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(54) Title: PLANTS HAVING MODIFIED GROWTH CHARACTERISTICS AND A METHOD FOR MAKING THE SAME

(57) **Abrégé/Abstract:**

The present invention concerns a method for modifying the growth characteristics of plants by modifying expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein and/or modifying level and/or activity in a plant of a 2xC2H2 zinc finger protein. The invention also relates to transgenic plants having modified growth characteristics, which plants have modified expression of a nucleic acid encoding a 2xC2H2 zinc finger protein. For example yield of crop plants are improved by the methods of the present invention.

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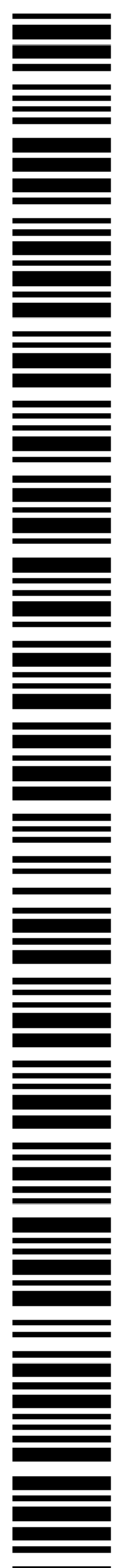
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(54) Title: PLANTS HAVING MODIFIED GROWTH CHARACTERISTICS AND A METHOD FOR MAKING THE SAME

(57) Abstract: The present invention concerns a method for modifying the growth characteristics of plants by modifying expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein and/or modifying level and/or activity in a plant of a 2xC2H2 zinc finger protein. The invention also relates to transgenic plants having modified growth characteristics, which plants have modified expression of a nucleic acid encoding a 2xC2H2 zinc finger protein. For example yield of crop plants are improved by the methods of the present invention.



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Plants having modified growth characteristics and a method for making the same

The present invention concerns a method for modifying plant growth characteristics. More specifically, the present invention concerns a method for modifying the growth characteristics of a plant by modifying expression of a nucleic acid encoding a zinc finger protein and/or by modifying the level and/or activity of a zinc finger protein in a plant, which zinc finger protein has two zinc finger domains of the type C2H2 (2xC2H2). The present invention also concerns plants having modified expression of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or modified levels and/or activity of a 2xC2H2 zinc finger protein, which plants have modified growth characteristics relative to corresponding wild type plants.

Given the ever-increasing world population, it remains a major goal of agricultural research to improve 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 in a specific and controlled way. 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 led to the development of plants having various improved economic, agronomic or horticultural traits. A trait or growth characteristic of particular economic interest is high 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. Other important growth characteristics include modified architecture, modified growth rate, among others.

The ability to influence one or more of the abovementioned growth characteristics, would have many applications in areas such as crop enhancement, plant breeding, production of ornamental plants, arboriculture, horticulture, forestry, production of algae or plants (for example for use as bioreactors, for the production of substances such as pharmaceuticals, antibodies, or vaccines, or for the bioconversion of organic waste or for use as fuel in the case of high-yielding algae and plants).

The term "zinc finger" describes a nucleic acid-binding domain in a protein that is folded around a tetrahedrally coordinated Zinc ion (Miller et al. 1985. EMBO, 4, 1609-1614). The amino acids that coordinate the zinc ion, are always cysteine or histidine residues, however, diversity occurs in the sequence and length of the zinc finger domain. Zinc finger proteins may contain several zinc finger domains of the same or different type. Further variability is encountered in nature by association of zinc finger domains with other domains. For example, some zinc finger proteins are found in association with ring finger or coil-coil domains, to form a so-called tripartite domain. There are several types of zinc fingers, such as C2H2, C2HC, C2C2. C2H2 is known as the classical zinc finger domain. There are typically two criteria used to classify zinc finger proteins, the first being the type of zinc finger and the second being the number of zinc fingers present in the protein. Zinc finger proteins having a single C2H2 domain have been characterised, for example Superman from *Arabidopsis* and Ramosa I from maize. A well-characterised zinc finger protein having three C2H2 domains is the Indeterminate 1 protein from Maize. Although the first report of this gene (Colasanti et al., Cell. 1998 May 15;93(4):593-603) only mentions the presence of two zinc finger domains, a more sophisticated analysis, using pFAM domain search, revealed the presence of three C2H2 zinc finger domains. Also known are zinc-finger proteins having only two C2H2 domains, for example ZAT10 (STZ) and SCOF-1. This subset of plant zinc finger proteins having two C2H2 domains have been implicated in plant responses to various stresses (Sakamoto *et al.*, Gene 248 (1-2) 23-32 (2000)). Both STZ and SCOF-1 have been used to enhance abiotic stress tolerance. When over-expressed, STZ has been reported to increase salt tolerance in yeast (Lippuner *et al.*, J Biol Chem. 271 (22) 12859-12866 (1996)) and over-expression of the SCOF-1 gene under control of the CaMV 35 S promoter has been reported to enhance cold tolerance in *Arabidopsis thaliana* (Kim *et al.*, Plant J. 25 (3) 247-259 (2001)). Reports of plants having modified expression of a zinc finger encoding gene (whether the zinc finger gene is mutated, over-expressed or otherwise) describe plants having abnormal growth characteristics, none of which (with the exception of cold stress tolerance in transgenic plants expressing SCOF-1) are desirable for crops or describe effects that are only detectable under particular stress conditions.

It has now been found that modifying expression in a plant of a 2xC2H2 zinc finger gene and/or modifying the level and/or activity in a plant of a 2xC2H2 zinc finger protein gives plants having modified growth characteristics. In particular it has been found that introduction into a plant of a 2xC2H2 zinc finger nucleic acid gives plants modified growth characteristics, such as increased yield, modified leaf architecture and altered cycle time, each relative to wild type plants.

Therefore according to one embodiment of the present invention there is provided a method for modifying the growth characteristics of a plant, comprising modifying expression in a plant of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or modifying level and/or activity in a plant of a 2xC2H2 zinc finger protein.

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The term "modifying" as used herein is taken to mean enhancing, decreasing and/or changing in place and/or time. Modifying expression of a nucleic acid encoding a 2xC2H2 zinc finger protein or modifying the level and/or activity of the 2xC2H2 zinc finger protein itself encompasses altered expression of a gene and/or altered level and/or activity of a gene product, namely a polypeptide, in specific cells or tissues, when compared to expression, level and/or activity of a 2xC2H2 zinc finger gene or protein in corresponding wild-type plants. The modified gene expression may result from modified expression of an endogenous 2xC2H2 zinc finger gene and/or may result from modified expression of a 2xC2H2 zinc finger gene previously introduced into a plant. Similarly, modified levels and/or activity of a 2xC2H2 zinc finger protein may be due to modified expression of an endogenous 2xC2H2 zinc finger nucleic acid/gene and/or due to modified expression of a 2xC2H2 zinc finger nucleic acid/gene previously introduced into a plant. Modified expression of a gene/nucleic acid and/or modified level and/or activity of a gene product/protein may be effected, for example, by chemical means and/or recombinant means.

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Therefore there is provided by the present invention, a method for modifying the growth characteristics of a plant, comprising modifying expression, level and/or activity of a 2xC2H2 zinc finger gene or protein by recombinant means and/or by chemical means.

Advantageously, modifying expression of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or modifying level and/or activity of the 2xC2H2 zinc finger protein itself may be effected by chemical means, i.e. by exogenous application of one or more compounds or elements capable of modifying activity of the 2xC2H2 zinc finger protein and/or capable of modifying expression of a 2xC2H2 zinc finger gene (which may be either an endogenous gene or a transgene introduced into a plant). The term "exogenous application" as defined herein is taken to mean the contacting or administering of a suitable compound or element to a plant. The compound or element may be exogenously applied to a plant in a form suitable for plant uptake (such as through application to the soil for uptake via the roots, or in the case of some plants by applying directly to the leaves, for example by spraying). The exogenous application may take place on wild-type plants or on transgenic plants that have previously been transformed with a 2xC2H2 zinc finger nucleic acid/gene or other transgene.

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Suitable compounds or elements for exogenous application include 2xC2H2 zinc finger proteins or 2xC2H2 zinc finger nucleic acids. Alternatively, exogenous application of compounds or elements capable of modifying levels of factors that directly or indirectly activate or inactivate a 2xC2H2 zinc finger protein will also be suitable in practising the invention. Also
5 included are antibodies that can recognise or mimic the function of 2xC2H2 zinc finger proteins. Such antibodies may comprise "plantibodies", single chain antibodies, IgG antibodies and heavy chain camel antibodies, as well as fragments thereof.

Additionally or alternatively, the resultant effect may also be achieved by the exogenous
10 application of an interacting protein or activator or an inhibitor of a 2xC2H2 zinc finger gene/gene product. Additionally or alternatively, the compound or element may be a mutagenic substance, such as a chemical selected from any one or more of: N-nitroso-N-ethylurea, ethylene imine, ethyl methanesulphonate and diethyl sulphate. Mutagenesis may also be achieved by exposure to ionising radiation, such as X-rays or gamma-rays or ultraviolet light.
15 Methods for introducing mutations and for testing the effect of mutations (such as by monitoring gene expression and/or protein activity) are well known in the art.

Additionally or alternatively, and according to a preferred embodiment of the present invention, modifying expression of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or modifying
20 level and/or activity of the 2xC2H2 zinc finger protein may be effected by recombinant means. Such recombinant means may comprise a direct and/or indirect approach for modifying expression of a nucleic acid and/or level and/or activity of a protein.

For example, an indirect approach may comprise introducing, into a plant, a nucleic acid
25 capable of modifying expression of the gene in question (a gene encoding a 2xC2H2 zinc finger protein) and or capable of modifying the level and/or activity of the protein in question (a 2xC2H2 zinc finger protein). Examples of such nucleic acids to be introduced into a plant include nucleic acids encoding transcription factors or activators or inhibitors that bind to the promoter of a 2xC2H2 zinc finger gene or that interact with a 2xC2H2 zinc finger protein.
30 Methods to test these types of interactions and methods for isolating nucleic acids encoding such interactors include yeast one-hybrid or yeast two-hybrid screens in which the 2xC2H2 zinc finger gene/protein is used as bait. One example of such a transcription regulator is LOS2, described as a transcription regulator for the STZ gene. Therefore, the method of the invention may also be performed using LOS2, wherein expression of a 2xC2H2 zinc finger gene may be
35 increased or further increased by decreasing expression of LOS2 in plants.

Also encompassed by an indirect approach for modifying expression of a 2xC2H2 zinc finger gene and/or for modifying level and/or activity of a 2xC2H2 zinc finger protein is the provision of, or the inhibition or stimulation of regulatory sequences that drive expression of a native 2xC2H2 zinc finger gene or transgene. Such regulatory sequences may be introduced into a
5 plant. For example, the regulatory sequence to be introduced into a plant may be a promoter capable of driving expression of an endogenous 2xC2H2 zinc finger gene.

A further indirect approach for modifying expression of a 2xC2H2 zinc finger gene and/or for modifying level and/or activity of a 2xC2H2 zinc finger protein in a plant encompasses
10 modifying levels in a plant of a factor capable of interacting with a zinc finger protein. Such factors may include ligands of a 2xC2H2 zinc finger protein. Therefore, the present invention also provides a method for modifying growth characteristics of a plant, comprising modifying expression of a gene coding for a protein which is a natural ligand of a 2xC2H2 zinc finger protein. Furthermore, the present invention also provides a method for modifying growth
15 characteristics of a plant, comprising modifying expression of a gene coding for a protein which is a natural target/substrate of a 2xC2H2 zinc finger protein. Examples of such targets/substrates include stretches of DNA that are bound by the zinc-finger domains.

A direct and preferred approach on the other hand comprises introducing into a plant a nucleic
20 acid encoding a 2xC2H2 zinc finger protein or a portion thereof or sequences capable of hybridising therewith, which nucleic acid preferably encodes a 2xC2H2 zinc finger protein or a homologue, derivative or active fragment thereof. The nucleic acid may be introduced into a plant by, for example, transformation.

25 Therefore, there is provided a method for modifying growth characteristics of a plant, comprising introducing into a plant a 2xC2H2 zinc finger nucleic acid or a portion thereof.

The 2xC2H2 zinc finger nucleic acid may be derived (either directly or indirectly (if subsequently modified)) from any source provided that the sequence, when expressed in a
30 plant, leads to modified expression of a 2xC2H2 zinc finger-encoding nucleic acid/gene and/or modified level and/or activity of a 2xC2H2 zinc finger protein. The 2xC2H2 zinc finger gene or protein may be wild type, i.e. the native or endogenous nucleic acid or polypeptide. Alternatively, it may be a protein or nucleic acid derived from the same or another species. The nucleic acid/gene may then be introduced into a plant as a transgene, for example by
35 transformation.

The nucleic acid may be isolated from a bacteria, yeast or fungi, or from a plant, algae, insect or animal (including human) source. This nucleic acid may be substantially modified from its native form in composition and/or genomic environment through deliberate human manipulation. The nucleic acid is preferably obtained from a plant, whether from the same plant species in which it is to be introduced or whether from a different plant species. Further preferably, the nucleic acid is from a dicot, preferably from the family *Brassicaceae*, further preferably from *Arabidopsis thaliana*. More preferably, the nucleic acid is essentially similar to a nucleic acid as represented by SEQ ID NO 1, or a portion of SEQ ID NO 1, or a nucleic acid capable of hybridising therewith or is a nucleic acid encoding an amino acid sequence essentially similar to an amino acid as represented by SEQ ID NO 2, or a homologue, derivative or active fragment thereof.

Advantageously, the methods according to the invention may also be practised using variant 2xC2H2 zinc finger nucleic acids and variant 2xC2H2 zinc finger amino acids, preferably wherein the variant nucleic acids are variants of SEQ ID NO 1 and wherein the variant amino acids are variants of SEQ ID NO 2. Examples of variant sequences suitable in performing the methods of the invention include:

- (i) Functional portions of a 2xC2H2 zinc finger nucleic acid/gene;
- (ii) Sequences capable of hybridising with a 2xC2H2 zinc finger nucleic acid/gene;
- (iii) Alternative splice variants of a 2xC2H2 zinc finger nucleic acid/gene;
- (iv) Allelic variants of a 2xC2H2 zinc finger nucleic acid/gene;
- (v) Homologues, derivatives and active fragments of a 2xC2H2 zinc finger protein.

The abovementioned variants may also be described as being "essentially similar" to a 2xC2H2 zinc finger nucleic acid/gene, particularly to the 2xC2H2 zinc finger encoding nucleic acid of SEQ ID NO 1, or essentially similar to a 2xC2H2 zinc finger amino acid/protein, particularly that of SEQ ID NO 2. The term "essentially similar to" also includes variants of SEQ ID NO 1 in the form of a complement, DNA, RNA, cDNA or genomic DNA. The variant nucleic acid encoding a 2xC2H2 zinc finger protein or the variant of a 2xC2H2 zinc finger protein may be synthesized in whole or in part, it may be a double-stranded nucleic acid or a single-stranded nucleic acid. Also, the term encompasses a variant due to the degeneracy of the genetic code; a family member of the gene or protein; and variants that are interrupted by one or more intervening sequences.

An example of a variant 2xC2H2 zinc finger nucleic acid is a functional portion of a 2xC2H2 zinc-finger gene. Advantageously, the method according to the present invention may also be practised using portions of a DNA or nucleic acid encoding a 2xC2H2 zinc finger protein. A

functional portion refers to a piece of DNA derived or prepared from an original (larger) DNA molecule, which DNA portion, when expressed in a plant, gives plants having modified growth characteristics. The portion may comprise many genes, with or without additional control elements or may contain spacer sequences. The portion may be made by making one or more deletions and/or truncations to the nucleic acid. Techniques for introducing truncations and deletions into a nucleic acid are well known in the art. Portions suitable for use in the methods according to the invention may readily be determined by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the portion to be tested for functionality.

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An example of a further variant 2xC2H2 zinc finger nucleic acid is a sequence that is capable of hybridising to a 2xC2H2 zinc finger nucleic acid, for example to any of SEQ ID NO 1, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 41, 43, 45, 47 or 49. Advantageously, the methods according to the present invention may also be practised using these variants.

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Hybridising sequences suitable for use in the methods according to the invention may readily be determined for example by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the hybridising sequence.

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The term "hybridisation" as defined herein is a process wherein substantially homologous complementary nucleotide sequences anneal to each other. The hybridisation process can occur entirely in solution, i.e. both complementary nucleic acids are in solution. Tools in molecular biology relying on such a process include the polymerase chain reaction (PCR; and all methods based thereon), subtractive hybridisation, random primer extension, nuclease S1 mapping, primer extension, reverse transcription, cDNA synthesis, differential display of RNAs, and DNA sequence determination. 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. Tools in molecular biology relying on such a process include the isolation of poly (A+) mRNA. 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 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). Tools in molecular biology relying on such a process include RNA and DNA gel blot analysis, colony hybridisation, plaque hybridisation, *in situ* hybridisation and microarray hybridisation. 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. The stringency of hybridisation is influenced by conditions such as temperature, salt concentration and hybridisation buffer

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composition. High stringency conditions for hybridisation include high temperature and/or low salt concentration (salts include NaCl and Na₃-citrate) and/or the inclusion of formamide in the hybridisation buffer and/or lowering the concentration of compounds such as SDS (detergent) in the hybridisation buffer and/or exclusion of compounds such as dextran sulphate or polyethylene glycol (promoting molecular crowding) from the hybridisation buffer. Conventional hybridisation conditions are described in, for example, Sambrook (2001) *Molecular Cloning: a laboratory manual*, 3rd Edition Cold Spring Harbor Laboratory Press, CSH, New York, but the skilled craftsman will appreciate that numerous different hybridisation conditions may be designed in function of the known or the expected homology and/or length of the nucleic acid sequence. Sufficiently low stringency hybridisation conditions are particularly preferred (at least in the first instance) to isolate nucleic acids heterologous to the DNA sequences of the invention defined supra. An example of low stringency conditions is 4-6x SSC / 0.1-0.5% w/v SDS at 37-45°C for 2-3 hours. Depending on the source and concentration of the nucleic acid involved in the hybridisation, alternative conditions of stringency may be employed, such as medium stringency conditions. Examples of medium stringency conditions include 1-4x SSC / 0.25% w/v SDS at ≥ 45°C for 2-3 hours. An example of high stringency conditions includes 0.1 to 2x SSC / 0.1% w/v SDS at 60°C for 1-3 hours. The skilled man will be aware of various parameters which may be altered during hybridisation and washing and which will either maintain or change the stringency conditions. The stringency conditions may start low and be progressively increased until there is provided a hybridising nucleic acid, as defined hereinabove. Elements contributing to heterology include allelism, degeneration of the genetic code and differences in preferred codon usage.

