACCCAGTTTAAATTTATATTTATTTCTAATTTGGGTGACATGTAA
 ATTTGGTTTCGAGAAACATTGAAGTACCCATAATGTTAGTTCATGTATCAGATATAGTAAACACTTTGG
 ATTAATAAAAAAACCTCCTAATATTTTATTTGTAAAAA

SEQ ID NO: 226, AAV85777.1| EREB1 transcription factor [Gossypium hirsutum]

MRLCGRCYKSTNQLNKGRSETIQKTSRVTKNVEKTQRTKRFYRGIRQRPWGKWAEEIRDPQKGVVRVW
 LGTHNTAEAAARAYDEAAKRIRGDKAKLNFPQTPTKNQAASPALIQLPPAKKRCIVPELTQPSFQTD
 PPYPMGLGSGRSEDYKPIEVVESELELKEQIWSLESFLGLEPDETTTELSGSAEPDSVDLWMLDDLVT
 HHQQQPQLFY

SEQ ID NO: 227, AY781119.1| Gossypium hirsutum ethylene-responsive element binding protein ERF6 mRNA, complete cds

ATAACCGTCGGTCTATAAATCCTAGACCCCAATACCAAAGCTTTTTCCATCTGAAAAAAAACAGGTT
 TTCTTTTAAAGATAACACCCAAAAATGTGTGGAGGTGCAATTATTTCCGATTTCTGTCGCCCCCAATAT
 GACCGGAAATTGACCGGCGATGACCTTTGGTCTGAACTTGACATATTCTCCGACCTCCTAGGTTTTCGA
 CAACAATGGCAAAAGCTTTGTCAATCATCAGTTTCATAACAACAACAACAAGCTCATTAATCCAA
 AAGACAATCAACTTAACAAAGAGAGAAGCGAGACGATTGAGAAGACAAGCCAAGTCACTAAAAAGGTT
 GAAAAGACTCAGCGAACTCGGAAAACTTTTACAGAGGAATAAGACAAAGACCATGGGGCAAATGGGC
 AGCTGAGATTAGAGACCCTCAAAAAGGCGTCCGAGTTTGGCTCGGTACCTATAACACAGCCGAAGAAG
 CGGCTCGAGCCTACTATGAAGCCGCCAAGCGTATCCGTGGTGATAAAGCCAAGCTCAACTTCCCTCAA
 ACGCCACCAAAAATCAAGCAGCTTACCAGCTCTTACTCAGCTTCCTCCTGCTAAGAAAAGGTGCAT
 CGTTCCCGAGTTAACTCAACCGAGTTTCCAGACTGACTCACCACCTTATCCTATGGGTCTTGGGTATG
 GAAGAAGTGAAGATTATAAGCCGATTGAAGTGGTGGAGAGTGAGTTGGAGTTGAAAGAACAATCTGG
 AGCCTGGAATCATTCCTGGGTTTGGGAGACTAACCATGAGACTATGACTCAGCTGAGTGGTAACGGTGG
 GACTGACTCACTGGAGCTTTGGACACTTGATGACCTCGTAACTCAGTATAAGCAACGGCGCTAACATG
 TTCATTAGTGGGGGCGAAAATTAAATAATAGTTAGCGTTAATCAATGTTTTTGTGTTACTTAGGGTTT
 TTTTATTTATGCTATCATGCATTATATATATATATATGAGAATAAAGGATTAACGCTTTGCTCTTGCA
 TGGATTAGTTAGCGTTAATCAATATTTGTGTGTTAATTAGGGTTTTTTATTATGTTGTTATATATGTA
 TATGCTTAAGGACTTTCATGTTTGTATCAATGCATTAGTTGCATTATATATATTAAGAATAAAGGGAT
 TTTACACGTTGCAGTTTGAAAAA

SEQ ID NO: 228, AAX07460.1| ethylene-responsive element binding protein ERF6 [Gossypium hirsutum]

MCGGAIISDFVAPKYDRKLTGDDLWSELDFSDLLGFDNNGKSFVNHQFHNNNNKLNPKDNQLNKE
 RSETIQKTSQVTKKVEKTQRTKRFYRGIRQRPWGKWAEEIRDPQKGVVRVWLGTYNTEAAARAYYEA
 AKRIRGDKAKLNFPQTPTKNQAASPALIQLPPAKKRCIVPELTQPSFQTDSPYPMLGYGRSEDYKP
 IEVVESELELKEQIWSLESFLGLETNHETMTQLSGNGGTDSELELWTLDDLVTQYKQRR

FIGURE 28 (continued)

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SEQ ID NO: 229, AY973613.1| *Manihot esculenta* ethylene response factor mRNA, complete cds

CTGCAGCGACAACCACCATGTGTGGCGGTGCTATCATCTCCGACTTCATCCCTGCCACCGCTGCTGGC
 CGATCCTCGCGACGGTTGACAGCGGACTTTCTCTGGCCTGATCTAAAGAAGCCCATTGGGAAAATCGT
 TGGTGACCTTGACGATGATTTTCGAGGCTGATTTCCAGGAGTTTAAGGATGAGTCTGATGTCGATGAGG
 AAGATGACGTTTTGTTTGATGTCAAGCCTTTCTCTTTCTCTGCTACTGCTTCTCCTCCTCCTCGCAAT
 CGCAGTCCTTCACGTGGTTCTACAGCTGTAAAGTCTGTGGAATTTAATGGGCTAGCTGAAAAATCTGC
 AAAGAGAAAAGAGAAAAAACCAGTACAGAGGAATCCGGCAGCGCCCATGGGGAAAATGGGCTGCTGAGA
 TTCGTGACCCCGAGGAAAGGGGTGCGTGTCTGGCTAGGAACATTCAATACTGCTGAAGAAGCTGCAAGA
 GCGTATGATGCTGAGGCACGTAGAATTCTGTTGGCAAGAAAGCTAAAGTGAACCTTTCTGATGAAGCTCC
 ACGTGCTTCCCCAAAGCGGACAATGAAGGCAAACCTCAGAAACCACTTCCTAAGAGAAATGCTACTG
 AGAGTATGAGTTACTTGAACAATCCAGATCAGGACTACTTCAATACTTTGGGCTCTGTTGATGAGAAA
 CCACTAGTGAGCCAGTTTGATTTGATGGACTCTTTTCTGCCAATGGAGATGCTACAGTCAAATCTAT
 TCCTCCATGTGATAATGTTCCACGTTTTTCAATTCTGATCAGGGAAGCAACTCATTTGAATGTTCCG
 ACTTTGGATGGGGGGAGCAGGCCTCAAAGACTCCTGAAATCTCATCTGTTCTTTTCAGCTACTCCAGAA
 ATTGATGAATCACTTTTCATGGATGATGCTAACCCTAAAAAGAAGATGAAGTCTGACTCTGAAAATGC
 AGTTCCTATAGAAGAAAGCAATGGAATATCTCTATCAGAGGAGTTGTTGGCTTTTGACAACCAGATGA
 ACTTTTCAGATGCCTTATCTTGAGGGAAGTTGGGAGGCTTCACTTGATGGCTTCCTTAATGGAGACGTG
 ACTCAGGATGGTGGAAATCCAATGGACCTGTGGAGCTTTGATGACCTCCCTAATATGGTTGGGGGAGT
 TTATTGAGCAAAATCATAATTGCCGGTTGGCTTCTGTAAATAAGGCTACATGGATGGTTTTCTCTCTG
 AAATGTATTACAAGCACATCTGAACATGCTTAATCCTTTGAGGAGAGTGTCCTAGGGAGCTTTTGGTA
 CAAGAGTTGTAGTAAATAGGAATATTTAGTTTCCCTTTTACATTTTGAGACACTGGACTTGGGTTGTT
 CAATTTAATAACTGTAATTGACAATGTGCGTGTGATTTGTGTTTAAACTGATATAAATTTTATCTCT
 ACTGTTGTTTTTAAAAAATAAAAAAAAAAAAAA

SEQ ID NO: 230, AAX84670.1| ethylene response factor [*Manihot esculenta*]

MCGGAIISDFIPATAAGRSSRRLTADFLWPDLLKPIGKIVGDLDDDFEADFQEFKDESDVDEEDDVLF
 DVKPFSSSATASPPPRNRSPSRGSTAVKSVFENGLAEKSAKRKRKNQYRGIRQRPWGKWAAEIRDPRK
 GVRVWLGTENTAEAAARAYDAEARRIRGKKAKVNFPEAPRASPKRTMKANPQKPLPKRNATESMSYL
 NNPDQDYFNTLGSVDEKPLVSQFDLMDSFPANGDATVKSIPPCDNVPTFFNSDQGSNSFECSDFGWGE
 QASKTPEISSVLSATPEIDESLFMDANPKKKMKSDSENAVPIEESNGKSLSEELLAFDNQMNFMQMPY
 LEGSWEASLDGFLNGDVTQDGGNPMDLWSFDDLPMVGGVY

SEQ ID NO: 231, *Populus alba* x *Populus tremula* apetala2/ethylene responsive factor (ERF1) mRNA, complete cds

ATAATCACCATCAATCAACATGTGTGGCGGTGCTATCATCTCAGGCTTCATCGCTCCGACAACCACCG
 CTCGATCTTCTCGGCGGTGACCTCGGGCTTTGAGTGGCTTGAGCCGAAGAAACCTTCAACAACAAG
 CACTTGAAGCCAGTTGTTGCTGATCCCGAAGATGATTTTGAGGCTGATCTTCAAGAGTTTAAGGACGA
 GTCTGATGTGACGAGGATTATGATGTCTTTGCTGATGCCAAGCCTTTTGCTTTCTCTGCCAGTGCTT
 CTGAACCTGCTAAAAACGTGGGCTCCCTCGTGGTCTACTGCTGTAAATCTGCTGGATTCAGTGGA
 CTTGCTAAAAACTCAGCAAAGAGGAAGAGAAAGAACCAAGTTTAGAGGAATTAGGCAGCGTCCATGGGG
 AAAATGGGCTGCTGAGATTCGTGATCCCAGGAAGGGGTACGTGTCTGCTTGGG

FIGURE 28 (continued)

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AACATTCAATACTGCAGAAGAAGCTGCTAGAGCATATGATTCTGAGGCACGTAGAATTCTGTTGGCAAGA
AAGCGAAGGTGAACTTCCCTGATGAAGCTCCATGTGCTTCAGCAAGGCATCCAATTAAGGAAAACCTCA
CAGAAACGACTTACAAAGGCAAATTTAAGCCAGGATTTTAGTTACTTGAGCAACCCAGAAACGGATTA
TAATAATATGGGCTTTGTGGAAGAGAAACCACAAGTGAGCCAGTTTGAATAATGAATTCTATCCCGG
TCAATGGAGATTCTGGGGTGACGCCCTTAACCTCTGACAATGCTTCTATGTATTTCAATTCTGAC
AAGGGGAGCAACTCATTTGATTGTGACTTTGGGTGGGGAGAACAAGGCGCTGAAATCTTGTCTGTTCT
TGCAGCAACTCCAGAAGTTGATGAATCCGTCTTTGTGGAAGCTAATCCTAAGAAGTTGAAATCATACA
CTGAGTATGCAGTGCCTGTTGAAGAGAGGAATGGAAAATCTCTGTCCGAAGAGTTGCTGGCTTTTGAC
AATCAGTTGATGAACCTTCAGATGCCAGATCTTGTGGGTAACCTGGGAGGCTTCTCTTGATAGCTTCCT
TAATGGAGACACAACCTCAGGATGGCACAAACGCAGTGGACTTGTGGAGCTTCGAAGACTTCCCCTCCA
TGTTGGGGGAGTTTATTGAGCCAACCTTTCTGTGCTTGCCAGGTTTTGTAAATAATAAGGCTACATG
AATGGTTGTTTATCTGAGATGGGAATGGAGTGCAACACAGATGAACATGCTTAGCCTTGGTGTGGGAG
AAGCATTCTCAGGAGCATTTTCCATATAAAAGTAGTACATCGGTTTCCCGTTTCATTACATTTGGAGT
CACTGGACTTTGGAAGTTGGATTGCATGACTGTAATTTGACAATGTGGTGTGACTTATTTAGA

SEQ ID NO: 232, AAW33881.1] *apetala2*/ethylene responsive factor [Populus alba x Populus tremula]

MCGGAIISGFIAPTITARSSRRLTSGFEWLEPKKPFNNKHLKPVVADPEDDFEADLQEFKDESDVDED
YDVFADAKPFAFSASASEPAKKRGLPRGSTAVKSAGFSGLAKNSAKRKRKNQFRGIRQRPWGKWAAEI
RDPRKGVVRVLGTFTAEAAARAYDSEARRIRGKKAKVNFPDEAPCASARHPIKENSQKRLTKANLSQ
DFSYLSNPETDYNMGMFVEEKPQVSQFGIMNSIPVNGDSGVTPLTPSDNASMYFNSDKGSNSFDCDFG
WGEQGAELSLVLAATPEVDESVEANPKKLKSYTEYAVPVEERNKSLSEELLAFDNQLMNLQMPDL
VGNWEASLDSFLNGDITQDGTNAVDLWSFEDFSPMVGGVY

SEQ ID NO: 233, AB236754.1] *Trifolium pratense* RNA for putative transcription factor EREBP, complete cds, clone: C1500

GAATCAATCAACAAAACAAAACCCAGTAAAAATTTCAATCCTTTTTTAACAAAATCTTCAATTGGGTAT
AAGAAAGTTTCAATCTTTTTCTTGTTAAGATAAAGACAAAGATCTGACAAAACAGAAAGATGTGTGG
TGGTGCTATTATTTCCGACTTCATTCCAGCTGCGGCGGCGGTGGGTGGTTCGCCCGCTGTCACTGCTG
ATATCTTGTGGCCAAATTTGAGGAAAACCTGGTTCCAAAAAATCATCTTTTTTGCTTGACGATGATTTT
GAAGCTGGTTTCAGACAGTTTAAGGATGATTCTGATTTTCATGAAGACGAGGATGAAGATGACGATGA
AGGGTTGTGGTTCGGTGTCAAAGGTTTTACCTTTGCTGCTTCTAACAACAAATCTTCAAGGAACCTCT
CTCGTGGCTCGGCTGGTGCAAAATCCGTGGCATCGAAATCAAATGAGCAAGCTGAAAAGGAATCAAAG
AGAAAGAGGAAGAATCAGTATAGGGGTATCCGCCAACGTCCATGGGGAAAATGGGCAGCTGAGATCCG
TGATCCAAGGAAGGAGTCCGTGTTTGGCTCGGAACTTTCAACACTGCTGAAGAAGCTGCAAGAGCTT
ACGATGCTGAAGCTAGGAGAATCCGTGGCAAGAAAGCCAAGGTGAATTTCCCGATGAGGCTCCAAAT
GCTTCCTCAAAACGTCTGAAGACAAATCCTGATAACCAGCTGTTGAACAAAATCTGAACCTTTTCAA
GCCGAACGGAAACAACAAAATGTTCAATTTAGCGAGAATATGGAGAACTTCTATTCTCCTATGGATC
AGGTTGAACAGAAACCATTTGGTTAACAACCAATATGGTGCTGCTGACATTGGAGCCTTCACTGGAAAC
GGAGTTCACCTTGACCTGCTGATGTTAATGCTTATTTAGTTCTGAGCATTCAAGCAACTCGTTTGA
TTATTCTGATTTATGTTGGGGGAACAAGGCCCGAAAACCCCTGAGATTTCTCGGTGTTTTCTGCTC
CTCTCGAAGCTGAACCTCAGATGAACATGCAGTCTAACAACCTCTCAGGATATGCTACCTATGCAAGCT
GAATCTGCAAAGACACTCTCTGAGGAGCTTGAGATATCGAATCCAGCTGAAGTTCTTCGAGAACTC
ATTCGATGATAACTGGAGTGATGCTTCACTTG

FIGURE 28 (continued)

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CGTCTTTGCTCGGTGCTGATGTAACCTCAGGATGCTGGAAACACAATGAACCTTTGGAGCTTTGATGAC
 CTGCCTTCCATCGCAGGCGGAGTTTTCTGAACAACTTTCGCCTCACCGGTTATGTAAATAAAGCTACA
 AGTTAGTAACTTTCAGTTTACATTCGGTTTGGTTCATTTTGTTTTTACAAGGTGGATAATTAAATTGT
 TTTGTTTTTTCAGGATTGTTGGTTTATTTTTATATTGTTGATGGAATCAGAAACAAGAACAAGTTACCAG
 CTTTAATTAAGCGTGGAGTTTTATTCTCTTGTGGCAAAAATAAATTATTATAGGTTTTTTATT

SEQ ID NO: 234, BAE71206.1| putative transcription factor EREBP [Trifolium pratense]

MCGGAIISDFIPAAAAVGGSRRTADILWPNLRKTGSKKSSFLDDDFEAGFRQFKDDSDFFDEDEDED
 DDEGLLVGVKGFTFAASNKSSRNFSRGSAGAKSVASKSNEQAEKESKRKRKNQYRGIRQRPWGKWAA
 EIRDPRKGVRVWLGTENTAEAAARAYDAEARRIRGKKAKVNFPEAPNASSKRLKTNPDNQLLNKNLN
 SFKPNGNNKMFNFSENMFYSPMDQVEQKPLVNNQYGAADIGAFTGNGVHLAPADVNAYFSSEHSSN
 SFDYSDLCWGEQGPKTPEISSVFSAPLEAEPQNMNQSNNQSQDMLPMQAESAKTLSEELADIESQLKFF
 ENSFDDNWSASLASLLGADVTQDAGNTMNLWSFDDLPSIAGGVF

SEQ ID NO: 235, AF537220.1| Glycine max ethylene responsive protein (EREB) mRNA, complete cds

ATTGAGCCAAAGCTTTGTATTTTCTGCGATAATTTTCCATTGGGTGGAAGAAAGTCTCAACCTTTATT
 CGAAAGAGCAAGGATCTGAGTTGAGTTGAGTGATCATGTGTGGTGGTGCGATTATCTCCGACTTCATA
 CCGGCAGGTCCCGCCAGCGGGGCGCGGCGCTGACCGCCGACATCCTGTGGCCGAGTTTGAGGAAGCG
 CTTCTCGAAGCCGCTGCTGGACGATGATTTTCAGAGGCTGGGTTCAGAGAATTCAAGGATGATTCGGA
 TCGAGGATGTTGATGACGAGGACGATGAAGACGAGGAGGAGTTGAAGAAGAAGCCCTTTGGGTTCTCT
 CGCTCCAGCAACAAGGCTGCTTCTAAGCCTCTCTCTCGTGGAGCAACAACCTGTGAAATCTGTGGAATC
 AAAGGGGCAAGCTGAGAAGTGTGCCAAGAGAAAGAGGAAGAACCAGTATCGCGGAATCCGCCAGCGTC
 CATGGGGAAAGTGGGCTGCTGAGATTTCGCGACCCAAGAAAGGGGGTTCGTGTTTGGCTTGGAACCTTC
 AGCACTGCTGAAGAAGCTGCAAGAGCTTACGATGCTGAAGCAAGGAGGATCCGTGGCAAGAAAGCCAA
 GGTGAATTTCCCTGATGAGCCTTCAGGCGCTGCTTCCTCAAAACGTCTCAAGGCGAATCCAGAGGCTC
 AGCCAATGAAGAAAAATCTGAACTCTGTGAAGCCGAAAATAAACAGATGTTCAATTTTGGTGACAAT
 CTTGAGGGGCTACTACAGCCCTATAGATCAGGTGGAACAGAAACCACTGGTTAACCAGTATGTTAACCG
 TGCCCCGTTTGCTGGAAATGGAGTTCAAGTCTCACCTGTTACTCCATCTGCTGATGTTACTGCTTACT
 TCAGCTCTGAGCATTCGAGCAACTCGTTTGATTATTCTGACCTTGGATGGGGTGAACAAGTCCCCAAG
 ACCCCCGAGATCTCATCCTTGCTTTCTGCTGCTCCTTTGGAGGGTGTGCTGATCAGGTTTCAAGAC
 CAACAACCTCGCAGGATGTGGTGGCTGCACAAGATGATTCTGCAAAAACCTTTCCGAAGAGCTTGACG
 ACATTGAATCCCAGCTCAAGTTCTTTGAGACCCCTTCTTTTCTTGATGAAGCCTGGGCTGATGCTACA
 TTGGCGTCTTTGCTCGGCGGAGACGCAACTCATGACGCCGCCGGAACCCCTATGAACCTTTGGAGCTT
 CGACGACCTGCCTTCCATGGCAGGAGTCTTCTGAACACCCCTTTATCTCCCTTTTATGTAAATAAAGC
 TACAAGAATTGTGATCGTGATGTTGGTGATGGAGTCCACAGCCAAGAAACCTGCTTAAAGCTTATGTG
 GAGTTTATTTTATCTTGTAGCTAATGCAGTAGTATAGGACTATATAGGTTTTTTATTATAGGGTATC
 CTTTTGTGAACCTCAAAGACCTCGTTTTTCAGGGGATTTTCTGTTTGATGTCCTTAAGGATTATCAATTA
 TGTTATATATAGGTCTTGATAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 28 (continued)

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SEQ ID NO: 236, AAQ10777.1| ethylene responsive protein [Glycine max]

MCGGAIISDFIPAGPASGARRVTADILWPSLRKRFSKPLLDDDFEAGFREFKDDSEIEDVDDEDEDE
EELKKKPFGFSRSSNKAASKPLSRGATTVKSVESKQAEKCAKRKRKNQYRGIRQRPWGKWAAEIRDP
RKGVRVWLGTFTSTAEAAARAYDAEARRIRGKKAKVNFPEPSGAASSKRLKANPEAQPMKKNLNSVKP
KINQMFNFNGDNLEGYYSPIDQVEQKPLVNQYVNRAPFAGNGVQVSPVTPSADVTAYFSSEHSSNSFDY
SDLGWGEQVPKTPEISSLLSAAPLEGAADQVQKTNNSQDVVAAQDDSAKTLSEELADIESQLKFFETP
SFLDEAWADATLASLLGGDATHDAAGNPMNLWSFDDLPSMAGVF

SEQ ID NO: 237, AF459404.1| *Narcissus pseudonarcissus* DAFSAG9 AP-2 domain containing protein mRNA, partial cds

ATGTGTGGAGGAGCAATAATCTCTGATTTTCATACCTCCATCAAGGTCAAGGAAGCTCACTGCCGATTA
CTTGTGGCCCAATCTCAACAAGGGGAAGGACAAGAAGAAGAGCTTTGGGTTTGAAGATGACTTTGAAG
CTGACTTCAATGAGTTTGAAGATGAGTCTGAGGAGGGGGAATCTGAAGCTGTTGATGTCAAACCCCTTT
AAGTTTGGGGCTAAAGCTGGCTTTTCTAGAGAGGGATCGACTTATCTGAAACCCATCGAACTCAATGG
AGCTGCTGAACGATCATCCAAAAGGAAGAGGAAGAACCAATACAGAGGTATCCGTCAGCGTCCATGGG
GTAAATGGGCAGCTGAGATAAGAGATCCTAACAAAGGAGTTCGTGTTTGGCTGGGAACCTTTTAACACA
GCTGAAGAAGCTGCGAGAGCCTATGATGATGAAGCCCGTAGGATCCGTGG

SEQ ID NO: 238, AAL67489.1|AF459404_1 AP-2 domain containing protein [*Narcissus pseudonarcissus*]

MCGGAIISDFIPPSRSRKLTDYLPNLNKGKDKKKSFGFEDDFEADFNEFEDESEEGESEAVDVKPF
KFGAKAGFSREGSTYLPKPIELNGAAERSSKRKRKNQYRGIRQRPWGKWAAEIRDPNKGVRVWLGTENT
AEEAARAYDDEARRIRG

SEQ ID NO: 239, AJ001911.1| *Arabidopsis thaliana* mRNA for ethylene-responsive element binding protein

AGTAATTTAGCAGCAACAAACAGAGAAAAATGTGTGGCGGTGCTATTATTTCCGATTATGCCCCCTCTCG
TCACCAAGGCCAAGGGCCGTAAGCTCACGGCTGAGGAACTCTGGTCAGAGCTCGATGCTTCCGCCGCC
GACGACTTCTGGGGTTTCTATTCCACCTCCAACTCCATCCCACCAACCAAGTTAACGTGAAAGAGGA
GGAGGCGGTGAAGAAGGAGCAGGCAACAGAGCCGGGGAAACGGAGGAAGAGGAAGAATGTTTATAGAG
GGATACGTAAGCGTCCATGGGGAAAATGGGCGGCGGAGATTGAGATCCACGAAAAGGTGTCAGAGTT
TGGCTTGGTACGTTCAACACGGCGGAGGAAGCTGCCATGGCTTATGATGTAGCGGCGAAGCAGATCCG
TGGTGAGAAAGCCAAGCTCAACTTCCAGATCTGGATCATCATCCTTCTACTCCTCCGCCATCGTCTA
CTTCACTAAGATTATCCGATCAGCCACCGGCGAAGAAGGTTTGCCTTGTCTCTCAGAGCGAGTTAGCT
CAGCCGAGTTTCCCGGTGGAGTGTGTTGGATTTGGAAAGGGGGAAGAGTTTCAGAACCTGATGTACGG
ATTTGAACCGGATTATGATTTGAAACAGCAGATATCGAGCTTGGAGTCGTTTCTTGAGCTTGACGGTA
CCACGGCGGAGCAACCGAGTCAACTAGATGAGTCTGTTTGCATGTGGATATGTGGATGCTTGATGAT
GTCATTGCGTCGTATGAGTAAAAGGAAAAAAAACAGAAGATAATGTAATATGTAAAAAAAACCTA
AATTACT

FIGURE 28 (continued)

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SEQ ID NO: 240, CAA05084.1| putative Ckc2 [Arabidopsis thaliana] similar but different from SEQ ID NO: 40

MCGGAIISDYAPLVTKAKGRKLTAEELWSELDAASAADDFWGFYSTSKLHPTNQVNVKEEEAVKKEQAT
EPGKRRKRKNVYRGIRKRPWGKWAAEIRDPRKGVVRVWLGTFTNTAEAAAMAYDVAAKQIRGEKAKLNFP
DLDHHPTSTPPSSSTSLRLSDQPPAKKVCVVSQSELAQPSFPVECVGFGKGEEFQNLMYGFEPDYDLKQ
QISSLESFLELDGTTAEQPSQLDESVCDVDMWMLDDVIASYE

SEQ ID NO: 241, (gi|84662889:105357-105537, 105673-106409) Medicago truncatula clone mth2-18n7, complete sequence