Another variant 2xC2H2 zinc finger nucleic acid useful in practising the methods according to the present invention is an alternative splice variant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein. The term "alternative splice variant" as used herein encompasses variants of a nucleic acid sequence in which selected introns and/or exons have been excised, replaced or added. Such splice variants may be found in nature or may be manmade. Methods for making such splice variants are well known in the art. Splice variants suitable for use in the methods according to the invention may readily be determined for example by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the splice variant.

Another variant 2xC2H2 zinc finger nucleic acid useful in practising the methods according to the present invention is an allelic variant of a nucleic acid encoding a 2xC2H2 zinc finger protein. Allelic variants exist in nature and encompassed within the methods of the present invention is the use of these natural alleles. Allelic variants also 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. Allelic variants suitable for use in the methods according to the invention may readily be determined for example by following the methods described in the Examples section by simply substituting the sequence used in the actual Example with the allelic variant.

The present invention provides a method for modifying plant growth characteristics, comprising modifying expression in a plant of an alternative splice variant or expression in a plant of an allelic variant of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or by modifying level and/or activity in a plant of a 2xC2H2 zinc finger protein encoded by the alternative splice variant or allelic variant.

Examples of variant 2xC2H2 zinc finger proteins useful in practicing the methods of the present invention are homologues, derivatives or functional fragments of a 2xC2H2 zinc finger protein.

"Homologues" of a 2xC2H2 zinc finger 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. To produce such homologues, amino acids of the protein may be replaced by other amino acids having similar properties (such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break α -helical structures or β -sheet structures). Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company). The homologues useful in the method according to the invention have at least in increasing order of preference 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 52%, 54%, 56%, 58%, 60%, 62%, 64%, 66%, 68%, 70%, 72%, 74%, 76%, 78%, 80%, 82%, 84%, 86%, 88%, 90%, 92%, 94%, 96%, 98% sequence identity or similarity to an unmodified protein.

The percentage of identity may be calculated by using an alignment program well known in the art. For example, the percentage of identity may be calculated using the program GAP, or needle (EMBOSS package) or stretcher (EMBOSS package) or the program align X, as a module of the vector NTI suite 5.5 software package, using the standard parameters (for example GAP penalty 5, GAP opening penalty 15, GAP extension penalty 6.6).

According to another embodiment of the present invention, the nucleic acid sequence useful in the methods of the present invention is a nucleic acid encoding a protein homologous to SEQ ID NO 2.

5 Methods for the search and identification of 2xC2H2 zinc finger protein homologues, for example STZ zinc finger homologues, would be well within the realm of a person skilled in the art. Such methods, involve screening sequence databases with the sequences provided by the present invention, for example SEQ ID NO 2 (or SEQ ID NO 1), preferably in a computer readable format. This sequence information may be available in public databases, that include but are not limited
10 to Genbank, the European Molecular Biology Laboratory Nucleic acid Database (EMBL) or versions thereof or the MIPS database. Different search algorithms and software for the alignment and comparison of sequences are well known in the art. Such methods include GAP, BESTFIT, BLAST, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453, 1970) to find the alignment of two complete sequences that maximises
15 the number of matches and minimises the number of gaps. The BLAST algorithm calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The suite of programs referred to as BLAST programs has 5 different implementations: three designed for nucleotide sequence queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, Trends in Biotechnology: 76-80, 1994; Birren et al., GenomeAnalysis, 1: 543, 1997). The
20 software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information.

Default blast parameters to find useful homologues of any of SEQ ID NO 1, SEQ ID NO 2 or any
25 of SEQ ID NO 10 to SEQ ID NO 50, are, when comparing nucleotide sequence G (Cost to open a gap) 5, E (Cost to extend a gap default) 2, q (Penalty for a mismatch) -3, r (Reward for a match) 1, e (Expectation value (E)) 10.0, W (Word size) 11, V (Number of one-line descriptions) 100 and B (Number of alignments to show) 100. When comparing protein sequences, the default parameters are preferably G 11, E 1, e value 10.0, W 3, V 100 and B 100.

30 The above-mentioned analyses for comparing sequences, for the calculation of sequence identity and for the search for homologues, is preferentially done with full-length sequences or within a conserved region of the sequence. Therefore, these analyses may be based on a comparison of certain regions such as conserved domains, motifs or boxes.

The identification of such domains or motifs for examples the motif and boxes as represented by SEQ ID NO 5, 6, 7, 8 and 9, would also be well within the realm of a person skilled in the art and involves for example, a computer readable format of proteins of the present invention, the use of alignment software programs and the use of publicly available information on protein domains, conserved motifs and boxes. This protein domain information is available in the PRODOM, PIR or pFAM database. For the identification of Zinc finger domains, such as the 2xC2H2 zinc finger domain, pFAM is preferred. Sequence analysis programs designed for motif searching may be used for identification of fragments, regions and conserved domains as mentioned above. Preferred computer programs would include but are not limited to MEME, SIGNALSCAN, and GENESCAN. A MEME algorithm (Version 3.0) may be found in the GCG package;

At present, zinc finger motifs are subdivided in more than 40 different classes as can be found in the Pfam database of protein families present at the Sanger institute.

The C2H2 zinc finger (Zf-C2H2) motif is the classical zinc finger domain. It was first recognized in the transcription factor IIIA (TFIIIA) of *Xenopus* (Miller et al. 1985). The domain is typically 25 to 30 amino-acid residues in length. The following pattern describes the zinc finger *X-C-X(1-5)-C-X3-*X5-*X2-H-X(3-6)-[H/C] where X can be any amino acid, and numbers in brackets indicate the number of residues. The positions marked * are those that are important for the stable folding of the zinc finger. The final position can be either his or cys, while still being a C2H2 zinc finger domain. In view of recent publications on the design of zinc finger domains it becomes feasible also to replace one or more of the Cys or His amino acids, whilst still retaining the original functionality of the C2H2 domain. The residues separating the second Cys and the first His are mainly polar and basic. The canonical C2H2 zinc finger is composed of two short beta strands followed by an alpha helix. DNA binding of the zinc finger motif is mediated by amino terminal part of the alpha helix which binds the major groove in DNA binding zinc fingers. C2H2 domains have been shown to interact with RNA, DNA and proteins. The tetracoordination of a Zinc ion by the conserved cysteine and histidine residues determines the conserved tertiary structure of the motif. Conserved hydrophobic residues are commonly found at positions -2 and also at 4 amino acids after the second cysteine (that participates in zinc binding) and at position three before the first histidine (that participates in zinc binding). In

plant multi zinc finger proteins, spacing between the C2H2 domains is generally about 15 to about 65 amino acids.

Thus, plant zinc finger proteins are characterized by long spacers of diverse lengths between adjacent fingers. Moreover, they are characterised by a highly conserved sequence of six amino acids, located within a putative DNA-contacting surface of each finger. Two forms of such conserved sequence are most commonly found in plant C2H2 zinc fingers, the QALGGH (SEQ ID NO 5) and the NNM/WQMH (SEQ ID NO 6). Despite the high sequence conservation of the QALGGH, some variants or the so-called 'modified type' occur in nature where one or two amino acids can have a different form, most typically the +1 "Q" can be a "G", "K" or "R" (these amino acids share the same turn-like characteristic), the +2 "A" can be "S" (both of which share the characteristic of being small amino acids) or the +3 "L" can be "F" (these two amino acids are both hydrophobic). The QALGGH-motif as used herein comprises all these variants. In the NNM/WQMH motif at position 3 there is mostly an "M" or a "W".

Therefore, the present invention provides a method as described hereinabove, wherein said 2xC2H2 zinc finger protein comprises a QALGGH motif. Further, the present invention provides as described hereinabove, wherein said 2xC2H2 zinc finger protein comprises a NNM/WQMH motif.

According to one embodiment of the invention, both C2H2 domains are of the same type. More preferably, both C2H2 zinc finger domains have the same conserved GALGGH or NNM/WQMH motif. According to another embodiment, each C2H2 zinc finger domain has a different conserved motif.

According to one embodiment, the 2xC2H2 protein useful in the methods of the present invention is characterized by an EAR motif, which is an ERF-Associated amphiphilic repression motif. This motif has been recognized in two unrelated types of transcription factors, namely the ERF transcription factors of the AP2 type and in the zinc finger transcription factors. In the latter class, the EAR motif is generally located at the C-terminus of the protein. The pattern for the EAR motif has the conserved sequence hDLNh(X)P (SEQ ID NO 7), where "h" is a hydrophobic residue (any one of A,C,F,G,H,I,K,L,M,R,T,V,W,Y) most typically L/F/I and where "X" can be one (any amino acid) or no amino acid. A characteristic feature of the EAR motif is the alternation of hydrophilic and hydrophobic residues with the aspartic acid (D) residue being amphiphilic. Ohta et al. (The plant cell, 2001, 13, p1959-1968), previously characterized EAR motifs present in 2xC2H2 zinc finger proteins.

Therefore, the present invention provides a method as described hereinabove, wherein the 2xC2H2 zinc finger protein comprises an EAR motif. According to one embodiment, the EAR motif is located in the C-terminal region of the protein, preferably between the second zinc finger domain and the C-terminus.

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According to a further embodiment, the zinc finger proteins used in the methods of the present invention have two zinc finger domains and a nuclear localization signal (B-box). A cluster of basic amino acids that resembles the B-box (Basic box) were described by Chua et al. (EMBO 1992- 11, 241-9) and were hypothesized to be a nuclear localization signal for the protein.

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These have been recognized in 2xC2H2 proteins (Sakamoto et al., Gene 248 (2000) 23-32). The cluster is rich in Lysine (K) and Arginine (R) residues. A consensus sequence defining the most frequent form of the B-box in 2xC2H2 genes is KR(S)KRXR (SEQ ID NO 8) where "S" at the 3rd position may be absent or present. However other variants may occur in nature that still retain the characteristic of being a charged region rich in basic amino acids. The location of the basic box is most frequently at the N-terminus of the protein, but can also occur in other locations. It has been speculated that due to its basic nature the B-box could also participate in DNA binding.

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Accordingly, the present invention provides a method as described hereinabove, wherein the 2xC2H2 zinc finger protein further comprises a B-box. According to one embodiment the B-box is located in the N-terminal region of the zinc finger protein. Preferably the proteins useful in the methods of the present invention have a B-box located between the N-terminus and the first zinc finger domain.

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According to a further embodiment, the zinc finger proteins useful in the methods of the present invention have two C2H2 zinc finger domains and an L-box. A conserved motif, named L-box, of yet unknown function has been identified in 2xC2H2 proteins and has been described previously by Sakamoto et al. (Gene 248 (2000) 23-32). The L-box is typically located at the N-terminus, between the B-box and the first C2H2 zinc finger. The L-box is represented by the sequence EXEXXAXCLXXL (SEQ ID NO 9). This region may be involved in protein-protein interactions. Zinc finger proteins lacking the L-box, may for example have serine rich regions at a similar position, which regions are putative sites for protein-protein interactions.

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Therefore, the present invention provides a method as described hereinabove, wherein the 2xC2H2 protein comprises an L-box.

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Particular zinc finger homologues useful in the methods of the present invention have one or more of the conserved motifs as depicted in SEQ ID NO 5, 6, 7, 8 and 9, or motifs that are 80% identical to these motifs or motifs that have conserved substitutions of amino acids. The 2xC2H2 protein as set forth in SEQ ID NO 2 comprises all the boxes as set forth in SEQ ID NO 5, 7, 8 and 9. All its paralogues and orthologues also comprise all of these boxes.

Homologues of a 2xC2H2 protein as presented in SEQ ID NO 2 and isolated from *Arabidopsis thaliana*, that are useful in the constructs and the methods of the present invention are also identified in other plant species.

Two special forms of homologue, orthologues and paralogues, are evolutionary concepts used to describe ancestral relationships of genes. The term "paralogue" relates to a gene-duplication within the genome of a species leading to paralogous genes. The term "orthologue" relates to a homologous gene in different organisms due to ancestral relationship. The term "homologue" as used herein also encompasses paralogues and orthologues of the proteins useful in the methods according to the invention.

Orthologues in other plant species may easily be found by performing a so-called reciprocal blast search. Orthologous genes can be identified by querying one or more gene databases with a query gene or protein of interest (SEQ ID NO 1 or 2), using for example BLAST program. The highest-ranking subject genes that result from the search are then again subjected to a BLAST analysis, and only those subject genes that match again with the query sequence (SEQ ID NO 1 or 2) are retained as true orthologous genes. For example, to find a rice orthologue of an *Arabidopsis thaliana* gene, one may perform a BLASTN or TBLASTX analysis on a rice database such as (but not limited to) the *Oryza sativa Nipponbare* database available at the NCBI website or the genomic sequences of rice (cultivars *indica* or *japonica*). In a next step, the obtained rice sequences are used in a reverse BLAST analysis using an *Arabidopsis* database. The results may be further refined when the resulting sequences are analysed with ClustalW and visualised in a neighbour joining tree. The method can be used to identify orthologues from many different species.

The closest homologues in other species (orthologues of the protein of SEQ ID NO 2), include those from a variety of dicot and monocot plants, for example from *Datisca glomerata* (AF119050_1, AAD26942, SEQ ID NO 10 and 11), from soybean (T09602, SCOF-1, SEQ ID NO 12 and 13), *Medicago sativa* (CAB77055.1, SEQ ID NO 14 and 15), from tobacco (T01985, SEQ ID NO 16 and 17) from rice, (AF332876_1, AAK01713.1, SEQ ID NO 18 and 19), from petunia (BAA05079.1, SEQ ID NO 20 and 21), from wheat (S39045 and BAA03901,

WZF1, SEQ ID NO 22 and 23), from *Capsicum annum* (SEQ ID NO 24 and 25), from turnip (T14408, T14409) and from sugarcane (CA279020).

Close homologues of the same species (paralogues of the protein of SEQ ID NO 2 from
5 *Arabidopsis thaliana*) are described below.

The MIPS database contains the sequence of the *Arabidopsis thaliana* genome with prediction and functional annotation of the proteins encoded. Searching this database with the STZ gene of SEQ ID NO 1 (MIPS accession number At1g27730), showed that in the *Arabidopsis* genome there are 2 genes encoding very close homologues of SEQ ID NO 2, At5g43170
10 (NM_123683, SEQ ID NO 32 and 33) and At5g04340 (NM_120516 SEQ ID NO 28 and 29), and 3 others with high similarity: At3g19580 (NM_112848, SEQ ID NO 26 and 27), At5g67450 (NM_126145, SEQ ID NO 34 and 35) and At3g49930 (NM_114853, SEQ ID NO 30-31). These genes are spread over 3 chromosomes, 1, 3 and 5. Similarly, a number of paralogues of the orthologue in *Petunia* have been isolated and sequenced. Advantageously, paralogues from
15 the same species may be used in the methods of the present invention.

Furthermore, a number of family members of the STZ protein of SEQ ID NO 2 have been found in *Arabidopsis*. The STZ gene and protein of SEQ ID NO 1 and 2 have been previously published in the database under the MIPS accession number At1g27730 or in Genbank under
20 the accession numbers NP_174094.1, X95573 or CAA64820. Additionally, several other cDNA's, isolated from other tissues or at different developmental stages of *Arabidopsis* have been reported and encode the same protein as that of SEQ ID NO 2. Such sequences sequences deposited under the Genbank accession number AY034998, NM_102538, AC12375, X95573, AY063006, X98671, X98670, or AF250336. These isolates illustrate the
25 differential expression of the STZ gene in different plant tissues at different developmental stages. The differential regulation of these different cDNA's is reflected by the differences at their 5'UTR and the 3'UTR regions, while the encoded protein remains the same. Advantageously, the members of the same gene family as SEQ ID NO 1 or the members of the same family of any of the orthologues of SEQ ID NO 1, may be used in the methods of the
30 present invention.

Other close homologues useful in the methods of the present invention are the sequences as deposited in the public database under the following accession numbers, which sequences are herein incorporated by reference: homologues isolated from *Petunia*: BAA21923.1,
35 BAA21922.1, BAA21926.1, BAA21925.1, BAA19110.1, BAA19926.1, BAA21924.1, BAA19111.1, BAA21921.1, BAA19114.1, BAA05076.1, BAA05079.1, CAA43111.1, BAA21920.1, BAA21919.1, BAA05077.1, BAA05078.1, BAA20137.1; homologues isolated

from *Arabidopsis*: CAA67229.1, BAC43454.1, NP_196054.1, AAM67193.1, NP_199131.1, NP_188592.1, NP_201546.1, NP_190562.1, NP_182037.1, BAC43008.1, Q8VWG3, CAC86393.1, CAC86168.1, CAC86167.1, CAC86166.1, CAB67667.1, CAC01747.1, CAB90936.1, CAB90935.1, CAB80245.1, CAB41188.1, CAA18741.1, CAA67234.1, CAA67236.1, CAA67231.1, CAA67230.1, CAA67228.1, CAA67235.1, CAA67233.1, CAA67232.1, CAA67229.1, CAA64820.1 and homologues isolated from rice: BAB16855.1, AAO06972.1, CAC09475.1, BAB63718.1, P0683F02.21, BAB67885.1, P0031D11.19, BAB64114.1, AAK01713.1, AF332876_1, AAL76091.1, BAB67879.1, P0031D11.12 and BAC15513.1.

A phylogenetic tree may be constructed with all the homologues, paralogues and orthologues are defined herein above. Multiple alignment may be made using clustal W present in the VNTi (version 5.0) program with for example Gap opening penalty 10 and Gap extension 5. For making a phylogenetic tree the Phylic software package may be used. Sequences clustering around SEQ ID NO 1 or SEQ ID NO 2, identify genes or proteins suitable for use in the methods of the present invention.

The sequence of SEQ ID NO 2 and its rice orthologue AF332876 (SEQ ID NO 19) have 36% sequence identity when using the program Needle with the parameters Gap penalty 5 and Gap extension penalty 6. Therefore, homologues particularly useful in the methods of the present invention are homologues having 36% or more sequence identity with the 2xC2H2 zinc finger protein as presented in SEQ ID NO 2 or having 36% or more sequence identity to the closest orthologue of SEQ ID NO 2 from another species.

Preferred homologues useful in practicing the methods of the present invention are plant homologues, i.e. proteins obtained from a plant nucleic acid. More preferably, the nucleic acid sequence is from a dicot, more preferably from the family *Brassicaceae*, further preferably from *Arabidopsis thaliana*.

Preferably the 2xC2H2 zinc finger protein useful in the methods of the present invention belongs to the same gene family as the salt tolerant zinc finger protein (STZ) of *Arabidopsis thaliana*, or is a homologue thereof. The name ZAT10 can also be used to identify the STZ zinc finger protein of *Arabidopsis thaliana*.

Another variant of a zinc finger protein useful in the methods of the present invention is a substitutional variant. The term "Substitutional variants" of a protein refers to those variants in

which at least one residue in an amino acid sequence has been removed and a different residue inserted in its place. 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 1-10 amino acid residues, and deletions will range from about
5 1-20 residues. Preferably, amino acid substitutions comprise conservative amino acid substitutions. Particular substitutional variants of the C2H2 zinc finger protein are substitutional variants in which one or more of the conserved Cys and/or His residues is replaced, whilst retaining the same zinc finger functionality. To retain the same functionality, the residues around these conserved Cys or His residues may also be substituted.

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"Insertional variants" of a protein are those in which one or more amino acid residues are introduced into a predetermined site in said protein. Insertions can comprise amino-terminal and/or carboxy-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 amino- or
15 carboxy-terminal fusions, of the order of about 1 to 10 residues. Examples of amino- or carboxy-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
20 peptide), HA epitope, protein C epitope and VSV epitope.

"Deletion variants" of a protein are characterised by the removal of one or more amino acids from the protein. Amino acid variants of a protein may readily be made using peptide synthetic techniques well known in the art, such as solid phase peptide synthesis and the like, or by
25 recombinant DNA manipulations. 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-
30 mediated site-directed mutagenesis or other site-directed mutagenesis protocols.

The term "derivatives" refers to peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise substitutions, deletions or additions of naturally and non-naturally occurring amino acid residues compared to the amino acid sequence of a naturally-occurring
35 form of the 2xC2H2 protein such as for example the 2xC2H2 zinc finger protein as presented in SEQ ID NO 2. "Derivatives" of a 2xC2H2 zinc finger protein encompass peptides, oligopeptides, polypeptides, proteins and enzymes which may comprise naturally occurring

altered, glycosylated, acylated or non-naturally occurring 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 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, for example, 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.

Another variant of a 2xC2H2 zinc finger protein useful in the methods of the present invention is an active fragment of a zinc finger protein. "Active fragments" of a 2xC2H2 zinc finger protein encompasses at least five contiguous amino acid residues of a protein, which residues retain similar biological and/or functional activity to the naturally occurring protein. For example, useful fragments comprise at least 10 contiguous amino acid residues of a 2xC2H2 zinc finger protein. Other preferred fragments are fragments of a 2xC2H2 zinc finger protein starting at the second or third or further internal methionin residues. These fragments originate from protein translation, starting at internal ATG codons. Functional fragments of a 2xC2H2 zinc finger protein useful in practising the methods of the present invention may have one, two or no C2H2 domains, without affecting its functionality in the methods of the present invention.

According to a preferred feature of the present invention, enhanced or increased expression of a nucleic acid encoding a 2xC2H2 zinc finger protein is envisaged. Methods for obtaining enhanced or increased expression of genes or gene products are well documented in the art and include, for example, over-expression driven by a strong promoter, the use of transcription enhancers or translation enhancers. The term over-expression as used herein means any form of expression that is additional to the original wild-type expression level. Preferably the nucleic acid to be introduced into the plant and/or the nucleic acid that is to be overexpressed in the plant is in the sense direction with respect to the promoter to which it is operably linked. Preferably, the nucleic acid sequence represented by SED ID NO 1 is over-expressed in a plant. However, it should be clear that the applicability of the invention is not limited to use of the nucleic acid represented by SEQ ID NO 1 nor to the nucleic acid sequence encoding the amino acid sequence of SEQ ID NO 2, but that other nucleic acid sequences encoding homologues, derivatives or active fragments of SED ID NO 1 or SED ID NO 2 may be useful in the methods of the present invention. Examples of nucleic acids or proteins are provided in SEQ ID NO 10 to SEQ ID NO 50.

Alternatively and/or additionally, increased expression of a 2xC2H2 encoding gene or increased level and/or activity of a 2xC2H2 protein in a plant cell, is achieved by mutagenesis.

For example these mutations may be responsible for altered control of the 2xC2H2 gene, resulting in more expression of the gene, relative to the wild-type gene. Mutations can also cause conformational changes in a protein, resulting in more activity and/or higher levels of the 2xC2H2 protein.

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Modifying gene expression (whether by a direct or indirect approach) encompasses altered transcript levels of a gene. Altered transcript levels may be sufficient to induce certain phenotypic effects, for example via the mechanism of cosuppression. Here the overall effect of introduction of a transgene is that there is less activity in the cell of the protein encoded by a native gene having homology to the introduced transgene. Therefore, according to another embodiment of the present invention, there is provided a method for modifying growth characteristics in a plant, comprising decreasing expression of a gene encoding a 2xC2H2 zinc finger protein or decreasing level and/or activity of a 2xC2H2 zinc finger protein. Examples of decreasing expression, level and/or activity of a protein in a cell are well documented in the art and include, for example, downregulation of expression by anti-sense techniques, RNAi techniques, small interference RNAs (siRNAs) and microRNA (miRNA) .

Another method for downregulation of gene expression or gene silencing comprises use of ribozymes, for example as described in Atkins et al. 1994 (WO 94/00012), Lenée et al. 1995 (WO 95/03404), Lutziger et al. 2000 (WO 00/00619), Prinsen et al. 1997 (WO 97/3865) and Scott et al. 1997 (WO 97/38116).

Gene silencing may also be achieved by insertion mutagenesis (for example, T-DNA insertion or transposon insertion) or by gene silencing strategies as described by, among others, Angell and Baulcombe 1998 (WO 98/36083), Lowe et al. 1989 (WO 98/53083), Lederer et al. 1999 (WO 99/15682) or Wang et al. 1999 (WO 99/53050).

Expression of an endogenous gene may also be reduced if it contains a mutation. Such a mutation or such a mutant gene may be isolated and introduced into the same or different plant species in order to obtain plants having modified growth characteristics. Examples of such mutants are dominant negative mutants of a 2xC2H2 zinc finger gene.

Genetic constructs aimed at silencing gene expression may comprise the 2xC2H2 zinc finger nucleic acid, for example as represented by SEQ ID NO 1 (or one or more portions thereof or a sequence capable of hybridising therewith), in a sense and/or antisense orientation relative to the promoter sequence. The sense or antisense copies of at least part of the endogenous gene in the form of direct or inverted repeats may also be utilised in the methods according to

the invention. The growth characteristics of plants may also be modified by introducing into a plant at least part of an antisense version of the nucleotide sequence represented by SEQ ID NO 1.

5 According to a further embodiment of the present invention, genetic constructs and vectors to facilitate introduction and/or to facilitate expression of the 2xC2H2 zinc finger nucleotide sequences useful in the methods according to the invention are provided. Therefore, according to the present invention, there is provided a construct comprising:

- 10 (i) a nucleic acid capable of modifying expression of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or modifying level and/or activity of a 2xC2H2 zinc finger protein;
- (ii) one or more control sequence capable of driving expression of the nucleic acid sequence of (i); and optionally
- 15 (iii) a transcription termination sequence.

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 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.
20 Preferably the genetic construct is a plant expression vector.

The nucleic acid according to (i) is advantageously any of the nucleic acids described hereinbefore. A preferred nucleic acid is the nucleic acid represented by SEQ ID NO 1 or a variant thereof as hereinbefore defined, or is a nucleic acid sequence encoding a sequence
25 represented by SEQ ID NO 2 or a variant as hereinbefore defined. For example such variants encode a protein as presented in any of SEQ ID NO 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 42, 44, 46, 48 and 50.

The terms "regulatory element" and "control sequence" are used herein interchangeably and
30 are to be taken in a broad context to refer to regulatory nucleic acids capable of effecting expression of the sequences to which they are operably linked. Encompassed by the aforementioned terms are promoters. A "promoter" encompasses 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
35 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 which confers, activates or enhances expression of a nucleic acid molecule in a cell, tissue or organ. 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. Preferably, the gene of interest is operably linked to a promoter in a sense direction.

Advantageously, any type of promoter may be used to drive expression of the nucleic acid sequence depending on the desired outcome.

Promoters useful for the present invention are described in EP 03075331.3.

Other examples of preferred promoters are presented in Table I (a) to (c), which promoters or derivatives thereof are useful in the methods and/or in making the constructs of the present invention. Accordingly, genetic constructs comprising of the nucleic acids of (i), for example a 2xC2H2 nucleic acid, and at least part of a promoter from Table I (a) to (c) or from EP 03075331.3, preferably, wherein said parts are operably linked, are also provided by the present invention.

According to another embodiment, the nucleic acid of (i) is operably linked to a constitutive promoter. The term "constitutive" as defined herein refers to a promoter that is expressed substantially continuously. Furthermore, preferably the constitutive promoter is a ubiquitous promoter, which is expressed in more than one, preferably in most or substantially all tissues of the plant. Preferably, the constitutive promoter to be used in the methods of the present invention, or cloned in the genetic constructs of the present invention, is a plant promoter, preferably a constitutive promoter, such as a GOS2 promoter or a promoter with similar strength and/or similar expression pattern. Preferably plant promoters derived from a plant nucleic acid are used. Alternatively, promoters operable in plant, such as promoters derived from plant pathogens are used.

According to another embodiment of the invention, the nucleic acid of (i) is operably linked to a plant promoter, preferably a tissue-preferred promoter. The term "tissue-preferred" as used herein refers to a promoter that is expressed predominantly in at least one tissue or organ. For example, the tissue-preferred promoter is a seed-preferred promoter, such as a pWS18 (Joshee et al. Plant Cell Physiol. 1998 Jan;39(1):64-72.) or a promoter of similar strength and/or similar expression pattern.

Promoters with similar strength and/or similar expression pattern may be found by coupling the promoter to a reporter gene and checking the function of the reporter gene in different tissues of a plant. One suitable reporter gene is beta-glucuronidase and the colorimetric GUS staining to visualize the beta-glucuronidase activity in a plant tissue is well known to a person skilled in the art.

Table I (a): flower preferred promoters useful in the present invention. Sequences of these promoters are described in the cited reference.

Gene	Expression	Reference
AtPRP4	flowers	Fowler et al: Plant Physiol. 1999 Dec;121(4):1081-92
chalcone synthase (chsA)	flowers	Van der Meer, <i>et al.</i> , <i>Plant Mol. Biol.</i> 15, 95-109, 1990.
LAT52	anther	Twiss <i>et al</i> Mol. Gen Genet. 217:240-245 (1989)
<i>apetala-3</i>	flowers	

Table I (b): seed-preferred promoters useful in the present invention. Sequences of these promoters are described in the cited reference.

Gene	Expression	Reference
seed-specific genes	seed	Simon, <i>et al.</i> , <i>Plant Mol. Biol.</i> 5: 191, 1985; Scofield, <i>et al.</i> , <i>J. Biol. Chem.</i> 262: 12202, 1987.; Baszczyński, <i>et al.</i> , <i>Plant Mol. Biol.</i> 14: 633, 1990.
Brazil Nut albumin	seed	Pearson, <i>et al.</i> , <i>Plant Mol. Biol.</i> 18: 235-245, 1992.
legumin	seed	Ellis, <i>et al.</i> , <i>Plant Mol. Biol.</i> 10: 203-214, 1988.
glutelin (rice)	seed	Takaiwa, <i>et al.</i> , <i>Mol. Gen. Genet.</i> 208: 15-22, 1986; Takaiwa, <i>et al.</i> , <i>FEBS Letts.</i> 221: 43-47, 1987.
zein	seed	Matzke <i>et al</i> Plant Mol Biol, 14(3):323-32 1990
napA	seed	Stalberg, <i>et al</i> , <i>Planta</i> 199: 515-519, 1996.

wheat LMW and HMW glutenin-1	endosperm	Mol Gen Genet 216:81-90, 1989; NAR 17:461-2, 1989
wheat SPA	seed	Albani <i>et al</i> , Plant Cell, 9: 171-184, 1997
wheat α , β , γ -gliadins	endosperm	EMBO 3:1409-15, 1984
barley <i>ltr1</i> promoter	endosperm	
barley B1, C, D, hordein	endosperm	Theor Appl Gen 98:1253-62, 1999; Plant J 4:343-55, 1993; Mol Gen Genet 250:750-60, 1996
barley DOF	endosperm	Mena <i>et al</i> , The Plant Journal, 116(1): 53-62, 1998
<i>blz2</i>	endosperm	EP99106056.7
synthetic promoter	endosperm	Vicente-Carbajosa <i>et al</i> , Plant J. 13: 629-640, 1998.
rice prolamin NRP33	endosperm	Wu <i>et al</i> , Plant Cell Physiology 39(8) 885-889, 1998
rice α -globulin Glb-1	endosperm	Wu <i>et al</i> , Plant Cell Physiology 39(8) 885-889, 1998
rice OSH1	embryo	Sato <i>et al</i> , Proc. Natl. Acad. Sci. USA, 93: 8117-8122, 1996
rice α -globulin REB/OHP-1	endosperm	Nakase <i>et al</i> . Plant Mol. Biol. 33: 513-522, 1997
rice ADP-glucose PP	endosperm	Trans Res 6:157-68, 1997
maize ESR gene family	endosperm	Plant J 12:235-46, 1997
sorgum γ -kafirin	endosperm	PMB 32:1029-35, 1996
KNOX	embryo	Postma-Haarsma <i>et al</i> , Plant Mol. Biol. 39:257-71, 1999
rice oleosin	embryo and aleuron	Wu <i>et al</i> , J. Biochem., 123:386, 1998
sunflower oleosin	seed (embryo and dry seed)	Cummins, <i>et al</i> ., Plant Mol. Biol. 19: 873-876, 1992

Table I (c): constitutive promoters useful in the present invention. Sequences of these promoters are described in the cited reference.

Gene	Expression	Reference
Actin	constitutive	McElroy <i>et al</i> , Plant Cell, 2: 163-171, 1990
CAMV 35S	constitutive	Odell <i>et al</i> , Nature, 313: 810-812,

		1985
CaMV 19S	constitutive	Nilsson <i>et al.</i> , <i>Physiol. Plant.</i> 100:456-462, 1997
GOS2	constitutive	de Pater <i>et al.</i> , <i>Plant J</i> Nov;2(6):837-44, 1992
ubiquitin	constitutive	Christensen <i>et al.</i> , <i>Plant Mol. Biol.</i> 18: 675-689, 1992
rice cyclophilin	constitutive	Buchholz <i>et al.</i> , <i>Plant Mol Biol.</i> 25(5): 837-43, 1994
maize H3 histone	constitutive	Lepetit <i>et al.</i> , <i>Mol. Gen. Genet.</i> 231:276-285, 1992
actin 2	constitutive	An <i>et al.</i> , <i>Plant J.</i> 10(1); 107-121, 1996

Optionally, one or more terminator sequences may also be used in the construct introduced into a plant. 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. Additional regulatory elements may include transcriptional as well as translational enhancers. Those skilled in the art will be aware of terminator and enhancer sequences which may be suitable for use in the invention. Such sequences would be known or may readily be obtained by a person skilled in the art.

- 5 The genetic constructs of the invention may further include an origin of replication sequence which 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.

15

The genetic construct may optionally comprise a selectable marker gene. As used herein, the term "selectable marker gene" includes any gene which confers a phenotype on a cell in which it is expressed to facilitate the identification and/or selection of cells which are transfected or transformed with a genetic construct of the invention. Suitable markers may be selected from markers that confer antibiotic or herbicide resistance. Cells containing the recombinant DNA will thus be able to survive in the presence of antibiotic or herbicide concentrations that kill untransformed cells. Examples of selectable marker genes include genes conferring resistance to antibiotics (such as nptII encoding neomycin phosphotransferase capable of phosphorylating neomycin and kanamycin, or hpt encoding hygromycin phosphotransferase

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capable of phosphorylating hygromycin), to herbicides (for example bar which provides resistance to Basta; aroA or gox providing resistance against glyphosate), or genes that provide a metabolic trait (such as manA that allows plants to use mannose as sole carbon source). Visual marker genes result in the formation of colour (for example beta-glucuronidase, GUS), luminescence (such as luciferase) or fluorescence (Green Fluorescent Protein, GFP, and derivatives thereof). Further examples of suitable selectable marker genes include the ampicillin resistance (Ampr), tetracycline resistance gene (Tcr), bacterial kanamycin resistance gene (Kanr), phosphinothricin resistance gene, and the chloramphenicol acetyltransferase (CAT) gene, amongst others

10

The present invention also encompasses plants obtainable by the methods according to the present invention. The present invention therefore provides plants obtainable by the method according to the present invention, which plants have modified growth characteristics, which plants have altered 2xC2H2 zinc finger protein level and/or activity and/or altered expression of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein.