ATGTGTGGTGGTGCTATCATCGCTGACTTCATTCCCTCGCCGTGACGGCCGCGTCTCACCGCCTCGGA
GCTCTGGCCTAACTCATTTGGCCAACAGATTGACTCCTCAAACCTTCGGTTTTTCTCATACTGCTGCTG
ATCAACAACCACCCAGCACTCTCAAAGATCACAGCCTCCCAAAGTTAATGAACGAGTTGAGAAGCCA
CTGAAAAACAGAGGAAGAATCTCTATAGAGGAATTCGACAGCGTCCATGGGGAAAATGGGCTGCAGA
GATTCGTGATCCAAGAAAAGGAGTTCGTGTTTGGCTTGGTACATTCAACACTGCTGAAGAAGCTGCTA
GAGCTTACGACAAAGAAGCTCGAAAAATCCGTGGCAAAAAGCTAAGGTTAATTTTCCTAACGAAGAT
GATGAATATACCATTGCTACTCGTCGCTACAATAATAATCCTCCACCGATTGACACAGAAAGCT
TCCTCTATATCATCAACAACACTATCAGAAGAATCTGAACCTGGAATTTGGTTATGATCTGAACCAA
CTGACACAATTGCTATCAATACTGGTCTGGTGGTGGTATGAGAATTCCTTTATTTGGGTCTGGTTCA
GTTTCAGAGGTTGGTTTTTCTGTGATGGAGTTCAATGGTGGTTCGAATCAGAATGAATTCGGTTATTT
TGGTGGTGTGTGAATGAACATGAAAAAGAGAAAGAGAAAGTGGTAGAACAAGAAACACATGTTGTTG
AACAAGCTGAAGCTGAATTAGCAAAAAATGAGGTACAAGAATTGTCTGATGAATTGTTGGCATAACGAG
GATTACATGAAGTTTTATCAGATTTACTATGATGGACAATCAGTGATGCCACCTAATAATGTTTCAGGA
ACATGTGGTGGAGATTTATGGAGCTTTGATTGA

SEQ ID NO: 242, ABE84970.1| Pathogenesis-related transcriptional factor and ERF [Medicago truncatula]

MCGGAI IADFI PRDRGRRLTASELWPNSFGQQIDSSNFGFSHTAADQQPPSTLKRSPPPKVNERVEKP
LKKQRKNLYRGIRQRPWGKWAAEIRDPRKGVVRVWLGTFTNTAEAAARAYDKEARKIRGKKAKVNFNED
DEYTIHATRRYNNNPPPIRPQKLPLYHQHYQKNLNLEFGYDLNQDTIHAINTGSGGDENSLFGSGS
VSEVGFSVMEFNGGSNQNEFGYFGGVVNEHEKEKEKVVEQETHVVEQAEELAKNEVQELSDELLAYE
DYMKFYQIYYDGQSVMPNNVQEHVVGDLWSFD

SEQ ID NO: 113, gi|50300636:c114504-113782 Medicago truncatula clone mth2-28b4, complete sequence

ATGTCACCCCCTAAACCGTATATAAACCAACTCAAATCTCTGACTTTCCTTCAACTTCAAAATCTTC
TAAACCTTCAAAAACCTCAGTTTCCATACATGAACTACGCCTTCTCCACTACCACCTCACCTCCGATC
AAGAACTCTCAGTCATCGTCGCTGCCCTAACCAACGTAGTCTCCGTTCCACCTCCACCGTCGGCTTA
GATCGAATAGTTCAACCGGTGAACATAGAAACCTGTCGGGAATGCAACATAGCAGGATGTTTAGGATG
CAATTTCTTCCCTGAAGAGAAAAAACAAAAACAAAAACAAAAACAAAAAGAGAGCTAAGAATAATAAGT
ACAGAGGAGTGAGGCAGAGACCATGGGGAAAATGGGCTGCTGAGATTCGTGACCCGAGACGTGCGGTT
CGTGTTTGGCTTGGAACCTTTACCACGGCGGAGGAAGCTGCTAGAGCTTACGAC

FIGURE 28 (continued)

AATGCCGCTATCGAGTTCGCGGGGCCGAGAGCCAAGCTTAATTTTCCACTTGTTGATGAATCTCTTAA
GCGTACTGTTGAGGATCCAGAATTGGTTGTTGATGTAAAGGATGAAGAAATGCAAATTGAGACAACGA
TGGGATTTGGGAATAATACGACTGAATGTGATTTTTGGGATAGTATTGGGGAAGAAGCTGATTTTCAA
CAACTTATGAGGTTTATGGATTCTTCTCATTCTAGAACAGGAAACACTTTTAATTAG

MSPPKPYINQLKSLTFPSTSKSSKPSKTQFPYMNYAFSTTTLTSDQELSVIVAALTNVVGSTSTVGL
DRIVQPVNIETCRECNIAGCLGCNFFPEEKKQKQKQKQKRAKNNKYRGVRQRPWGKWA AEIRDPRRAV
RVWLGTFTTAEAAARAYDNAAIEFRGPRAKLNFLPLVDES LKRTVEDPELVVHV KDEEMQIETTMGFGN
NTTECDFWDSIGEEADFQQLMR FMDSSHSRTGNTFN

[illegible]

MCGGAILYDIIPRRRLSSTDLWPSSADFWQTSSFSKPISTQNVPPKPKRAQLSRGSEQMKKRQRKNL
 YRGIRQRPWGKWAAEIRDPRKRVRVWLGTFTAEAARAYDREARKIRGKKAKVNFNEDDDHYSHPE
 PPPLNIVYESYDTTSTYNQESNNCPFHSENTPEVMEFAIANKNSSGSAYNGIEDQNVEGEEQTVKN
 SNNRIVEEEEEKTEDEVQILSDELMAYESLMKFYEIPYVDGQSVAAATVNPAADTEVGGGSMELWSFDDV
 SRLQPSYNVSLIIVLFLKLLHLFSLLN

FIGURE 28 (continued)

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SEQ ID NO: 247, AB085820.1| *Solanum tuberosum* cip353 mRNA for AP2/ERF-domain protein, complete cds

CTTTCAC TCAAAAAAAAAAAGGAAAAAATTAAGAGTAACAAAAGATGTGTGGAGGTGCCATAATCTCC
GATTATGAGCCCGCCGGAACCTTCTACCGGAACCTCTCTGCTCGTGACCTGTGGGCTGAGCTGGACCC
TATCTCCGACTACTGGTCCTCTTCCTCCTCATCCTCAACTGTCGAAAACCCTTATTCGCTCAGTCGC
CGGTGACTCACTCCGTCGATAAGCCTAAGAAATCAGATTCCGGCAAATCTAATCAACTCAAAAAAGGT
AATAAGACTGTGAAGGTTGAGAAGGAGAAGAGTACTGGACCAAGGCAGAGAAAGAACAAGTACAGAGG
AATAAGGCAGAGACCATGGGGAAAATGGGCTGCTGAGATTCGCGATCCTCAGAAGGGTGTCCGTGTTT
GGCTTGGTACATTCAACACAGCAGAGGATGCTGCCAGAGCCTATGATGAGGCTGCTAAGCGCATTTCGT
GGTAACAAGGCCAACTCAACTTCCCTGCCCCATCACCACCTGCTAAGCGACAGTGCCTAGCACTGT
CGCTGCTGATCCTCCACCAGCACTACTCCTTGAGAGTTCTAACATAATATCTTATAACAATTCTCCTT
TAATGAACCTTCGGATATGATGTTTCAAGGCCAACTCCCTACTACCCAATGGAAATGCCCGTTGCTAGT
GATGATTATGAACCAAGGAACAGATTTCCAACCTTGAATCGTTCCTGGAATTGGAGCCAGCAGATTC
ATCTGATCAGTTTTTCAGGGATCGTCGATCCTGATCCTCTTAATGTTTTTCTGATGGAGGATTTTGCTT
CAACTCAGCATCAGTTCTATTGATCCTGAGTTGTTTGGTGAGTGATGAGTGACTAGTTTATTAGCTTT
TGGCTGTAGTAGTAGTAATAGAGAAAAAAGTACATATGATATGATAATAATAAGTTGCGTGCCTTAGC
CTGCAATTGTAATAGTATCAATGTTTGTGTCTTGTGTTGTTTATGCTTTCTAAATCTTGGATTTACC
TTATAATGTTTGGTCATTTGGTGTATGTATTGTAACATATATGGAGTACTTTATTACTAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 248, BAC56862.1| AP2/ERF-domain protein [*Solanum tuberosum*]

MCGGAIISDYEPAGNFYRKLSARDLWAE LDPISDYWSSSSSSSTVENPYS AQSPVTHSV D KPKKSDSG
KSNQLKKGNKTVKVEKEKSTGPRQRKNKYRGIRQRPWGKWAAEIRD PQGVRVWLGT FNTAEDAARAY
DEAAKRIRGNKAKLNFAPSPPAKRQCTSTVAADPPPALLLESSNII SYNNSPLMNFYD VQSQT PYY
PMEMPVASDDYELKEQISNLESFLELEPADSSDQFSGIVDPDPLNVFLMEDFASTQH QFY

SEQ ID NO: 249, AY522505.1| *Coffea canephora* ERF-like transcription factor mRNA, complete cds

AAGTACCGCAAATTTGTAAGCTTAGATCATCAAAAATGTGTGGCGGTGCAATCCTCGAAGGCCTCATC
CCGCCCCGCAACAACAACGACGGCACTCGCCGTCTCTCCTCCGCTGACCTCTGGCCCTCCGCTGCTGA
TTTTTGGCCCAACTCTCACCTTGCCAAGCCCAGCCGCTCCAACCAACTGATGCCCCCACAAAGCCA
CGCACGAAACTTGTACGATCCACATGATGAAGCTGGTGGAAAGCAGCAAGTCCTTCCCAAGGGTGCC
AAGAGGCAGAGGAAAACTTATACAGGGGGATCAGGCAGCGACCATGGGGGAAATGGGCTGCTGAGAT
TCGAGACCCTAGGAAAGGCGTGAGAGTCTGGTTGGGCACTTTCAACACTGCCGAAGAAGCTGCCAGAG
CCTACGACAAAGAAGCTCGAAAAATCAGAGGCAAGAAAGCCAAGGTAACTTCCCAAACGAGGATTCG
ACCAGTTATCCCACATGCATCCCTTCGCAAACCCAGTACCAACAGGTACACATCCCCAGCCCTCCCAC
TTTCTGTGGTCCCTCCTCCTCCAATTGCAAGTTCAATCAGCTCCGTGTTGGGTGCTCTGATTGCAGTG
CCAGTGACTGCTATCACGCGAACAGCATCGATGATTGTGCCCGTTTCACCAATATGATGGGTTTTCGA
AATCCAAGCGAAGAGGTTTCTGGTTCTGGTAGTTTCGGATAATGAGTGTTTTCTTGGCCACCTTAAACA
AGTAGCCAAGGCGGCGGCGGAGGAGGAGGCGGCTTCGGTTATAACTGAAAATGATACGAAAGACAATA
ACAAAGCAGCTGAAAGCGAGGAGTACCAAGTGGAAAAGCTGTCTGAGGAGCTGCTGGCCTATGAGTCC
TTCATGAAGTTCTATCAGATTCCTTATATAGATGGGCAGT

FIGURE 28 (continued)

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CCGCAGCTGCATCGGCCAACCTGCTCAAGAGCTGGCAACTTCTATTAGCTTTGGAGCTTTGATGAT
GTCTCACCCGCCAATCGCCCAATGCCTCTGTAACCGCCAATCGCCCAAGTTCGATGGTCTTTTTTTTGG
GGAGTCCCAATTGCGTTTTTGGTGCCTAGTTTTTGTAGGTTTTGCTATGTAATTGACATTAACCTTCTTA
AAACATTGTAGGAAATTGTTGTTAGGTTGCAGGTTGGTACTCTTGACCGGCTTGTTTAGTTAAAATAC
CTATATGTAGGTTGGCACTTTGTAATTACTGTTTTTGTGGACAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 250, AAS01337.1| ERF-like transcription factor [*Coffea canephora*]

MCGGAILEGLIPPRNNNDGTRRLSSADLWPSAADFWPNSHLAKPSRSNPTDAPHKATHETCHDPHDEA
GGKQQVLPKGAQRQRKNLYRGIRQRPWGKWAAEIRDPRKGVVWLGTFTAEAAARAYDKEARKIRGK
KAKVNFNEDSTSYPTCIPSQTYQQVHIPSPPTFCGPSSSNCKFNQLRVGSSDCSASDCYHANSIDD
CARFTNMMGFRNPSEEVSGSGSSDNECFLGHLKQVAKAAAEAAASVITENDTKDNNKAAESEEYQVE
KLSEELLAYESFMKFYQIPYIDGQSAAASANPAQELATSIQLWSFDDVSPANRPMPL

SEQ ID NO: 251, DQ102383.2| *Hordeum vulgare* root abundant factor (RAF) mRNA, complete cds

CAGGAAGAGAAAACAATGTGTGGCGGCGCCATCCTAGCGCAGCTGATCCCGCCGTCGGCGGGCCGTCC
GTCGAAGCAGGCGGCAGCGGGCGGCCGGGCCCCGCCACGAGCTCCAAGAAGGGCGGCGTGAGCAAGA
GCCGCCACAGCAGCACCCCAGATGCCGACGACGACGTCTTCGAGGCGGCCTTCGAGGACTTCGATGAC
CACTTCGACCTGCGGGCGGAGGAGGACGGCGGCGACGACCATGTCGTCTTTGCATCCAAGCCTGCCTT
CTCTCCACGTCCGGCCTACGACGGTGGCCGCGCGGCGCATGCGGCGAGCAGGAAGAAGCGCACCGGCC
ACCTCCATGGCATCCGGCAGCGGCCGTGGGGCAAGTGGGCGGCGGAGATCCGCGACCCGCACAAGGGC
ACCCGCGTCTGGCTCGGCACGTTCGACACGGCCGATGATGCCGCCCGGGCCTACGACGTGCGCGCCCG
TCGCCTCCGTGGCAGCAAGGCCAAGGTCAACTTCCCCGACGCGGCCAGGACCGGGGCTCGCCCGCGCC
GCGCCAGCCGTAGAACC GCGCAGAAACCGCAATGCCCCCTGCGCGGACGACGGCGTACTCTGCCACC
GCAGCAGCACGCGCACAGCCGGAGCAGGACGCTATGATGGTCAAACCCGAGCTGATGGAGTTTTTCAA
CGTGGACGCCATCGTCCACCTGACCACTGCCGTGCGCGCGCTACCGCCTGTACGGCGAGCACCTTCG
CCGACACGATGCCGAGGGTCGACGAGGACTCTTCTGTGGGGAGCGGCGGCGGCCATGCTGGGGTTC
GCCGACGAGCTTGGGTTCGATCCGTTTCATGATGTTCCAGCTACCCTGCTCGGACATGTACGAATCCGC
CGACAGCATCTTCGCCGGAGACGCTGTCATCCCGGATGCCCTCAGCGTGGACAGTGGCATGGACGCCG
TCAGCCTCTGGAGCTTCGACGAGTTCCCCATGGACAGCGCCATTTTCTGACGCTTCCGTGTGATGCA
CTGCACTCTGTTGGTTGTAAGAATCTCCACCTGGCCTCTACGTAGTTCCTTGTAATGCCCGCGCACA
GAACCTTGCTCAGACCAGATTCTGTTTCTTGCCAGGAACGAAAGGAAGGGTTGCTGCCGATGCATGA
TTGCTTCCTCGATGAACGCAGATTCGAAATGTATTCTACTGTTTGAGTTTCTTGTTCTGTCACACACTG
TACCAAACTGTATTGTACCCTATCATAATTTCTGCTCGGTACCTCTCTGTACTGCTGGTACCAAACTG
TATTGTACTCTGTCATGATCTGTACTAGTCTTTGGTACTGCTGGTCAATAGTCTACGAATTGATCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 252, AAZ14085.2| root abundant factor [*Hordeum vulgare*]

MCGGAILAQLIPPSAGRPSKQAAAGGRAPPTSSKKGGVSKSRHSSTPDADDDVFEEAFEDFDDHFDLR
AEEDGGDDHVVFASKPAFSPRPAYDGGRAHAASRKRKTGHLHGIRQRPWGKWAAEIRDPHKGTRVWL
GTFDTADDAARAYDVAARRLRGSKAKVNFDAARTGARPRRASRRTAQKPPPARTTAYSA

FIGURE 28 (continued)

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TAAARAQPEQDAMMVKPELMEFFNVDAIVHLTTAVAALPPVTASTFADTMPRVDEDSSVSGGGGAMLG
FADELGFDPFMMFQLPCSDMYESADSI FAGDAVIPDALSVDSGMDAVSLWSFDEFPMDSAI F

SEQ ID NO: 253, AB125976.1| Cucumis melo CMe-ERF2 mRNA for ERF-like protein, complete cds

AATTCTCTAATCATGTGTGGCGGCGCCATTATCGCCGACTTAATCCCTCGCCGTGACGGCCAACGCGT
TACCGCTTCCGACATTTGGCCTAACTCCTCCTTCTTCCATTTCAACAAAATTCGCTCCGATCAAGTTT
CAACTCCCCCTCAACGAACCCCCCTCCCGGCTCTTCCGAGGCTTCGAAGCCCAAGAAGAGGCAGAGG
AAGAATCTTTACAGAGGAATTCGTCAGCGCCCGTGGGGAAAATGGGCGGCTGAGATTCGTGACCCAG
GAAGGGGATCCGTGTCTGGCTTGGGACTTTCAATACTGCTGAGGAAGCCGCTCGAGCTTACGATCGAG
AAGCTCGCAAGATTCGTGGAAAGAAAGCTAAGGTCAATTTCCCTAATGAAGATGATGCATATTCATT
CAAGCTCCCATTCTCAATTTACCCCTCATCTTTACACTGTCCCTGAGAATTCGGAATTCCTTACGA
TCTCAACCAATCGGTGATTTACCGGCACTCACTTTCCCGTGGCGATTGAGGAACAATCCGGCTCTG
GGTCGGAGGATTCTTATTCTCCACCGAAAAGATTTCGGTGTGAAAGAGGCTGAAGATCAGAAGCCGGAG
CAGAAGGTTAGCGTTATTGCCGCGGCGGAGGAAGAGAACGAGGTGCAAAGCTTTCTGAGGAATAAT
GGCGTATGAGAACTACATGAAGTTCTACCAAATTCCATACCTCGACGGTCAATCGACGGTGACGAATC
CGGCTGAAGAACAAGTGGTGGGCGATCTCTGGAGCTTCGACGACGAGGATGGGCTTCACGGCTCTGTT
TCGTCGTCTGAATTATGATGATTGATGATCCAATAACTTCTCCATATCTCAAACCGGTTTCTCCATT
TTCTATTGTTGTTTTGTTATTTAATTCCAGAATGTGTTTTATGTAATTTCTGTCTGTTGAACGATGTC
AATTTGTTGATATGAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 254, BAD01556.1| ERF-like protein [Cucumis melo]

MCGGAI IADLI PRRDGQ RVTASDI WPNSSFFHFNKIRSDQVSTPLKRTPLPASSEASKPKKRQRKNLY
RGIRQRPWGKWA AEIRDPRKGIRVWLGT FNTAE EAARAYDREARKIRGKKAKVNFNEDDAYS IQAPI
PQFHPHLYTV PENSEFPYDLNQIGDFTGTHFPVAIEEQSGSGSEDSYSPPKRFGVKEAEDQKPEQKVS
VIAAAEEENEVQKLSEELMAYENYMKFYQIPYLDGQSTVTNPAEEQVVGDLWSFDDDEDGLHGSVSSSE
L

SEQ ID NO: 255, AB288347.1| Malus x domestica MdERF1 mRNA for ethylene response factor, complete cds

CTGAGAGGGCTCTTTTTTCTCTCTAAGTTTCTACAAGTGGCAATATAAACATGTGTGGTGGTGCTATC
ATTTCCGACTTCATCGCCGTCAAGCGCGCCCTGAAGCTGACGGCGGAGGACCTCTGGTCAGATCTTGA
CACCATCTCTGACCTCCTTGGCATAGACTACTCCAACAGCATCAACAAACAGCCGGAATCACAAGG
TGGTCCAAAAGCCGAAACCATCTATCACCAAAGTAGTGACAAGTGATGAGAAGCCCAAGCAGGCGAGC
GGGTCTGCTGCTGCCGCAAAGGCAAGAGAGTGAGAAAAAACGTGTACAGAGGAATAAGGCAGAGGCC
GTGGGGCAAATGGGCGGCTGAGATTTCGCGACCCCTACAAAGCCGTCCGGGTCTGGCTCGGCACCTATG
ACACCGCTGAGGAAGCCGCCCGCGCTTACGATGAAGCCGCCGTGCGCATCCGCGGGGACAAGGCCAAG
CTCAACTTTGCCCAACCACCATCCTCTTCACCGCTTCCATCTCTGGCGCCGGATACGCCGCCGCCGAC
AAAGAGGCGGTGCATTGTTGCTGAGTCAACTCGGGTGGAGCCGACTCAAC
CGAGTTTCCAGACCGGTTCTTACTATTATGATCCATTATATCACGGCGGTGGTGGTGGGGAAATGTAT
GCTAAGAAAGAGGTGGCGGGTGGGGACGAGGTGGTGGTAGAGCAGCTGAGTCAGGTGGTGAAGTGAAG
CGGAGAGTCGACTCGTTGTACCTGTGGATGCTGGATGACCTGGTGGCATATCAGCAACAAG
GGCAGCTTCTGTATTAAGGCAGCGGAATTGTTCTAGCTAAATATTTGTATGGCTAGGAATTAAAA

FIGURE 28 (continued)

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CATATTAATTAAAGGGTATGTATGTTTAATTTACGTGTGTGAAATGCGAGTGTTGAGTATGTCTATGA
CTGGGTTTGTGTAACGTGTGTTGTTTGCTACGGTGTATGTTTAATAGTAACTGCTTTTGTCTTTGA
AAAAAAAAAAAAAAAA

SEQ ID NO: 256, BAF43419.1| ethylene response factor [Malus x domestica]

MCGGAIISDFIAVKRALKLTAEDLWSDLDTISDLLGIDYSNSINKQPENHKVVQKPKPSITKVVTSD
KPKQASGSAAAAGKRVKRVYRGIRQRPWGKAAEIRDPYKAVRVWLGTYDTAEAAARAYDEAAVRI
RGDKAKLNFAQPPSSPLPSLAPDTPPPTKRRRCIVAESTRVEPTQPSFQTGSYYYDPLYHGGGGGEMY
AKKEVAGGDEVVVEQLSQVVSGSGESDSLYLWMLDDLVAAYQQQGQLLY

FIGURE 28 (continued)

SEQ ID NO 257, *Oryza sativa* – DNA

SEQ ID NO 258, *Oryza sativa* – protein

SEQ ID NO 259, *Oryza sativa* – DNA

FIGURE 29

SEQ ID NO 260, *Oryza sativa* – protein

MATTVDWCGRGSLPAAMYDMVVDSEKELMGALAPSMVVSFSYPCSEQSASSLLAGANYLTPAQVLHVQA
QLQLRLRRPGAASGCLAAPPLPMKRHGAVAVAAAAAARAPVKLYRGVRQRHWGKWVAEIRLPRNRTRL
WLGTFTDAEEAALAYDSAAFRLRGESARLNFPELRRGGAHLGPPHAAVDAKLHAICHGMDLPQPQPQ
TQSNATTTTMTSTATNTSPFFSSESPVVKSEPVCSASESSSSADGDVSTGSSDVVPEMQLLDFSEA
PWDESESFLLHKYPSLEIDWDAILS

SEQ ID NO 261, Oryza sativa – DNA

ATGGCGACGACAGTGGATTGGTGTGGCCGTGGCAGCAATCTTCCTGCTGCGATGTATGACATGGTGGT
GGATAGCAAGGAGCTAATGGGCGCGCTTGCTCCGTCCATGGTGTCTCTTCTCCTACCCGTGTTCCGAGC
AGAGCGCGAGCTCGCTTCTTGCTGGCGCCAACCTACCTGACTCCCGCGCAGGTGCTCCATGTCCAGGCG
CAGCTACAGCGCCTGCGCCGCCCGGGCGCGGCGAGCGGCTGCCTCGCCGCGGCGCCGCCGCTGCCGAT
GAAGCGGCATGGCGCGGTGGCGGTGGCGGCGGCGGCGGCGCGGGCGCCGGTCAAGCTGTACCGCG
GCGTCAGGCAGCGGCATTGGGGCAAGTGGGTGGCGGAGATCCGCCTGCCGCGCAACCGCACCCGCCCTC
TGGCTGGGCACCTTCGACACCGCCGAGGAGGCCGCGCTGGCGTACGACAGCGCCGCGTTCCGCCCTCCG
CGGCGAGTCCGCGAGGCTCAACTTCCCCGAGCTCCGCCGCGGCGGCGCCACCTCGGCCCGCCGCTCC
ACGCCGCGGTTCGACGCCAAGCTCCACGCCATCTGCCACGGGATGGACCTGCCCCAACCCCAACCCCAA
ACCCAGAGCAATGCGACGACGACGACGATGTGACGACGCGGACGAACACCCCAAGCCCCCTTCTTCTC
CTCGGAGAGCCCGGTGGTCAAGAGCGAGCCCGTCTGCTCCGCCTCCGAGAGCTCTTCTCGGCCGACG
GCGACGTGTCATCGACGGGCTCCTCCGACGTCTGCCGAGATGCAGCTGCTCGACTTCTCGGAGGCG
CCATGGGACGAGTCCGAGAGCTTCCTGCTGCACAAGTACCCGTGCTGGAGATCGACTGGGACGCGAT
CCTTTCTCTGA

SEQ ID NO 262, *Oryza sativa* – protein

MATTVDWCGRGSNLPAAMYDMVVDSEKELMGALAPSMVSFSYPCSEQSASSLLAGANYLTPAQVLHVQA
QLQRLRRPGAASGCLAAPPLPMKRHGAVAVAAAAAARAPVKLYRGVRQRHWGKWVAEIRLPRNRTRL
WLGTFDTAEAAALAYDSAAFRLRGESARLNFPELRRGGAHLGPPHAAVDAKLHAICHGMDLPQPQPQ
TQSNATTTTMTSTATNTSPFFSSESPVVKSEPVCSASESSSSADGDVSSTGSSDVPEMQLLDFSEA
PWDESESEFLLHKYPSLEIDWDAILS

SEQ ID NO 263, *Triticum aestivum* – DNA

GCTCTCCTCGGCTTCCCTTCCCTCCAATCGTCGGCGTTTCTTGATCGACGAGGGCATGGCGACGACGCG
TGGACTGGCGCAGCTATAGGCCCGATCTTCCTGCCGCGATGTATCACATGGTGGACAGCAGGGACCAG
GTAATGCACGCGTTTGCTCCGGCGACGGCGCAGGGCGCGGCTCCGACCATCTCGTTCGCCTTCCCTTG
CCCCGGCGCGGAGCAGAGCGCCGGCCTGCTTCGTGGCGCCAGCTACCTCACTCCCAGCGCAAATCCTCC
AGCTCCAGTCGCAGCTGCACCACGTGCGCCGGGCGCCGGGCGCGGCCATGGCCGCGGTGGGGCAGCCG
ATGAAGCGGCACGGCGTGGCAGCGCTCCCGGCGCGGCCGGCGACCAAGCTTTACCGCGGGCGTAAGGCA
GCGGCATTGGGGGAAGTGGGTGCGCCGAGATCCGCCTGCCCCGCAACCGCACCCGCCTCTGGCTCGGCA
CCTTCGACACCGCCGACGAGGCCGCGCTGGCC'TACGACGCCGCGCCCTTCCGGCTCCGCGGGCAGTCC
TCCAGGCTCAACTTCCCCGAGCTCAGGCGCGGGCGGCGAGCACCACGGCCCGCGCTCGACGCCGCGAT
CGACGCCAAGCTCCGCTCCATCTGCCACGGGGAAGACATGCCCCAGAGCCAGAGCGATGAGACGCCGG
CGCCGACGACGACACTGACGCCGATTTCTTTCCCGGACGTCAAGAGCGAGCCAGTCTGCTCCGTCTCC
GAGAGCTCGTCGTGCGGTGACGGCGAGGTGTCCTCGTGCTCCGACGTGTCCTCCGGAGATGCAGCTTCT
TGATTTCTCGGAGGCTCCATGGGACGAGTTCCTGCTGCGCAAGTACCCGTCGCTCGAGATCGACTGGG
ACGCGATCCTTTCTTGAATCAAGTTCATGCTCGATCCACAGCTCG