15

Therefore, according to one aspect of the present invention, there is provided a method for the production of plants, having modified growth characteristics, comprising introducing, into a plant, a nucleic acid capable of modifying activity of a 2xC2H2 zinc finger protein and/or capable of modifying expression of a 2xC2H2 zinc-finger gene. According to a further embodiment of the present invention, there is provided a method for the production of transgenic plants having modified growth characteristics, comprising introduction and expression in a plant of a 2xC2H2 nucleic acid.

20

More specifically, the present invention provides a method for the production of transgenic plants having modified growth characteristics, which method comprises:

25

- (i) introducing into a plant or plant cell a 2xC2H2 zinc finger nucleic acid;
- (iii) cultivating the plant cell under conditions promoting plant growth.

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The growth characteristic may be any of the characteristics defined hereinunder.

The 2xC2H2 zinc finger nucleic acid includes all variant nucleic acids as described herein before and includes all nucleic acids encoding all variant proteins as described herein before. Cultivating the plant cell under conditions promoting plant growth, may or may not include regeneration and or growth to maturity.

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

5

The term "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 therefrom. 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 can then be used to regenerate a transformed plant in a manner known to persons skilled in the art.

20 Transformation of a plant species is now a fairly routine technique. Advantageously, any of several transformation methods may be used to introduce the nucleic acid of interest (e.g. the 2xC2H2 nucleic acid) into a suitable ancestor cell. 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., June 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 T.M. et al., 1987, Nature 327, 70) infection with (non-integrative) viruses and the like. A preferred transformation method is an *Agrobacterium* mediated transformation method.

Transgenic rice plants expressing a 2xC2H2 gene are preferably produced via *Agrobacterium*-mediated transformation using any of the well-known methods for rice transformation, such as the ones described in any of the following: published 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. 1996 Jun; 14(6): 745-50) or Frame et al. (Plant Physiol. 2002 May; 129(1): 13-22).

- 5 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.

- 10 Following DNA transfer and regeneration, putatively transformed plants may 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 undertaken using Northern and/or Western analysis, both techniques being well known to persons having ordinary skill in the art.

- 15 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 to give homozygous second generation (or T2) transformants, and the T2 plants further propagated through classical breeding techniques.

- 20 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).

- 25 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
- 30 phenotypic characteristic(s) as those produced in the parent by the methods according to the invention. The invention also includes host cells having modified expression and/or level and/or activity of a 2xC2H2 zinc finger protein. Such host cells for example comprise genetic constructs as mentioned above. Preferred host cells according to the invention are derived from a plant, algae, bacterium, fungus, yeast, insect or animal. The invention also extends to
- 35 harvestable parts of a plant such as but not limited to seeds, leaves, fruits, flowers, petals, stamen, stem cultures, stem, rhizomes, roots, tubers, bulbs or cotton fibers.

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, roots (including tubers), and plant cells, tissues and organs. The term "plant" also encompasses suspension cultures, embryos, meristematic regions, callus tissue, leaves, gametophytes, sporophytes, pollen, and microspores. 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 crop, tree, or shrub 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*, *Baikiaea plurijuga*, *Betula* spp., *Brassica* spp., *Bruguiera gymnorhiza*, *Burkea africana*, *Butea frondosa*, *Cadaba farinosa*, *Calliandra* spp., *Camellia sinensis*, *Canna indica*, *Capsicum* spp., *Cassia* spp., *Centroema pubescens*, *Chaenomeles* spp., *Cinnamomum cassia*, *Coffea arabica*, *Colophospermum mopane*, *Coronilla varia*, *Cotoneaster serotina*, *Crataegus* spp., *Cucumis* spp., *Cupressus* spp., *Cyathea dealbata*, *Cydonia oblonga*, *Cryptomeria japonica*, *Cymbopogon* spp., *Cynthea dealbata*, *Cydonia oblonga*, *Dalbergia monetaria*, *Davallia divaricata*, *Desmodium* spp., *Dicksonia squarosa*, *Diheteropogon amplexans*, *Dioclea* spp., *Dolichos* spp., *Dorycnium rectum*, *Echinochloa pyramidalis*, *Ehrartia* spp., *Eleusine coracana*, *Eragrestis* spp., *Erythrina* spp., *Eucalyptus* spp., *Euclea schimperi*, *Eulalia villosa*, *Fagopyrum* spp., *Feijoa sellowiana*, *Fragaria* spp., *Flemingia* spp., *Freycinetia banksii*, *Geranium thunbergii*, *Ginkgo biloba*, *Glycine javanica*, *Gliricidia* spp., *Gossypium hirsutum*, *Grevillea* spp., *Guibourtia coleosperma*, *Hedysarum* spp., *Hemarthria altissima*, *Heteropogon contortus*, *Hordeum vulgare*, *Hyparrhenia rufa*, *Hypericum erectum*, *Hyperthelia dissoluta*, *Indigo incarnata*, *Iris* spp., *Leptarrhena pyrolifolia*, *Lespedeza* spp., *Lettuca* spp., *Leucaena leucocephala*, *Loudetia simplex*, *Lotonus bainesii*, *Lotus* spp., *Macrotyloma axillare*, *Malus* spp., *Manihot esculenta*, *Medicago sativa*, *Metasequoia glyptostroboides*, *Musa sapientum*, *Nicotianum* spp., *Onobrychis* spp., *Ornithopus* spp., *Oryza* spp., *Peltophorum africanum*, *Pennisetum* 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*, *Populus* spp., *Prosopis cineraria*, *Pseudotsuga menziesii*, *Pterolobium stellatum*, *Pyrus communis*, *Quercus* spp., *Rhaphiolepis umbellata*, *Rhopalostylis sapida*, *Rhus natalensis*, *Ribes grossularia*, *Ribes* spp., *Robinia pseudoacacia*, *Rosa* spp., *Rubus* spp., *Salix* spp., *Schyzachyrium sanguineum*, *Sciadopitys verticillata*, *Sequoia sempervirens*, *Sequoiadendron giganteum*, *Sorghum bicolor*, *Spinacia* spp., *Sporobolus fimbriatus*, *Stiburus alopecuroides*, *Stylosanthos humilis*, *Tadehagi* spp., *Taxodium distichum*, *Themeda triandra*, *Trifolium* spp., *Triticum* spp., *Tsuga heterophylla*, *Vaccinium*

spp., *Vicia spp.*, *Vitis vinifera*, *Watsonia pyramidata*, *Zantedeschia aethiopica*, *Zea mays*, amaranth, artichoke, asparagus, broccoli, brussel sprout, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugarbeet, sugar cane, sunflower, tomato, squash, and tea, trees and algae amongst others.

5 According to a preferred embodiment of the present invention, the plant is a crop plant such soybean, sunflower, canola, alfalfa, rapeseed, cotton, tomato, potato or tobacco. According to another preferred embodiment of the present invention, the plant is a monocotyledonous plant, such as sugar cane, further preferably a cereal, most preferably the plant is selected from the group consisting of rice, maize, wheat, barley, millet, rye or oats.

10

In a particular embodiment of the present invention, proteins of one plant species (for example *Arabidopsis*) are introduced in another plant species (for example rice). It has been shown in the present invention that plant growth characteristics are improved by introduction of a 2xC2H2 zinc finger gene or protein from a dicot into a monocot.

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According to a particular embodiment of the invention, there are provided methods as described above, wherein the plant is a monocot. More preferably the plant is rice or corn.

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Advantageously, performance of the methods according to the present invention leads to plants having modified growth characteristics.

The term "growth characteristic" as used herein, preferably refers to anyone or more of, but is not limited to, yield, architecture and cycle time.

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The term "yield" means the amount of harvested material. For crop plants yield also means the amount of harvested material per acre of production. Depending on the crop the harvested part of the plant may be a different part or tissue of the plant, such as seed (e.g. rice, sorghum or corn when grown for seed); total above-ground biomass (e.g. for corn, when used as silage), root (e.g. sugarbeet), fruit (e.g. tomato), cotton fibers, or any other part of the plant which is of economic value. "Yield" also encompasses yield stability of the plants, meaning that year after year, one can obtain the same yield from the progeny of the plants, without too much interference of external factors, such as weather conditions. "Yield" also encompasses yield potential, which is the maximum obtainable yield.

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Yield maybe dependent on a number of yield components. The parameters for these components are well known by a person skilled in the art. For example breeders are well aware of the specific yield components and the corresponding parameters for the crop they are aiming to improve.

For example key yield components for corn include number of plants per hectare or acre, number of ears per plant, number of rows (of seeds) per ear, number of kernels per row, and thousand kernel weight. For silage corn typical parameters are the above ground biomass and energy content.

- 5 Key yield components for rice include number of plants per hectare or acre, number of panicles per plant, number of spikelets per panicle, seed filling rate (number of filled seeds) and thousand kernel weight. Preferentially methods for increasing yield of rice encompass increased number of flowers per panicle and an increased number of filled seeds. The parameter of increased total number of seeds may be linked to increased number of flowers.
- 10 "Yield" further encompasses typical biomass components, such as above ground parts of a plant and the root system. General biomass parameters are area and dry weight. Specific parameters for above ground biomass further encompass above ground area and plant height. Specific parameters for the root system encompass root ratio, root length and penetration depth, root branching, root hair density, root pulling resistance and aerenchyma formation.

- 15 The plants of the present invention are characterized by increased number of filled seeds, increased total seed weight, increased total number of seeds and increased harvest index. Therefore the methods of the present invention are particularly favorable to be applied in cereals such as rice and corn (maize). Accordingly, a particular embodiment of the present invention relates to a method to increase yield of corn, comprising modifying expression of a
- 20 nucleic acid encoding a 2xC2H2 zinc finger protein.

- The plants of the present invention are characterized by an increase in thousand kernel weight and therefore the seed size or seed volume and/or the seed content and/or seed composition
- 25 are altered by the methods of the present invention. The seeds provided by the methods of the present invention may have more nutritional value, more starch and/or more oil, possibly due to their bigger size.

- The plants of the present invention are characterized by more above ground area. Therefore,
- 30 the methods of the present invention are particularly favorable for crops grown for their green tissue and/or grown for their above ground biomass. The methods of the present invention are particularly useful for grasses, forage crops (such as forage corn (maize), clover, medicago etc.), trees, sugar cane etc.

- 35 The improvement in yield as obtained by the methods of the invention, may be obtained as a result of improvement of one or more of the above mentioned yield components and/or parameters.

The term "architecture" as used herein encompasses the appearance or morphology of a plant, including any one or more structural features or combination of structural features thereof. Such structural features include the shape, size, number, position, texture, arrangement, and pattern of any cell, tissue or organ or groups of cells, tissues or organs of a plant, including the root, leaf, shoot, stem, petiole, trichome, flower, petal, stigma, style, stamen, pollen, ovule, seed, embryo, endosperm, seed coat, aleurone, fibre, cambium, wood, heartwood, parenchyma, aerenchyma, sieve element, phloem or vascular tissue, amongst others. Particular architectural characteristics that may be modified by the methods of the present invention are increased plant height, increased number or size of stems or stalks or tillers or panicles or pedicles, increased number or size of inflorescences, increased branching of for example of tassels and ears or altered flowering characteristics. A preferred architectural characteristic that may be modified by the methods of the present invention is leaf architecture. The term "leaf architecture" as used herein comprises typical leaf characteristics such as length, width, thickness, cell number, cell size and greenness.

Typically, the plants of the present invention display increased leaf surface area and /or increased leaf blade width. This trait is particularly important as it allows the plant to optimize the shape of its leaf to maximize the area used for photosynthesis. For that purpose, preferably the leaf blade is widened, but alternatively, the leaves are longer or smaller or rounder. These effects may lead to more healthy plants. Alternatively, this trait attributes aesthetic properties to the plant such as greenness and stronger leaves.

"cycle time" of the plant as used herein means the time wherein a plant reaches 90% of its maximum total area. This parameter is an indication of the duration of the vegetative growth. Prolonged vegetative growth was only displayed in some of the plants according to the present invention and may be controlled by choice of the transformation event and/or by choice of the promoter driving the 2xC2H2 nucleic acid. For example this characteristic was not displayed when a seed-preferred promoter was used.

Other "growth characteristics" that may be improved by the methods of the present invention are growth rate, early vigour, modified Tmid, T90 or A42 or altered growth curve.

It is clear from the data as presented in the examples that one or more of the growth characteristics as defined herein above, may be combined in one plant. Alternatively, depending on the chosen transformation event and/or depending on the promoter used, one

or more of these growth characteristics may be present or absent or more or less pronounced in the plant.

5 The methods of the present invention may also be used to confer stress tolerance to plants. In particular, a 2xC2H2 of the STZ type may be used to confer to a plant salt stress tolerance and/or drought stress tolerance. According to a specific embodiment, a tissue preferred promoter, such as a seed-preferred promoter" is used in these methods.

10 The present invention also relates to use of a nucleic acid sequence encoding a zinc finger protein and homologues, derivatives and active fragments thereof in modifying the growth characteristics of plants, preferably in increasing yield, further preferably increasing seed yield. The present invention also relates to use of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein and homologues, derivatives and active fragments thereof and to the 2xC2H2 zinc finger protein itself and to homologues, derivatives and active fragments thereof as a growth regulator. The sequences represented by SEQ ID NO 1, and portions thereof and SEQ
15 ID NO 2, and homologues, derivatives and active fragments thereof are useful in modifying the growth characteristics of plants, as hereinbefore described. The sequences would therefore find use as growth regulators, such as herbicides or growth stimulators. The present invention also provides a composition comprising a protein represented by SEQ ID NO 2, or a
20 homologue, derivative or active fragment thereof for the use as a growth regulator. A growth regulator is used herein as meaning a regulator that increased yield and is therefore also referred to as yield regulator.

In particular, the present invention provides a yield regulating composition comprising a nucleic acid encoding a 2xC2H2 protein, and/ or comprising a 2xC2H2 protein, and/or comprising a
25 construct as defined herein above. Such a yield regulating composition further comprises additives normally use in yield regulating compositions, such as a solvent or carrier.

Conversely, the sequences according to the present invention may also be interesting targets for agrochemical compounds, such as herbicides or growth stimulators. Accordingly, the
30 present invention encompasses use of a nucleic acid encoding a 2xC2H2 protein, of a 2xC2H2 protein and/or of a construct as defined in any of claims 20 to 22 as target for an agrochemical, such as a herbicide or a growth stimulator.

The methods according to the present invention may also be practised by co-expression of a gene encoding a 2xC2H2 zinc finger protein in a plant with at least one other gene that
35 cooperates with the gene encoding a 2xC2H2 zinc finger protein. Such a gene may be a gene encoding a target protein of the 2xC2H2 zinc finger protein. Co-expression may be effected by cloning the genes under the control of a plant expressible promoter in a plant expressible

vector and introducing the expression vector(s) into a plant cell using *Agrobacterium*-mediated plant transformation. Therefore, the methods according to the present invention may result in plants having modified growth characteristics, particularly increased yield, as described hereinbefore in combination with other economically advantageous traits, such as further yield-enhancing traits, tolerance to various stresses, traits modifying various architectural features and/or biochemical and/or physiological features.

Since the plants of the present invention have excellent growth characteristics and have high yield, they are suitable for the production of enzymes, pharmaceuticals or agrochemicals. Also, there are suitable to produce food or feed products.

The invention clearly extends to enzymes, pharmaceuticals or agrochemicals as well as food or feed products isolated from these plants.

Further a nucleic acid encoding a 2xC2H2 protein, a 2xC2H2 protein and/or the constructs of the present invention may be used breeding programs aiming at the development of plants with increased yield.

Particularly, the use of allelic variants as defined above in particular conventional breeding programmes, such as in marker-assisted breeding is also encompassed by the present invention; this may be in addition to their use in the methods according to the present invention. Such breeding programmes sometimes require the introduction of allelic variations in the plants by mutagenic treatment of a plant. One suitable mutagenic method is EMS mutagenesis. Identification of allelic variants then takes place by, for example, PCR. This is followed by a selection step for selection of superior allelic variants of the sequence in question and which give rise to altered growth characteristics in a plant. Selection is typically carried out by monitoring growth performance of plants containing different allelic variants of the sequence in question, for example, SEQ ID NO 1. Monitoring growth performance may be done 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

According to another type of breeding programme a DNA marker is identified which may be genetically linked to a gene capable of modifying expression of a nucleic acid encoding a 2xC2H2 zinc finger protein in a plant, which gene may be a gene encoding the 2xC2H2 zinc finger protein itself or any other gene which may directly or indirectly influence expression of the gene encoding a 2xC2H2 zinc finger protein and/or activity of the 2xC2H2 zinc finger protein itself. This DNA marker may then be used in breeding programs to select plants having altered growth characteristics.

The methods according to the present invention may also be practised by introducing into a plant at least a part of a (natural or artificial) chromosome (such as a Bacterial Artificial Chromosome (BAC)), which chromosome contains at least a gene encoding a 2xC2H2 zinc
 5 finger protein, optionally together with one or more related gene family members. Therefore, according to a further aspect of the present invention, there is provided a method for modifying growth characteristics of plants by expressing in a plant at least a part of a chromosome comprising at least a gene encoding a 2xC2H2 zinc finger protein.