FIGURE 29 (CONTINUED)

139/173**SEQ ID NO 264, *Triticum aestivum* – protein**

MATTVDWRSYRPDLPAAMYHMDSRDQVMHAFAPATAQGAAPTISFAFPCPGAQEQSAGLLRGASYLTP
AQILQLQSQLHHVRRAPGAAMAAVGPMPKRHGVAAALPARPATKLYRGVRQRHWGKWVAEIRLPRNRTR
LWLGTFTDADEAALAYDAAAFRLRGESSRLNFPFLRRGGEHHGPPLDAAIDAKLRSICHGEDMPQSQS
DETPAPTTTLTPISFPDVKSEPVCSVSESSSSADGEVSSCSDVVPQMQLLDFSEAPWDEFLLRKYPSL
EIDWDAILS

SEQ ID NO 265, *Triticum aestivum* – DNA

GCTCTCCTCGGCTTCTCTTCTCCTCAAATCGTCGGCGTTTCTTGATCGACAGGGCATGGCGACGACGGT
GGACTGGCGCAGCTATAGGCCCGATCTTCTGCGGCGATGTACCGCATGGTGGACAGCAGAGACCAGG
TAATGCACGCGTTTCGCTCCGCCGACGGCGCAGGGCGCGGCTCCGACCATCTCGTTTCGCCTTCCCATGC
CCCGGCGCGGATCAGAGCGCCGGCCTGCTTCGTGGCGCCACCTACCTCACTCCCGCGCAAATCCTCCA
GCTCCAGTCGCAGCTCCACCACGTGCGCCGGGCGCGCGGCGCGCCCATGGCCGCGGTGGGGCAGCCGA
TGAAGCGGCACGGCGTGGCGGCGCTCCCGGCGCGGCGGCGGCGACCAAGCTGTACCGCGGCGTGCAGCAG
CGGCATTGGGGGAAGTGGGTGCGCGGAGATCCGCCTGCCCCGCAACCGCACCCGCCTCTGGCTCGGCAC
CTTCGACACCGCCGACGAGGCCGCGCTGGCCTACGACGCCGCCGCCTTCCGGCTCCGCGGCGAGTCCG
CCAGGCTCAACTTCCCCGAGCTCAGGCGCGGCGGCGAGCACACGCCCCGCCGCTCGATGCCGCGATC
GACGCCAAGCTCCGCTCCATCTGCCACGGGGAAGACATGCCGCAGAGCCAGAGCAATGAGACGCCGGC
GCCGACGCCGACACTGACGCCGATTTCTTTCCCGGACGTCAAGAGCGAGCCAGTCTGCTCCGTCTCCG
AGAGCTCTTCGTGCGGCTGACGGCGAGGTGTCCTCGTGCTCCGACGTGCTCCCGGAGATGCAGCTTCTT
GATTTCTCGGAGGCTCCATGGGACGAGTCCCTGCTGCGCAAGTACCCGTCGCTCGAGATCGACTGGGA
CGCGATCCTTCCTTGAATCAAGTTCATGCTCGATCCACAGCTCGTCCAAAGTGATTACTTCGGCTTCC
ACTTAGGCTCGATCGAGTATACGCGTGTAGCATCAACCCCTCCCTGC

SEQ ID NO 266, *Triticum aestivum* – protein

MATTVDWRSYRPDLPAAMYRMVDSRDQVMHAFAPPTAQGAAPTISFAFPCPGADQSAGLLRGATYLTP
AQILQLQSQLHHVRRAPGAPMAAVGPMPKRHGVAAALPARPATKLYRGVRQRHWGKWVAEIRLPRNRTR
LWLGTFTDADEAALAYDAAAFRLRGESARLNFPFLRRGGEHHGPPLDAAIDAKLRSICHGEDMPQSQS
NETPAPTPTLTPISFPDVKSEPVCSVSESSSSADGEVSSCSDVVPQMQLLDFSEAPWDESLLRKYPSL
EIDWDAILP

SEQ ID NO 267, *Triticum aestivum* – DNA

TCCTCCAGCTCCAGTCGCAGCTCCACCACGTGCGCCGGGCGCCGGGCGCGGCCATGGCAGTGGCGGGG
CAGCCCATGAAGCGGCACGGCGTTGCGGCGCTCCCGGCGCAGCCGGCGGCCAAGCTGTACCGCGGCGT
GCGGCAGCGGCATTGGGGGAAGTGGGTGCGCGAGATCCGCCTGCCCCGCAACCGCACCCGCCTCTGGC
TCGGCACCTTCGACACCGCCGACGAGGCCGCGCTGGCCTACGACGCCGCCGCCTTCCGGCTCCGCGGC
GAGTCCGCCAGGCTCAACTTCCCCGAGCTCAGGCGCGGCGGCGAGCACACGCCCCGCCGCTCGACGC
CGCGATCGACGCCAAGCTCCGCTCCATCTGCCACGGGGAGGACCTGCCGCAGAGCCAGAGCAATGCGA
CGCCGGCGCCGACGCCGACCTGACGCCGAGCTCTTTCCCGGACGTCAAGAGCGAGCCAGGCTGCTCC
GTCTCCGAGAGCTCGTTCGTGCGCCGACGGCGAGGTGTCCTCGTGCTCCGACGTGCTCCCGGAGATGCA
GCTTCTTGATTTCTCGGAGGCTCCATGGGACGAGTCCCTGCTGCGCAAGTACCCGTCGCTCGAGATCG
ACTGGGACGCGATCCTTTCTTGAACCGAGTTCATGCCCGATCCACAGCTCGTTCAAAGTGATTGCTTC
TGCTTTCGTTAGGCTCTTAGATAGGTTATTATGGGTTTGTATCAAGTATTCTTGTGTAACATCAATCCC
TGCTCTGCTTGTTTTTTGAATGGCATTGCCAGGAAGGAGGTTTTATGTAGAAATTTTAAGTATGTCAT
GTAGTTTGTGATTCATTTTTTTTTTTTTTTTTT

FIGURE 29 (CONTINUED)

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SEQ ID NO 268, *Triticum aestivum* – protein

MAVAGQPMKRHGVAALPAQPAAKLYRGVRQRHWGKWVAEIRLPNRNTRLWLGTFTADEAALAYDAAA
FRLRGESARLNFPELRRGGEHHGPPLDAAIDAKLRSICHGEDLPQSQSNATPAPTPTLTPSSFPDVKS
EPGCSVSESSSSADGEVSSCSVDVPEMQLLDFSEAPWDESLLRKYPSLEIDWDAILS

SEQ ID NO 269, *Oryza sativa* – DNA

TTTTTCTCTTCTGGATTCTTGCCGATTTTTAGGCTTCCTTTGCTTTTCTAAGGCCAGAAAGGGTTGTT
TTGCAATACCCTTCTAGTTCATCCTCTCAAATTTTTCTTCTTCTATTCAAAGCTCTTTCTTTCTTT
GCACCCTTTGTTTCTCTACTTTTATTGAGGAACAGGGCTGATTTTTCACTTCTTGCATCCAAAAAGCA
CCCCTTTTTCTTTCTGTTTTTAAGATTTCCATACCCTTGCCATCTTCATCTTCTACCTCCATCCAG
TCCTCATGGCCGAGCAATAGACATGTACAAGTATAACACTAGCACACACCAGATCGCATCCTCGGAT
CAGGAGCTCATGAAAGCGCTCGAACCTTTTATTAGGAGCGCTTCTTCTTCTCCGCTTCCTCCCCCTG
CCACCACTACTACTCTTCTTCTCCTTCCATGAGCCAAGATTCTTACATGCCCACCCCATCTTATCCCA
CTTCTCTATCACAACCGCCGCCGCCACCACCACCTCGTCTTCTCGCAGCTACCTCCGCTGTACTCT
TCGCAGTATCATGCTGCTTACCTGCGGCGTGGCGACGAACGGGCGGATGGGGCTGACCCACCTGGG
CCCAGCCCAGATCCAGCAGATCCAGGCCAGTTCTTGGCCAGCAGCAGCAGCAGAGGGGCCCTGGCCG
GCGCCTTCTTTCGGCCGCGTGGCCAGCCGATGAAGCAGTCCGGGTGCGCCGCCGCGCGGGGCCGTTT
GCGGCGGTGCGCGGGGCGGCGCAGTCGAAGCTCTACCGCGGAGTGCGGCAGCGCCACTGGGGGAAGTG
GGTGGCGGAGATCCGCCTCCCGAAGAACCGGACGCGGCTGTGGCTCGGCACCTTCGACACCGCCGAGG
ACGCCGCGCTCGCCTACGACAAGGCCGCCTTCCGCCTCCGCGGCGACCTCGCGCGGCTCAACTTCCCC
ACCCTCCGCGCGGCGGCCGCCACCTCGCCGGCCCGCTCCACGCCTCCGTGCGACGCCAAGCTCACCGC
CATCTGCCAGTCCCTCGCCACGAGCTCGTCCAAGAACACCCCCGCCGAGTCAGCGGCCTCCGCGGCGG
AGCCGGAGTCCCCCAAGTGCTCGGCGTGCAGGAAGGGGAGGACTCGGTGTCCGCGGCTCCCCTCCT
CCGCCCACGCCGCTGTGCCCCCGGTGCCGGAGATGGAGAAGCTGGACTTCACGGAGGCGCCATGGGA
CGAGTCGGAGACATTCCACCTGCGCAAGTACCCGTCTGGGAGATCGACTGGGACTCAATCCTCTCAT
AAACAAGCAGAAGCAGCTACTACTAGTCTATTACTAGTACTAGTAGTCTTCGTCAAGCTAGAGTC
ACTCAACTCAACTAGCTGTGTAATCTTCTCTGAATCCGTGGCTTCCATGGCTCGGTGGCATTTTAGA
CGTCGGCCATGGCTGCTGCGAGTAGCAGTAAGTACTAGTACTAGTAGTAAGGTGCTTGGTATT
ACGTCGTGCTGCAAGTGTGCTTGGTGTACTCAGTGATCTGATCTCCTGTTGAGCTGCCGGTTGTTTT
TTTCACGGCGCGGCCGGTGCAGAATTAAGCTGTAATCCCTTGTTACATGTTGGAAATTGAGTAGCTTA
TGTAACATATGTACCTTTCTC

SEQ ID NO 270, *Oryza sativa* – protein

MAAAIDMYKYNTSTHQIASSDQELMKALEPFIRSASSSSASSPCHHYSSSPSMSQDSYMPTPSYPTS
SITTAAATTTSSFSQLPLYSSQYHAASPAASATNGPMGLTHLGPQIQQIQAQFLAQQQQQRALAGA
FLRPRGQPMKQSGSPPRAGPFAAVAGAAQSKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFTDAEDA
ALAYDKAAFRLRGDLARLNFPTLRRGGAHLAHLASVDAKLTAICQSLATSSSKNTPAESAAAEPAEP
ESPKCSASTEGEDSVSAGSPPPPTPLSPPVPEMEKLDFTAPWDESETFHLRKYPSWEIDWDSILS

FIGURE 29 (CONTINUED)

SEQ ID NO 271, Arabidopsis thaliana – DNA

SEQ ID NO 272, Arabidopsis thaliana – protein

SEQ ID NO 273, *Oryza sativa* – DNA

FIGURE 29 (CONTINUED)

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SEQ ID NO 274, *Oryza sativa* – protein

MAAIDLYKYQLSSSSSSSSSDQELMKALEPFIRSASPTSTSTSTPLFYSSSSIISTTTTTTFFSYSSPLP
QESYYLPASSSYAAIIVPPPTTTTNTTTTSFSELPPLPPSSSSSFASPANAAVGLAHLGPEQIQQIQVQF
LMQQQLQQRGMAASASASAAASYLGPRAPQPMKQAGAAAAAAGGKMYRGVRQRHWGKWVAEIRLPKNR
TRLWLGTFTDAEDAALAYDKAAFRLRGDAARLNFPFLRRGGAGLAGPLHASIDAKLTAICHSLAAAPP
ASSKKAAAAAHPDSPKGSASTTTTTTSEGDESAISACSPPLPPPPPPPAALPEMANLDFTEAPWDES
DAFHLYKCPSWEIDWDSILS

SEQ ID NO 275, *Asparagus officinalis* – DNA

CCACCTTTGATCACTCCTCGCCATCAAACCTCCAGTCTTTTGAGCATGGACCAGCCTGATCTGAGCCAA
GTTGGGCCAGTTGGGCTGACCCAACTGAGCCCACTTCAAATCCAGCAGATCCAAGCTCAAATCCAGCT
CAACCACCAACACCAGCTAATGGTCTCCAGAACCCTGCAAGCTAGAAATTACCATAACACCCTCGGTG
TAAAGCCCCAGCCCATGAAGCTCCAGGCCTCGGTGCTGCACCTCAGTCAAAACCCACGAAGCTCTAC
AGAGGGGTGAGGCAAAGGCACTGGGGTAAATGGGTGTCAGAGATCAGACTGCCGAAGAATCGAACCAG
GCTTTGGCTTGAACCTTTGACACTGCTGAAGAAGCTGCCTTGGCCTATGACAAGGCTGCTTACAAAT
TGAGAGGGGACTACGCGAGGCTCAATTTCCCTAACCTGAAGCATACCCATCTGGCTGGCAACCCTCTG
CACTCGTCTGTTGATGCCAAGCTCGAAGCAATTTGCCAGACCCTGGAGAGCCCTGGGAAGAAGAAGGT
TAGCACCGGGTGAAGCCTGAGCCGGTTGTTTCATCGCCGACTGTTGAGACCGAGGAGGAGTCTTCCT
CTTCTTCTTCGGTGACGGGGGCGACGAATTTCTCCGGTTTCAGAGATCGAGAGCTTGGATTTCAATGAG
GTGCCGTGGGATGAGACTGAGGACTTTGTGTTGAGGAAATACCCATCCTATGAGATTGATTGGGATTC
TATATTGTCTTCAGCTTAGTAGTGTCTGGTTTGTGCTTGTGTTGTTAGATTTGGGGGTCTTTAGTGG
CTGTTGCAAATGGAGTTTTTGGCATTTCGCTAGCCTTGTTTCAGGGATTTTGTAGTTAGTTTATTTTTT
TTTCTTTCTTTTAGAGTGTAAGAACTCATGGCCTCTGCTGATTATTTTGTCTTGGCGAGGCCGTTGAG
GGGTAAAGTGTACTACTATTGTGAGTTCAGGTGTAAGTCTTCTCTGTTGCAGCTTTGTAAGTATGAG
TGTATCTTGTGTTTAATTAAGGTATATTTGTAGCTTTTGAIAAAAAAAAAAAAAAAAAA

SEQ ID NO 276, *Asparagus officinalis* – protein

MDQPDLSQVGPVGLTQLSPLQIQQIQAQIQLNHQHQLMVSRTLQARNYHNTLGVKPQPMKLQASVAAP
QSKPTKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFTDAEEAALAYDKAAYKLRGDYARLNFNPKH
THLAGNPLHSSVDAKLEAICQTLESPGKKKVSTGSKPEPVVSSPTVETEESSSSSVTGATNSPVSE
IESLDFNEVPWDETEDFVLRKYPSYEIDWDSILSSA

SEQ ID NO 277, *Aloe vera* - DNA

AAATCCAATCTTTGACCGCCGACCTGAGCCAGCTGTGCCCCGATAGGTTTGAATCACCTGAGCTCGCT
CCAGATCCAACAAATTCAAGCCCAGATCCAGCTCAACCAGCAGCAGCAGCTCATGATATCGAGAGCCA
TGCAAGCAAGGAACATAACCTCGGGGTGAGATCTCAGCCCATGAAGCTCGCCGCCGCTGCAGCGCCG
CCTCAGCCGAAGCCGACGAAGCTCTACAGGGGCGTGAGGCAGCGGCACTGGGGCAAGTGGGTGGCCGA
GATCAGACTACCGAAGAACAGGACAAGGCTCTGGCTCGGCACTTTTGACACAGCCGAGGAGGCCGCCT
TGGCCTACGACAAGGCCGCCTACAAGCTGAGGGGGGACTACGCCAGGCTCAACTTCCCCACCTGAAG
CACACCGGTGCCACCTGGCTCCCGGCGGCCCCCTGCACTCCTCTGTGGACGCCAAGCTGCAGGCCAT
CTGCCAGAGCTTGGAGCAGAATAAGAGCTCAAACCTCAAACCTCATCAAAGAAAGAGAAGAGGGGGGATG
CAGTAGAAGAAAAATCTGACAAGGTGGTGGTTGTTGTTGCCGAGGGCGAG

FIGURE 29 (CONTINUED)

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GAGTCTTGCTCATCTTCTTCGATGAACACGGGGAGTGCGAGCTCGCCATCGTCCGAGATAGAGAGCCT
GGACTTCACGGAGGTGCCATGGGATGAGTCTGAGGACTTTGTGCTGAGGAAATACCCTTCATGGGAGA
TTGATTGGGATGCTATACTGTCTTAATGTTTTGGTAGTCGTTGTGTTTTGTGGTTTTGTTCTAGGGTT
TTTAGTCGTTGGTGGCTGGTTGCAAATGGAGTTTTTGGCATTGTCACAGCCTTTTAGAGCTCAAGGTC
TTTGCTGGTTATTTTTTCTTGGCAAAGGACTGGGTGGGGGGAGTAGTTCTGTTTCAGATTTTCAGGTTG
TTGTTATTGTCATCTTGTAGTAGCTTTGTATTATAATCAGTTTATTTGTGTTCCAGTTCTTAAAAA
AAAAAAAAAAAA

SEQ ID NO 278, Aloe vera - protein

MISRAMQARNYNLGVRSQPMKLAAAAAPPQPKPTKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFTD
AEEAALAYDKAAYKLRG DYARLNFPHLKHTGAHLAPGGPLHSSVDAKLQAICQSLEQNKSSNSNSSKK
EKRGDAVEEKS DKVVVVVAEGEESCSSSSMNTGSASSPSSEIESLDFTEVPWDESEDFVLRKYPSEI
DWDAILS

SEQ ID NO 279, Gossypium hirsutum - DNA

ACCTCTTTTAATCCGTTCTGGATTTAGGACCTGTTCTTCAAGTTTTGGTAAGAAACAGGTTAATTTTT
TATTAATTTGGTCTCATCTTATTTCTAGTTTTAGTGTAATGGCAGCTGCAATGGATTTTATTAGT
ATTGGAGTAGATCAATCAGATCTATATGGGGGAGAATTGATGGAAGCTCTCGAACCTTTTATGAAAAG
TGTTTCCTCCTCTTCCCCTTCCCCTTCCCCTTCCCCTTCCCCTTCTTCTCTTCTTCTTCTTCTTACC
TTTCTTTCTCTTCTTCCGAAACACAACCTAATTTTTTACCCAGATAGCTGTTGTTACCCTTACCCTACA
CCAATGGACTCAGTATCATGTCCCCAACAGCCTCAAACCTGGTTCAACAATTGGGCTAAATAGCTTGAC
ACAAGCTCAGATCCATCAGATCCAGCTTCAATTCCACCTCCACAACAACCAACCAAGCTACCTTTGCC
AAAGTCCCCAACCCAACACCATCAGCGCCAATAGTAACCCGATGGTTAGCTTTCTTTGCCCTAAACCT
GTCCCAATGAAACACGTGGGTGCGCCATCCAAACCCACCAAACTTTACAGAGGAGTTAGGCAACGCCA
CTGGGGAAAATGGGTGCTGAGATCCGGTTACCTAGAAACCGGACACGTCTTTGGTTAGGCACTTTTG
ACACTGCTGAGGAAGCAGCCTTGGCTTATGACAAAGCAGCTTATAAACTAAGAGGTGACTTTGCGAGA
CTCAACTTCCCTAACCTTTCGTCACCACGGTTCCCACGTAGGTGACTACAAGCCTTTGCCTTCCTCTGT
TGACGCTAAGCTTCAAGCCATTTGTGAGAGCTTGGTACAAAACCCTAAGCAAGGGAGCAAGAAGAAAT
CATCCAAGGTTACGGCAGACACCAAAAGCAGGAACAACAAAAATCCGACATGGCAGAGCCAAAGCCC
GAGGAGAATACAGCGAAAGTGGAGAACTCCTCATCTTTGTCTACGGTTCAATCCGAGAGTGAGGGTTC
GGCTGTATCTTACCTTTATCAGATCTTACATTCTCGGATTTGACGAACAACCATGGCCGGAAGTCG
TTTCTTCTTCGGAAACTTTTATGTTGTCCAAGTACCCTTCAGAGATCGATTGGGATTCATTCTAAAA
GCCTGAAGGGAAAAACCCAAGTTTCGTTTTCTGTGTAACAGTCTTTTGTGTTTAGGAGTTTCCTTTC
GTGTATTTTTTTTTGTAAAGCTAGCTGCAATGGAGTTTTTGGCAGTTGCAGTGGCATGTATTTTAGGT
TATTAAGAGTCTGTTAATGAGTGTAAGTGCTTGTGTTTATAAGAATTTGTGATTTTCTCCATGCTGGT
CAGCTCGTTTTTTTTACTTGCTGAACCAAAAGGTGAAATTTGTAGTGTCTATAAAAAAAGTTTATAGC
TTTTGTATTTTGTACGAATTAAATGTTATTTATGTTGTTGTATTCTCTGGTATCGTGTTCCTTC

SEQ ID NO 280, Gossypium hirsutum - protein

MAAAMDFISIGVDQSDLYGGELMEALEPFMKSVSSSSPSPSPSPSSLPSTSYLSFSSSETQPNFYF
DSCCYPYPTPMDSVSCPQQPQTGSTIGLNSLTQAQIHQIQQLQFHLHNNQPSYLCQSPQPNNTISANSNP
MVSFLCPKPVPMKHVGAPSKPTKLYRGVRQRHWGKWVAEIRLPNRNTRLWLGTFTDAEEAALAYDKAA
YKLRGDFARLNFNLRHHGSHVGDYKPLPSSVDAKLQAICESLVQNPQKQSKKKSSKVTADTKSRNNK
KSDMAEPKPEENTAKVENSSSLSTVQSESEGSASVSSPLSDLTFSDFDEQPWPPEVSSSETFMLSYP
EIDWDSILKA

FIGURE 29 (CONTINUED)

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SEQ ID NO 281, Arabidopsis thaliana - DNA

ATGAATTTGTACACTTGTAGCAGATCGTTTCAAGACTCTGGTGGTGAACATCATGGACGCGCTTGTACC
TTTTATCAAAAGCGTTTCCGATTCTCCTTCTTCTTCTGTCAGCGTCTGCGTCTGCGTTTCTTCACC
CCTCTGCGTTTTCTCTCCCTCCTCTCCCCGGTTATTACCCGGATTCAACGTTCTTGACCCAACCGTTT
TCATACGGGTCGGATCTTCAACAAACCGGGTCATTAATCGGACTCAACAACCTCTCTTCTTCTCAGAT
CCACCAGATCCAGTCTCAGATCCATCATCCTCTTCTCCTCCGACGCATCACAACAACAACCTCTTTCT
CGAATCTTCTCAGCCCCAAAGCCGTTACTGATGAAGCAATCTGGAGTCGCTGGATCTTGTTTCGCTTAC
GGTTCAGGTGTTCCCTTCGAAGCCGACGAAGCTTTACAGAGGTGTGAGGCAACGTCACTGGGGAAAATG
GGTGGCTGAGATCCGTTTGCCGAGAAATCGGACTCGTCTCTGGCTTGGGACTTTTGACACGGCGGAGG
AAGCTGCGTTGGCCTATGATAAGGCGGCGTACAAGCTGCGCGGCGATTTCGCCCCGGCTTAACCTCCCT
AACCTACGTCATAACGGATCTCACATCGGAGGCGATTTCGGTGAATATAAACCTCTTCACTCCTCAGT
CGACGCTAAGCTTGAAGCTATTTGTAAAAGCATGGCGGAGACTCAGAAACAGGACAAATCGACGAAAT
CATCGAAGAAACGTGAGAAGAAGGTTTCGTCGCCAGATCTATCGGAGAAAGTGAAGGCGGAGGAGAAT
TCGGTTTCGATCGGTGGATCTCCACCGGTGACGGAGTTTGAAGAGTCCACCGCTGGATCTTCGCCGTT
GTCGGACTTGACGTTTCGCTGACCCGGAGGAGCCGCCGAGTGGAACGAGACGTTCTCGTTGGAGAAGT
ATCCGTCGTACGAGATCGATTGGGATTCGATTCTAGCTTAG

SEQ ID NO 282, Arabidopsis thaliana - protein

MNLYTCSRSEFQDSGGELMDALVPFIKSVSDSPSSSSAASASAFSLHPSAFSLPPLPGYYPDSTFLTQPF
SYGSDLQQTGSLIGLNNLSSSQIHQIQSQIHHPPLPTHNNNNSFSNLLSPKPLLMKQSGVAGSCFAY
GSGVPSKPTKLYRGVRQRHWGKWVAEIRLPRNRTRLWLGTFTAEAAALAYDKAAYKLRGDFARLNFP
NLRHNGSHIGGDFGEYKPLHSSVDAKLEAICKSMAETQKQDKSTKSSKKREKKVSSPDLSEKVKAEEN
SVSIGGSPPVTEFEESTAGSSPLSLDTFADPEEPPQWNETFSLEKYPSYEIDWDSILA

SEQ ID NO 283, Arabidopsis thaliana – DNA

ATCGGTGAGGTTGAGAGTAATTCCTACACACACACAAAAATAAATTGAGTGCCTCCCCCAAAAACA
AAATTGGTAGATAACGAGCAATTGTTTTTTTTTTCAGATTTGATCCTGAATTTTTTACATTTTTTTTTTTG
CAATCTCCCCCTAATCTGTTGTTTCTCGCTTCTTCTTCTGTTAATCATCTGTCTTTCAAAAAGAAAGA
AAAAAGAAAAATTGATTTCTGGGTTTGTGTTTGTGTCATACAGAAAAAATCAAGCTTATGAATTTGTG
TTTAATTTTTTGTGTTTAATTTGAAAGGCAGGTTTTTTCAGAACGAGATCGTTTTTTCAAATTTCTTCT
GATTTTACCTCTTTTTTTCTTCTTAGATTTTAGTGAATCGAGGGTGAAATTTTTGATTCCCTCTTTTC
GGATCTACACAGAGGTGCTTATTTCAAACCTTTTAGATCCATTTTTTTTTTAATTTTCTCGGAAAAAT
CCCTGTTTCTTTACTTTTTTATAAGTCTCAGGTTCAATTTTTTTCGGATTCAAATTTTTATTTTAAATG
GCAGCTGCTATGAATTTGTACACTTGTAGCAGATCGTTTCAAGACTCTGGTGGTGAACATCATGGACGC
GCTTGTACCTTTTATCAAAAGCGTTTCCGATTCTCCTTCTTCTTCTTCTGTCAGCGTCTGCGTCTGCGT
TTCTTCACCCCTCTGCGTTTTCTCTCCCTCCTCTCCCCGGTTATTACCCGGATTCAACGTTCTTGACC
CAACCGTTTTTCATACGGGTCGGATCTTCAACAAACCGGGTCATTAATCGGACTCAACAACCTCTCTTC
TTCTCAGATCCACCAGATCCAGTCTCAGATCCATCATCCTCTTCTCCTCCGACGCATCACAACAACA
ACTCTTTCTCGAATCTTCTCAGCCCCAAAGCCGTTACTGATGAAGCAATCTGGAGTCGCTGGATCTTGT
TTCGCTTACGGTTCAGGTGTTCCCTTCGAAGCCGACGAAGCTTTACAGAGGTGTGAGGCAACGTCACTG
GGGAAAATGGGTGGCTGAGATCCGTTTGCCGAGAAATCGGACTCGTCTCTGGCTTGGGACTTTTGACA
CGGCGGAGGAAGCTGCGTTGGCCTATGATAAGGCGGCGTACAAGCTGCGCGGCGATTTCGCCCCGGCTT
AACTTCCCTAACCTACGTCATAACGGATCTCACATCGGAGGCGATTTCGGTGAATATAAACCTCTTCA
CTCCTCAGTCGACGCTAAGCTTGAAGCTAT

FIGURE 29 (CONTINUED)

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TTGTAAAAGCATGGCGGAGACTCAGAAACAGGACAAATCGACGAAATCATCGAAGAAACGTGAGAAGA
AGGTTTCGTGCGCCAGATCTATCGGAGAAAAGTGAAGGCGGAGGAGAATTCGGTTTCGATCGGTGGATCT
CCACCGGTGACGGAGTTTGAAGAGTCCACCGCTGGATCTTCGCCGTTGTCGGACTTGACGTTGCTGA
CCCGGAGGAGCCGCCGAGTGGAACGAGACGTTCTCGTTGGAGAAGTATCCGTGCTACGAGATCGATT
GGGATTGATTCTAGCTTAGGGGCAAAATAGGAAATTCAGCCGCTTGCAATGGAGTTTTTGTGAAATT
GCATGACTGGCCCAAGAGTAATTAATTAAATATGGATTAGTGTTAAATTCGTATGTTAATATTTGTA
TTATGGTTTGTATTAGTCTCTCTGTGTGCGGTCCAGCTTGCGGTTTTTTTGTGAGGCTCGACCATGCCAC
AGTTTTTCATTTTATGTAATCTTTTTTTCTTTTGTCTTATGTAATTTGTAGCTTCAGTTTCTTCATCTA
TAATGCAATTTTATTATGATTATGTAA

SEQ ID NO 284, Arabidopsis thaliana - protein

MAAAMNLYTCSRSEFQDSGGELMDALVPFIKSVSDSPSSSSAASASAFHLHPSAFSLPPLPGYYPDSTFL
TQPFYSYGSDDLQQTGSLIGLNNLSSSQIHQIQSQIHHPLPPTHNNNNNSFSNLLSPKPLLKQSGVAGS
CFAYGSGVPSKPTKLYRGVRQRHWGKWVAEIRLPNRTRLWLGTFTAEAAALAYDKAAYKLRGDFAR
LNFNLRHNGSHIGGDFGEYKPLHSSVDAKLEAICKSMAETQKQDKSTKSSKKREKVVSSPDLSEKVK
AEENSVSIGGSPPVTEFEESTAGSSPLSLDTFADPEEPPQWNETFSLEKYPSYEIDWDSILA

SEQ ID NO 285, Arabidopsis thaliana - DNA

AAAAAACAAATATTTAGAAACAAAAAATGCTATAATTCTTCCTTTTTCTTGTTCTTTCAGAGATTTTG
ATTTCTATTCAATCGACTAAGAGGGTGTGTTTTTAATCCCTCTCTGTTTTAATTTTGTTCCTAGTCT
TTAAAGATCCATGGCAGCCATAGATATGTTCAATAGCAACACAGATCCTTTTCAAGAAGAGCTCATGA
AAGCACTTCAACCTTATACCAACACTGATTCTTCTTCTCCTACGTATTCAAACACAGTCTTCGGT
TTCAATCAAACCACATCTCTCGGTCTAAACCAGCTCACACCTTACCAAATCCACCAAATCCAAAACCA
GCTTAACCAGAGACGTAACATAATCTCTCAAATCTAGCCCCAAAGCCTGTCCAATGAAGAACATGA
CCGCTCAGAACTCTATAGAGGAGTTAGACAAAGGCACTGGGGAAAATGGGTAGCTGAGATCCGTTTA
CCCAAGAACCGGACCCGACTCTGGCTTGGAACCTTCGACACAGCTGAAGAAGCAGCCATGGCTTATGA
CCTAGCTGCTTACAAGCTAAGAGGCGAGTTCGCGAGACTTAATTTCCACAGTTCAGACACGAGGATG
GATACTACGGAGGAGGTAGCTGTTTCAATCCTCTTCATTCCCTCTGTGCGACGCAAAGCTCCAAGAGATT
TGTCAGAGCTTGAGAAAAACAGAGGATATTGACCTCCCCTGTTCTGAAACAGAGCTTTTCCCGCCAAA
AACAGAGTATCAAGAAAGTGAATATGGGTCTTGAGATCTGATGAGAATTCGTTTTTCAGATGAGTCTC
ATGTGGAATCTTCTTCGCCGGAATCTGGTATTACTACGTTCTTGGACTTTTCGGATTCTGGATTTGAT
GAGATTGGGAGTTTCGGGCTGGAGAAGTTTCCTTCTGTGGAGATTGATTGGGATGCGATTAGCAAATT
GTCCGAATCTTAAACAAAGCAAAGAGAAGACTTTTTCTTTTAGGAGTTTGTCTTTCAATTTTCAGTGTC
TTATATTAATCTCTCTGCAACTGAAATTTTTTAACAGTTGCGGAGAGAATCGTCTCTAGGGTTTGTTC
TCTTCCTCCATGTTTTGGTCTGACTGGTTAATGTCTTTTTTTTTTTTTTTGAAGTTTCAAAAACCTTTG
TCATTGACCAATCGGAGAAGTTTCCATGTATTCTCTCATCTTTAAATTTCTAATGAAGAATGTAAATT

SEQ ID NO 286, Arabidopsis thaliana - protein

MAAIDMFNSNTDPFQEELMKALQPYTTNTDSSSPTYSENTVFGFNQTTSLGLNQLTPYQIHQIQNLNQ
RRNIISP NLAPKPVPMKNMTAQKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFTAEAAAMAYDLAA
YKLRGEFARLNFPPQFRHEDGYGGGSCFNPLHSSVDAKLEICQSLRKTEDIDLPCSETELFPPKTEY
QESEYGFLRSDENSFSDESHVESSPESGITTFLDSDSGFDEIGSFGLEKFPSVEIDWDAISKLSSES

FIGURE 29 (CONTINUED)

SEQ ID NO 287, *Oryza sativa* - DNA

SEQ ID NO 288, Oryza sativa - protein

SEQ ID NO 289, Broussonetia papyrifera - DNA

CACCACACACAGTTTTCTCTGATCCCTTTAGAGAAGAGCTCATGAAAGCACTTGAACCTTTTATGAAAA
GTGCTCATAATAATATCAACAACAACATTTACCAATCTCTTCTTCTTCTTCTTCTTCTTACCTTTCT
AGTGAGCCCAACTTTTACCCTGAATCTGAAACTTGCTCACCTTCAACTACCCAAATGTTTTCCAGTGG
GTTGTTCTCCAGCTTTAACCACATGGGTCTGAGCAGACTGGTTCTTTAGGCTTAAACCAGCTCACCC
AATCCCAGATTCTCCAAATTCAGCCCAATCTACTTCCAACAACAACAGCAACAGCAACAAAATCTA
CTCATGACCACCATAACTCCGCCCAAAACAGCCTCAACTACCTCGGTCCGAGGGCGGTTCGGATGAA
GAACGTCGGCGCCAATTCAAAGCCCAACAACTCTACAGAGGAGTGAGGCAGAGGCATTGGGGCAAAT
GGGTGCGCGAGATCAGACTCCCCAAGAACCGGACCCGCCTCTGGCTGGGCACCTTCGACACCGCCGAG
GAAGCCGCCTTGGCCTACGACAAGGCGGCGGTACAAGCTCCGCGGGGACTTCGCCCGCCTCAACTTCCC
CCACCTCCGCCACGAAGGCGCCACGTCTCTGGCGAGTTCGGCGAGTACAAGCCCCTCCATTCTCTCG
TCGACGCCAAGCTTCAGGCGATTTGCCAAAGCCTGGCGAATTTCGCAGAAGCAGGGGAGTGCCAAGGAG
GCTTGTTCCGAGCCGGAGGTGAAGCCAGTCATCGAGCCCAAGATGGCGTCCGATAATTCTCCGAAAG
CGAATTGGAGGTGTCGTCTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGT
CGCCGTTGTCGGATGAGTCTTCGGCGGGGTATCCTCGCCGGAGTCCGATGTCACGTTGTTGGACTTC
TCGGATTCTCATTGGGATGGGAATGAGAATTTTGGGCTAGGGAAGTACCCTTCAGTGGAGATCGACTG
GGATGCTCTGTGATCGTAATAAATGTTGGTTATGTTGTCATTTTCTTTTTTTATTTTTTCTGCGTTA
TTAGTTGTTTTTAAAGTTTTTTTTTTTTTAGTTGTACAAGCACGGCTTCTGCGATGGAATTTTTTAACATG
GCAGGGGTTTTAGCTCAGTTTTTTTAAATTTAGG

FIGURE 29 (CONTINUED)

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AAGGGTCAGTAAGTCAGTCAGTCAGTCAGATGTTTTATGTTGTAATATTTGATGTCGTTTGATATCT
CCTATGTTGGTCAGCTGGTAGTTTTTTTTCCCTGCTAGGCCTGGCCATGGGAGATCTCTCTGGGTTGTA
TTACTACTTTTTGAATGTAATTAGGCAAGTCTACTTTATATAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO 290, *Broussonetia papyrifera* - protein

MKALEPFMKSANNNNINNNISPISSSSSSSYLSSEPNFYPESETCSPSTTQMFSSGLFSSFNHMGSEQT
GSLGLNQLTQSQILQIQAIYFQQQQQQQNLMTTITPPQNSLNYLGPRAVPMKNVANSKPNKLYR
GVRQRHWGKWVAEIRLPKNRTRLWLGTFTAEAAALAYDKAAYKLRGDFARLNFPHLRHEGAHVSGEF
GEYKPLHSSVDAKLQAICQSLANSQKQGSAAKEACSEPEVKPVIKPKMASDNSPKGELEVSSSSSLSSSS
SLSLSLSLSSPLSDESSAGSSSPESDVTLLDFSDSHWDGNENFGLGKYPSEIDWDAL

SEQ ID NO 291, *Jatropha curcas* - DNA

GGACTCAGATAGTTGCTCCACATCGACTGCCCTTCCATTTTCAAATGGGTTCTCGATCCAAGACCCCA
ACCGTCTTCAGCAACCTACTTGTTCATTCGGGCTATGTCTTACTCCAACCCAGATCCACCAGATCCAG
ACCCAAATCCATTACCAGAATCAAATGGATTCAATTTCCAGAATTTCCACACCCAAAACCAACATGG
CTTAACCTTTTTAGGTCCGAAACCCGTGCCCATGAAGCAGGTGGGTTTACCACCAAAACCCACTAAGCT
CTACAGAGGAGTAAGGCAGCGACATTGGGGCAAATGGGTTGCCGAGATCCGACTACCCAAGAACCGTA
CAGACTCTGGCTTGGTACTTTTGACACAGCAGAAGAAGCCGCTTTAGCTTATGACAAAGCGGCGTAC
AAACTCCGTGGCGACTTCGCGAGACTTAACTTCCCTAACCTCCGCCACCAAGGGTCCACATTGAAGG
CAGCTTCGGCGAGTATAAGCCTCTCCATTCCTCGGTGATGCGAAACTGCAAGCTATTTGTCAAAGCT
TAGCAGAATCGCAGAAACAAGGAGGAAAAGCAGAGAAGCAATCAAATCGTCAGCGAAAAAGAAGACT
TCGGTGGGGACTACTCCAGCGACGGCGGAGAAGGTTAAGGAAGCTAAGGCACCGCAACAGGTTGTTCC
GGACAAGTGTTGCAAGGTCGAGACACCATCGTCAGTGTTGACAGAAAGTGAAGCCTCTGGCGGATCTT
CACCGTTGTCGGATCTTACGTTTCCGGATCTAGAAGAGGCACCATTTGGATGTTGATTCTGGAAATTTT
AATTTGGAGAAGTACCCATCTTATGAAATTGATTGGGCTTCTCTTTTATCTTCTTAGATTTGGTTATG
TTATGTTATTTATCTTTTATCTTTATTTTGCAGTTATGTTTAGTTCTTAGGCGTGTGGTTGCTGCAAT
GAGTTTTTGGCAGTTGCAGAGCCAAAAAAAAAAAAAAAAAAAA

SEQ ID NO 292, *Jatropha curcas* - protein

MSYSNPDPDPDPNPLPESKWIQFPEFFPHPKPTWLNFLGPKPVPKQVGSPPKPTKLYRGVRQRHWGK
WVAEIRLPKNRTRLWLGTFTAEAAALAYDKAAYKLRGDFARLNFNLRHQGSHIEGSFGEYKPLHSS
VDAKLQAICQSLAESQKQGGKAQKQSNSSAKKTSVGTTPATAEKVKEAKAPQQVVPDKCKVETPSS
VLTESEASGGSSPLSDLTFPDLEEAPLDVDSGNFNLEKYPSYEIDWASLLSS

SEQ ID NO 293, *Arabidopsis thaliana* - DNA

TCTTCCTCCGACGCATCACAACAACAACACTCTTTCTCGAATCTTCTCAGCCCAAAGCCGTTACTGA
TGAAGCAATCTGGAGTCGCTGGATCTTGTTTCGCTTACGGTTCAGGTGTTCTTTCGAAGCCGACGAAG
CTTTACAGAGGTGTGAGGCAACGTCACTGGGGAAAATGGGTGGCTGAGATCCGTTTGCCGAGAAATCG
GACTCGTCTCTGGCTTGGGACTTTTGACACGGCGGAGGAAGCTGCGTTGGCCTATGATAAGGCGGCGT
ACAAGCTGCGCGGCGATTTTCGCCGGCTTAACTTCCCTAACCTACGTCATAACGGATTTACATCGGA
GGCGATTTTCGGTGAATATAAACCTCTTCACTCCTCAGTCGACGCTAAGCTTGAAGCTATTTGTAAAAG
CATGGCGGAGACTCAGAAACAGGACAAATCGACGAAATCATCGAAGAAACGTGAGAAGAAGGTTTCGT
CGCCAGATCTATCGGAGAAAGTGAAGGCGGAGGAGAATTTCGGTTTCGATCGG

FIGURE 29 (CONTINUED)

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TGGATCTCCACCGGTGACGGAGTTTGAAGAGTCCACCGCTGGATCTTCGCCGTTGTCGGACTTGACGT
TCGCTGACCCGGAGGAGCCGCCGAGTGGAAACGAGACGTTCTCGTTGGAGAAGTATCCGTCGTACGAG
ATCGATTGGGATTGATTCTAGCTTAGGGGCAAAATAGGAAATTCAGCCGCTTGCAATGGAGTTTTTG
TGAAATTGCATGACTGGCCCAAGAGTAATTAATTAATATGGATTAGTGTTAAATTTTCGTATGTTAAT
ATTTGTATTATGGTTTGTATTAGTCTCTCTGTGTGTCGGTCCAGCTTGCGGTTTTTTGTCAGGCTCGACC
ATGCCACAGTTTTTCATTTTATGTAATCTTTTTTTCTTTTGTCTTATGTAATTTGTAGCTTCAGTTTCT
TCATCTATAATGCAATTTTATTATGATTATGTG

SEQ ID NO 294, Arabidopsis thaliana - protein

LPPTHNNNNNSFSNLLSPKPLLMKQSGVAGSCFAYGSGVPSKPTKLYRGVRQRHWGKWVAEIRLPNR
TRLWLGTFTAEAAALAYDKAAYKLRGDFARLNFNLRHNGFHIGGDFGEYKPLHSSVDKLEAICKS
MAETQKQDKSTKSSKKREKKVSSPDLSEKVKAEENSVSIGGSPPVTEFEESTAGSSPLSLDTFADPEE
PPQWNETFSLEKYPSYEIDWDSILA

SEQ ID NO 295, Oryza sativa - DNA

CTTGGTTAGGTTGCTTGCAGAGAGCGAGAGACCCAGGGCCTTTTAGATCCAGGGCTCCCAGATCTGCT
GTTTTTCTTTCATCTTCTTTGTGTTCTAGTGTTAGGTTGGTAGCCAAGAGGGGTCTTTTTCCACACC
TCACTTGCTAGATCTACCACCAAAAAGCCATCTGTTTTTTTACTGTGGCTGTGATTTCTCCCTCCTT
CCTGCCTGTTCTTGATTTTGGATTTCGGAACCAGGCAAATCTTGTACTACTGTTTTAGTATCAGAAA
AAAAAATCCAAAAAAAAGAGTGAGTAGATGGCTGCAGCTATAGATCTGTCAGGGGAGGAGCTGATGA
GAGCACTCGAGCCTTTTATCCGAGATGCCTCCGGCTCGCCTCCGGTTTGTTCAGTTTAGTCCCACC
TCGCCATTCTCCTTCCCGCACGCGTTTCGCGTACGGTGGCGGGCTGGCCCAGCAGCCAGAGCTCAGCCC
GGCCCAGATGCACTACATCCAGGCCCCGCTCCACCTCCAGCGGCAGGCGGCGCAGGCCGGCCGCTCG
GCCGCGCGCGCAGCCGATGAAGGCGTCGTCGTCGTCGGCTTCGGCGGCGGGGGCGGCGGCGACGCCG
CCGCGGCCGCGAGAAGCTGTACCGCGGCGTGCGGCAGCGGCACTGGGGGAAGTGGGTGGCGGAGATCCG
CCTCCCGCGGAACCGCACGCGGCTCTGGCTCGGCACCTTCGACACAGCCGAGGAGGCGGCGCTTGCT
ACGACCAGGCGGCGTACCGCCTCCGCGGCGACGCGGCGCGGCTCAACTTCCCCGACAACGCCGCTCC
CGCGGCCCGCTCCACGCCTCCGTGACGCCAAGCTCCAGACGCTCTGCCAGAACATCGCCGCCGCCAA
GAACGCCAAGAAGTCTCTGTCTCCGCCTCCGCCGCCGCAACATCCTCCGCGCCACCAGCAACTGCT
CGTCGCCGCTCCTCCGACGACGCGTCGTCCTGCCTGGAGTCCGCCGACTCGTCGCCCTCCTGTGCGCG
TCCTCCGCCGCCACCACGGCCGAGACGCCGCGGACCGTGCCGGAGATGCAGCAGCTCGACTTCAGCGA
GGCGCCGTGGGACGAGGCCGCCGCTTCGCCCTACCAAGTACCCGTCCTACGAGATCGACTGGGACT
CCCTCCTCGCCGCCAATTAACACCACCACCACTTCTTGGCTAGTACTCACGCCGTCGTTAGCCTAATC
GTCGCCGCCGCCGCCGCGTGCAGATGGGATTTTAGACATTCTGCACCGCACGGACGGGCATGGATTA
GCAGTTTTATAGTCCCTAATCCTTTTGGTTTGGTTCGTTTGTGTACGTAGATCGATCTCTCTCCGGAC
TTGTTTCCTCTGTAGATGCTAGGGTTGGTTGGTGTTCCTCAACC

SEQ ID NO 296, Oryza sativa - protein

MAAAIDLSGEELMRALEPFIRDASGSPPVCSQFSPTSPFSFPHAFAYGGGLAQQPELSPAQMHIYIQR
LHLQRQAAQAGPLGPRAQPMKASSSSASAAGAAATPPRPQKLYRGVRQRHWGKWVAEIRLPNRTRLW
LGTFTAEAAALAYDQAAAYRLRGDAARLNFDPNAASRGPLHASVDKLTLCQNIAAAKNAKSSVSA
SAAATSSAPTSNCSSPSSDDASSCLESADSSPSLSPSSAATTAETPATVPPEMQQLDFSEAPWDEAAAF
ALTKYPSYEIDWDSLLAAN

FIGURE 29 (CONTINUED)

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SEQ ID NO 297, *Oryza sativa* - DNA

AACCCAAACGACGGAGACCCACTACTCCGAGCCATCAAGAACACACACACATCCAGAAAGCCTAATCC
AATCCAAAAGCCCTAATCAGCCAGACTCCATCTCTGTGAGGTTTGAGAGAGGTAGGTGAGCCGTAGAT
CTGAGCGAGTTCTTGGGTCTTCCAGCAGGTAGATCACTTCATCTGAGGATCAATCTTTTTTTTTTTTCC
TTTGTTTTTGAGCTTCTGTTGGTGTACAGGACAGAGAGTTCCAGAGCCTTTTAGTTTCTGGTGTTCTG
ATCTGTTCTTGGTGTAAGATTATTGGTCTGATTTGGTAGCCAAGAGGGTTAATTTTTTCCACACCTCC
TTGTGCTAGTTAGCTTAGCTTATACCCCCCTTGTAAGTGATTAGTAGATCTAGAACTTCTCTTTTCG
TCTGCCAGTTCTTGGATTTTGGAAGAAGAGGTGGTTTGTATTTCAGATTTTTAGGTTAGAAAAATC
CACAAAAAAAAGATATTCGATGGCAGCTGCTATAGAAGGAAATCTGATGCGGGCGCTGGGAGAGGCT
CCGTCGCGCGCAGATGCAGAAGATCGCGCCGCCCGCTTTCATCCCGGCTTGCCGCCGGCGCCGGCGAA
CTTCTCCTCGGCCGGAGTCCACGGGTTCACATACATGGGCCCGGCCAGCTCAGCCCGGCCAGATCC
AGCGCGTCCAGGCCCACTCCACATGCAGCGGCAGGCCAGTCCGGGGCTCGGCCCGCGGGCCAGCCC
ATGAAGCCCGCTTCGGCGGCTGCTCCGGCGGCGGCGGCGGCGGCGGCGCAGAAGCTGTACCGCGGCGT
GCGGCAGCGGCACTGGGGCAAGTGGGTGGCGGAGATCCGGCTGCCGCGCAACCGCACCAGGCTCTGGC
TCGGCACCTTCGACACCGCCGAGGAGGCGGCGCTCACCTACGACCAGGCCGCGTACCGCCTCCGCGGC
GACGCGGCGCGGCTCAACTTCCCGACAACGCCGCGTCCGCGGGCCCGCTCGACGCCGCCGTGGACGC
CAAGCTCCAGGCCATCTGCGACACCATCGCCGCGTCCAAGAAGCCTCATCCAGGTCCAGGGGCGGCG
CCGGCAGGGCCATGCCATCAACGCGCCCTGGTCCGCGCGGCGTCTGTCGTCCTCCGGCTCCGACCAC
TCCGGCGGCGGCGACGACGGCGGCTCGGAGACGTCGTCGTCGTCGTCGCGGCGGCGTCCGCGTGGCGGA
GATGGAGCAGCTGGACTTCAGCGAGGTGCCGTGGGACGAGGCGGAGGGGTTTCGCGCTCACCAAGTACC
CGTCGTACGAGATCGACTGGGACTCGCTGCTCAACAACAATACTAGCTCTTCTCTTCCATAGCCCCG
CATTGCCGCGCGGCGCAGATGAGGTTTTAGGCATTCTGCGCGGCGGCGAGGCGATGGATTATATGTTT
GTTCTTGTGTAGATCCTTTTCTTTTGTGTTGGTTTTTTAGGTTCCGGAGGCTGCTCGCCGGCGTCTG
TTTTGTGTCCGGCGTCTCCGATGTCTAGTAAGCAGTGACTCGTTAGTGTAGTAGTTGTACAACCTCTAC
AAATGTACAAATACTTGTGCATGTAGGTTGTTGTAATCAATTGTTGGTAACTACCTGTAATAGAACTA
CTGTGAATTAAGTATTAATGTGC

SEQ ID NO 298, *Oryza sativa* - protein

MAAAIEGNLMRALGEAPSPQMOKIAPPPFHPGLPPAPANFSSAGVHGFHYMGPALSPAQIQRVQAQL
HMQRQAQSGLPRAQPMKPASAAAPAAAAARAQKLYRGVRQRHWGKWVAEIRLPRNRLRLWLGTFDTA
EEAALTYDQAAYRLRGDAARLNFPDAAASRGPLDAVDAKLQAICDTIAASKNASSRSRGAGRAMPI
NAPLVAAASSSSGSDHSGGDDGGSETSSSSAAASPLAEMEQLDFSEVPWDEAEGFALTKYPSYEIDW
DSLLNNNN

SEQ ID NO 299, *Lycopersicon esculentum* – DNA

GTTTGTTCCTTCCACAGAGATGAATTCCCAAATCTTTTCAACTGGGTTTTCTGGGTATGGAATGGA
GCAACAGGGTTCAATTGGGCTGAATCAGTTAACCCCAATTCAGATCCAGCAAATTCAGCTCAAATCA
ACTTTCAAAACCAACAACAACAGCAGCAGCAGATGATGTTACAGACTGCCCATCATGCTTCCACC
ATGAATTTCTTGGCTCCAAAGCCGTTCCAATGAAGCAATCTGGGTGCGCACCAAAACCCACGAAGCT
CTACAGAGGTGTTAGACAACGCCACTGGGGTAAGTGGGTGCGTGAGATCCGTTTGCCTAAGAACCGAA
CCCGCCTTTGGCTTGGTACATTTGACACCGCTGAAGAAGCTGCTCTGGCTTACGACAAGGCGGCGTAT
ATGCTTCGTGGCGACTTTGCTCGACTGAACCTCCCTCAACTCCGCCACAACGGCAACCTAATCGGCGG
CGACTTTGGTGAATACAATCCATTGCATTCTCAGTTGATGCTAAGCTAAAGGACATATGCCAAAGCT
TGGCACAGGGGAAGAGCATTGACTCTAAGAAGAAGAAAACCAAGGGTTG

FIGURE 29 (CONTINUED)

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TCGGCGGAGAAAGCGGCGGTGGTGAAGATGGAGGAAGAGGAGAGCAAAACAGCAGAAGTTGGATCCGA
AAGTGACGGGTCCCATTCCGGTTCGGTGGATCATCGCCGGTGACCGAACTGATATTCGCGGAGTTCA
CTGAGGAAGAGCCAACCTGGGACATGTCAGAAAATTTTTTGTGTCAGAAGTATCCATCTCATGAAATT
GATTGGGCTCTCTATAAAATTAGAAAATAATTAAGA