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

Fig. 1 is a map of an expression vector for the expression in plants of a 2xC2H2zinc finger protein under the control of a GOS2 promoter. CDS1536 is the internal code for the *Arabidopsis thaliana* salt tolerant zinc finger (STZ) protein cDNA. The zinc finger protein
 15 expression cassette has a GOS2 promoter and a double terminator sequence (T-zein and T-rbcS-deltaGA) located within the left border (LB repeat) and the right border (RB repeat) of the Ti plasmid. Cloned within these T-borders are also a screenable marker and a selectable marker, each under the control of a constitutive promoter (Prom), followed by a terminator sequence (poly a and t-NOS). Furthermore, this vector also contains an origin of replication
 20 (pBR322 (ori + bom)) for bacterial replication and a selectable marker (Sm/SpR) for bacterial selection.

Fig. 2A shows digital images from a T1 positive line transformed with an STZ zinc finger transgene under control of a GOS2 promoter and **Fig. 2B** shows digital images of
 25 corresponding nullizygotes plants.

Fig. 3 lists sequences useful in the methods of the present invention. SEQ ID NO 1 is an STZ encoding nucleic acid isolated from *Arabidopsis thaliana*; the start and the stop codon are highlighted in bold. SEQ ID NO 2 is the STZ protein sequence encoded by SEQ ID NO 1. In
 30 the STZ protein the nuclear localization signal also called the KRS motif or B-box is annotated (bold, italics, underlined), as well as the L-box (bold, underlined), the EAR motif (bold, italics), and the two C2H2 zinc finger domains with QALGGH motif (bold and boxed). SEQ ID NO 10 to SEQ ID NO 25 provides the sequences of various orthologs of the *Arabidopsis thaliana* STZ protein from other plant species. SEQ ID NO 26 to SEQ ID NO 35 provides the sequences of
 35 various paralogs (from *Arabidopsis*) of the STZ protein. SEQ ID NO 36 to SEQ ID NO 50 provides the sequences of related 2xC2H2 genes and proteins useful in the methods of the present invention.

Fig. 4 is a photograph of T3 plants grown in a greenhouse (A) or in a field (B). The photograph shows yield increase (especially in aboveground biomass and plant height) in subsequent generations of STZ transformed plants.

5

Fig. 5 shows the binary vector for expression in *Oryza sativa* of the *Arabidopsis thaliana* STZ gene (CDS1536) under the control of a seed preferred WSI18 promoter (PRO0151). This vector contains a T-DNA derived from the Ti Plasmid, limited by a left border (LB repeat, LB Ti C58) and a right border (RB repeat, RB Ti C58)).

- 10 The zinc finger protein expression cassette has a WSI18 (PRO0151) promoter and a double terminator sequence (T-zein and T-rbcS-deltaGA) located within the left border (LB repeat) and the right border (RB repeat) of the Ti plasmid. Cloned within these T-borders are also a screenable marker and a selectable marker, each under the control of a constitutive promoter (Prom), followed by a terminator sequence (poly a and t-NOS). Furthermore, this vector also
- 15 contains an origin of replication (pBR322 (ori + bom)) for bacterial replication and a selectable marker (Sm/SpR) for bacterial selection.

Examples

- The present invention will now be described with reference to the following examples, which
- 20 are by way of illustration alone.

DNA Manipulation

- Unless otherwise stated, recombinant DNA techniques are performed according to standard protocols described in Sambrook (2001) Molecular Cloning: a laboratory manual, 3rd Edition
- 25 Cold Spring Harbor Laboratory Press, CSH, New York or in Volumes 1 and 2 of Ausubel *et al.* (1988), Current Protocols in Molecular Biology, Current Protocols. Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfase (1993) by R.D.D. Croy, published by BIOS Scientific Publications Ltd (UK) and Blackwell Scientific Publications (UK).

30

Example 1: Gene Cloning

- A gene encoding an STZ protein was amplified by PCR from an *Arabidopsis thaliana* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was
- 35 1.5 kb, and original number of clones was of 1.59×10^7 cfu. Original titer was determined to be 9.6×10^5 cfu/ml, after first amplification of 6×10^{11} cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 µl PCR mix. Sequences of the primers used for PCR amplification

were, including the attB sites for Gateway recombination (in bold) were PRM3204 (sense, start codon in italics) 5' **GGGGACAAGTTTGTACAAAAAAGCAGGCTTCACAA**TGGCGCTCGAGGCTC 3' (SEQ ID NO 3) and PRM3205 (reverse, complementary stop codon in italics) 5' **GGGGACCACTTTGTACAAGAAAGCTGGGT**AATTTCTTAAAGTTGAAGTTTGA 3' (SEQ ID NO 4).

PCR was performed using Hifi Taq DNA polymerase in standard conditions. The PCR fragment (CDS1536) was amplified and purified using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment was recombined *in vivo* with the pDONR plasmid to produce, according to Gateway terminology, an "entry clone", p3359. PDONR was purchased from Invitrogen, as part of the Gateway technology.

Example 2: Vector construction for rice transformation with pGOS2::AtSTZ

The entry clone p3359 was subsequently used in an LR reaction with p0640, a destination vector used for rice transformation. This vector contains as functional elements within the T-DNA borders a plant selectable marker and a Gateway cassette intended for LR *in vivo* recombination with the sequence of interest already cloned in the donor vector. Upstream of this Gateway cassette lies the rice GOS2 promoter for constitutive expression of the zinc finger gene (De Pater *et al.*, Plant J. 2 (6) 837-844, 1992). After the recombination step, the resulting expression vector with the expression cassette CD4398 (Figure 1) was transformed into *Agrobacterium* strain LBA4404 and subsequently into plants. Transformed rice plants were allowed to grow and then examined for various parameters as described in Example 3.

Example 3: Evaluation of T0, T1 and T2 transgenic rice plants transformed with pGOS2::AtSTZ (CD4398)

Approximately 15 to 20 independent T0 transformants were generated. The primary T0 transformants were transferred from tissue culture chambers 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 homo-zygotes), and approximately 10 T1 seedlings lacking the transgene (nullizygotes), were selected by PCR. Based on the results of the T1 evaluation three events were chosen, for further characterisation in the T2 generation, one event being very positive for a number of parameters, a second event being positive for a number of parameters, but less pronounced, and a third event being neutral. Seed batches from the positive plants (both hetero- and homozygotes) in T1, were screened by monitoring marker expression. For each chosen event, the heterozygote seed batches were then selected

for T2 evaluation. An equal number of positives and negatives within each seed batch were transplanted for evaluation in the greenhouse (i.e., for each event 40 plants were grown of which there were about 20 positives for the transgene and about 20 negative). Therefore, the total number for the three events amounted to 120 plants for evaluation in the T2 generation.

5

T1 and T2 plants were transferred to the greenhouse and evaluated for vegetative growth parameters and seed parameters, as described hereunder.

(I) Statistical analysis of phenotypic characteristics

10 A two factor ANOVA (analyses of variance) was used as statistical model for the overall evaluation of plant phenotypic characteristics. An F-test was carried out on all the parameters measured, for all the plants of all the events transformed with the gene of interest. 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 or "global gene effect". Significant data, as determined by
15 the value of the f-test, indicates a "gene" effect, meaning that the phenotype observed is caused by more than the presence or position of the gene. In case of the F-test, the threshold for significance for a global gene effect is set at 5% probability level.

To check for an effect of the genes within an event, i.e., for a line-specific effect, a t-test was
20 performed within each event using data sets from the transgenic plants and the corresponding null plants. "Null plants" or "Null segregants" 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 homozygous negative transformant plants. The threshold for significance for the t-test is set at 10% probability level. Within one population of transformation events, some
25 events may be under or above this t-test 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 may also be referred to as a "line effect of a 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 stand
30 for the probability that the null hypothesis (null hypothesis being "there is no effect of the transgene") is correct.

(II) Vegetative growth measurements

The selected plants were grown in a greenhouse. Each plant received a unique barcode label
35 to link unambiguously the phenotyping data to the corresponding plant. The selected plants were grown on soil in 10 cm diameter pots under the following environmental settings: photoperiod= 11.5 h, daylight intensity= 30,000 lux or more, daytime temperature= 28°C or

higher, night time temperature= 22°C, relative humidity= 60-70%. Transgenic plants and the corresponding nullizygotes were grown side-by-side at random positions. From the stage of sowing until the stage of maturity (which is the stage where there is no more increase in biomass) the plants were passed weekly through a digital imaging cabinet (examples of pictures are shown in Figures 2A and 2B). At each time point digital images (2048x1536 pixels, 16 million colours) were taken of each plant from at least 6 different angles. The parameters described below were derived in an automated way from the digital images using image analysis software.

10 (a) **Aboveground area**

Plant above ground area was determined by counting the total number of pixels 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.

Results of the maximum above ground area values of the lines selected for T2 evaluation are summarized in Table 1. The plants of the best performing line showed an increase in biomass of 34 % , compared to the nullizygotes.

When an F-test was carried out on all the plants of all the T2 events it became clear that the transgenic plants show a significant increase in above ground area, in average an increase of approximately 18%. A significant increase in above ground biomass is also displayed by STZ transformed plants grown under field conditions (see figure 4).

25

Table 1: *Aboveground area of STZ transgenic T2 plants. Each row corresponds to one event, for which the average maximum aboveground area (expressed in mm²) was determined for the transgenics (TR) and the null plants (null). The difference in absolute values between the transgenic population and the nullizygotes of each event are presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test for each event. The last row presents the average numbers calculated from all the events. Here the p-value is produced by the F-test.*

30

Total above ground Area Max (mm ²)					
Line	TR	null	dif	% dif	p-value
CD4396 L1	63947	47606	16341	34	0.0021
CD4396 L2	42509	41342	1167	3	0.8063
CD4396 L3	41116	33687	7429	22	0.1107
Overall	49178	41657	7522	18	0.0047

(b) Plant height measurements

Plant height was determined by the distance between the horizontal lines going through the upper pot edge and the uppermost pixel corresponding to a plant part above ground. This value was averaged for the pictures taken on the same time point from the different angles and was converted, by calibration, to a physical distance expressed in mm. Experiments showed that plant height measured this way correlate with plant height measured manually with a ruler.

The increase in plant height was displayed very clearly in STZ transformed plants when measured at the end of the vegetative growth (see figure 4A). Also, this parameter, was displayed by STZ transformed plants when grown in the field (see figure 4B) at the time of harvest.

(c) Total area cycle time measurements

Plants were imaged weekly along the complete cell cycle and the maximum total area of the plants was determined as mentioned above. Total Area Cycle Time is the time when a plant reaches 90% of its maximum total area. This parameter is an indication of the duration of the vegetative growth.

Only in some transgenic lines there was an effect on cycle time. These few lines showed a prolonged vegetative growth.

(III) Measurement of seed-related parameters

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 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 seed-related parameters described below.

(a) Total number of filled seeds per plant

The number of filled seeds was determined by counting the number of filled husks that remained after the separation step.

- 5 **Total numbers of filled seeds per plant are summarized in Table 2. The t-test shows that for two events, transgenic plants produce 106% and 130% more filled seeds than the nullizygotes.**

10 Table 2: *Number of filled seeds of STZ transgenic T2 plants. Each row corresponds to one event, for which the average number of filled seeds was determined for the transgenics (TR) and the null plants (null). The difference in absolute values between the transgenic population and the nullizygotes of each event are presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test for each event. The last row presents the average numbers calculated from all the events. Here*

15 *the p-value is produced by the F-test.*

Number of filled seeds					
Line	TR	null	dif	% dif	p-value
CD4396 L1	387.9	188.7	199.19	106	<0.0001
CD4396 L2	163.8	156.5	7.22	5	0.8382
CD4396 L3	236.9	102.9	133.98	130	0.0004
Overall	264.9	159.7	105.25	66	<0.0001

(b) Total seed weight per plant

The total seed weight was measured by weighing all filled husks harvested from a plant.

- 20 The total seed weight values of STZ transformed plants are summarized in Table 3. STZ transgenic plants produce significantly more seed weight than the corresponding nullizygotes. The difference in seed weight of the transgenics may be as high as 138% or higher.

25 Table 3: *Total seed weight per plant of STZ transgenic T2 plants. Each row corresponds to one event, for which the average total seed weigh (in gram) was determined for the transgenics (TR) and the null plants (null). The difference in absolute values between the transgenic population and the nullizygotes of each event are presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test for each event. The last row presents the average numbers calculated*

30 *from all the events. Here the p-value is produced by the F-test.*

Total weight of seeds					
Line	TR	null	dif	% dif	p-value
CD4396 L1	9.8	4.5	5.25	116	<0.0001
CD4396 L2	3.4	3.3	0.1	3	0.908
CD4396 L3	6.1	2.6	3.56	138	0.0001
Overall	6.5	3.7	2.75	74	<0.0001

(c) Harvest index

The harvest index 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.

5

The harvest index values of the STZ-transgenic plants are summarized in Table 4. STZ transgenic plants have a significant increase in harvest index. The increase in harvest index of the transgenic plants may be as high as 66%, when compared to the corresponding nullizygotes.

10

Table 4: *Harvest index of STZ transgenic T2 plants. Each row corresponds to one event, for which the average harvest index was determined for the transgenics (TR) and the null plants (null). The difference in absolute values between the transgenic population and the nullizygotes of each event are presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test for each event. The last row presents the average numbers calculated from all the events. Here the p-value is produced by the F-test.*

15

Harvest index					
Line	TR	null	dif	% dif	p-value
CD4396 L1	149.1	90	59.11	66	<0.0001
CD4396 L2	74	73.4	0.55	1	0.9574
CD4396 L3	121.3	75.9	45.32	60	<0.0001
Overall	114.8	82.6	32.16	39	<0.0001

(d) Thousand kernel weight (TKW) of plants

20

Thousand Kernel Weight (TKW) is a parameter extrapolated from the number of filled seeds counted, and their total weight.

The weight values of thousand kernels of STZ transgenic plants are presented in Table 5. STZ transgenic plants have increased thousand kernel weight. The increase of TKW of transgenic plants may be as high as 6% when compared to the corresponding nullizygotes.

Table 5: Thousand kernel weight of STZ transgenic T2 plants. Each row corresponds to one event, for which the average TKW was determined for the transgenics (TR) and the null plants (null). The difference in absolute values between the transgenic population and the nullizygotes of each event are presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test for each event. The last row presents the average numbers calculated from all the events. Here the p-value is produced by the F-test.

TKW					
Line	TR	null	dif	% dif	p-value
CD4396 L1	25.2	23.8	1.46	6	0.0128
CD4396 L2	20.6	20.7	-0.14	-1	0.7963
CD4396 L3	25.5	24.5	0.99	4	0.0812
Overall	23.7	23	0.71	3	0.0213

10 (e) Total number of seeds

The total number of seeds per plant was measured by counting the number of husks harvested from a plant.

The total numbers of seeds per plant are summarized in Table 6. STZ transformed plants have an increase in total number of seeds. The increase of total number of seeds may be as high as 68%, when compared to the corresponding nullizygotes.

Table 6: Total number of seeds of STZ transgenic T2 plants. Each row corresponds to one event, for which the average total number of seeds was determined for the transgenics (TR) and the null plants (null). The difference in absolute values between the transgenic population and the nullizygotes of each event are presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test for each event. The last row presents the average numbers calculated from all the events. Here the p-value is produced by the F-test.

Total number of seeds					
Line	TR	null	dif	% dif	p-value
CD4396 L1	483.5	367.4	116.03	32	0.0146
CD4396 L2	353.9	327.5	26.42	8	0.5473
CD4396 L3	383.6	228.2	155.48	68	0.0009
Overall	406	312.5	93.52	30	0.0002

Conclusion

It may be concluded that vegetative growth is increased in the STZ transgenic plants when compared to the control non-transgenic plants, as reflected by parameters such as above ground area, where the increase is above 20 %. This effect may be attributed to the expression of the STZ gene in the transgenic plants. Additionally, in some transformation events, the length of the vegetative growth is altered in the STZ transgenic plants. For those transformation events in which this effect occurs, in average the vegetative growth was prolonged with about 4 to 6 days, under the conditions tested.

Furthermore, yield was increased in STZ transgenic plants. Several seed parameters reflect this yield increase. The total number of seeds harvested was at least 100% higher in the transgenics than in the control plants, for those events showing a differential. For these events, there was also an increase in the total number of seeds of the transgenics, which increase was higher than 30 %. Seed filling in those transgenics was greatly improved, reaching differences above 100% in the number of filled seeds.

Seed of the transgenic plants were also heavier, and probably bigger, as suggested by the higher values obtained for the thousand kernel weigh. The TKW parameter is a very stable parameter in rice cultivars, such as nipponbare, and in the growth conditions here used. This means that this parameter is not easily influenced and makes it an important yield parameter. Therefore a TKW increase of 6 % represents a significantly increase in yield.

Harvest index, another important yield parameter, was increased in the transgenic plants with more than 50 %.

In summary, based on the evaluation of STZ transgenic plants in the T1, T2 and further generations, it may be concluded that the presence of an STZ transgene, has a positive effect on the size of the plant and/or its organs, as well as a positive effect on the final yield harvested.

(III) Root growth measurements

Transgenic plants are grown next to their corresponding non-transgenic null segregant in transparent pots. In average, for each construct comprising a particular promoter-2xC2H2 combination, a minimum of 5 independent transformation events are evaluated for root growth, root development and root architecture. Typically, per transformation event, 10 transgenics are compared to 10 nullizygotes. Root pictures are taken weekly during plant growth. The pictures are processed and analyzed to extract the values for the root parameters as detailed below. Statistical analysis as described above are applied to these data.

a) Root Area

Total root area is calculated from the summed number of pixels of each root images. A positive linear correlation between root area and dry weight and root biomass of the root has been previously established by similar experiments. Therefore, root area is a good approximation for root biomass.

b) Root Length

The total perimeter of the roots of a plant is calculated as the sum of the perimeter of all roots in the images. A linear correlation between this measurement and root length has been previously established. Thus, root length is extrapolated from the total root perimeter.

c) Root Width

Average root width of a plant is expressed as the ratio between the Root Area and the Root Length.

STZ transgenic plants of the invention show a superior performance when compared to control plants. Transgenic plants are altered in one or more the root parameters detailed above. In particular the transgenic have increased root biomass, for example due to increased root dry weight or area, and/or increased root length and/or increased root width.

Example 4: Leaf Blade Width Measurement.

Leaves of STZ transgenic plants appeared bigger and wider when compared to the corresponding control non-transgenic plants. To quantify the increase in leaf width, leaf blade width (length of transversal axe) of the flag leaf was measured with a ruler at the widest point of the leaf, which is approximately at half of the length, in plants that have reached the end of the vegetative growth phase. The results shown in the Table 7, indicate that the increase in the leaf blade width in at least the event here measured was around 15 % when compared to the corresponding nullizygote.

Table 7: Leaf blade width of STZ transgenic T2 plants. The average leaf blade width was determined for the transgenics (TR) and the null plants (null) of the selected event. The difference in absolute values between the transgenic population and the nullizygotes of the event is presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test .

Leaf blade width					
Line	TR	null	dif	% dif	p-value
CD4396 L1	1.56	1.35	0.21	15	0.098

Example 5: Vector construction for rice transformation with pWSI18::AtSTZ

Vector construction for transformation with the pWSI18 (PRO0151) - AtSTZ (CDS1536) cassette was carried out essentially as in example 2. The entry clone p3359, described earlier, was subsequently used in an LR reaction with p05653, a destination vector used for rice transformation. This destination vector contains as functional elements within the T-DNA borders a plant selectable marker and a Gateway cassette intended for LR in vivo recombination with the sequence of interest already cloned in the donor vector. A WSI18 promoter for seed preferred expression (PRO0151) is located upstream of this Gateway cassette. After the recombination step, the resulting expression vector with the expression cassette CD4398 (Figure 5) was transformed into *Agrobacterium* strain LBA4404 and subsequently this vector was transformed to *Oryza sativa* plants. Transformed rice plants were allowed to grow and then examined for various parameters as described in example 3.

15

Example 6: Evaluation of T0 and T1 transgenic rice plants transformed with the seed preferred expression cassette pWSI18::AtSTZ (CD4398)

Preparations of calli and of the *Agrobacterium tumefaciens* strain containing the expression vector with the CD4398 expression cassette, were carried out as described in example 3, as were the calli transformation and plant regeneration.

20

Approximately 15 to 20 independent T0 rice transformants were generated. The primary transformants were transferred from tissue culture chambers to a greenhouse for growing and harvest of T1 seed. 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 homo-zygotes), and approximately 10 T1 seedlings lacking the transgene (nullizygotes), were selected by monitoring marker expression.

25

Transgenic plantlets were grown next to control nullizygotes, seeds were harvested and thousand kernel weight determined as previously described.

30

Transformed plants comprising the expression cassette CD8490 (seed preferred pWSI18::STZ), had a normal and healthy appearance and were harvested at the same time as the control plants. The seeds harvested from the transgenic plants had an increase in

thousand kernel weight when compared to the control plants. As shown in Table 8 increase in thousand kernel weight was above 10%.

Table 8: *Thousand kernel weight of STZ transgenic T1 plants. The average 1 thousand kernel weight was determined for the transgenics (TR) and the null plants (null) of the selected event. The difference in absolute values between the transgenic population and the nullizygotes of the event is presented (dif.) as well as the percentage of difference between the two populations (% dif). P stands for the probability produced by the t-test .*

Thousand kernel weight					
Line	TR	null	dif	% dif	p-value
CD8490 L1	29.6	26.8	2.82	11	0.001

Example 7: Cloning, transformation and evaluation of other 2xC2H2 encoding genes.

In Table 9 an overview is given of constructs with STZ or other 2xC2H2 zinc finger proteins, under control of various promoters, which constructs are made for use in the methods of the present invention. The coding regions of the 2xC2H2 genes to be cloned (GOI, Gene of Interest) are amplified by PCR from cDNA , following the protocol as in Example 1. Specific primers for each 2xC2H2 gene were designed at the start and stop codons of the gene sequence as present in the public database under the accession number as indicated in Table 9. These cloned sequences are also herein incorporated under the SEQ ID NO number as mentioned in the table. Moreover, the isolated PCR fragments were also given a unique CDS number.

The PCR fragment with a 2xC2H2 gene is then cloned under the control of a particular promoter. Different combinations for different genes are made (see Table 9). Chimeric constructs are made and CD numbers represent bacterial strains carrying the chimeric construct. Corresponding transgenic plants are obtained by transforming the plants with the chimeric constructs, following the protocols as mentioned herein before. Evaluation of the transgenic events reveals an increase in yield, and increase in leaf surface area and/or an increase in duration of vegetative growth in the transgenic plants when compared to the control non-transgenic plants.

CD-070-PCT**Table 9:** examples of 2xC2H2 chimeric constructs useful for the methods of the present invention. *see Table 1

CDS	Accession number (cDNA on which primers were designed to amplify the CDS region)	Prot ACC number	SEQ ID NO	PRO0129*	PRO0170*	PRO0061_2*	PRO0123*	PRO0207*	PRO0110*
CDS1536 STZ Arabidopsis	X95573	CAA64820	1 + 2	CD4398	CD11371	CD11382	CD10960	CD10959	CD10313
CDS2200 Paralog Arabidopsis	AF022658 NM_120516	AAB80922.1At5g04340	28 + 29	CD11576			CD11413		CD11540
CDS2205 Paralog Arabidopsis	NM_123683	At5g43170	32 + 33	CD11325			CD11414		CD11387
CDS2775 Ortholog Oryza sativa	AF332876	AAK01713.1	36 + 37	CD09948					CD10313
CDS1677 Homolog Arabidopsis	AL132966 REGION: 116202..116729	CAB67667	38 + 39	CD06462			CD		CD
CDS3337 Homolog Sugarcane	CA279020		40	CD			CD		CD
CDS2416 Homolog Arabidopsis	AF254447	At3g57670	41 + 42	CD			CD		CD
CDS2377 Homolog Arabidopsis	AJ311810	CAC86167	43 + 44	CD			CD		CD
CDS Homolog Arabidopsis	AL355775 REGION: complement(7957..8451)	CAB90935	45 + 46	CD			CD		CD
CDS Homolog Arabidopsis	AL391143 REGION: complement(31730..32938)	CAC01747	47 + 48	CD			CD		CD
CDS3641 Homolog Arabidopsis	X98678	CAA67236	49 + 50	CD			CD		CD

Table 10: examples promoters used in combination with 2xC2H2 for the methods of the present invention.

Promoter	Preferred expression type	Origin species	Gene
PRO0151	Seeds (mainly embryo and aleurone). Strong expression.	Oryza sativa	WSI18
PRO0110	Root	Oryza sativa	RCc3
PRO0207	Green tissue. Moderate expresssion levels	Saccharum officinarum	Prp
PRO0123	Green tissue. Strong expression levels.	Oryza sativa	Protochlorophyllide reductase
PRO0090	Seed specific (mainly endosperm)	Oryza sativa	Prolamin RP6
PRO0170	Constitutive. Strong Expression.	Oryza sativa	High Mobility Group protein
PRO0218	Seeds (mainly embryo and aleurone)	Oryza sativa	oleosine 18kda
PRO0061_2	Young expanding tissues	Oryza sativa	beta-expansine EXPB9
PRO0129	Constitutive. High expression levels.	Oryza sativa	GOS2

5

Example 8: use of the invention in corn.

The methods of the invention described herein are also used in maize. To this aim, an STZ encoding gene, for example a maize or other STZ ortholog, is cloned under control of a promoter operable in maize, in a plant transformation vector suitable for Agrobacterium-mediated corn transformation. Methods to use for corn transformation have been described in literature (Ishida et al., Nat Biotechnol. 1996 Jun;14(6):745-50; Frame et al., Plant Physiol. 2002 May;129(1):13-22).

Transgenic plants made by these methods are grown in the greenhouse for T1 seed production. Inheritability and copy number of the transgene are checked by quantitative real-time PCR and Southern blot analysis and expression levels of the transgene are determined by reverse PCR and Northern analysis. Transgenic lines with single copy insertions of the transgene and with varying levels of transgene expression are selected for T2 seed production.

20

Progeny seeds are germinated and grown in the greenhouse in conditions well adapted for maize (16:8 photoperiod, 26-28°C daytime temperature and 22-24°C nighttime temperature)

as well under water-deficient, nitrogen-deficient, and excess NaCl conditions. Null segregants from the same parental line, as well as wild type plants of the same cultivar are used as controls. The progeny plants resulting from the selfing or the crosses are evaluated on different biomass and developmental parameters, including, plant height, stalk/stem thickness, stem size, number of leaves, total above ground area, leaf greenness, time to maturity, time to silking, flowering time, time to flower, ear number, ear length, row number, kernel number, kernel size, kernel oil content, grain maturity, harvesting time. The seeds of these lines are also checked on various parameters, such as grain size, total grain yield per plant, and grain quality (starch content, protein content and oil content).

10

Lines that are most significantly improved compared to corresponding control lines are selected for further field-testing and marker-assisted breeding, with the objective of transferring the field-validated transgenic traits into commercial germplasm. The testing of maize for growth and yield-related parameters in the field is conducted using well-established protocols.

15

The corn plants are particularly evaluated on yield parameters, such as for example, amount of plants per acre, amount of ears per plant, amount of rows per ear, amount of seeds per row and TKW. Subsequent improvements for introgressing specific loci (such as transgene containing loci) from one germplasm into another is also conducted using well-established protocols.

20

SEQUENCE LISTING

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                20              25              30

Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Asp Phe His His Gln Asn
35              40              45

Leu Thr Glu Glu Glu Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg
50              55              60

Asp Asn Arg Gln Pro Pro Pro Pro Pro Ala Val Glu Lys Leu Ser Tyr
65              70              75              80

Lys Cys Ser Val Cys Asp Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly
85              90              95

Gly His Lys Ala Ser His Arg Lys Asn Leu Ser Gln Thr Leu Ser Gly

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100					105					110					
Gly	Gly	Asp	Asp	His	Ser	Thr	Ser	Ser	Ala	Thr	Thr	Thr	Ser	Ala	Val
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Thr	Thr	Gly	Ser	Gly	Lys	Ser	His	Val	Cys	Thr	Ile	Cys	Asn	Lys	Ser
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Phe	Pro	Ser	Gly	Gln	Ala	Leu	Gly	Gly	His	Lys	Arg	Cys	His	Tyr	Glu
145					150					155					160
Gly	Asn	Asn	Asn	Ile	Asn	Thr	Ser	Ser	Val	Ser	Asn	Ser	Glu	Gly	Ala
				165					170					175	
Gly	Ser	Thr	Ser	His	Val	Ser	Ser	Ser	His	Arg	Gly	Phe	Asp	Leu	Asn
			180					185					190		
Ile	Pro	Pro	Ile	Pro	Glu	Phe	Ser	Met	Val	Asn	Gly	Asp	Asp	Glu	Val
		195					200					205			
Met	Ser	Pro	Met	Pro	Ala	Lys	Lys	Pro	Arg	Phe	Asp	Phe	Pro	Val	Lys
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Leu	Gln	Leu													
225															

<210> 3
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 <213> Artificial sequence

<220>
 <223> primer PRM3204

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<210> 4
 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer PRM3205

<400> 4
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<210> 5
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> QALGGH motif

<400> 5
 Gln Ala Leu Gly Gly His

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<210> 6
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> NNM box

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa can be either methionine or tryptophan

<400> 6
Asn Asn Xaa Gln Met His
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<210> 7
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> EAR motif

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa can be any hydrophobic amino acid (Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr, Val, Trp or Tyr)

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be any hydrophobic amino acid (Ala, Cys, Phe, Gly, His, Ile, Lys, Leu, Met, Arg, Thr, Val, Trp or Tyr)

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa can be any amino acid or no amino acid

<400> 7
Xaa Asp Leu Asn Xaa Xaa Pro
1 5

<210> 8
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> B-Box

<220>
<221> MISC_FEATURE

<222> (3)..(3)
 <223> Ser can be serine or no amino acid

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Xaa can be any amino acid

<400> 8
 Lys Arg Ser Lys Arg Xaa Arg
 1 5

<210> 9
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>
 <223> L-Box

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> Xaa can be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (4)..(5)
 <223> Xaa can be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> Xaa can be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(11)
 <223> Xaa can be any amino acid

<400> 9
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<210> 10
 <211> 1006
 <212> DNA
 <213> Datisca glomerata

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 gacgacccca gcttgaatta ccttgagcca tggaccaagc gtaagcggtc caagcgtagc 180
 cgcttagata gccccatacc gaggaagagt accttgcttt ctgcctcatc atgctcgctc 240
 gtggccgcgt tgcctctgca aatcgacggg attctcagtc ttccattcag attcagcctg 300
 aagcaacgac ttcggctacc aaagtcagtt ataagtgtc tgtgtgcat aaggcctttt 360
 cgtcttatca ggctttgggt gggcacaagg ccagccacag aaagctcgct ggcggcgaag 420
 atcaatcgac ttcctttgcc accacgaatt cagccaccgt cactaccacc acagcctccg 480

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accacaacaa taccaccaac agcgggaagca acggtggcat gagcatgacc tccgaagtag 660
gttccacaca cacagtcagc cacagtcacc gtgacttcga tctcaacatc ccggccttgc 720
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ccaagaaacc ccgtatattg atgaaataaa acatttctca agatcactga accaggcttt 840
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attaatatat ttcgtgtaca taaatttgta gttctttaac acactctgtt tcattttctt 960
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<210> 11
 <211> 247
 <212> PRT
 <213> *Datisca glomerata*

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 His Tyr Asp Asp Pro Ser Leu Asn Tyr Leu Glu Pro Trp Thr Lys Arg
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 35 40 45
 Tyr Leu Ala Phe Cys Leu Ile Met Leu Ala Arg Gly Arg Val Ala Ser
 50 55 60
 Ala Asn Arg Arg Asp Ser Gln Ser Ser Ile Gln Ile Gln Pro Glu Ala
 65 70 75 80
 Thr Thr Ser Ala Thr Lys Val Ser Tyr Lys Cys Ser Val Cys Asp Lys
 85 90 95
 Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
 100 105 110
 Lys Leu Ala Gly Gly Glu Asp Gln Ser Thr Ser Phe Ala Thr Thr Asn
 115 120 125
 Ser Ala Thr Val Thr Thr Thr Thr Ala Ser Gly Gly Gly Gly Arg Ser
 130 135 140
 His Glu Cys Ser Ile Cys His Lys Ser Phe Pro Thr Gly Gln Ala Leu
 145 150 155 160
 Gly Gly His Lys Arg Cys His Tyr Glu Gly Ser Ile Gly Gly Asn Ser
 165 170 175
 Ile His His His Asn Asn Thr Thr Asn Ser Gly Ser Asn Gly Gly Met
 180 185 190
 Ser Met Thr Ser Glu Val Gly Ser Thr His Thr Val Ser His Ser His
 195 200 205
 Arg Asp Phe Asp Leu Asn Ile Pro Ala Leu Pro Glu Phe Arg Ser Asn
 210 215 220

Phe Phe Ile Ser Gly Asp Asp Glu Val Glu Ser Pro His Pro Ala Lys
 225 230 235 240

Lys Pro Arg Ile Leu Met Lys
 245

<210> 12
 <211> 996
 <212> DNA
 <213> Glycine max

<400> 12
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 ttgacgaccc aactattcca tgggcgaaac gaaaacgttc aaagcgttct cgcgaccatc 180
 cttctgaaga agagtacctc gccctctgcc tcatcatgct cgctcgcggc ggcaccacca 240
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 cccccagcac caccacttcc tccgcgcgcg ccaccagctc cgcctccgga ggtaaggccc 480
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 tcgcctcgga aggcgtgggc tccaccacac ctgtcagtcg cggccaccac cgcgacttcg 660
 atctcaacat cccggccttt ccggattttt cgaccaaggt cggagaagac gaggttgaga 720
 gccctcaccc tgtcatgaag aagcctcgcc tcttcgtcat tccaagatc gaaatcccc 780
 aatttcaatg aactcgttga atttttagtt tatttttcga ctatatattt tggagaattt 840
 tgagagttac tataatttga ttttgtacat agtacttgga agttttgttg gaccgtaccg 900
 gaccagttc tctggttgag gttgtacttt cacaacagtg gcagatttgc aattcaattc 960
 aatttatattg tttattttta aaaaaaaaaa aaaaaa 996

<210> 13
 <211> 240
 <212> PRT
 <213> Glycine max

<400> 13
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 20 25 30
 Arg Ser Arg Asp His Pro Ser Glu Glu Glu Tyr Leu Ala Leu Cys Leu
 35 40 45
 Ile Met Leu Ala Arg Gly Gly Thr Thr Thr Val Asn Asn Arg His Val
 50 55 60
 Ser Pro Pro Pro Leu Gln Pro Gln Pro Gln Pro Thr Pro Asp Pro Ser
 65 70 75 80
 Thr Lys Leu Ser Tyr Lys Cys Ser Val Cys Asp Lys Ser Phe Pro Ser
 85 90 95
 Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Leu Ala Gly
 100 105 110
 Ala Ala Glu Asp Gln Pro Pro Ser Thr Thr Thr Ser Ser Ala Ala Ala

115	120	125
Thr Ser Ser Ala Ser Gly Gly Lys Ala His Glu Cys Ser Ile Cys His		
130	135	140
Lys Ser Phe Pro Thr Gly Gln Ala Leu Gly Gly His Lys Arg Cys His		
145	150	155
Tyr Glu Gly Asn Gly Asn Gly Asn Asn Asn Asn Ser Asn Ser Val Val		
165	170	175
Thr Val Ala Ser Glu Gly Val Gly Ser Thr His Thr Val Ser His Gly		
180	185	190
His His Arg Asp Phe Asp Leu Asn Ile Pro Ala Phe Pro Asp Phe Ser		
195	200	205
Thr Lys Val Gly Glu Asp Glu Val Glu Ser Pro His Pro Val Met Lys		
210	215	220
Lys Pro Arg Leu Phe Val Ile Pro Lys Ile Glu Ile Pro Gln Phe Gln		
225	230	235
		240