SEQ ID NO 300, *Lycopersicon esculentum* - protein

MNSQIFSTGFSGYGMEQQGSIGLNQLTPIQIQIQIAQINFQNNQQQQQQMMMLQTAHHASTMNFLAPK
PVPKQSGSPPKPTKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFTAEAAALAYDKAAYMLRGDFA
RLNFPQLRHNGNLIGGDFGEYNPLHSSVDAKLKIDICSLAQGKSIDSKKKTKGLSAEKAAYVKMEEE
ESKTAEVGSESDGSHSGSGSSPVTELIFFETEEPTWDMSENFLQKYPSEIDWASL

SEQ ID NO 301, *Zea mays* - DNA

CACGAGCAATCCCCCTTCAACAAACGCACCGCACTCCACGGCAGCCAGAAAACACATCCCACGGGGCCC
AGACCCGGCGACCCACCTGAGCCCGGCGCAGATGCAGTTCATCCAGGCCAGCTCCACCTGCAGCGGA
ACCCGGGGCTGGGCCCGCGGGCGCAGCCCATGAAGCCCGCCGTCCAGTGCCGCCGGCGCCGGCGCCG
CAGCGGCTGTGAAGCTGTACCGCGGCGTGCGGCAGCGTCACTGGGGCAAGTGGGTGGCCGAGATCCG
GCTCCCCCGGAACCGCACCCGCCTGTGGCTCGGGACCTTCGACACCGCCGAGCAGGCAGCGCTGGCCT
ACGACCAGGCGGCGTACCGCCTCCGCGGGGACGCGGCGCGGCTCAACTTCCCCGACAACGCGGAGTCC
AGGGCGCCGCTCGACCCCGCCGTGGACGCCAAGCTGCAGGCCATCTGCGCCACCATCGCCGCCGCGTC
GTCGTCATCCAAGAATTCCAAGGCCAAGAGCAAGGCGATGCCAATCAACGCGTCCGTTCTGGAAGCGG
CAGCGGCGTCTCCGAGCAACAGCTCCTCCGACGAAGGTTCCGGCTCCGGGTTCCGGTTCGGACGACGAG
ATGTCCTCGTCTTCCCCGACGCCGGTGGTGGCGCCCGCGGTGGCGGACATGGGACAGTTGGATTTTCA
CGAGGTTCCGTGGGACGAGGACGAGAGCTTCGTGCTCCGCAAGTACCCGTCCTACGAGATCGACTGGG
ACGCGCTGCTCTCAACTAGTCGCCCTTCGCCGACAGATGTGCTGTTGTAGTTTCACTAGTGGCAGTAT
CTCTGGCCGCCGAGATGAGGTTTTAGGCAATCTGCAGGCCGCCGCCCATGTGTATTAAGTAGGTTT
TGCTCAGTTGTTGGCCCCGGAATTCGCCGCGGTTTTTGTGACCGGCGTCCCCGAGTGCATGATTGG
TGTAAGTGGTCTGTCTGTAAAAAAAATGGATCTGTGTACTTCTATAGTGTGTATTCAACCATTTGTTCT
TAAAAAAA

SEQ ID NO 302, *Zea mays* - protein

MQFIQAQLHLQRNPLGPRAPQPMKPAVPVPPAPAPQRPVKLYRGVRQRHWGKWVAEIRLPNRTRLWL
GTFDTAEQAALAYDQAAYRLRGDAARLNFPDNEASRAPLDPVDAKLQAICATIAAASSSSKNSKAKS
KAMPINASVLEAAAASPSNSSSDESGSGFGSDDEMSSSSPTPVVAPPVADMGQLDFSEVPWDEDESF
VLRKYPSYEIDWDALLSN

SEQ ID NO 303, *Oryza sativa* - DNA

GGAAAGAACAGGTGGTTTGTATTTCAGATTTTTAGGTTAGAAAAAATCCACAAAAAAAAGATATTTCG
ATGGCAGCTGCTATAGAAGGAAATCTGATGCGGGCGCTGGGAGAGGCTCCGTCCGCCGAGATGCAGAA
GATCGCGCCGCCCGGTTTCATCCCGCTTGCCGCCGGCGCCGGCGAACTTCTCCTCGGCCGGAGTCC
ACGGGTTCCACTACATGGGCCCGGCCAGCTCAGCCCGGCCAGATCCAGCGCGTCCAGGCCCACTC
CACATGCAGCGGCAGGCCAGTCGGGGCTCGGCCCGCGGGCCAGCCCATGAAGCCGCTTCGGCGGC
TGCTCCGGCGGCGGCGGCGGCGGCGGCGCAGAAGCTGTACCGCGGCGTGCGGCAGCGGCACTGGGGCA
AGTGGGTGGCGGAGATCCGGTGCCGCGCAACCAACCCAGGCTCTGGCTCGGCACCTTCGACACCGCC
GAGGAGGCGGCGCTACCTACGGCCAGGCCGCGTACCGCCTCCGCGGCGACG

FIGURE 29 (CONTINUED)

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CGGCGCGGCTCAACTTCCCGGACAACGCCGCGTCGCGGGGCCCCGCTCGACGCCGCGTGGACGCCAAG
CTCCAGGCCATCTGCGACACCATCGCCGCGTCCAAGAACGCCTCATCCAGGTCCAGGGGCGGCGCCGG
CAGGGCCATGCCCATCAATGCGCCCCTGGTCGCCGCGGCGTCGTCGTCTCCGGCTCCGACCACTCCG
GCGGCGGCGACGACGGCGGCTCGGAGACGTCGTCGTCGTCTGCGGCGGCGTCGCCGCTGGCGGAGATG
GAGCAGCTGGACTTCAGCGAGGTGCCGTGGGACGAGGCGGAGGGGTTGCGGCTCACCAAGTACCCGTC
GTACGAGATCGACTGGGACTCGCTGCTCAACAACAATAACTAGCTCTTCTCTCCATAG

SEQ ID NO 304, *Oryza sativa* - protein

MAAAIEGNLMRALGEAPSPQMOKIAPPPFHPGLPPAPANFSSAGVHGFHYMGPALSPAQIQRVQAQL
HMQRQAQSGLGPRAPQPMKPASAAAPAAAAARAQKLYRGVRQRHWGKWVAEIRLPNHPRLWLGTFDTA
EEAALTYGQAAYRLRGDAARLNFPDAAASRGPLDAAVDAKLQAICDTIAASKNASSRSRGAGRAMPI
NAPLVAAASSSSGSDHSGGGDDGGSETSSSSSAAASPLAEMEQLDFSEVPWDEAEGFALTKEYPSYEIDW
DSLLNNNN

SEQ ID NO 305, *Atriplex hortensis* - DNA

AATTTACTTACCCCCAAGCCCAGCCCCAACAAATGAGCTACTCATACCCACCTCCACTTCCTAGTAAT
ACCCTTAACAACCTTTCTATCTCCCAAGCCTGTGACCATGAAAACAACCTGGTGGGCGCCCAAGCCCAC
TAAGCTTTATCGTGGGGTTAGGCAACGTCACTGGGGTAAATGGGTTGCTGAGATCCGTTTACCCAAGA
ACAGGACCCGGCTTTGGTTGGGTACCTTTGATACAGCTGAGGAAGCTGCTTTGGCTTACGACAAGGCG
GCTTACAAGCTGAGAGGTGACTTTGCGAGGTTGAATTTTCTTAATCTCCGCCATGAAGGGTCCCACAT
CGGTGGCGAATTCGGCGAATACAAACCCCTTCATTCCTCCGTAAACGCAAACTCGAAGCCATTTGCG
AGAGTCTAGCCAAACAGGGGAATGAAAAACAGGGGAAATCAGGAAAGTCCAAGAAGAAAGATGTTGCT
AATAATAACAATAATACTTCATCTTCGTCATCTTCAAGCTGTTGTACAACAGCTACTGCTGCGGCCGA
TGCACCGCAGCAGCAGCAGCGGATGCCGAAAACGGCGGCGATGTAAAAACCGAGAGCACCTCCGATA
GTGAGGTGGGGTCCGGTGGATCGTCGCCGTTGTGCGGATTTGACATTTCGGAGATAATGAAGAAATGGGA
TCGGAGAATTTCTTGTGGAGTCATGCCCATCTCATGAGATTGATTGGGATGCTATATTATCATCTGA
ATCTTAATAATTTTCAATTTGTGGTCTTAAGTATGGGTAAATAAGGAGTATTAATTAATTAATTAAGG
AGTTATAAAATGTGTCATCATAATATAAGTCATGTAATGTTGTGTAAATTTTTTCTTTTTTTTTTTTT
AATTTTAATTAATAATTAGTAGGTTGGTAGTGGGTAGTTTCAGGGAGGAGTGATCTCTGCAATGAAGTT
TTTGGAATTTGTAGGGACTCCATATTTGGTCTTCTTTGGTGAGGCAAGTGTTTTTTTGATCTTGCCTT
TGATCAATTGAAGAGTAGTTTTTTTTTCTTATTGTTTATTTTATGTTTATAGTAGAAAAAATTTAGG
ATTGTAATTTGATGATCATTTTTTAGTGAAGTATTATTATTAATATTTTTTATTAGTATAAAAAAAATTT
GGACTGTTATCAAGGTAAGTGCTTATTTTGACTTCCATATTTGTATGTTGCTCTCTTTCTTTGATTCT
TTCATATTTCTAGTGAGATCTGAACTATAATTAATATGGATTAAACCTTAAATTACTAGTGGTTTGTG
TAACAGGATATGCTTGATGTTCTGTTTTATACATAATCGGAGCTTTTGTCCCTGCAACAATGATTGC
AGTGCTCTATTATTTTGATCACAGTGTGGCATCTCAACTTGCTCAGCAGCGACAGCAACGGAATTCGG
CCCTCG

SEQ ID NO 306, *Atriplex hortensis* - protein

MSYSYPPPLPSNTLNNFLSPKPVTMKTGGPPKPTKLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFD
TAEAAALAYDKAAYKLGRDFARLNFPNLRHEGSHIGGEFGEYKPLHSSVNAKLEAICESLAKQGNEKQ
GKSGKSKKKDVANNNNNTSSSSSSSCCTTATAAADAPQQQQRMPENGDDVKTESTSDSEVSGSGSSPL
SDLTFGDNEEMGSENFLESCPSHEIDWDAILSSES

FIGURE 29 (CONTINUED)

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SEQ ID NO 307, *Arabidopsis thaliana* - DNA

AACAAGAGCCAAGCTAATGAGATAAGTGTATCGGTGAGGCTGAGAGTTATTCACCTACAAAAAAAAAA
AAAACTTGAGTGTAACCAAAAAAAAAAAGTTGATATACTTTCTGGTTTTCTCCTTAACCTTTATTCTT
TACAAATCCATCCCCCTTAGATCTGTTTATTTCCCGCTACTTTGATTCAATTTCTGTTAGTAATCTGTC
TTTCGTATAGAAGAAAACCTGATTTCTTGGTTTTGTATTTTCTTAAAGAGATCAATCTTTTTTTATTTTT
GATCTTCTTGTGTTTTTTTTTTCTTTGTAGAATTAATCGTTTGTGAGGGTATTTTTTTAATTCCCTCCT
CTCAGAAATCTACACAGAGGTTTTTTATTTTATAAACCTCTTTTTTCGATTTTCTTGAAAACAAAAAAT
CCTGTTCTTTACTTTTTTTTACAAGAACAAGGGAAAAAATTTCTTTTTATTAGAAATGACAACCTTCTA
TGGATTTTTACAGTAACAAAACGTTTCAACAATCTGATCCATTCGGTGGTGAATTAATGGAAGCGCTT
TTACCTTTTATCAAAAGCCCTTCCAACGATTCATCCGCGTTTGCCTTCTCTACCCGCTCCAATTTT
ATACGGGTCGGATCTCCACTCATTTTCTCACCATCTTAGTCTAAACCGGTCTCAATGAAACAAACCG
GTACTTCCGCGGCTAAACCGACGAAGCTATACAGAGGAGTGAGACAACGTCACCTGGGGAAAAATGGGTG
GCTGAGATTCGTTTACCGAGGAATCGAACTCGACTTTGGCTCGGAACATTCGACACGGCGGAGGAAGC
TGCTTTAGCTTATGACAAGGCGGCGTATAAGCTCCGAGGAGATTTTGCGCGGCTTAATTTCCCTGATC
TCCGTCATAACGACGAGTATCAACCTCTTCAATCATCAGTCGACGCTAAGCTTGAAGCTATTTGTCAA
AACTTAGCTGAGACGACGCAGAAACAGGTGAGATCAACGAAGAAGTCTTCTTCTCGGAAACGTTTCATC
AACCGTCGCAGTGAAACTACCGGAGGAGGACTACTCTAGCGCCGGATCTTCGCCGCTGTTAACGGAGA
GTTATGGATCTGGTGGATCTTCTTCGCCGTTGTGCGAGCTGACGTTTGGTGATACGGAGGAGGAGATT
CAGCCGCCGTGGAACGAGAACGCGTTGGAGAAGTATCCGTCGTACGAGATCGATTGGGATTCGATTCT
TCAGTGTTTCGAGTCTTGTAATTAGATGTTGCCATAGGGGTATTTAGGGACTTTAGAGCTCTCTGCG
ATGGAGTTTTTGGTCATTGCAGAGATTTTATTATTATTAAGGGGGTTTGTATGTTAATATCAAATAA
GTTTATCTACTTTGATGTTAATTAGTGTTAATCTCTGCGTCGGTCCAAGCTGTTTTTTTTTGGCATGC
TTCGACCGTGTGAGATTTCTTATGTAATTTTTGTAGTTCCTTGATTTTCTTAGTTCAAGTTAAATTGG
CACAAAAGAAC

SEQ ID NO 308, *Arabidopsis thaliana* - protein

MTTSMDFYSNKTFAQSDPFGGELMEALLPFIKSPSNDSSAFSLPAPISYGSDLHSFSSHLSPKPVS
MKQTGTSAAKPTKLYRGVRQRHWGKWVAEIRLPRNRRLWLGTFTAEAAALAYDKAAYKLRGDFARL
NFPDLRHNDYQPLQSSVDAKLEAICQNLAEITQKQVRSTKKSSSRKRSSTVAVKLPEEDYSSAGSSP
LLTESYSGSGSSSPLSELTFGDTEEEIQPPWNENALEKYPSYEIDWDSILQCSSLVN

SEQ ID NO 309, *Arabidopsis thaliana* - DNA

ATAACGAGAGATTTTTTATATATAAAAAATAAAGGAAGCACGAGTTCACCTTAAAAATTTGAGTTTCT
CTTTTCTTGACCCTGAAGTTTCGTTTTGATCAATTTACCCATTTCTTTGTTTCGTCGTCTTTTCTTTC
AAAAGGGTTTCATCTTTGTATTATAAAAAATCCAACTTTATATCTTCACAAGCAGCAAAGATCTCTAT
TTCAATCCTCTCATGGAACTGCTTCTCTTTCTTTCCCTGTCCCAAACACGAGCTTCGGTGTAACAA
ATCTATGCCTCTCGGTCTAAACCAGCTCACACCATAACCAATTCATCAGATTGAGAACCAGCTTAACC
ATAGACGTAGCACAATCTCAAACCTCTCTCCAAACCGTATCAGAATGAAGAACTTAACACCTTCTACC
TCCAAAACCAAGAATCTCTACAGAGGCGTAAGGCAAAGGCACTGGGGGAAATGGGTGCTGAGATCCG
TTTGCCCAAGAACCAGGACCCGTCTCTGGCTCGGGACATTGCAAACCGCCGAAAAAGCCGCTTAGCTT
ACGACCAAGCTGCTTTTCAGCTCCGTGGAGATATCGCGAAGCTTAACCTCCCAAACCTCATACACGAA
GACATGAATCCTCTCCCTTCTCTGTTGATACCAAGCTTCAAGCTATCTGCAAAAGTTTGAGAAAAAC
AGAGGAAATTTGCTCTGTTTCTGATCAAACAAAGGAGTACTCTGTTTACTCTGTTTCAGATAAAACAG
AGCTTTTCTGCCAAAAGCAGAGCTTTTCTTGCTTAAAGAGAGCATTTGGAGACAAATGAGCTCTCT
AATGAGTCACCGAGAAGCGATGAGACCTCGTTGTTGGATGAG

FIGURE 29 (CONTINUED)

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TCGCAGGCGGAATATTCATCGTCGGATAAAACATTCCTGGATTTCTCGGATACTGAGTTTGAAGAGAT
 TGGAAGTTTCGGGCTTCGGAAGTTTCCTTCGGTGGAGATTGATTGGGATGCAATTAGTAAACTGGCCA
 ATTCCTTAAAGTCTTCTATTTTATATTAATCTTCTGTGCAACTGAAATTTTCAACAAGTTGCAGATGAG
 TTTATTAGGTTTGAATCTGTCCTAGTTTTCTTTGTTGGTTCGTATAGAGTTTTACTATGTAGCTAATCT
 CCATGTTTGGTTTGGCTTGGTAAGTTTTTAAGGTCTCGTCATCAACAAACCGGAGAAAGTTTATGTA
 TTCAAAGCTATGTATTATATCCTCACATCTACTTATGAGAGTGAGATCAAAGTTTGTAAAATGAAGT
 CTTGATTTCTTCTTTTAGTTCTCTCTTTTT

SEQ ID NO 310, Arabidopsis thaliana - protein

METASLSFPVPNTSFGVNKSMPLGLNQLTPYQIHQIQNLNHRSTISNLSPNRIRMKNLTPTSTSKTK
 NLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFFETAEKAAALAYDQAAFQLRGDIAKLNFPNLIHEDMNP
 LPSSVDTKLQAICKSLRKTEEICSVSDQTKKEYSVYSVSDKTEFLPKAELFLPKREHLETNELSNESP
 RSDETSLLEDSEAQAEYSSSDKTFLDFSDTEFEEIGSFGLRKFPSVEIDWDAISKLANS

SEQ ID NO 311, Glycine max – DNA

ATAACGAGAGATTTTTTATATATAAAAAATAAAGGAAGCACGAGTTCACCTTAAAAATTTGAGTTTCT
 CTTTTCTTGACCCTGAAGTTTCGTTTTGATCAATTCACCCATTTCTTTGTTTCGTCGTCTTTTCTTTC
 AAAAGGGTTTCATCTTTGTATTATAAAAAATCCAACTTTATATCTTCACAAGCAGCAAAGATCTCTAT
 TTCAATCCTCTCATGGAACTGCTTCTCTTTCTTTCCCTGTCCCAAACACGAGCTTCGGTGTAACAA
 ATCTATGCCTCTCGGTCTAAACCAGCTCACACCATAACAAATTCATCAGATTCAGAACCAGCTTAACC
 ATAGACGTAGCACAAATCTCAAACCTCTCTCCAAACCGTATCAGAATGAAGAAGCTTAACACCTTCTACC
 TCCAAAACCAAGAATCTCTACAGAGGCGTAAGGCAAAGGCACTGGGGGAAATGGGTCGCTGAGATCCG
 TTTGCCCAAGAACCGGACCCGTCTCTGGCTCGGGACATTGGAACCGCCGAAAAAGCCGCCTTAGCTT
 ACGACCAAGCTGCTTTTCAGCTCCGTGGAGATATCGCGAAGCTTAACTTGCCAAACCTCATACACGAA
 GACATGAATCCTCTCCCTTCTCTGTTGATACCAAGCTTCAAGCTATCTGCAAAAGTTTGAGAAAAAC
 AGAGGAAATTTGCTCTGTTTCTGATCAAAACAAAGGAGTACTCTGTTTACTCTGTTTCAGATAAAACAG
 AGCTTTTCTGCCAAAAGCAGAGCTTTTTCTTGCCATAAAGAGAGCATTTGGAGACAAATGAGCTCTCT
 AATGAGTCACCGAGAAGCGATGAGACCTCGTTGTTGGATGAGTCGCAGGCGGAATATTCATCGTCGGA
 TAAACATTCCTGGATTTCTCGGATACTGAGTTTGAAGAGATTGGAAGTTTCGGGCTTCGGAAGTTTC
 CTTCGGTGGAGATTGATTGGGATGCAATTAGTAAACTGGCCAATTCTTAAAGTCTTCTATTTTATATT
 AATCTTCTGTGCAACTGAAATTTTCAACAAGTTGCAGATGAGTTTATTAGGTTTGAATCTGTCCTAGT
 TTTCTTGTTGGTTCGTATAGAGTTTTACTATGTAGCTAATCTCCATGTTTGGTTTGGCTTGGTAAGTTT
 TTAAGGTCTCGTCATCAACAAACCGGAGAAAGTTTATGTATTCAAAGCTATGTATTATATCCTCAC
 ATCTACTTATGAGAGTGAGATCAAAGTTTGTAAAATGAAGTCTTGATTTCTTCTTTTAGTTCTCTCTT
 TTTC

SEQ ID NO 312, Glycine max - protein

MAALMDFYSSSTEFQLHSDPFRGELMEVLEPFMKSPFSTPSPNSCFLSTSYSPPNNYSPSLYSNGL
 SSIPNTTQNLIGFGQGQPTSLVGLNHLTPSQISQIQAQIQIHNHSNTLSFLGPKPIPMKHVGMPPKPT
 KLYRGVRQRHWGKWVAEIRLPKNRTRLWLGTFDTAEEAALAYDKAAYKLRGDFARLNFPNLRHQSSV
 GGDFGEYKPLHSAVDAKLQAICEGLAELQKQKTEKPPRKTRSKLASPPENDNNNDNNSCKVEAAPPL

FIGURE 29 (CONTINUED)

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SEQ ID NO 313, *Arabidopsis thaliana* - DNA

GTACATTTTTTTTTGTATTTTCAGGAACTCCGATGGCGGATCTCTTCGGTGGTGGCCACGGCGGCGAG
CTTATGGAAGCACTTCAACCTTTTTACAAAAGTGCTTCCACGTCTGCTTCAAATCCTGCGTTTGCCTC
CTCAAACGATGCGTTTGCCTCTGCCCCAACGACCTATTTTCTTCTTCTTCTTACTATAATCCTCATG
CATCTTTATTCCCTTCACATTCCACAACCTCTTACCCGGATATTTATTCTGGATCCATGACCTATCCA
TCTTCATTTCGGGTCGGATCTTCAACAACCCGAAAACCTACCAATCTCAGTTCCATTACCAAAACACTAT
CACTTACACTCACCAAGACAACAACACTTGCATGCTTAACTTCATTGAGCCGAGCCAACCGGGTTTTA
TGACCCAACCGGGTCCGAGTTCGGGTTTCGGTTTCAAACCGGCTAAGCTCTATAGAGGAGTGAGGCAA
AGACATTGGGGAAAATGGGTGCGCGGAGATCCGTTTACCCAGGAACCGAACCCGACTTTGGCTCGGAAC
ATTCGACACGGCTGAAGAAGCCGCGTTGGCTTATGATCGCGCCGCGTTTAAAGCTTCGTGGTGACTCGG
CTCGGCTTAACTTCCCAGCTCTCCGATACCAAACCGGCTCGTCTCCGTCTGATACCGGCGAATATGGT
CCTATTCAAGCTGCCGTAGACGCTAACTAGAACCCATATTAGCTGAGCCGAAGAATCAGCCGGGCAA
AACGGAGAGGACGTCGAGGAAACGAGCTAAAGCCGCGGCTTCTTCAGCTGAGCAGCCGTCAGCGCCAC
ACAACATTCCGGGTCGGGTGAAAGTGATGGGTTCGGGTTTACCGACTTCGGATGTTATGGTGCAGGAG
ATGTGCCAAGAGCCAGAGATGCCATGGAATGAAAATTTTCATGCTCGGCAAGTGTCCTTCTTATGAGAT
AGATTGGGCTTCAATTTTATCGTGA

SEQ ID NO 314, *Arabidopsis thaliana* - protein

MADLFGGGHGGELMEALQPFYKSASTSASNPAFASSNDAFASAPNDLFSSSSYYNPHASLFPSHSTTS
YPDIYSGSMYTPSSFGSDLQQPENYQSQFHYQNTITYTHQDNNTCMLNFIEPSQPGFMTQPGPSSGSV
SKPAKLYRGVRQRHWGKWVAEIRLPRNRRLWLGTFTAEAAALAYDRAAFKLRGDSARLNFPALRYQ
TGSSPSDTGEYGPIQAAVDAKLEAILAEPKNQPGKTERTSRKRAKAAASSAEQPSAPQQHSGSGESDG
SGSPTSDVMVQEMCQEPMPWNNENFMLGKCPSEIDWASILS

SEQ ID NO 315, *Arabidopsis thaliana* - DNA

AACAAATCTCTCTGTTTCTCCCGCTCTTGCTCTGTTTTCTCAAAGACAAAAGAGGACATCGTCGTTGA
CTCCTCTTCTCTATGGCTACTGCTAAGAACAAGGGAAAATCAATCAGGGTCCTTGGTACCAGTGAAGC
AGAGAAAAAGGATGAGATGGAGTTGGAGGAGGAGTTCCAGTTTAGTAGCGGCAAGTATAAAGATTTCGG
GTCCTGGCTCGGACATGTGGTTAGGAGATGCTTCTCTACGTCTCCAAGAAGTCTTAGGAAGACTAGA
ACCTTTGACCGACATAATCCCTATCTCGTATCTTCTTATGCTACTCCTCAGCCGCCAACAACTAC
ATGCTCTGTCTCTTTTCCCTTTTACCTCCCTCCAGCGATTCAAATCAACAACGATTTTTTACACCCGA
ATGACCCTTCAGGACAAAGACAGCAACAAATGATCTCGTTTGATCCTCAACAACAGGTGCAACCATAT
GTTGCACAACAGCAGCAACAACAACATCTATTGCAGTACTGGAGAGACATTCTGAAGCTGAGTCC
GAGCGGAAGAATGATGATGATGAACATGTTAAGACAAGAAAGCGATCTGCCACTGACGAGGCCACCGG
TTCAACCCTTCAGCGCCACCAAGCTATATAGAGGTGTCAGGCAACGCCACTGGGGAAAATGGGTTGCC
GAGATCCGTAAGCCACGAAACAGGACACGTCTCTGGCTAGGGACATTCGATACAGCAGAAGAAGCCGC
CATGGCCTACGACCGCGAGGCCTTCAAGTTGAGGGGAGAGACCGCTAGGCTCAATTTCCCTGAACCTT
TTCTCAATAAACAAGAGCCAACCTCCCGTGCATCAGAAACAATGTGAGACGGGGACTACTAGTGAAGAC
TCAAGCAGAAGAGGAGAGGATGATTTCGAGCACGGCATTGGCAGTAGGAGGGGTGAGTGAGGAGACGGG
TTGGGCTGAGGCATGGTTCAATGCAATTCCAGAGGAATGGGGACCTGGAAGCCCTCTATGGGATGATT
ACCACTTTCCCATTTCTAACCATAAGGACGATCTTGACGCCACACAAAACCTCTTCTTCTGATACAATT
TAGGACCTTTGTTAGAATATAGATATGCTTAGTTGTATGACTGATCTAGCTTGTGTTTTTTTTTTGGG
TGGAGACAGTTTTTGTCTCTTCCACATTTTAGATTCTATTTTCGACCATCATTTTTTTCTTGATCGG
TGACTATGAATCTAATGGGGTCAATCATTTTACATATAAACTTAAGTATTTGGTGTGTTGTAATTC