<210> 14
 <211> 1006
 <212> DNA
 <213> Medicago sativa

<400> 14

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tggaagcact	taactcacc	accactgcta	ctcctttcac	accctttgag	gaaccaaadc	180
tgagttatct	tgaaacaccg	tggacgaaag	gtaaacgatc	aaagcgttct	cgcattggatc	240
aatcttcatg	cactgaagaa	gagtattctg	ctcttttgtct	catcatgctt	gctcgcagcgc	300
gtaacaacaa	cgacaaaaag	tctgattcgg	tggcgacgcc	gctaaccacc	gttaaaactca	360
gtcacaaatg	ctcagtctgc	aacaaagctt	tctcatctta	tcaagcccta	ggtggacaca	420
aagccagtca	ccggaaagct	gttatgtccg	caaccaccgc	tgaagatcag	atcaccacca	480
cttcatccgc	cgtgactacc	agctctgctt	ccaacggtaa	gaacaagact	catgagtgtt	540
ccatctgtca	caaatccttc	cctactggac	aggctttggg	aggacacaag	cgttgtcact	600
acgaaggcag	cgttggtgcc	ggtgccggtg	ctggaagtaa	cgctgtaact	gcctctgaag	660
gagttggatt	gtcacacagc	caccaccgtg	attttgatct	taacctcccg	gcttttccgg	720
acttttcaaa	gaagtttttc	gtggatgacg	aggtttttag	tcctttacct	gctgcaaaga	780
agccctgtct	tttcaagctg	gaaattcctt	ctcattactg	atcaataata	gatccaattt	840
tattgttatt	attattaata	attattatcg	cttagggcat	agttattttc	ttttttcttt	900
caattatttc	ggatcaattt	gttctgtaca	tacaaattgg	gattggtttt	agaatttagg	960
acggttgtag	acaatggaaa	ttcaattcaa	ttatttaatt	ttgtgt		1006

<210> 15
 <211> 235
 <212> PRT
 <213> Medicago sativa

<400> 15

Met Ala Met Glu Ala Leu Asn Ser Pro Thr Thr Ala Thr Pro Phe Thr
1 5 10 15
Pro Phe Glu Glu Pro Asn Leu Ser Tyr Leu Glu Thr Pro Trp Thr Lys
20 25 30

Gly Lys Arg Ser Lys Arg Ser Arg Met Asp Gln Ser Ser Cys Thr Glu
 35 40 45
 Glu Glu Tyr Leu Ala Leu Cys Leu Ile Met Leu Ala Arg Ser Gly Asn
 50 55 60
 Asn Asn Asp Lys Lys Ser Asp Ser Val Ala Thr Pro Leu Thr Thr Val
 65 70 75 80
 Lys Leu Ser His Lys Cys Ser Val Cys Asn Lys Ala Phe Ser Ser Tyr
 85 90 95
 Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Ala Val Met Ser
 100 105 110
 Ala Thr Thr Ala Glu Asp Gln Ile Thr Thr Thr Ser Ser Ala Val Thr
 115 120 125
 Thr Ser Ser Ala Ser Asn Gly Lys Asn Lys Thr His Glu Cys Ser Ile
 130 135 140
 Cys His Lys Ser Phe Pro Thr Gly Gln Ala Leu Gly Gly His Lys Arg
 145 150 155 160
 Cys His Tyr Glu Gly Ser Val Gly Ala Gly Ala Gly Ala Gly Ser Asn
 165 170 175
 Ala Val Thr Ala Ser Glu Gly Val Gly Leu Ser His Ser His His Arg
 180 185 190
 Asp Phe Asp Leu Asn Leu Pro Ala Phe Pro Asp Phe Ser Lys Lys Phe
 195 200 205
 Phe Val Asp Asp Glu Val Phe Ser Pro Leu Pro Ala Ala Lys Lys Pro
 210 215 220
 Cys Leu Phe Lys Leu Glu Ile Pro Ser His Tyr
 225 230 235

<210> 16
 <211> 1061
 <212> DNA
 <213> Nicotiana tabacum

<400> 16
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 ggattcttgg gctaaaggaa aacgatcaaa acggccccgt attgatgccc caccgactga 180
 agaagagtat ttagccctct gtctcatcat gctcgtctgc agcgggaaccg gaaccagaac 240
 cgggtttaact gatgctacta cttcccaaca acctgccgat aaaaaaacg ccgagttgcc 300
 gccggttcat aagaaagagg tggcaacaga gcaagcagag caatcttaca agtgtagcgt 360
 gtgtgacaag gctttttctt cttatcaagc actcgggtggg cataaagcaa gtcaccgtaa 420
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 ccacaaggct tttcctactg gccaaagcttt ggggtgggcac aagcgccgcc actatgaagg 600
 caaactcggg ggtaacagcc gcgacttagg cggcgccggc ggcggcggtc atagtgaag 660
 cgtcttgact acttcagacg gcggcgcgct gactcacacg ctacgtgact ttgacctgaa 720

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gttttcgttg ggttgaaact tctttagggg aattgaattg attgtgtttt agccaaatta 900
gtaaattggg tcatgtgatt ttatttttag gaaaaggaat tattgattgt tttaccggtt 960
tattcttagg gtggtattat gtacagggag tgaatcattc attggtttta cactttctta 1020
attatatatt cttttttttt acacataaaa aaaaaaaaaa a 1061

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<210> 17
 <211> 273
 <212> PRT
 <213> Nicotiana tabacum

<400> 17
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 1 5 10 15
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 20 25 30
 Ala Lys Gly Lys Arg Ser Lys Arg Pro Arg Ile Asp Ala Pro Pro Thr
 35 40 45
 Glu Glu Glu Tyr Leu Ala Leu Cys Leu Ile Met Leu Ala Arg Ser Gly
 50 55 60
 Thr Gly Thr Arg Thr Gly Leu Thr Asp Ala Thr Thr Ser Gln Gln Pro
 65 70 75 80
 Ala Asp Lys Lys Thr Ala Glu Leu Pro Pro Val His Lys Lys Glu Val
 85 90 95
 Ala Thr Glu Gln Ala Glu Gln Ser Tyr Lys Cys Ser Val Cys Asp Lys
 100 105 110
 Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
 115 120 125
 Lys Thr Thr Thr Thr Ala Thr Ala Ala Ser Asp Asp Asn Asn Pro Ser
 130 135 140
 Thr Ser Thr Ser Thr Gly Ala Val Asn Ile Ser Ala Leu Asn Pro Thr
 145 150 155 160
 Gly Arg Ser His Val Cys Ser Ile Cys His Lys Ala Phe Pro Thr Gly
 165 170 175
 Gln Ala Leu Gly Gly His Lys Arg Arg His Tyr Glu Gly Lys Leu Gly
 180 185 190
 Gly Asn Ser Arg Asp Leu Gly Gly Gly Gly Gly Gly His Ser Gly
 195 200 205
 Ser Val Leu Thr Thr Ser Asp Gly Gly Ala Ser Thr His Thr Leu Arg
 210 215 220
 Asp Phe Asp Leu Asn Met Pro Ala Ser Pro Glu Leu Gln Leu Gly Leu
 225 230 235 240

Ser Ile Asp Cys Gly Arg Lys Ser Gln Leu Leu Pro Met Val Gln Glu
245 250 255

Val Glu Ser Pro Met Pro Ala Lys Lys Pro Arg Leu Leu Phe Ser Leu
260 265 270

Gly

<210> 18
<211> 1213
<212> DNA
<213> Oryza sativa

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agcagcagca gcacgaggtg gaggaggcga cggtcgtgac gagcagcagc gccacgagcg 240
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gcgtccaggc gccgcctccg ctctcggctt cggcgccccc gccggcaggt gcggagttca 420
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ccgacggcat gaccaacaga gtccacaggt gttccatctg ccagaaggag ttccccaccg 660
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gcaacggcca gtccgccacc cgggcgttcg acctcaacct cccggccgtg ccggagttcg 840
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agccatacat acagtcatac agatataggt ctagctcttc cttggttctt tgtaacactg 1140
gaactgtacc tgtatctttt acactttgtt ctttgacagt catatattgt agaccaaaaa 1200
aaaaaaaaaaa aaa 1213

<210> 19
<211> 269
<212> PRT
<213> Oryza sativa

<400> 19

Met Ser Ser Ala Ser Ser Met Glu Ala Leu His Ala Ala Val Leu Lys
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Glu Glu Gln Gln Gln His Glu Val Glu Glu Ala Thr Val Val Thr Ser
20 25 30
Ser Ser Ala Thr Ser Gly Glu Glu Gly Gly His Leu Pro Gln Gly Trp
35 40 45
Ala Lys Arg Lys Arg Ser Arg Arg Gln Arg Ser Glu Glu Glu Asn Leu
50 55 60
Ala Leu Cys Leu Leu Met Leu Ala Arg Gly Gly His His Arg Val Gln
65 70 75 80

Ala Pro Pro Pro Leu Ser Ala Ser Ala Pro Pro Pro Ala Gly Ala Glu
85 90 95

Phe Lys Cys Ser Val Cys Gly Lys Ser Phe Ser Ser Tyr Gln Ala Leu
100 105 110

Gly Gly His Lys Thr Ser His Arg Val Lys Leu Pro Thr Pro Pro Ala
115 120 125

Ala Pro Val Leu Ala Pro Ala Pro Val Ala Ala Leu Leu Pro Ser Ala
130 135 140

Glu Asp Arg Glu Pro Ala Thr Ser Ser Thr Ala Ala Ser Ser Asp Gly
145 150 155 160

Met Thr Asn Arg Val His Arg Cys Ser Ile Cys Gln Lys Glu Phe Pro
165 170 175

Thr Gly Gln Ala Leu Gly Gly His Lys Arg Lys His Tyr Asp Gly Gly
180 185 190

Val Gly Ala Gly Ala Gly Ala Ser Ser Thr Glu Leu Leu Ala Thr Val
195 200 205

Ala Ala Glu Ser Glu Val Gly Ser Ser Gly Asn Gly Gln Ser Ala Thr
210 215 220

Arg Ala Phe Asp Leu Asn Leu Pro Ala Val Pro Glu Phe Val Trp Arg
225 230 235 240

Pro Cys Ser Lys Gly Lys Lys Met Trp Asp Glu Glu Glu Glu Val Gln
245 250 255

Ser Pro Leu Ala Phe Lys Lys Pro Arg Leu Leu Thr Ala
260 265

<210> 20

<211> 1020

<212> DNA

<213> Petunia x hybrida

<400> 20

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aatacaaaca	agaaaatfff	ctctctatac	ttgattgagt	ttagtaaggc	aaacaagaaa	180
actatcatgg	cacttgaagc	attgaattct	ccaactacaa	caacaccacc	atcattccaa	240
tttgagaaca	acgggcttaa	gtaccttgag	agttggacaa	aaggtaaaaag	atcaaaaagg	300
caacgcagca	tggaacgaca	gtgtactgaa	gaagagtatt	tagcactttg	tcttatcatg	360
ctagcacgta	gcgatgggtc	tgtaataaac	tcacgggtctc	taccaccacc	accactacca	420
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agtcaccgga	aacttgtcag	catgggagga	gatgaacaat	ctactacttc	cactactact	600
aacgtaacgg	gaactagttc	cgctaacggt	aacggtaacg	gaagaactca	cgaatgttca	660
atgtgtcaca	agtgttttcc	tactggacaa	gcttttaggtg	gtcataaaaag	gtgccactat	720
gacgggtggt	acggtaacgg	taacggaagt	gtaagtgttg	gggtgacgtc	atctgaaggt	780
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ttttggccgg	gatttggttc	cggcgaggat	gaggtggaga	gtcctcatcc	agcaaagaag	900

tcaaggctat ctcttccacc taaacttgaa ttattcaaag gattatagag ggaatattga 960
 tttgttacag gaagatttat taggattcac gaattttttg ttgactagtt tatgtaatat 1020

<210> 21
 <211> 253
 <212> PRT
 <213> Petunia x hybrida

<400> 21
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 Gly Lys Arg Ser Lys Arg Gln Arg Ser Met Glu Arg Gln Cys Thr Glu
 35 40 45
 Glu Glu Tyr Leu Ala Leu Cys Leu Ile Met Leu Ala Arg Ser Asp Gly
 50 55 60
 Ser Val Asn Asn Ser Arg Ser Leu Pro Pro Pro Pro Leu Pro Pro Ser
 65 70 75 80
 Val Pro Val Thr Ser Gln Ile Asn Ala Thr Leu Leu Glu Gln Lys Asn
 85 90 95
 Leu Tyr Lys Cys Ser Val Cys Gly Lys Gly Phe Gly Ser Tyr Gln Ala
 100 105 110
 Leu Gly Gly His Lys Ala Ser His Arg Lys Leu Val Ser Met Gly Gly
 115 120 125
 Asp Glu Gln Ser Thr Thr Ser Thr Thr Thr Asn Val Thr Gly Thr Ser
 130 135 140
 Ser Ala Asn Val Asn Gly Asn Gly Arg Thr His Glu Cys Ser Ile Cys
 145 150 155 160
 His Lys Cys Phe Pro Thr Gly Gln Ala Leu Gly Gly His Lys Arg Cys
 165 170 175
 His Tyr Asp Gly Gly Asn Gly Asn Gly Asn Gly Ser Val Ser Val Gly
 180 185 190
 Val Thr Ser Ser Glu Gly Val Gly Ser Thr Ile Ser His His Arg Asp
 195 200 205
 Phe Asp Leu Asn Ile Pro Ala Leu Pro Glu Phe Trp Pro Gly Phe Gly
 210 215 220
 Ser Gly Glu Asp Glu Val Glu Ser Pro His Pro Ala Lys Lys Ser Arg
 225 230 235 240
 Leu Ser Leu Pro Pro Lys Leu Glu Leu Phe Lys Gly Leu
 245 250

<210> 22
 <211> 786
 <212> DNA
 <213> Triticum aestivum

<400> 22
 atgtcgctcgt cggccatgga agcgctccac gccctgatcc cggagcagca ccagctggac 60
 gttgaggcgg ctgcggctgt cagcagcgcc accagcggcg aggagagcgg ccacgtgctg 120
 caggggtggg ccaagaggaa gcgatcgcg cgcagcgct ccgaggagga gaacctcgcg 180
 ctctgcctcc tcatgctctc gcgcggcggc aagcagcgtg ttcaggcgcc gcagccggag 240
 tcgttcgctg cgccgggtgcc tgccgagttc aagtgtctcg tctgcggcaa gtccttcagc 300
 tcctaccagg cgctcggagg ccacaagacg agccaccggg tgaagcagcc gtctcctccc 360
 tctgatgccg ctgctgcccc actcgtggcc ctcccggccg tcgcggccat cctgcggtcc 420
 gccgagccgg ccacgtcgtc caccgcccgc tcctccgacg gcgcgaccaa cagagtccac 480
 aggtgctcca tctgcaaaaa ggagttcccg actgggcagg cgctcggcgg gcacaagagg 540
 aagcactacg acggaggcgt gggcgccgcc gcctcgtcga ccgagcttct ggccgccgcg 600
 gccgccgagt ctgaggtggg gagcaccggc aacgggagct ccgccgcccg ggccttcgac 660
 ctgaacattc cggccgtgcc ggagttcgtg tggaggccgt gcgccaaggg caagatgatg 720
 tgggaggacg atgaggaggt gcagagcccc ctgccttca agaagcctcg gcttctcacc 780
 gcttga 786

<210> 23
 <211> 261
 <212> PRT
 <213> Triticum aestivum

<400> 23
 Met Ser Ser Ser Ala Met Glu Ala Leu His Ala Leu Ile Pro Glu Gln
 1 5 10 15
 His Gln Leu Asp Val Glu Ala Ala Ala Val Ser Ser Ala Thr Ser
 20 25 30
 Gly Glu Glu Ser Gly His Val Leu Gln Gly Trp Ala Lys Arg Lys Arg
 35 40 45
 Ser Arg Arg Gln Arg Ser Glu Glu Glu Asn Leu Ala Leu Cys Leu Leu
 50 55 60
 Met Leu Ser Arg Gly Gly Lys Gln Arg Val Gln Ala Pro Gln Pro Glu
 65 70 75 80
 Ser Phe Ala Ala Pro Val Pro Ala Glu Phe Lys Cys Ser Val Cys Gly
 85 90 95
 Lys Ser Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Thr Ser His
 100 105 110
 Arg Val Lys Gln Pro Ser Pro Pro Ser Asp Ala Ala Ala Ala Pro Leu
 115 120 125
 Val Ala Leu Pro Ala Val Ala Ala Ile Leu Pro Ser Ala Glu Pro Ala
 130 135 140
 Thr Ser Ser Thr Ala Ala Ser Ser Asp Gly Ala Thr Asn Arg Val His
 145 150 155 160
 Arg Cys Ser Ile Cys Gln Lys Glu Phe Pro Thr Gly Gln Ala Leu Gly

[illegible]