FIGURE 29 (CONTINUED)

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SEQ ID NO 316, Arabidopsis thaliana - protein

MATAKNKGKSIRVLGTSEAEKKDEMELEEEFQFSSGKYKDSGPGSDMWLG DASSTSPRSLRKRTRTFDR
HNPYLVS SYATPQPPTTTTCSVSFPFYLPPIQNRFLHPNDPSGQRQQQMISFDPQQQVQPYVAQQ
QQQQQHLLQYWRDILKLSPSGRMMMMNMLRQESDLPLTRPPVQPF SATKLYRGVRQRHWGKWVAEIRK
PRNRTRLWLGTFDTAEEAAMAYDREAFKLRGETARLNFPELFLNKQEPTPVHQKQCETGTTSEDSSRR
GEDDSSTALAVGGVSEETGWAEAWFNAIPEEWGPGSPLWDDYHFPISNHKDDL DATQNSSSDTI

SEQ ID NO 317, Arabidopsis thaliana - DNA

ATGATCACACCAATACACACACAACACTCCTTAATTCTCGTATATATAAACATTTATTCTCCACCTAT
TTTGTCAAAATTAAGAACAGGCTTCATTCTCTGGACAAACACTCAAAAAACAAACAAAAAAGGAACA
TGGAAGATCAGTTTCTCTAAATAGAACTAGCTTCATGCACGACAAGCTCTTGTCTTCTGGAATCTAC
GGGTTCTTGAGTTCTTCGACGCCGCCACAACCTTCTCGGTGTTCCAATATTTTTGGAAGGTATGAAATC
TCCTCTTCTTCTGCTTCTTCGACTCCGAGCTACTTTGTGTGCGCTCATGATCATGAGCTCACATCTT
CTATTCATCCATCTCCGGTAGCTTCTGTTCTTGGAACTTTCTAGAATCTTTTCCTCAGTCTCAACAT
CCTGATCATCATCTTCTAAACCTCCAAACCTTACTTTGTTCTTAAAGAACCAAAGCTACTAGAACT
TTCTCAATCCGAAAGCAACATGAGCCCTTACCATAAATACATCCCAAACCTCTTTTATCAATCAGACC
AAAACAGAAACGAATGGGTAGAGATCAATAAACTCTAACCAACTATCCCTCGAAAGGTTTTGGAAC
TATTGGCTAAGTACCACCAAGACTCAACCCATGAAGTCAAAAACAAGAAAGGTTGTTTCAGACGACGAC
CCCAACAAAACGTATAGAGGAGTGAGACAAAGACACTGGGGCAAATGGGTGCGCAGAGATTAGGCTTC
CAAGGAACAGAACCCGTGTTTGGCTCGGCACTTTTGAAACCGCTGAGCAAGCAGCAATGGCTTACGAT
ACAGCAGCTTATATCCTTCGTGGCGAATTCGCACACCTCAACTTTCCTGATCTTAAACACCAGCTCAA
GTCCGGTTCTTTGCGATGCATGATCGCCTCACTTTTGGAGTCCAAGATTCAACAGATCTCATCTTCCC
AAGTAAGTAACTCTCCTTCTCCTCCTCCTCCAAAAGTGGGAACACCGGAGCAAAAGAATCATCACATG
AAGATGGAGTCAGGAGAAGACGTGATGATGAAGAAACAGAAAAGCCATAAGGAAGTGATGGAAGGAGA
TGGTGTACAATTGAGTAGGATGCCTTCTTTGGATATGGATCTCATTTGGGATGCTCTCTCATTTCTC
ATTCTTCTTGACTTCAAATTAATATTTGTCAAACCTATTTTACTTACTTCTACCCTTTTTTATATCAA
AAGTTTCCACCAAAGAAAGAAATTCATATTATGATGCCAAGATTGGTTTGCATTTGGGGTTGAACACA
TTGTAATTCTTCTTACGACCACATAATCAAGTGGTTCTCCTTTTTTTGTCTGCTAATTAATTGTTCTT
TTCTTTGCGGTTACTAGTAACCATAAAATAGAAAAGTGTTTGTT

SEQ ID NO 318, Arabidopsis thaliana - protein

MITPIHTQHSLILVYINIYSPILSKLRTGFILWNTNQKTNKRNMEDQFPKIETSFMDKLLSSGIY
GFLSSSTPPQLLGVPFLEGMKSPLLPASSTPSYFVSPHDHELTSSIHPSVASVPWNFLESFPQSQH
PDHHPKPPNLTFLKEPKLLELSQSESNMSPYHKYIPNSFYQSDQNRNEWVEINKTLTNYPKGFN
YWLSTTKTQPMKSKTRKVVQTTPTKLYRGVRQRHWGKWVAEIRLPRNRTRVWLGT FETA EQAAMAYD
TAAYILRGEFAHLNFPDLKHQLKSGSLRCMIASLLESKIQQISSQVSNSPSPPPPKVGTPEQKNHHM
KMESGEDVMMKKQKSHKEVMEGDGVQLSRMPSLDMDLIWDALSFPHSS

SEQ ID NO 319, Oryza sativa - DNA

ATGGACGCGGTGGACAGAGGCGGAGGCGGAGGCGGTGGAGGAGCGCGCGGGCACGGGCGGAGATGGAA
GGGGAAGGGAGTGAGCGCGGCGATCTCCTCCTCCGCGGCCGAGACGCAGCAGCCGGTGCCAGTTTTAG
AAGACGCGCGCGGCGGCCGAGCATTGCTCCGTCCCCAGAAGAAGATCCGCAGCCCCGATCGT

FIGURE 29 (CONTINUED)

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CGCCTCCAGCGCTCCATCTCCTCGCTGTCGTCGGCCCCCTGCTTCCCCCGACTCGTCCTCTGTCTCCAA
CCCCATGTCTCCCCCGGCGATGTCCTTGCCGAATCAGCCGCCATCGTCGCGACATATATTTCCGTTTCG
CGTACGATCCGTCTCCGGGCGCGGCGGCACCAAGGCTCCTCCCGCTGCTGCAGTACTCCAGCTTGTAC
CCGCAGCCTCTGCTGCCGAGCAGCAATCACCCTTGAGAATCAGCAAATGATATCGTTCCGGCAGTAG
CCAGCAGCAGCAGCAGCAGCAGCCGCAGTTTGGGGCGGCGTCTCCTCTGTTCCCGCCGCAGTTCTTGC
CGCCGGAGGAGCAGCAGCGCCTGCTGCTGCGCTACTGGAGCGAGGCGCTGAACCTGAGCCCCCAGGC
GTGCGCGGCGGCGCCCTGCCGCCGTCGCTGTACCAGCACCTGCTGCGCGCGCCTGGGCGGCCAACT
GTACCGCGGCGTGCAGCAGCGCCACTGGGGGAAGTGGGTGGCGGAGATCCGCCTGCCGCGGAACCGCA
CCAGGCTGTGGCTCGGCACGTTTCGACACCGCCGAGGACGCAGCCATGGCGTACGACCGCGAGGCCTTC
AAGCTCCGCGGCGAGAACGCGCGGCTCAACTTCCCCGACCTCTTCCTTGGCAAAGGCCGACCGGCGG
GAGCGGACGCACCGAGCGCCAGCGCCGCGGCTCCTGCTCCTCCTCCTCCTCCTCGGCTCCGCCTACAC
CGGACGAGAGCCACACGCAGCAAGCTCAGCCGCAGCCGCAGCAGCCTACAGAAGAGTCATCCAACACT
GAACCGAAGCCTCTGCTCTTCGTAGCAGAGCAGGACGGCATTCAGAAACCCGAGCTGAATCCTCAGCT
CCAGACAGCTGAACAACATGGCAGCGACGGCAACACGGCCATGTTCCAGCCGTCGGTGACGTCCGGCG
GCATTTGGGGTCCGGCCGACGAGGCGTGTTTCAGCGCTTGGGGGCCAGGAAGCTCCGTCTGGGACTAC
GACATGGACAGCGCCACGGCCTCCTCCTCCAGTCTCGCTTGGCCGGTGAGCAGACCGGCATGGACTA
CGCCTACACCGCGCCGGAAGTCCTCGTGGCACCGGTGCCGGCGGCAGGGACAGCCATGGCCACTGCCG
CTTCCTCCTCTCTTCCTCCTCGTCCTCCCCCTCCTTGCCACAGTCCAACCTTCGCATGGAAGGACTAA

SEQ ID NO 320, *Oryza sativa* - protein

MDAVDRGGGGGGGGARGHGRRWKKGVSAAISSSAAETQQPVPVLEDAPAAAALLRPQKKIRSPDRRL
QRSISSLSAPASPDSSSVSNPMSPPAMSLPNQPPSSRHIFPFAYDPSPGAAAPRLLPLLQYSSLYPQ
PLLPQQQSPLQNQQMISFGSSQQQQQQQPQFGAASPLFPPQFLPPEEQRLLLRWSEALNLSPPGVR
GGALPPSLYQHLLRAPGPPKLYRGVRRQHWGKWVAEIRLPRNRTRLWLGTFTDAEDAAMAYDREAFKL
RGENARLNFDDLFLGKGRGTGSGRTSASAAASCSSSSSSAPPTPDESHTQQAQPQPQQPTEESSNTEP
KPLLFAEQDGIPEPELNPQLQTAEQHGSDGNTAMFQPSVTSGGIWPADAEAWFSAWGPSSVWDYDM
DSAHGLLLQSRLAGEQTGMDYAYTAPEVLVAPVPAAGTAMATAASSSLPPRPPPPCHSPTFAWKD

SEQ ID NO 321, *Oryza sativa* - DNA

ACGTTTGGCTGCACCCTGTCTCGCGGCTGATACGTTTGCACAGGCGTTCAGATACAGCCGATACACCG
GCGGCGCTAGCTGCGTTTCTTCTCCGCATGGACGCTCCGTCGTCGCCCTCGCCACCGTCGGCGCGACA
CATCTTCCCCTTCGCGTACGAGGCCTCCACGACGACGGTGGGTGGGAGCCCAAGGCTCCACCCGCTGT
CGTGGCAGCAATCCAGCATGTCCAGCCCGCGTCGCCACAGCAACAGCAGCAGCAGCCGTTGCAGCAC
CAGCAGATGATATCGTTCCGGCGCTCGCCTCCGTGCTCGACGACGCAGTTTCGTGCTCCCGGAGAACGC
GCAGCAGCAGCAGATGCTGCTGCGGTACTGGAGCGAGGCGCTGAACCTGAGCCCGCGCGGTGGCCCCG
GTGGCGTGCCACCGTGGCTGTACCAGCAGCTGCTCCGGGTCCCGCCACCGCCGAGAAAGCTTTACCGC
GGCGTGCGGCAGAGGCACTGGGGGAAGTGGGTGCGGAGATCCGCCTGCCACGGAACCGCACGCGGCT
GTGGCTTGGCACCTTCGACACCGCCGAGGACGCCGCATGGCGTACGACCGCGAGGCCTTCAAGCTCC
GCGGCGAGAACGCGCGGCTCAACTTTCCGGACCGGTTCTTGGGAAGGGCCGCGCCGGCGGGAAGGC
CGCACCAGCGTAAGCTCCTCGGCCGCTGCCGCCGCGTCGTGCTCGTCGTCGCTATCGCCACCGGA
GACACCTGACGACGCAACACGCAGCAACAAGCTCCTCAGCAGCGAGAACAGCGGGACACGGCAGGAG
TGTCCATGGAGAAGAAACAACCACAGCTCCAGCTCCAACCTCTCGTCAAGAAGGGTGCTCTGGCGGC
GACGCAGCTGCGCCGTACCCGGCCGAAATGCTTCACGCGCCGGCGGCGTGCGGCGGCATGTGGGTTC
TCCCGACGAGTCATGGTTTCAGCACGTGGGGCCCTGGCA

FIGURE 29 (CONTINUED)

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GCTCCTTCTGGGACGACTACGACATGGACAGCGCTCGCGGCCTCTTCCTCCACCCTCGCTTCACCGGT
GACGAAACTAGCATGGATCATTCCGGCACGCAAGCAACCGTGCCGGCAGTGGCAGCAACAGCGGCAGG
GATGAGCATGCCATGCGATGATGTTCCGGTAACCTCTTCTTCTTCAGATCTCCCTCCCCAAGGGACAC
CTCAGACTCCTACCTTCATGTGGAAGGAGGACTAAGCATGCATGCACACAGCCACGCACCTCGACGAG
ACGACTATCTCTTCCATCTCCCATCGACTTCGACGATCTCTTTCATTACTCATCGACTTCAACCACAA
AGGTATGATTAGGGTAGAGATGCTTGAGATTGCAGTTTTTAAAGACAATTTTGCAGCATCACACAGCT
CTACGTACAACAGCCACACCTATATCAATTCTCAAGACTTCTAAACCACAAGGGAACCCCTGTTCTAG
GCTGCGATTTTTAGGTCAGCTTGTGGGGTGACCACAGTACAATTCCTTTATTTTCGTATCTTCCCAA
GATTGTGTGTGTCAGATATTCGTTGAACTCGACTTCAAAGATTTGAAGTATTCATGTTTTCTTTTAC
TC

SEQ ID NO 322, *Oryza sativa* - protein

MDAPSSPSPPSARHIFPFAYEASTTTVGGSPRLHPLSWQQSSMSQPASPQQQQQQPLQHQQMISFGAS
PPCSTTQFVVPENAAQQQQMLLRVWSEALNLSPRGGPGGVPPWLYQQLLRVPPPPQKLYRGVRQRHWGK
WVAEIRLPRNTRLWLGTFTDAEDAAAYDREAFKLRGENARLNFPDRFLGKGRAGGKGRSTSVSSSAA
AAASCSSSSLSPPETPDDANTQQQAPQQREQRDTAGVSMKKQPQPPAPTSRQEGCSGGDAAAPYPAE
MLHAPAACGGMWVAPDESWFSTWGPSSFWDDYDMSARGLFLHPRFTGDETSMDHSGTQATVPAVAA
TAAGMSMPCDDVPVTSSSSDLPPQGTPTPTFMWKED

SEQ ID NO 323, *Oryza sativa* - DNA

ATGGACGCTCCGAGCGGGCGAGAGCGGGCGGGCGGGCGGGCGGGCGGTGGTGGCAGGAGGTGGAAGGGGAA
GGGGGTGACGCCCATAACAGCCGCGGGCGGCGAGCTGGGGACGGTTTTTGGAGGACTCGTCGGCGGCATTGC
TGCGGCCCGCTCAAGAAGATTGGGCGGAGCCCCGACCGCCTCCTCCGCTCCGCATCGTCGCTCTCCACG
TCCTCGTCGGCTCCGCCTTCGCCTCGCTCTTCTTCGGCTTCCGATGCTCCAGTCCGCGTCATCTCGTC
GTCGCCGTCGTCGCCCTCGCCACCGTCGGCGCGACACATCTTCCCCTTCGCGTACGAGGCCTCCACGA
CGACGGTGGGTGGGAGCCCAAGGCTCCACCCGCTGTCGTGGCAGCAATCCAGCATGTCCAGCCCCGCG
TCGCCACAGCAACAGCAGCAGCAGCCGTTGCAGCACCAGCAGATGATATCGTTTCGGCGCGTCGCCTCC
GTGCTCGACGACGCAGTTCGTCGTCCCGGAGAACGCGCAGCAGCAGCAGATGCTGCTGCGGTACTGGA
GCGAGGCGCTGAACCTGAGCCCGCGCGGTGGCCCCGGTGGCGTGCCACCGTGCTGTACCAGCAGCTG
CTCCGGGTCCCGCCACCGCCGCGAGAAGCTTTACCGCGGCGTGCGGCAGAGGCACTGGGGGAAGTGGGT
CGCGGAGATCCGCCTGCCACGGAACCGCACGCGGCTGTGGCTTGGCACCTTCGACACCGCCGAGGACG
CCGCCATGGCGTACGACCGCGAGGCCTTCAAGCTCCGCGGCGAGAACGCGCGGCTCAACTTTCCGGAC
CGGTTCTTGGGAAGGGCCGCGCGGGCGGGAAAGGCCGACACAGCGTAAGCTCCTCGGCCGCTGCCGC
CGCGTCGTGCTCGTCGTGCTCGTATCGCCACCGGAGACACCTGACGACGAAACACGCAGCAACAAG
CTCCTCAGCAGCGAGAACAGCGGGACACGGCAGGAGTGTCCATGGAGAAGAAACAACCACAGCCTCCA
GCTCCAACCTCTCGTCAAGAAGGGTGCTCTGGCGGCGACGCGAGCTGCGCCGTACCCGGCCGAAATGCT
TCACGCGCCGGCGGCGTGCGGCGGCATGTGGGTTGCTCCCGACGAGTCATGGTTTCAGCACGTGGGGCC
CTGGCAGCTCCTTCTGGGACGACTACGACATGGACAGCGCTCGCGGCCTCTTCTCCACCCTCGCTTC
ACCGGTGACGAACTAGCATGGATCATTCCGGCACGCAAGCAACCGTGCCGGCAGTGGCAGCAACAGC
GGCAGGGATGAGCATGCCATGCGATGATGTTCCGGTAACCTCTTCTTCTTCAGATCTCCCTCCCCAAG
GGACACCTCAGACTCCTACCTTCATGTGGAAGGAGGACTAA

FIGURE 29 (CONTINUED)

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SEQ ID NO 324, *Oryza sativa* - protein

MDAPSGESGGGGGGGGGRRWKKGKGVTPIQPRRQLGTVLEDSSAALLRPLKKIGRSPDRLLRSASSLST
SSSAPPSPRSSSASDAPVRVISSSPSSPSPPSARHIFPFAYEASTTTVGGSPRLHPLSWQQSSMSQPA
SPQQQQQQQPLQHQQMISFGASPPCSTTQFVVPENAOQQQMLLRWSEALNLSPRGGPGGVPPWLYQQQ
LRVPPPPQKLYRGVRQRHWGKWVAEIRLPNRNTRLWLGTFTDAEDAAMAYDREAFKLRGENARLNFPD
RFLGKGRAGGKGRTSVSSSSAAAAASCSSSSLSPPETPDDANTQQQAPQQREQRDTAGVSMEKKQPQPP
APTSRQEGCSGGDAAAPYPAEMLHAPAACGGMWVAPDESWFSTWGPSSFWDDYDMDSARGLFLHPRF
TGDETSMDHSGTQATVPAVAATAAGMSMPCDDVPVTSSSSDLPPQGTPTPTFMWKED

SEQ ID NO 325, *Arabidopsis thaliana* - DNA

ATTAAATAGATCTTTAAACAAAAAACCAAATTCTACTTTTCTTTCAAAAACAATCTCTCATTATCTC
AATCTTACTCTTGTTCAATCTCTTTTGAACCTGAAAAACCATCATTCTATCAAATCAAACACAATTGT
TAGGGTTTCTTTTTATCTTATACTCCACGAAACGTCTGGTTGAGAAAAAATGGAAGAAAGCAATGATA
TTTTTCAGAACAATTTCAAGTCCTAAAATCTCAGAAATCAGAGCATCTCTGTCTCAGATCATATTAGCA
GGAGGACCAACACACTCGACTCAATCTTCTCACTTCTCACTCCCTCCTCCGTAGAATCCGCCACAAC
ATCATTCAACACTCACAATCCTCCGCCACCGCCGAGCTCGGGTCTCCTCGTCTATCTCCGCCAACGAG
ATATCATCGAGAAGTCCACCTTCAGAACAGAGCAATCTCCACTCCTCATCCTCCTCTGTTTTCTCA
ACGTACGATCATCATCAAACCTCCGAGCTAATGCTCCAAGCGGCGGCCGGGTCTCCAGCCGCCGCTTT
CGCCGCTGCGTTAGCGGCTGGGAGGGTGACGAAAAAGAAGAACTTTACAGAGGAGTGAGGCAGAGAC
ATTGGGGAAAATGGGTTGCGGAGATAAGATTGCCGCAAAACAGAATGAGGGTTTGGTTAGGTACTTAC
GACACGGCGGAAGCCGCCGCTTACGCTTACGATCGCGCCGCTATAAGCTCCGTGGAGAATACGCTCG
TCTCAATTTTCCTAATCTCAAAGACCCGAGTGAGCTACTCGGACTCGGAGATTCTCTAAGCTAATAG
CTCTCAAGAACGCCGTCGACGGGAAGATCCAATCCATTTGCCAGAGAGTCAGAAAAGAGAGAGCAAAA
AAGAGCGTAAAAGTGAGCAAAAACCTCGTCGGCCACGGCGGATTCTTCGTGTTTGTTCATCGCCGGAGAT
TCTGTCTGTCGTCTCCGGTGACGACAATACTACTGCGGTTACTTCAGAGGATAGTTATTGGGTTTTCAC
CTATGGGTTTGTGTAACAGTGAAAATAGTTCTCCGGTATCAGTTTCGGTCCCTAGTGAAGTACCGGCG
ACGGCGGAGGAAGAGGCAATGATGGGAGTGGACACTGATGGGTTTTTTATTAGCGAGGATGCCATCGTT
CGATCCAGAGCTGATTTGGGAAGTTCTTGCCAATTAATACTACACAAAGAATGTGAATTTTGATCAAA
ATTGCAACAAGAAGAAGAAAAAAGTTTGAATTAGGACAAAATGATGAGAAAAATTAGGGTTT
TAGGTGTTAATTTAGGGTTTAAAGTAAACCGGATCTTTTGTAAATCATTGAAAGTTGTAAATA
ATATAATTAGGGTTTCTCAAATACAATGTAAAGCCTCGTGGTTTTTGAAGAGGTTGTGAAAGCTCCT
TTTTTTGAATTTCTGTTTTAGATCATCGAAGGACTTCTTTCTGATTGTACTTAGAAGAACAATTATA
TGTTACAGTGTTAATTTAATAAAATTGAGATT

SEQ ID NO 326, *Arabidopsis thaliana* - protein

MEESNDIFQNNFSPKISEIRASLSQIILAGGPNTLDSIFSLLPSSVESATTSFNTHNPPPPQLGSS
VYLRQRDIIEKFHLQNRAISTPHPLFSSTYDHHQTSLEMLQAAAGSPAAAFAAALAGRVTKKKKLY
RGVRQRHWGKWVAEIRLPQNRMRVWLGTYDTAEAAAYAYDRAAYKLRGEYARLNFPNLKDPSELLGLG
DSSKLIALKNAVDGKIQSICQVRKERAKKSVKVSKNSSATADSSCLSSPEILSSSPVTTTTTAVTSE
DSYWVSPMGLCNSSENSPVSVSPSEVPATAEEEEAMMGVDTDGFLARMPSFDEPELIWEVLAN

FIGURE 29 (CONTINUED)

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SEQ ID NO 327, *Oryza sativa* - DNA

ATGGCAGCTGCTATAGAAGGAAATCTGATGCGGGCGCTGGGAGAGGCTCCGTCGCCGCAGATGCAGAA
GATCGCGCCGCCCGGTTTCATCCCGGCTTGCCGCCGGCGCCGGCGAACTTCTCCTCGGCCGGAGTCC
ACGGGTTCCACTACATGGGCCCCGGCCAGCTCAGCCCCGGCCAGATCCAGCGCGTCCAGGCCCACTC
CACATGCAGCGGCAGGCCAGTCGGGGCTCGGCCCGGGGCCAGCCATGAAGCCCGCTTCGGCGGC
TGCTCCGGCGGGCGGCGGCGGCGGGCGCAGAAGCTGTACCGCGGCGTGCGGCAGCGGCACTGGGGCA
AGTGGGTGGCGGAGATCCGGCTGCCGCGCAACCGCACCAGGCTCTGGCTCGGCACCTTCGACACCGCC
GAGGAGGCGGCGCTCACCTACGACCAGGCCGCGTACCGCTCCGCGGCGACGCGGCGGGCTCAACTT
CCCGGACAACGCCGCGTCCGCGGGCCCGCTCGACGCCCGCGTGACGCCAAGCTCCAGGCCATCTGCG
ACACCATCGCCGCGTCCAAGAACGCCTCATCCAGGTCCAGGGCGGCGCCGGCAGGGCCATGCCCATC
AACGCGCCCCCTGGTCGCCGCGGCGTCTGTCCTCCGGCTCCGACCACTCCGGCGGGCGGCGACGACGG
CGGCTCGGAGACGTCTGTCGTCTGCGGCGGCGTCCCGCTGGCGGAGATGGAGCAGCTGGACTTCA
GCGAGGTGCCGTGGGACGAGGCGGAGGGTTTCGCGCTACCAAGTACCCGTCTGACGAGATCGACTGG
GACTCGCTGCTCAACAACAATAACTAG

SEQ ID NO 328, *Oryza sativa* - protein

MAAAIEGNLMRALGEAPSPQMOKIAPPPFHPGLPPAPANFSSAGVHGFHYMGPAQLSPAQIQRVQAQL
HMQRQAQSGLGPRAPQPMKPASAAAPAAAAARAQKLYRGVRQRHWGKWVAEIRLPNRNTRLWLGTFTDA
EEAALTYDQAAYRLRGDAARLNFPDAAASRGPLDAAVDAKLQAICDTIAASKNASSRSRGGAGRAMPI
NAPLVAAASSSSGSDHSGGGDDGGSETSSSSAAASPLAEMEQLDFSEVPWDEAEGFALTKYPSYEIDW
DSLNNNN

SEQ ID NO 329, *Oryza sativa* - DNA

ATGGACGCCAGCCTCCGCACACTGCCTCCGGCGATCTTCCCCGGCGAGGTCCGCTCCGCCGTCTCCTC
CCTCCTCCTCTCTCCCGGCGGCAGCGCCCTCGACACCGTGTCTCCACCTCCCGCCGCCCGTCCACCA
TCCCGCCGCTCGGCTCCAGCGTCTACTACCGCCAGAGCGAGCTCCTGCGCCACTTCGCCGCGTCCGAG
GCGGCGCAGGCGCAGAGCGCCACCGCCGCCAGCTCTTCGTCCGCCGCCGCGGCGGGTCTCGACGA
TGGCGCGCCCGGAAGCTGTACCGCGGCGTGCGGCAGCGGCAGTGGGGGAAGTGGGTGGCCGAGATCA
GGCTGCCGCGAACCAGGTGCGCGTGTGGCTCGGCACCTACGACTCGCCGGAGACCGCCGCGCACGCC
TACGACCGCGCCGCGTCAAGCTCCGCGGCGAGTACGCGCGCCTCAACTTCCCCGGCGTCATGGACGG
CCGCGACTGCCCCGACAACCTGCGCCAACTCCGCGACGCGCTCGACGCCAAGATCCAGGCCATCCGCG
TCCGCATGGCGCGCAAGCGCGCGCGCGCGCGCCAGCGGAGGAGAGCAAGAAGAGCCAACGCGCC
GAGGACGCGAAGGCGGCGACGCCGTCTCGCCCCGTGGCCTCCGAGCGCGCCGCGTCCGAGACGACGAC
GACGACAACCACGACGTCGTCTGTCGTACGGGTACCGGACGGCGTGCTCTCCATGAGCGCGGCGTCCG
TCGACGGCGACTGCCCCGCTCGAGCGGATGCCGTCTGATCCCGAGTTGATCTGGGAGATGCTTAAC
TTCTAG

SEQ ID NO 330, *Oryza sativa* - protein

MDASLRTLPPAIFPGEVRSVSSLLLSPPGGSALDVFVSHLPPPVTIPLGSSVYYRQSELLRHFAASQ
AAQAQSATAAASSSSAAAAGLDDGAPRKLYRGVRQRQWGKWVAEIRLPQNRVRVWLGTYSPEATAHA
YDRAAFKLRGEYARLNFPVMDGRDCPDNLRLQLRDAVDAKIQAIRVRMARKRARARRQREESKKSQRA
EDAKAATPSRPVASERAASETTTTTTTTSSSYGSPDGVLSMSAASVDGDCPLERMPSFDPPELIWEMLN
F

FIGURE 29 (CONTINUED)

160/173**SEQ ID NO 331, C-terminal region of SEQ ID NO: 258**

PFLMQWLNLLPLPVLDSSSWCPEHFHNSESDALP

SEQ ID NO 332, AP2 DNA-binding domain

YRGVRQRHWGKWVAEIRLPRNRTRLWLGTFTAEAAALAYDSAAFRLRGESARLNF

SEQ ID NO 333, Motif XVIIIRLPXNX¹RXXWLGT F/Y D/E T/S**SEQ ID NO 334, Motif XIX**

RG D/E

SEQ ID NO 335, Motif XX

WDESESFLLHKYPSLEIDWDAILS

SEQ ID NO 336, Motif XXI

GPPLHAAVDAKLHAICH

SEQ ID NO 337, Motif XXII

GANYLTPAQVLHVQAQLQRLRRP

SEQ ID NO 338, Motif XXIII

VDSKELMGALAPSMVSFSYPCSEQSASS

FIGURE 29 (CONTINUED)

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SEQ ID NO 339 – ORIZA SATIVA – GOS2 PROMOTER (NEW VERSION 013107)

aatccgaaaagtttctgcaccgttttcccccctaactaacaatatagggaacgtgtgctaaatataa
aatgagaccttatatatgtagcgctgataactagaactatgcaagaaaaactcatccacctacttttag
tggcaatcgggctaaataaaaaagagtcgctacactagtttcgttttcccttagtaattaagtgggaaa
atgaaatcattattgcttagaataacgttcacatctctgtcatgaagttaaattattcgaggtagcc
ataattgtcatcaaactcttcttgaataaaaaaatctttctagctgaactcaatgggtaaagagagag
atTTTTTTTTTaaaaaatagaatgaagatatctgaacgtattggcaaagatttaaacatataattata
taattttatagtttgtgcattcgctcatatcgcacatcattaaggacatgtcttactccatcccaattt
ttatttagtaattaaagacaattgacttatttttattattttatcttttttcgattagatgcaaggtag
ttacgcacacactttgtgctcatgtgcatgtgtgagtgacacctcctcaatacacggttcaactagcaac
acatctctaataatcactcgcctatttaatacatttaggtagcaatatctgaattcaagcactccacca
tcaccagaccacttttaataatatctaaaatacaaaaaataattttacagaatagcatgaaaagtatg
aaacgaactatttaggtttttcacatacaaaaaaaaagaattttgctcgtgcgcgagcgccaatct
cccatattgggcacacaggcaacaacagagtggtgcccacagaacaacccacaaaaaacgatgatct
aacggaggacagcaagtcgcgaacaaccttttaacagcaggctttgcggccaggagagaggaggagag
gcaaaga!

aaaccaagcatcctccttctcccatctataaattcctcccccttttccctctctatataggaggca
tccaagccaagaagaggaggagcaccagacacgcgactagcagaagccgagcgaccgccttctcga
tccatatcttccggtcgagttcttggtcgatctcttccctcctccacctcctcctcacagggtatgtg
cctcccttcggttggttcttggatttattgttctaggttggtgtagtacgggcggttgatgttaggaaagg
ggatctgtatctgtgatgattcctgttcttggatttgggatagaggggttcttgatgttgcatgttat
cggttcgggttgattagtagtatggttttcaatcgctctggagagctctatggaaatgaaatggtttag
ggatcggaatcttgcgattttgtgagtagcttttgggttggagtaaaatcagagcaccggtgattttgc
ttggtgtaataaaagtacggttggttgggtcctcgattctggtagtgatgcttctcgatttgacgaagct
atcctttgtttattccctattgaacaaaaataatccaactttgaagacgggtcccggttgatgagattga
atgattgattcttaagcctgtccaaaatttcgcagctggcttggttagatacagtagtccccatcacg
aaattcatggaaacagttataatcctcaggaacaggggattccctgttcttccgatttgcttttagtcc
cagaatTTTTTTTTTcccaaatatcttaaaaagtcactttctggttcagttcaatgaattgattgctaca
aataatgcttttatagcgttatcctagctgtagttcagttaataggtaatacccctatagtttagtca
ggagaagaacttatccgattttctgatctccatttttaattatatgaaatgaactgtagcataagcagt
attcatttgattatttttttttattagctctcacc!

cttcattattctgagctgaaagtctggcatgaactgtcctcaattttgttttcaaattcacatcgatt
at

ctatgcattatcctcttgtatctacctgtagaagtttctttttgggttattccttgactgcttgattac
agaaagaaatttatgaagctgtaatcgggatagttatactgcttggttcttatgattcatttcctttgt
gcagttcttgggtgtagcttgccactttcaccagcaaagttc

FIGURE 29 (CONTINUED)

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SEQ ID NO 340, *Oryza sativa* – PRO0110_RCc3_2 (new sequence 050307)

tcgacgctactcaagtgggtgggagggccaccgcatgttccaacgaagcgccaaagaaagccttgacagac
tctaattgctattagtcgcctaggatatatttggaatgaaaggaaccgcagagtttttcagcaccaagagc
ttccgggtggctagtctgatagccaaaattaaggaggatgccaaaacatgggtcttggcgggcgcgaaa
caccttgataggtggccttaccttttaacatgttcggggccaaaggccttgagacggtaaaagttttctat
ttgcgcttgcgcatgtacaattttattcctctattcaatgaaattgggtggctcactgggttcattaaaa
aaaaaagaatctagcctgttcgggaagaagaggattttgttcgtgagagagagagagagagagagaga
gagagagagagagaaggaggaggaggattttcaggcttcgcattgcccacctctgcttctgttggcc
caagaagaatcccaggcgcccatgggctggcagtttaccacggacctacctagcctaccttagctatc
taagcggggccgacctagtagccacgtgcctagtgtagattaaagttgccggggccagcaggaagccacg
ctgcaatggcatcttcccctgtccttcgcgtacgtgaaaacaaaccaggttaagcttagaatcttctt
gcccgttggactgggacacccaccaatcccaccatgcccgcgatattcctccgggtctcggttcattgtga
tgtcctctcttgtgtgatcacggagcaagcattcttaaaccggcaaaagaaaatcaccaacttgctcac
gcagtcacgctgcaccgcgcgaagcgacgcccgataggccaagatcgcgagataaaataacaaccaat
gatcataaggaacaagcccgcgatgtgtcgtgtgcagcaatcttggtcatttgcgggatcgagtgc
tcacagc!
taaccaaataattcggccgatgatttaacacattatcagcgtagatgtacgtacgatttggttaattaat
ctacgagccttgctagggcagggtgttctgccagccaatccagatcgccctcgatgcacgctcacatg
atggcagggcaggggtcacatgagctctaacggtcgattaattaatcccggggctcgactataaatac
ctccctaatcccatgatcaaaaccatctcaagcagcctaatacatctccagctgatcaagagctcttaa
ttagctagctagtgattagctgcgcttgtgatc

FIGURE 29 (CONTINUED)

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SEQ ID NO: 341; HVAP2-2 Hordeum vulgare c62815824hv270303@7626

CCGCTTCATTAAAACTGCCCATTTTTCCAGTTCCGACGAGGCGCCTCCCCCCTCCCCG
GCGACGACTAGGACGAGGCACCGCCGGCAACAACCATGTGCGGCGGCGCGATCCTCAAGG
ACCTCAAGGTCCCCGCGGTGACGCGGAAGGTGACGGAGGCGGCGCTGTGGCCCCGAGAAGA
AGAAGCCCAGGCAGGCCGACGGCGGGGCCCGGCGCCTCGGGCTGGTCGACGGCGAGGAGG
ACTTCGAGGCCGACTTCGAGGAGTTTCGAGGCCGACTCCGGGGACTCCGACCTGGAGCTCG
GGCGCGGCCGGGCGGCTGAGAAGGACGACGACGAGGTCGTGAGATCAAGCCCTACGCCG
CCGTCAAGAGGCCCTCTCCCAAGATGACTTCAGCATCATTACTACTGCTGGTTGTGATG
GTCCTGCACAAAGGTCAGCAAAAAGGAAGAGAAAGAACCAATTACGGGGTATCCGTCAGC
GCCCCCTGGGGTAAGTGGGCTGCTGAAATCAGAGATCCTAGCAAAGGTGTCCGTGTTTGGC
TTGGTACTTTCAACAGTGCTGAAGAAGCTGCAAGAGCCTACGATGTTGAAGCACGCAGGA
TCCGTGGCAAGAAGGCCAAGGTAAACTTTCCAGAGGAACCAACAGTTCCTCAGAAGCGCC
GTGTTTCGCCCTGCTCCTCTTAAAGCACCCAAGCTAAGCGCATCACAGGAACCTACCGTCA
TACCAGCAGTCAACAACCTTGCCAACCCAAATGCTTTTCGTCTACCCATCTGCTGACTTTG
CATCAAACCAGCCACCTGTTGAGCCTGATAACGTGCCATTTGTTCCCTGCAATGAAGTTTG
CTGCCCCCTGTTGAAGCTCCTGTTATGAATATGTACTCTGACCAGGGAAGCAACTCTTTTG
GCTGTTCTGACTTGGGCTGGGACTATGAGACCAAGACTCCAGATATATCATCCGTTGCTC
CCATTTCCACCATTGCTGAAGGAGCAGAATCTGCGCTTATCCAGAGCAACACCTACAAC
CAGTGGTGCCTCCTGTTATGGAGAACAATGCTGTGATTTTGAACCTTGGACGAGGTTTC
TTATGGATGATGGCGTGGATGAGCCGATTGACAGCCTTCTGAACTTTGGTGTGCCTCAGG
ATGTCATTAGCAACATGGACCTTTGGAGCTTCGATGACATGCCATCTGTGGAGAATTAT
GCTGAGGGATTCAAACCCCTGTATATAAAGACAAAGGGAATAAGACTATGGGAGATTGGG
AAGCACCTGTGTCAACTTCGGCTAGCATATGCTTATGTCCAAGCTTAGATGCAAAAAA
GTTGCATCCTGAGTCTCTTTTGTAAATCAACCCTTTTCCTAGCTGACTGTCGATGAACCGT
TGTCATTTATGAGTCTGATGAACCGTTGTCTTTATCTTTTGTCAACTTATATGTCGTCGC
TACCATTTCTGAATGTGAATGGCATGGATCTATGTCCAGTTTGCTTTAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**SEQ ID NO: 342; HVAP2-2 Hordeum vulgare c62815824hv270303@7626,
deduced protein sequence**

MCGGAILKDLKVPVTRKVTAAALWPEKKKPRQADGGARRLGLVDGEEDFEADFEFEAD
SGDSDLLELRGRAAEKDDDEVVEIKPYAAVKRPLSQDDFSIITTAGCDGPAQRSKRKRK
NQFRGIRQRPWGKWAAEIRDPSKGVVRVLTGFNSAEAAARAYDVEARRIRGKKAKVNFPE
EPTVPQKRRVRPAPLKAPKLSASQEPTVIPAVNNLANPNAFVYPSADFASNQPPVQPDNV
PFVPAMKFAAPVEAPVMNMYSDQGSNSFGCSLDLWDYETKTPDISSVAPISTIAEGAESA
LIQSNTYNSVPPVMENNAVDPEPWTRFLMDDGVDEPIDSLNFGVPQDVISNMDLWSFD
DMPICGELC

**SEQ ID NO: 343; ZmAP2-2 Zea mays AP2-2 homologue
c65144673gm030403@12827**

CACCATTTGCTCCCGCAAGCACCGATTTGTTTACTGCTCTCTCCGACGCGCGGCGGCGG
AGCTCCCTACGACGACTGAACCATGTGCGGCGGCGCGATCCTTGCCAACCTCCGCGAGCC
GGCGCCGCGCGGCTCACAGAGCGGGACATCTGGCAGCAGAAGAAGAAGCCCAAGAGGGG
CGGCGCCGGCGGGAGGCGCTCGTTTCGCGCGGAAGACGATGAGGACTTCGAGGCCGACTT

FIGURE 30

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CGAGGACTTTCGAAGCCGACTCCAGTGATTTCAGATTTGGAGCTCAGGGAAGGGACTGACGA
CGACGTCATCGAGATCAAGCCCTTCACCGCCAAGAGGACTTTCTCCAGAGATGGCTTAAG
CACCATGACTACTGCTGGTTAGCAAGGTCAGCCAAAAGGAAGAGGAAGAATCAATACAGG
GGTATCCGCCAGCGCCCTTGGGGTAAGTGGGCTGCTGAGATCAGAGATCCCCAGAAGGGC
GTTTCGTGTTTGGCTTGGTACTTTCAATAGTCCGGAGGAAGCTGCAAGAGCTTATGATGCT
GAAGCGCGCAGGATTTCGTGGCAAGAAGGCCAAGGTTAACTTTCTCTGATGCACCAGCAGTT
GGTCAGAAGTGCCGTTTCTAGTTCAGCTTCTGCTAAAGCACTCAAGTCATGTGTTGAACAG
AAGCCAATTGTCAAAACAGATATGAACATCCTTGCCAACACAAATGCACCCTTCTACCAA
TCTGTTAATACTACGCATCCAATTTATTTGTTTCAGCATGGCAATATGCCATTTGTTCCAGCA
ATGAACTCTACTGTTTCTTTTGATGATCCTATCATGAATCTGCACTCTGACCAGGGGAAGT
AACTCCCTTGGCTGCTCAGACTTGGGCTGGGAGAATGATACCAAGACACCAGACATCACA
TCCATTGCTCCCATTCCCCTATTGCTGAAGGCGATGAGTCTGTATTTGTCAACTCCAAT
TCAAACAGCTCGATGGTGCCCTCCTGTCCTGGAGAACAAATGCTGTTGATCTCACTGATGG
CTGACAGATTTAGAATCCTATATGAGGTTTCTTCTGGATGGCGGTGCAAGTGATTCAATT
GATAGCCTTCTGAACCTTGATGGATCGCAGGATGTTGGTAGCAACATGGACCTCTGGACC
TTCGATGACATGCCCATCGCTGGCGATTTCTTCTGAGGAATTTGAAGCTTGGCCATAGGA
CTATGTACATAGGGACTAGGGGAATAAAGACTGGGAGATTGGGAAGCACCTGCTTGGCAC
CTTGGGGGTAGCATATGCTCGTGTCTAGCTCAGATGCAGAAGTCGCATTCTGAAACTCTT
TGGTTATCGACCTGTTCCCTATTTTAACTATCTCTGTATGAGAGCCATTTATGAGACTGA
ACCATTTTGTTTTGCTTTCTTTTCGTTGTTACAATATATGGTTTTAACATTATGATTTATG
GATATGTGCCAAATATGGTGCTCAACAGTGGTCAAACATGCCTTTTAGA

**SEQ ID NO: 344; ZmAP2-2 Zea mays AP2-2 homologue
c65144673gm030403@12827, deduced protein sequence**

MNILANTNAPFYQSVNYASNLFVQHGNMPFVPAMNSTVSFDDPIMNLHSDQGSNSLGCSD
 LGWENDTKTPDITSIAPIPTIAEGDES FVNNSNSNSSMVPVLENNAVDLTDGLTDLESY
 MRFLLDGGASDSIDSLNLDGSQDVGSNMDLWTFDDMPIAGDFF

SEQ ID NO: 345; TaAP2-2 *Triticum aestivum* AP2-2 homologue c54788773

GACGAGGCACCGCCGGCAATCATGTGCGGCGGCGCGATCCTCAAGGACCTCAAGGTCCCCGCGCCGAC
GCGGAAGGTGACGGCGGCGGTGCTGTGGCCCGAGAAGAACAAGCCCAAGCGGGCCGACGGCGGCGCCC
GGCGCCTCGCGGGGCTCGGCCGGCGCGGGGGGCTCGGGCTGGACGACGGCGACGCGGACTTCGAGGCC
GACTTCGAGGAGTTCGAGGCCGACTCCGGGGACTCCGACCAGGAGCTCGGGCGCGCCGGGGTGGCTGA
GAAGGACGGCGACGACGAGGTCGTCGAGACCAAGCCCTTCGCCGCCGTCAAGAGGTCCCTCTCCCAAG
ATGACTTAAGCACCATGACCACTGCTGGTTTTGATGGTCCTGCACAAAGGTGAGCAAAAAGGAAGAGA
AAGAACGAATTACAGGGGTATCCGCCAGCGCCCCCTGGGGTAAGTGGGCTGCTGAAATCAGAGATCCTAG
CAAGGGTGTCCGTGTTTGGCTTGGTACCTTCAACAGTGCTGAAGAAGCTGCAAGAGCTTATGATGTTG
AAGCACGAAGGATCCGTGGCAAGAAGGCCAAGGTTAACTTTCCAGAGGAACCAACAGTTCCTCAGAAG
CGCCGTGCTTGCCCTGCTGCTCCTAAAGTTCCCAAGTCAAGCGCAGCACAGGAACCTACCGTCATACC
AGCAGTCAACAACCTTGCCAACCCAAATGCTTTCGTCTACCCGCCTGCTGACTTTGCATCAAAGCAGC
CACTTGTTTCAGCCTGACAACGTGCCATATGTTCCCTGCAAT

FIGURE 30 (CONTINUED)

165/173**SEQ ID NO: 346; TaAP2-2 Triticum aestivum AP2-2 homologue c54788773 deduced protein sequence**

MCGGAILKDLKVPAPTRKVTAAVLWPEKNKPKRADGGARRLAGLGRRGGLGLDDGDADFEADFEEFEA
DSGDSQELGRAGVAEKDGDDEVVETKPFPAVKRSLSQDDLSTMTTAGFDGPAQRSKRKRKNEFRGI
RQRPWGKWAAEIRDPSKGVVRVWLGTFNSAEEAARAYDVEARRIRGKKAKVNFPEEPTVPQKRRACPAA
PKVPKSSAAQEPTVIPAVNNLANPNAFVYPPADFASKQPLVQPDNVPYVPCN

FIGURE 30 (CONTINUED)

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**SEQ ID NO: 347; ZmNAC1 Zea mays NAC1 homologue
c58553294gm030403@3368**

GGGACACACACGCAGATCCGAGCTAACCACCATCGACGAGCGCCAGCGCCAGCAGCCGAG
CCGGATCGACCTTTTCTTTTCTTTTACACAGCGGGACAGAGAAAGGAGTCAGGCAGCC
AAAGCCACCCACCGCTTTTACCAACCGATCGTCCGATCGGCGTTGCCGCCACCGCTAGCA
TTGTGCGGCTTCAGCTCCATCCAAATCCACCGCCAGCAAGCAAGCCGGCGCCATGGGTCTG
CCGATGAGGAGGGAGAGGGACGCGGAGGCGGAGCTCAACCTGCCGCCGGGGTTCCGGTTTC
CAGCCGACGGACGAGGAGCTGGTGGCGCACTACCTCTGCGCGCGCGCCGGGGCGCCGC
CCGCCCCGTGCCATCATCGCCGAGGTCGACCTGTACCGCTTCGACCCCTGGGACCTGCCG
GAGCGCGCCCTCTTCGGGCGCCGCGAGTGGTACTTCTTCACGCCGCGGGACCGCAAGTAC
CCCAACGGCTCCCGCCCCAACCGCGCCGCGGGTTCGGGCTACTGGAAGGCCACGGGCGCG
GACAAGCCCGTGGAGCACGGGGGCGCGACGGCGGGGATCAAGAAGGCGCTCGTGTCTAC
CACGGCAAGCCCGCGCGCGGGTCAAGACGGAGTGGATCATGCACGAGTACCGCCTCGCC
GAAGCCGGCGGCGCCCGCGCCAAGAAGTCCGGCGCGCGCACGCTCAGGCTGGATGACTGG
GTGCTGTGCCGCTGTACAACAAGAAGAACGAGTGGGAGAAGATGCAGCAGCAGAAGGAG
AAGGAGAGAAGAAGGCGATGGAGTCGGAGGCGTCGCTCTCGCACTCCCACTCCGACACGC
GGACGCCGAATCGGAGATCGACGACGACCCGTTCCCGGAGCTGGGCTCTCTGCCGGCGT
TCGACGACATGGGCCAGCCCCAGCAGCAGCAGCCCTGCCGGCGTCGTCCTGCCCAAGG
AGGAGGTGGAGGACTTCGGCGACCTCGGCGGCGACGACTGGCTCGCGGGCATCAACCTCG
ACGACCTGCAGATGCCGGGGGACGCCGCCGATTTCTACGGCTCCATGCTCGTCTCGCCGA
TGGCCGCCAAGATGGAGCCGGACGGCGGCTTCCCTTCTTCTGAGATCCTTCGGCGACTC
CGGGGACGACCGGATGCAGCGCAACGCAAACTGTGTATAGTTCAGATTTTCTTCATGGAA
CCAACAACAACAACAAAAAAGTTCTGCTAATATCTTGTTCTAGTGGTGTAGTGAGAAG
TAGCAGCAGGCATGATTGAAGTCCATTGTAGTACTGATGTTTCATCGCCACTTGATCTGT
GACAAGTGACGGCATTTCTTCGTTTCTTGGCTGCAAATTCTTCGTTGTTTCAGAAATATAAT
TTCAGATGGGTAATGCCAA

**SEQ ID NO: 348; ZmNAC1 Zea mays c58553294gm030403@3368 deduced
protein sequence**

MGLPMRRERDAEAEINLPPGFRFHPTDEELVAHYLCARAAGRPPVPPIAEVDLYRFDPW
DLPERALFGRREWYFFTPRDRKYPNGSRPNRAAGSGYWKATGADKPVEHGGRTAGIKKAL
VFYHGKPPRGVKTEWIMHEYRLAEAGGARAKKSGAGTLRLDDWVLCRLYNKKNEWEKMQQ
QKEKERRRRWSRRRRSRTPTPTRGRNRNRSTTTRSRSWALCRRSTTWAQPQQQQPLPASS
CPRRRWRTSATSAATTGSRASTTTCRCRGTPPISTAPCSSRRWPWRWSRTAASPSSEIL
RRLRGRPDAAQRKLCIVQIFFMEPTTTTKVLLISCSSGVVQK

**SEQ ID NO: 349; Hordeum vulgare NAC3 homologue
c62818592hv270303@4035 revcomp**

TTTCATATGCAGTAGCCGTCTTCTCCTCCTCCTCCTCCTCCTGCCTTCCAGCTAGCTCAC
TATCGCATCATCCACACCACACCTACTACTCATACCGATTCCGTTCCACCCCGCTCGCCA
TCGCCATGCCAATGGGCAGCAGCAGCAGCAGCGCCGATGCCGGCCCTCCCTCCCGGCT
TCCGGGTCCACCCACCGACGAGGAGCTCATCGTCCACTACCTCGGCAGGCAGGCCGCGT
CCATGCCCAGCCCCGTGCCCATCATCGCCGAGGTCAACATCTACAAGTGCAACCCATGGG

FIGURE 31

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ACCTCCCCGGCAAGGCCTTGCTTGGGGAGAACGAGTGGTACTTCTTCAGCCCCCGGGATC
 GCAAGTACCCCAACGGCGCGCGCCCGAACCAGCGCCCGGGTCCGGCTACTGGAAGGCCA
 CCGGCACCGACAAGCCCATCCCGCCCAGGGAGAGCGGCGGCAGGACCGTCGGCATCAAGA
 AGGCGCTCGTCTTCTACTCCGGCAGGGCGCCAGGGGCGTCAAGACCGACTGGATCATGC
 ACGAGTACCGCATCGCCCAAGCCGACCGCACACCCGGCAAGAAGGGATCCCTCAAGCTGG
 ACGAATGGGTGCTGTGCCGGCTGTATAACAAGAAGAACAACCTGGGACAAGGTCAAGGTGG
 AGCAGGACATGGCTGTGGTGCAGGGACAGAATGGGGAGGTCATGGACGCGCTGGCCACCG
 ACGCCATGTCCGACAGCTTCCAGACGCACGACTCCTCGGAGATCGACAACGCCTCCGGCC
 TGCAGCAGCAGCACCACGGCTTCATGGACATGGCGCAGCGGCAGGCCAGGGAAGGCATGG
 TGACGGTCAAGGAGGACAGCGACTGGTTCACCGGCCTGAGTATGGACGACCTGCAGACTT
 GTTACATGAACATGGGGCAGATGGTGAATCCAGCGGCGATGCCTGTGCACGACGGCAGCG
 GCTATCTGCAGTCGATGAACTCGCCTCAGATGATGAGACCCATGTGGCAAACAATCTTGC
 CACCATTCTGAGATGGAAGAAGAAAGATATGGTGTAAATTATGTTTGAAATAGAAGTGAT
 TAGACAAATACTTACTTTGAACTAGAAAGAGATAGAAATTTCCCAGGCATGATTCTGAAG
 ATGTGGTGGTAGGCTTGTAGCAGTATTTATTTCTTTGGTTTCGATCTATAAATTTGGTATT
 CTAAACAAACATGTAATTTTATTTCCCATATCATCTCAAGTCTAAGAAAAAAAAAAAAAAAA
 AA

**SEQ ID NO: 350; Hordeum vulgare NAC3 homologue,
 c62818592hv270303@4035, deduced protein sequence**

MPMGSSSSSAAMPALPPGFRVHPTDEELIVHYLGRQAASMPSPVPIIAEVNIYKCNPWDL
 PGKALLGENEWYFFSPRDRKYPNGARPNRAAGSGYWKATGTDKPIPPRESGGRTVGIIKA
 LVFYSGRAPRGVKTDWIMHEYRIAQADRTPGKKGSLKLEWVLCRLYNKNNWDDKVKVEQ
 DMAVVQGNQGEVMDALATDAMSDSFQTHDSSEIDNASGLQQQHGFMDMAQRQAREGMVT
 VKEDSDWFTGLSMDDLQTCYMNMGQMVNPAAMPVHDGSGYLQSMNSPQMMRPMWQTILPP
 F

**SEQ ID NO: 351; TaNAC4 Triticum aestivum NAC4 homologue
 c54272640@10467**

GCAGCTAGAACTGCGGCGAGCTGATCCAGCTGAGAGAACTACAGCGAGGTTTGTGGATC
 GCCGACCCGACCGGAGATGAGCGGCGGACAGGAGCTGAATCTGCCGCGGGCTTCCGGTT
 CCACCCGACGGACGAGGAGCTGGTGACGCACTACCTCTGCCGCGGCTGCGCCGGCGCGCC
 CATCGCCGTCCCCATCATCACCGAGATCGACCTCTACAAGTTCGACCCCTGGCAGCTCCC
 AAAGATGGCGCTGTACGGCGAGAAGGAGTGGTACTTCTTCTCCCCGCGGGACCGCAAGTA
 CCCCACGGGTCCAGGCCCAACCGGGCCGCGGGTCCGGCTACTGGAAGGCCACCGGGGC
 CGACAAGCCCGTGGGCACCCCCAAGCCGCTGGCCATCAAGAAGGCGCTCGTCTTCTACGC
 CGGCAAGGCCCCCAAGGGCGAGAAGACCAACTGGATCATGCACGAGTACCGCCTCGCCGA
 CGTCGACCGATCCCGCCCCGCAAGAAGAACAGCCTCAGGTTGGATGATTGGGTGCTGTGC
 CGCATCTACAACAAGAAGGGCGGCATGGAGAAGCCGGCGGCGGCGCAGCCGTTCCGGGACTTC
 GCCATGGGCGGCTACGGGGGTGGCCCTGGGGCCATGGCGAGCTCCCCGCGGAGCAGAAG
 CCCGTTCATGGGGATGAACGCCAACGGCGGCGGCGGCGGCGCAGCCGTTCCGGGACTTC
 GCGGCGTACTACGACCGGCCGTCCGACTCGATGCCGCGGCTGCACGCGGACTCGAGCTGC
 TCGGAGCAGGTGCTGTGCGCGGAGTTCCCGGCGGGGAGGTGCAGAGCCAGCCCAAGATCA
 GCGAGTGGGAGCGCTCGTTCGCCTCCGGCGGCGACCCCGTGAACCCGGCGGCGGCTCCA

FIGURE 31 (Continued)

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TGCTCGAGCCCAACGGCGGCTTCGGCGGCGACCCGCTCCTCCAGGACATCCTCATGTACT
 GGGGCAAGCCGTTTCTAGGCAGCGAAGAAACCGATCGGTTCGGTCGAAGCGAGTACCTCCTA
 TCCTTGCGGCTTTGGGGCGATGAAACGGGCGAGCCGCCATTGTTGACCTGATGAAGGGGAG
 ATAAATTTAAGAAGATATTAGACGGGAGATAAGACAAAATCAGGTGCTTGATGACGACGA
 CGACGACGGCGAAGATCGGAAGGTGGCGGCGATGATACCGTGGGTCCCCGGCCTCTCACC
 AGCATGACATGTGACCGACGACGCCCAAGATGCTTCAAAGCGTTCGCCGCATTGCATCAT
 CGGGCGGGCGGTTCGTGCGCTAGCAAGCATGCATGTGCGTGTATATGGATGGGTGTACATA
 CATGGAGATCATGATTGGTTTCGGTGCAGGGGTTGCTGTTTCTTGATTGGTTAGTTGTAAT
 ATTTTTTTTTTTTTTTCGGGTGAGTTGTAAGGGTTTATTGATAAGTTGATACCATAACCATA
 CCAGTGCTAGCCGCCGTGCGTGGTGCTGGCTAGCTGTAGTCCGAGTGGTAGTAGTGTAAC
 TGTAAGCCATTTCATCAAATGAAACTGAATATATTATCTGCCCTCAAAAAAANAAAAAAA
 AAAA

SEQ ID NO: 352; TaNAC4 *Triticum aestivum* c54272640@10467, deduced protein sequence

MSGQELNLPFGFRFHPTDEELVTHYLCRRRCAGAPIAVPIITEIDLYKFDPWQLPKMALY
 GEKEWYFFSPDRKYPNGSRPNRAAGSGYWKATGADKPVGTPKPLAIKKALVFYAGKAPK
 GEKTNWIMHEYRLADVDRSRPARRTASGWMIGCCAASSTRRAAWRSRRPWTGSRRPWAAT
 GVALGPWRAPRRSRSPSWG

SEQ ID NO: 353; NAM2 *Zea mays* homologue 65089172_CORN

cttgacgtctaccagctgcataataacttggttcagaagaagaagatggacgctttcaca
 catgttcctcccggttttcgtttccaccctaccgacgaggaactcgttgactactacct
 agggaaaaggttagcactgaagaagatagatttggtatgtgataaaagatgtggatttgta
 aagattgagccttggtatctgcaagaaaagtgcaggatttgaagcgaagagcagaacgag
 tggtacttcttcagccacaaggacaagaagtacccaaccggcactcgcaccaacagagcg
 acgacggccggtttttggaaggccacggggagagacaagccgatctacgtgaagaactgc
 ctctgtagggatgaggaagacactgggttttctacaaaggccgggcccgaatggacagaag
 tcagactggatcatgcacgagtatcgctggagaccaacaacaatggaattccacatgag
 gaaggatgggttgatgcagggtgttcaggaagcgactcgcgactgtccaaagaatggtc
 ggggactcgccttactgggttcaatgaccacgcggggttcatggcgccggagctcggctca
 ccgaggcaggcggcgccaccatcagcagaacgtcatgatgtaccacaggcaacagagcagc
 tacagctacccttgcaagggtggagctggagtagcaccacacctccttcctcaggagcacttc
 ctgcagcagctccctcagctggagagccccaagctccctgaccttattggccaagtagac
 actactctccagccagcatgcggccttacacaggagcatgggtgcccctcgctacaccatg
 caggagcttcaggccgagcctctctatctggcgactggcggggacacagattggcgagct
 ctgcacaagttcatggcgtcccagcttagccacggagacatcacccttaataaggagtca
 gctaactactccaatccggcactgcagggtgattcagcagctctgaagagaaagaaggcc
 ttggactacgtgtcaacgtcagcctcctgtggaggggacaatgatttggtgaaataacag
 cgtcaatggtataatacatattcacatacgcactaaatcactggactagtgcattattccct
 cattacacagttataataacattgaggcgtgctggatgtaatgtaacgtagtatataaagta
 gccaaactgattcatgtgtcatgggtatagtagaatgggtatgtgcataacaaagtgtaccg
 agtaggtcacacgtccatgcataagttggcataatgtctggtgttaataataagggttagc
 taacagctgaagctaaggagcttcagcacctgatttgacaaaaaaaaaaaaaaaa

FIGURE 31 (Continued)

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SEQ ID NO: 354; NAM2 Zea mays homologue 65089172_CORN deduced protein sequence

MDAFTHVPPGFRFHPTDEELVDYYLRKKVALKKIDLDVIKDVDLYKIEPWDLQEKCRIGS
 EEQNEWYFFSHKDKKYPTGTRTNRATTAGFWKATGRDKPIYVKNCLVGMKRTL VFYKGRA
 PNGQKSDWIMHEYRLTNNNGIPHEEGWVVCRVFRKRLATVQRMVGDSFYWFNDHAGFMA
 PELGSPRQAAHHQQNVMMYHRQQSSSYSPCKVELEYHLLPQEHFLQQLPQLES PKLPDL
 IGQVDTTLQPACGLTQEHGAPRYTMQELQAEPLYLATGGDTDWRALDKFMASQLSHGDIT
 PNKESANYSNPALQVIQQSEEKEEALDYVSTSASCGGDNDLWK

SEQ ID NO: 355; HaNAM2 Helianthus annuus 66785923_SUNFLOWER

cttgcttttgtgttgatatgtctaaagaagaagtgaatttgtctgtgaatgtaaattggc
 agtctaaagtgcctccagggtttcggttccaccctaccgaagaagagcttcttcattact
 acttaaggaagaaagtgcggtatgaaaagatcgatcttgatgttattcgtgatattgatc
 ttaacaagctcgaaccatgggatatcaaagaaaagtgcagaattggatcaaccccgcaaa
 acgattggtatttttttagccacaaagacaagaaatacccgactggaacgcgtacaaatc
 gtgcaactgctgcagggttttttgaaagccaccggtcgagataaggtcatttatagtagca
 tgagaagaatcggtatgaggaagacactcgtgttctataaaggaagagcacctcatggac
 aaaagtcggattggattatgcacgaatatagactcgatgacaacacgattatctcccagg
 attatgcctcagggttctaatttatgtgattccactcaagaagacgggtgggtcgatgtc
 gcgttttttaaaaagaaaaactaccataaagcggttgagagtcaccaaaaggatcatcatcag
 caccttccattgattcaacagctcaaattgcaatctttaagaaagatggaactcaacttc
 ttgcatacatcaatggtactaaatcctgcaagcaagaaccgaatcactcgccaatatag
 caaccacccatgactatgaccctttgcaacaattcatcaaccgataagcgacagattcc
 tacacctcccaaggctccacaacacttcaagtgacttgatcacgtcagccacctttgatc
 aagattcaatctttccggcccataacacccatgactcatttgctaacggaagttgaacatt
 ctaggaatcataaacatcttgaaaactggtcagatgtggatcgactcggtggcctcccaac
 tcaatggccaaccgcgatcatccaggcagatgtacggttgctacgacgaaccaatgaag
 acatatgcttctcacttcacccatgatgatcagcaagaaccaccacaaccatcatccatgg
 ctaaaccacaaccaagcagcctatacaagcgagatagatatatggagctttgcacaatctt
 catcacaatcatcatcaccggatccattttaccatttgcggtatagttcacataagtaa
 tatactttttacttttatggaaaatacagatggaataaactgttatataatacttggtatga
 tatatagctctctttaattagctgggtgggttatggatcttgatgtgaagtgaagggtcat
 gacttatgaatgtattgtgtttgatgcaaaaaaaaaaaaaa

SEQ ID NO: 356; HaNAM2 Helianthus annuus 66785923_SUNFLOWER, deduced protein sequence

MSKEEVNLSVNVNGQSKVPPGFRFHPTTEEELLHYLRKKVAYEKIDLDVIRDIDLNKLEP
 WDIKEKCRIGSTPQNDWYFFSHKDKKYPTGTRTNRATAAGFWKATGRDKVIYSSMRIGM
 RKT LVFYKGRAPHGQKSDWIMHEYRLDDNTIISQDYASGSNLC DSTQEDGWVVCRVFKKK
 NYHKAVESPQRSSSAPSIDSTAQMQLKKDGTQLLAYINGTKSCKQETESLANIATTHDY
 DPLQQFINPISDRFLHLRLHNTSSDLITSATFDQDSIFPAHNTMTHLLTEVEHSRNHKKH
 LENWSDVDRLVASQLNGQPRSSRQMYGCYDEPNEDICFSLHDDQQEPPQPSSMAKPQA
 AYTSEIDIWSFAQSSSQSSSPDPFYHLSV

FIGURE 31 (Continued)

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**SEQ ID NO: 357; GmNAM2 Glycine max NAM2 homologue
GM02LC19289_SOYBEAN,**

tcacctcatcatctatcattatatctttctttcaattcctatcctcttcttctgtagtgtgta
cccattttgaatgtgttctctctctctctctctctttcttttaggtccctggtgaatatctag
aaccactctctagctagtttctctcttcttctgtagctagctatcgccgatcactctcttg
gtttaaaccacctgaatgccggaaaacatgagcatatcagtgaatggcgaatctcaagtc
cctcctggccttcagggtttcatccaactgaagaagagcttcttcagtactacttgaggaag
aaggtctcttacgagaagattgacctcgacgtgattcgtgacgttgatctcaacaagctc
gagccatgggacatacaagagaaatgcaaaataggaaccactccgcagaatgattggtac
ttcttcagccacaaagacaagaagtacccacacaggaacgcgcaccaatcgcgcaactgct
gcagggttctggaaggccactggccgcgacaaagtcatctacagcaatggaaagaggatt
ggaatgagaaagactctggttttctacaaaggaagagcgccacatggccagaaatccgat
tggatcatgcatgaatacagactagacgacaacaacaccaccgacaccaatattgtgtcc
aatgtgatgggggatgctgctcaggaagaagggtgggtgggtgtgcaggatattcaagaag
aagaaccatctgaaaaccctagacagccccttagcttcaggggaagatagaaggagccac
ttgttcgactcgtgacgagggagctttggagcaaatacttcagcaaatgggaaggggt
tgcaaggaggagagcagctatgaaggcaactacaacagctatggaagggtttacaaggccg
tatgagacaacagcgggcgaacaatggcgggcgatacaatgatagggttcatgaagctccc
agcctcgagagcccaaaatccgcaagcatggagaaccaccacaacaccaacaacaacaat
aacatgaatagtaataataataataatgggtgataacaacgagaacaacaataataatggg
taccatcccataattccagtagagatgggcacggacaatgaagggacattcacacgcac
caggtgagtgggtggtagcccaaacaacaacaacaacagcaacattgttcatccattg
gaggtaggatcaggtgggtggaggcctcaccaactgggctgcgctggaccgttttagttgca
tctcaactcaatggccaaaccgatgcctctaggcaactaggatgtgctttcaacgacccc
accatgtattgcaccagcgtcgaccatcatgatcttcatcatcaaatccccaccctccga
tcctcatcaacgtccgctaacacacgaccttcccctgcacccgcattcatcaacccccca
acacaggacttcaccagcgagattgacctttggaacttctcccgatccacgtcctcactg
ttggcatcctccgaaccactgtgccacgtgtccaacacgtcagtgtagcgagatcaataa
aataataataataaaaaaaaatatctcaagtcccccttttctccatgttcgattgttaaa
tatagaaataattagcccctacttcatcacatatcatgtttaatatattaattagttct
tcttctctcaagtctcagaggattattattacagactttaaatgtgataattctcctagt
atacatttttactttaattagcttatttgcactcaaaaaataatattccattgacaatt
gtctcttgtaaattcttaatt

**SEQ ID NO: 358; GMNAM2 Glycine max NAM2 homologue
GM02LC19289_SOYBEAN deduced protein sequence**

MPENMSISVNGQSQVPPGFRFHPTEEEELLQYYLRKKVSYEKIDLDVIRDVDLNLKLEPWDI
QEKCKIGTTPQNDWYFFSHKDKKYPTGTRTNRATAAGFWKATGRDKVIYSNGKRIGMRKT
LVFYKGRAPHGQKSDWIMHEYRLDDNNTDTNIVSNVMGDAAQEEGWVVCRIFKKKNHLK
TLDSPLASGEDRRSHLFDSCDEGALEQILQQMGRGCKEESYEGNYSYGRFTRPYETTA
ANNGGGYNDRFMKLPSLESPEKSASMENHHNTNNNNNMNSNNNNNGDNNENNNNGYHPII
PVEMGTDNEGTFTTHQVSGGDPNNNNNSNIVHPLEVSGGGGLTNWAALDRLVASQLNG
QTDASRQLGCAFNDPTMYCTSDVHDLHHQIPTLRSSSTSANTRPSAPAFINPPTQDFT
SEIDLWNFSRSTSSLLASSEPLCHVSNTSV

FIGURE 31 (Continued)

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SEQ ID NO: 359; ZmNAM2 Zea mays NAM2 homologue ZM02LC45780_CORN

tgacaacctgttactggatcattgtgatttttagcgcggaatagcacgagcgcaaaacgat
 atcaggtacttacaattgtttgcaaagtgcgaagaacatacaaggtgacatgaccacaa
 ttgtttgcagtgttgacacgagtgggctcacacaatagacaatacatatgtcgcacttcg
 atcccgctcctcttaacaaccagagcacaggaccgcatttaccatgggggtataccgtgtt
 cgatatcaagaggccgcggtgcggtgctttgaccggctagttgtcggattgcatgctcct
 gagcatgttcaggatggagaggaacagggttcaggatgtcggaggtacagcccaaccgacgc
 ccagatgtactcgtcgtaggtgtggcgcttgatcaggttctcgggtgtcgtacaggatgaa
 gcctgagaagaccagagcccctagaccaccgaacaagcccaccgacacgggtcacagtgg
 gaagaaaacctgcagcgcagaattccacacagaaccaataaaaagtttattgtgcaagca
 gtggattgtcgtcgttggttaacaaagcatcattcgcggatatacagagcgcgtttctttca
 gagcttgtcgtaggcattacctgaagaaagctagttaggacgaggatagtaagcgcggaa
 gacaggataggccccagggtacccgaattccttgcccttctttgacgcccagaaagcatac
 gcagtcagagaaaaccaccacgccagccgctcagcactaaagcctccagaacgattttccct
 tgggtgttagcacaagccacgccgatgctgaagctcaagcacaacgtgaacagaccagg
 aaaacggaattgtgtgggtgcttgtgctgataatgatacaatgggatcatcaggatgaag
 ggcaggacggcgagcacgagcgcgagggccggggagtcggagagcgtggcgttgagggtg
 ggggtggagaacgggtgagggcgagacggcggtgggtgaggagcagctgcgcagcgaggatg
 ccgtagaccttgcgagcaagccccatcggagggcgctctccccgcgcgagatccccggg
 tacagcgtctccccggtccccggcctccagggtccaccaccgacgcctccaccttctccttc
 atctccggcgcgcgcggtacccccgcggcgcgaggggctgcatctccgccaccgatgcc
 atctctctctccgacgggggttgggtgcggtgcggtgcggggaaggggaacccacgcgt
 ccgcccacgcgtccgcccacgcgtccgcccacgcgtccgcccacgcgtccgcccacgcgt
 ccgcccacgcgtccgcccacgcgtccgcccacgcgtgggatcgtcttctccctccat
 cctctggcctctggtcctccaccgtcctgctagccagagctgctcttgtagcgcgagctg
 gcctctgtgcatatcaccagcacacgcgcgaggggaaggaaattaacaagagaaaaggca
 aggagagcaggcaggcaaggaaagctgcagaagccaagggaaggagaaggaggatcatcaat
 gagcatctcgggtgaacgggcagtcgtgctgcccgcgggggttccgcttccaccccacgga
 ggaggagctgctcaactactacctccgcaagaaggtggcctcccaggagatcgacctcga
 cgtcatccgcgacgtcgacctcaacaagctcgagccatgggacatccaagagaaatgcaa
 gatcgggtcgggtccccagaacgactggtacttcttcagccacaaggacaagaagtacc
 gacggggacgcgcaccaaccgcgccacggccgcgggttctggaaggccaccggccgcga
 caaggccatctacaacgcggtcaagcgcacatcggcacgcaagacgctcgtcttctacaa
 gggccgcgcgcgcacggccagaagtccgactggatcatgcacgagtaccgcctcgacga
 ccccgctgctgctgctgctgctggatccggtgatgccgtggccaacgacgacgcagccgc
 cacggctgctgctgctgctgctgctcgctcgacggcgggcaggaggacggctgggtggt
 gtgcagggtgttcaagaagaagcaccaccacaaggagtcagggtggggcgggggcaacaa
 gcacggcagcagtaacagcgcagatgggcacggcgggcgccggcaaggcatcggctgcggc
 tgcggtgcggcgacaccagcaccagcaccatggaggcctgcagtactcctccagcgacga
 ggcgtggaccagatcctgcagtacatgggcaggctcgtgcaagcaggagcacgagctggt
 gtcgccggcgccggcgccgggaacggcgggcggtccaggtaacctccggcccatcga
 gaccgttctggggcgggcacgcgttcatgaagcttccgcgctcgagagcccgtcccagcg
 ccaagcccaccaccaggagcgcgcgagtagccgcggcgccggctgggacgacgacgacgcg
 ctggaccgcctcgccgcctacgaccacctcaacggcctctccaacgacgacgcgtccaag
 aacatggccgcgttcttcgacgtcgagcctagcgccgcggcgccgcggcgccgtggacggc

FIGURE 31 (Continued)

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gacctgtggagcctcgacgggtccgtgtcgccgctgcacgcggacttgaccatgaacaac
gtctagcttctgggtcccgaccaacaacaacagggcccccgaatccccgatacacatccat
atggcgtgtgcacgcatgcatgcatgcatgcatgccgcgcgcaccactaaccactcgac
cagcatgcatgcatacgtgcgcacccccaccggcgcccgcgccgctagtgcgtcggtgctc
ccgtagtgcgtgcatgcatggccgcgcacgtacgtattgcacgctcgctcgcgcgtagc
tacgtacgtgcgcgaataagctagctagccctaggatcggaacatatgtatgcatccat
tgcatggccggatatacatcaggagctgctgccgctggtgtatgtccgcccgcgtccaaa
ctccaaagtgcgtgagatcgatcgatcgagctcgctcgctccagggtgtgcagtacgtac
gtacgtaagcgcctgtgtatgtgtaagcagacagcggtgtagtagctctagctagtagaa
catacttacacacactatatactgcataccgtttgtacctatcatatatagattactact
gtattattgcaaaccgctttggggggttttaaaaaaaaaaaaaaaaaaaaa

**SEQ ID NO: 360; ZmNAM2 Zea mays NAM2 homologue ZM02LC45780_CORN,
deduced protein sequence**

MSISVNGQSCVPPGFRFHPTEEEELNYYLRKKVASQEIDLVDVIRVDLNLKLEPWDIQEKC
KIGSGPQNDWYFFSHKDKKYPTGTRTNRATAAGFWKATGRDKAIYNAVKRIGMRKTLVFI
KGRAPHGQKSDWIMHEYRLDDPAAAAAAGSGDAVANDDAAATAAAAAAASSDGGQEDGWV
VCRVFKKKHHHKESSGGGGGNKHGSSNSEHGHGGAGKASAAAAAAHQHQHGGGLQYSSSD
EALDQILQYMGRSCKQHEHLVSPAPAPPGRAAASRYLRPIETVLGGHAFMKLPALSPSQ
RQAHHQERASTPPPAGTTTTTRWTASPPTTSTASPTTTRPRTWPRSSTSSLAPPPPPPW
ATCGASHGPCRRCTRT

**SEQ ID NO: 361, GmNAM2 Glycine max NAM2 homologue
50450638_SOYBEAN**

ggcattggatcatttgtggcttgtaccgaactctgaatgccggagatgaagatgagcata
tgtgtgaatggagaatcccaagtccctccaggcttccggtttcatccaaccgaaggagaa
ctgttgcagtactattttaggaagaagggtgtccaacgagaagatcgacctcgacgtgatt
cgcgatgttgatctcaacagactcgaacctatgggacatacaagagatgtgcaaaatagga
agcagcccacaaaacgatttggtacttgttcagccacaaggacaagaagtacccccacggga
agccgcaccaaccgcgccatcattgttgggttctggaaggccacggggcgcgacaaggctc
atatatagcaacgggaagataattggaatgagaaaaacattggttttctacaaagggcgt
gcccccaatggccaaaagtctgattggatcattgcatgaatacaggctagacgacattaat
aacaccaatgagatggaacacgggtgggtggtctgtagagttttcaagaagaagaatgtc
cctctcaaaaccctagatagcccaaaatccatgacctgaatatgtttacagaaagcgac
tactgtggaggcttactaactgggaatcccttgatcagcttgtggcatcacaactgaat
ggacaaactgagacatattgcagtgatttgcaattccccgcatttctatcatcctcatac
attgctacaacaacacacattgctcccacaatacaggattaccccagctacgacattgac
ctgtggaaccactgtgcttcgcgcgtgtccaacactccaaatgtaacactctaataaat
ccttcttttaatttcttcccatgtcagattattactactattaaatcatccctaaaatat
tcattttcaaaaaaaaaaaaaaaaaaaaa

FIGURE 31 (Continued)

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**SEQ ID NO: 362; GmNAM2 Glycine max NAM2 homologue
50450638_SOYBEAN, deduced protein sequence**

MPPEMKMSICVNGESQVPPGFRFHPTEEEELQYYLRKKVSNEKIDLDVIRDVDLNRLEPWD
IQEMCKIGSSPQNDWYLF SHKDKKYPTGSRTNRAIIVGFWKATGRDKVIYSNGKIIGMRK
TLVFKGRAPNGQKSDWIMHEYRLDDINNTNEMEHGWVVC RVFKKKNVPLKTLDSPKSMT
MNMFTESDYCGGFTNWESLDQLVASQLNGQTETYCSDLQFP AFLSSSYIATTTTHIAPTIQ
DYPSYDIDLWNHCASRVSNTPNVTL

SEQ ID NO: 363; ZmNAM2 Zea mays NAM2 homologue ZM06LC18271_CORN

ggtcgtctaaaaaagcagcagctgctcttctcttctgctagcagctttatttgccctgcct
ccctaccggcgagggaggtacgtgcgcccgatcgagaagcagcagcagcaattaataacta
aacatggatcaggcgggcggaggagtcttggtgttccccagggttcagggtccaccctacg
gaggaagaactggtgggctactaccttgccaggaaggtggcctcccagaggatcgacctc
gacatcatccaggaggtggatctctacaggatagagccatgggatctgcaagagcgggtgc
aagccgcagcagccggcggtgggcacgacgagcagacacaggagtggctacttcttcagc
tacaaggaccgcaagtaccccagcgggacgaggacgaaccgcgccacggcgggccggttc
tggaaggccaccggcgagggacaaaccggtgctgctgctgctccaccaggaccaccaggtgt
agcagggtcatcggcgatgaggaagacgctggtgttctacaagggcagggcacccaacggc
aggaagagcgactggatcatgcacgagtagcactccaatccaacgagcagcagcaccggcg
caggaggaaggctgggtggtgtgcccgcgctttccagaagcctatccccaaccagcggccc
ttcttccccaccagctacgcccgtactacgaccacaacctctcaacgacggcagcggtg
cacgtagacggcgaccgccatttcttgccggggtcatcagcagcagcagcagcactgcta
cagcagccaccagggttgccaggcagcagcttcccgcagctgactccgacgacgacttg
gagtccaagaagcagctggtgagtatcccgcgctggagagccccactgccatggcctgc
tggtccgacgcccggcggtacgcgcagagaagcagctacgatgaacatgagatgatgatg
atgatgatccagcagggaggaggaggaggagagcaagctgcagccgccatcgactggaac
ttcttgacagcctgctgtccgcgacgtcgcaactccatggggccctcgggatccctgttg
cagtgcctccggccatcgatcgatccatcttctttgatccagcggagaacattat
tcattcatcggcattatacaatatatttattagttgcatacacacacagagtatacgtat
atgctaataattcagatgtgttcatacacacttccattgtcatgtgttagttcggttgcgac
ttacattacagactgccttagatgattcaggtatactgtatacaacatgatgcacagtat
agtaggagtaagtgcaccagctctcagcagctggtagctagctagctatgtaaaattcctc
cttaattacagctatgtaacatatatacagttattattacttactgatatgatctatc
tatcaaaaaaaaaa

**SEQ ID NO: 364; ZmNAM2 Zea mays NAM2 homologue
ZM06LC18271_CORN, deduced protein sequence**

MDQAAEESCVPPGFRFHPTEEEELVGYYLARKVASQRIDLDIIQEVDLYRIEPWDLQERCK
PQHAGGGHDEQTQEWFYFSYKDRKYPSTRTNRATAAGFWKATGRDKPVLSSSTRTRTCS
RVIGMRKTLVFKGRAPNGRKS DWIMHEYRLQSNEHAPAQEEGWVVCRA FQKPIPNQRP
FPTSYAGYYDHNLSSTARLHVDGDRHFLAGSSAAAAALLQQPPGLAGSSFPQLYSDDDLE
SKKQLLSIPPLESPTAMACCS DAGGYAQRSSYDEHEMMMMMIQQGGGGGEQAAAAIDWNF
LDSLLSATSQ LHGPSGSLLQ

FIGURE 31 (Continued)