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<210> 24
<211> 1026
<212> DNA
<213> Capsicum annum
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<400>	24						
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accgtttcaa	tttgagagcg	acggccaaca	gcttcgatat	atcgaaaact	ggaggaaggg		180
aaagagatct	aaaaggtcac	gcagcatgga	gcaccagcct	actgaggaag	aatacttagc		240
gctttgtttg	atcatgcttg	cacgtagcgg	tggctccgtt	aatcatcaac	gatctctacc		300
accgccggct	ccggtgatga	aactgcacgc	gccgtcgtca	tcatcggcgg	cggaggagga		360
gaaggagaag	atggtgtata	agtgttcggg	ttgtggttaag	ggatttgggt	cttatcaagc		420
tttaggtgga	cacaaagcta	gtcaccggaa	actcgtaccc	ggcggagatg	atcagtcaac		480
tacctccaca	accactaacg	caaccggaac	aacaacctcc	gttaacggca	acggcaacag		540
aagtggaagg	actcacgagt	gttcgatttg	tcacaagtgt	tttcccactg	gacaagcttt		600
aggtggacac	aaaaggtgtc	actacgacgg	cggtatcggg	aacggaaacg	ctaacagtgg		660
cgttagtgct	agcgttggag	tgacgtcadc	ggaggggtgtg	gggtccacag	tcagtcaccg		720
ggatttcgac	ttgaacattc	cggcgttgcc	ggaattctgg	ctgggatttg	gttcgggcga		780
agatgaggtg	gagagtccac	atccggcgaa	gaaatcgcgg	ttatgttttg	ctccaaaata		840
tgaattatth	caacattaat	gggaatttga	ttgttaggat	ttactattht	ggtagacaaa		900
attatactat	gtaagthtth	atthtcatth	tgggtgggag	caaatthtth	aatthtthtgt		960
ctatagacct	agctagtht	taatagcaaa	aattcaattg	attgattth	aaaaaaaaaa		1020
aaaaaa							1026

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<210> 25
<211> 261
<212> PRT
<213> Capsicum annum
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<400>    25
Met Ala Leu Glu Ala Leu Asn Ser Pro Thr Gly Thr Pro Thr Pro Pro
 1              5              10              15

Pro Phe Gln Phe Glu Ser Asp Gly Gln Gln Leu Arg Tyr Ile Glu Asn
      20              25              30

Trp Arg Lys Gly Lys Arg Ser Lys Arg Ser Arg Ser Met Glu His Gln

```

35	40	45
Pro Thr Glu Glu Glu Tyr Leu Ala Leu Cys Leu Ile Met Leu Ala Arg		
50	55	60
Ser Gly Gly Ser Val Asn His Gln Arg Ser Leu Pro Pro Pro Ala Pro		
65	70	75
Val Met Lys Leu His Ala Pro Ser Ser Ser Ser Ala Ala Glu Glu Glu		
	85	90
Lys Glu Lys Met Val Tyr Lys Cys Ser Val Cys Gly Lys Gly Phe Gly		
	100	105
Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Lys Leu Val		
	115	120
Pro Gly Gly Asp Asp Gln Ser Thr Thr Ser Thr Thr Thr Asn Ala Thr		
	130	135
Gly Thr Thr Thr Ser Val Asn Gly Asn Gly Asn Arg Ser Gly Arg Thr		
145	150	155
His Glu Cys Ser Ile Cys His Lys Cys Phe Pro Thr Gly Gln Ala Leu		
	165	170
Gly Gly His Lys Arg Cys His Tyr Asp Gly Gly Ile Gly Asn Gly Asn		
	180	185
Ala Asn Ser Gly Val Ser Ala Ser Val Gly Val Thr Ser Ser Glu Gly		
	195	200
Val Gly Ser Thr Val Ser His Arg Asp Phe Asp Leu Asn Ile Pro Ala		
	210	215
Leu Pro Glu Phe Trp Leu Gly Phe Gly Ser Gly Glu Asp Glu Val Glu		
225	230	235
Ser Pro His Pro Ala Lys Lys Ser Arg Leu Cys Leu Pro Pro Lys Tyr		
	245	250
Glu Leu Phe Gln His		
	260	

<210> 26
 <211> 1068
 <212> DNA
 <213> Arabidopsis thaliana

<400> 26
 acttcactct ctaatttctt tctctctatc tctcaccata ttcgcgatta aaaactctca 60
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 tggccctcga agcgatgaac actccaactt cttctttcac cagaatcgaa acgaaagaag 180
 atttgatgaa cgacgccgtt ttcattgagc cgtggcttaa acgcaaacgc tccaaacgtc 240
 agcgtttctca cagcccttct tcgtcttctt cctcaccgcc tcgatctcga cccaaatccc 300
 agaatcaaga tcttacggaa gaagagtatc tcgctctttg tctcctcatg ctcgctaaag 360
 atcaaccgtc gcaaacgcga tttcatcaac agtcgcaatc gttaacgccg ccgccagaat 420
 caaagaacct tccgtacaag tgtaacgtct gtgaaaaagc gtttccttcc tatcaggctt 480

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taggcggtca caaagcaagt caccgaatca aaccaccaac cgtaatctca acaaccgccg 540
atgattcaac agctccgacc atctccatcg tcgccggaga aaaacatccg attgctgcct 600
ccggaaagat ccacgagtgt tcaatctgtc ataaagtgtt tccgacgggt caagcttttag 660
gcggtcacia acgttgtcac tacgaaggca acctcggcgg cggaggagga ggaggaagca 720
aatcaatcag tcacagtgga agcgtgtcga gcacgggtatc ggaagaaagg agccaccgtg 780
gattcatcga tctaaacctt ccggcgttac ctgaactcag ccttcatcac aatccaatcg 840
tcgacgaaga gatcttgagt ccgttgaccg gtaaaaaacc gcttttgttg accgatcacg 900
accaagtcac caagaaagaa gatttatctt taaaaatcta atactcgact attaattctt 960
gtgtgatttt tttcgttaca accatagttt cattttcatt tttttagtta caaattttta 1020
attgttctga tttggattga atattggtat attgttaggg gttgatac 1068

```

<210> 27

<211> 273

<212> PRT

<213> Arabidopsis thaliana

<400> 27

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Met Ala Leu Glu Ala Met Asn Thr Pro Thr Ser Ser Phe Thr Arg Ile
1           5           10          15

```

```

Glu Thr Lys Glu Asp Leu Met Asn Asp Ala Val Phe Ile Glu Pro Trp
20          25          30

```

```

Leu Lys Arg Lys Arg Ser Lys Arg Gln Arg Ser His Ser Pro Ser Ser
35          40          45

```

```

Ser Ser Ser Ser Pro Pro Arg Ser Arg Pro Lys Ser Gln Asn Gln Asp
50          55          60

```

```

Leu Thr Glu Glu Glu Tyr Leu Ala Leu Cys Leu Leu Met Leu Ala Lys
65          70          75          80

```

```

Asp Gln Pro Ser Gln Thr Arg Phe His Gln Gln Ser Gln Ser Leu Thr
85          90          95

```

```

Pro Pro Pro Glu Ser Lys Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu
100         105         110

```

```

Lys Ala Phe Pro Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His
115         120         125

```

```

Arg Ile Lys Pro Pro Thr Val Ile Ser Thr Thr Ala Asp Asp Ser Thr
130         135         140

```

```

Ala Pro Thr Ile Ser Ile Val Ala Gly Glu Lys His Pro Ile Ala Ala
145         150         155         160

```

```

Ser Gly Lys Ile His Glu Cys Ser Ile Cys His Lys Val Phe Pro Thr
165         170         175

```

```

Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Asn Leu
180         185         190

```

```

Gly Gly Gly Gly Gly Gly Gly Ser Lys Ser Ile Ser His Ser Gly Ser
195         200         205

```

```

Val Ser Ser Thr Val Ser Glu Glu Arg Ser His Arg Gly Phe Ile Asp
210         215         220

```

Leu Asn Leu Pro Ala Leu Pro Glu Leu Ser Leu His His Asn Pro Ile
225 230 235 240

Val Asp Glu Glu Ile Leu Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu
245 250 255

Leu Thr Asp His Asp Gln Val Ile Lys Lys Glu Asp Leu Ser Leu Lys
260 265 270

Ile

<210> 28

<211> 976

<212> DNA

<213> Arabidopsis thaliana

<400> 28

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ttcaagataa tggcacttga aactcttact tctccaagat tatcttctcc gatgccgact    120
ctgtttcaag attcagcact agggtttcat ggaagcaaag gcaaacgatc taagcgatca    180
agatctgaat tcgaccgtca gagtctcacg gaggatgaat atatecgttt atgtctcatg    240
cttcttgctc gcgacggaga tagaaaccgt gaccttgacc tgccttcttc ttcgtcttca    300
cctcctctgc ttcctcctct tcctactccg atctacaagt gtagcgtctg tgacaaggcg    360
ttttcgtctt accaggctct tgggtggacac aaggcaagtc accggaaaag cttttcgtct    420
actcaatctg ccggaggaga tgagctgtcg acatcgtcgg cgataaccac gtctggtata    480
tccggtggcg ggggaggaag tgtgaagtcg cacgtttgct ctatctgtca taaatcgttc    540
gccaccggtc aagctctcgg cggccacaaa cggtgccact acgaaggaaa gaacggagggc    600
ggtgtgagta gtagcgtgtc gaattctgaa gatgtggggg ctacaagcca cgtcagcagt    660
ggccaccgtg ggtttgacct caacataccg ccgataccgg aattctcgat ggtcaacgga    720
gacgaagagg tgatgagtc tttgcccggc aagaaactcc ggtttgactt cccggagaaa    780
ccctaaacat aaacctagga aaaactttac agaattcatt ttataggaaa ttgttttact    840
gtatatacaa atatecgattt tgattgatgt tcttcttcac tgaaaaatta tgattctttg    900
ttgtataatt gatgtttctg aaaaagatat aactttttat tgtttcacac gtatcaaaat    960
ttgcttggat acatca                                     976

```

<210> 29

<211> 238

<212> PRT

<213> Arabidopsis thaliana

<400> 29

Met Ala Leu Glu Thr Leu Thr Ser Pro Arg Leu Ser Ser Pro Met Pro
1 5 10 15

Thr Leu Phe Gln Asp Ser Ala Leu Gly Phe His Gly Ser Lys Gly Lys
20 25 30

Arg Ser Lys Arg Ser Arg Ser Glu Phe Asp Arg Gln Ser Leu Thr Glu
35 40 45

Asp Glu Tyr Ile Ala Leu Cys Leu Met Leu Leu Ala Arg Asp Gly Asp
50 55 60

Arg Asn Arg Asp Leu Asp Leu Pro Ser Ser Ser Ser Ser Pro Pro Leu
65 70 75 80

Leu Pro Pro Leu Pro Thr Pro Ile Tyr Lys Cys Ser Val Cys Asp Lys
 85 90 95
 Ala Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser His Arg
 100 105 110
 Lys Ser Phe Ser Leu Thr Gln Ser Ala Gly Gly Asp Glu Leu Ser Thr
 115 120 125
 Ser Ser Ala Ile Thr Thr Ser Gly Ile Ser Gly Gly Gly Gly Gly Ser
 130 135 140
 Val Lys Ser His Val Cys Ser Ile Cys His Lys Ser Phe Ala Thr Gly
 145 150 155 160
 Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Glu Gly Lys Asn Gly
 165 170 175
 Gly Gly Val Ser Ser Ser Val Ser Asn Ser Glu Asp Val Gly Ser Thr
 180 185 190
 Ser His Val Ser Ser Gly His Arg Gly Phe Asp Leu Asn Ile Pro Pro
 195 200 205
 Ile Pro Glu Phe Ser Met Val Asn Gly Asp Glu Glu Val Met Ser Pro
 210 215 220
 Met Pro Ala Lys Lys Leu Arg Phe Asp Phe Pro Glu Lys Pro
 225 230 235

<210> 30
 <211> 718
 <212> DNA
 <213> Arabidopsis thaliana

<400> 30
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 ttcctccggtt gcctcgacga aaccgagccc gaaaacctcg aatcatggac caaaagaaaa 120
 cgtacaaaac gtcaccgtat agatcaacca aacctcctc cttctgaaga agagtatctc 180
 gctctttgcc tccttatgct cgctcgtggc tcctccgatc atcactctcc accgtcggat 240
 catcactctc tttctccact gtccgatcat cagaaagatt acaagtgttc cgtctgtggc 300
 aaatctttcc cgtcttacca agcgtaggt ggacacaaaa caagtcaccg gaaaccggtt 360
 agtgtcgatg ttaataatag taacggaacc gttactaata acggaaatat tagtaacggt 420
 ttagttggtc aaagtgggaa gactcataac tgctctatat gttttaagtc gtttccctct 480
 ggtcaagcat tgggtgggtca caaacgttgt cactatgatg gtggtaacgg taacagtaac 540
 ggtgacaata gccacaagtt tgacctaaat ttaccggctg atcaagttag tgatgagaca 600
 attggaaaaa gtcaactctc cgggtgaagaa acaaagtcgg tgttgtgatt attattattt 660
 tttaccgatc gggattagct agtggttgat cattagctga gtctgtaatg aaaatgat 718

<210> 31
 <211> 215
 <212> PRT
 <213> Arabidopsis thaliana

<400> 31
 Met Ala Leu Asp Thr Leu Asn Ser Pro Thr Ser Thr Thr Thr Thr Thr
 1 5 10 15

Ala Pro Pro Pro Phe Leu Arg Cys Leu Asp Glu Thr Glu Pro Glu Asn
 20 25 30
 Leu Glu Ser Trp Thr Lys Arg Lys Arg Thr Lys Arg His Arg Ile Asp
 35 40 45
 Gln Pro Asn Pro Pro Pro Ser Glu Glu Glu Tyr Leu Ala Leu Cys Leu
 50 55 60
 Leu Met Leu Ala Arg Gly Ser Ser Asp His His Ser Pro Pro Ser Asp
 65 70 75 80
 His His Ser Leu Ser Pro Leu Ser Asp His Gln Lys Asp Tyr Lys Cys
 85 90 95
 Ser Val Cys Gly Lys Ser Phe Pro Ser Tyr Gln Ala Leu Gly Gly His
 100 105 110
 Lys Thr Ser His Arg Lys Pro Val Ser Val Asp Val Asn Asn Ser Asn
 115 120 125
 Gly Thr Val Thr Asn Asn Gly Asn Ile Ser Asn Gly Leu Val Gly Gln
 130 135 140
 Ser Gly Lys Thr His Asn Cys Ser Ile Cys Phe Lys Ser Phe Pro Ser
 145 150 155 160
 Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Asp Gly Gly Asn
 165 170 175
 Gly Asn Ser Asn Gly Asp Asn Ser His Lys Phe Asp Leu Asn Leu Pro
 180 185 190
 Ala Asp Gln Val Ser Asp Glu Thr Ile Gly Lys Ser Gln Leu Ser Gly
 195 200 205
 Glu Glu Thr Lys Ser Val Leu
 210 215

<210> 32
 <211> 702
 <212> DNA
 <213> Arabidopsis thaliana

<400> 32
 aaatttttcta tagcaatggc gcttgaagct cttaattcac caagattggt cgaggatccc 60
 ttaagattca atggcggtga gcagtggacc aaatgtaaga aacgatccaa acgttcgaga 120
 tctgatcttc atcataacca ccgtctcact gaggaagagt atctagcttt ctgtctcatg 180
 cttcttgctc gggatggcgg cgatcttgac tctgtgacgg ttgcggagaa gccgagttat 240
 aagtgtggcg tttgttacia gacgttttcg tcttaccag ctctcggcgg tcataaagcg 300
 agccaccgga gcttatacgg tgggtggagag aatgataaat cgacaccatc caccgccgtg 360
 aaatctcacg tttgttcggt ttgcgggaaa tctttcgcca ccggtcaagc tctcggcggc 420
 cacaagcggg gccactacga tgggtggcgtt tcgaactcgg aagggtgtggg gtctactagc 480
 cacgtcagca gtagtagcca ccgtggattt gaccttaata ttataccggt gcagggattt 540
 tcgccggacg acgaagtgat gagtccgatg gcgactaaga agcctcgcct gaagtaagtc 600
 tttgttgaag acctggaagt ttatcaaag taaatatcaa atttcaattt caaggaacag 660
 ttttgttgat tctattacca atacacaata cgattcaatt cc 702

<210> 33
 <211> 193
 <212> PRT
 <213> Arabidopsis thaliana

<400> 33
 Met Ala Leu Glu Ala Leu Asn Ser Pro Arg Leu Val Glu Asp Pro Leu
 1 5 10 15
 Arg Phe Asn Gly Val Glu Gln Trp Thr Lys Cys Lys Lys Arg Ser Lys
 20 25 30
 Arg Ser Arg Ser Asp Leu His His Asn His Arg Leu Thr Glu Glu Glu
 35 40 45
 Tyr Leu Ala Phe Cys Leu Met Leu Leu Ala Arg Asp Gly Gly Asp Leu
 50 55 60
 Asp Ser Val Thr Val Ala Glu Lys Pro Ser Tyr Lys Cys Gly Val Cys
 65 70 75 80
 Tyr Lys Thr Phe Ser Ser Tyr Gln Ala Leu Gly Gly His Lys Ala Ser
 85 90 95
 His Arg Ser Leu Tyr Gly Gly Gly Glu Asn Asp Lys Ser Thr Pro Ser
 100 105 110
 Thr Ala Val Lys Ser His Val Cys Ser Val Cys Gly Lys Ser Phe Ala
 115 120 125
 Thr Gly Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Asp Gly Gly
 130 135 140
 Val Ser Asn Ser Glu Gly Val Gly Ser Thr Ser His Val Ser Ser Ser
 145 150 155 160
 Ser His Arg Gly Phe Asp Leu Asn Ile Ile Pro Val Gln Gly Phe Ser
 165 170 175
 Pro Asp Asp Glu Val Met Ser Pro Met Ala Thr Lys Lys Pro Arg Leu
 180 185 190
 Lys

<210> 34
 <211> 1157
 <212> DNA
 <213> Arabidopsis thaliana

<400> 34
 cacacttcac tcttttcttca tctttcttctt cttaaatagc tcgaaatcac atctcacaga 60
 attaaatctt atggctctcg agactctcaa ttctccaaca gctaccacca ccgctcggcc 120
 tcttctccgg tatcgtgaag aaatggagcc tgagaatctc gagcaatggg ctaaaagaaa 180
 acgaacaaaa cgtcaacggt ttgatcacgg tcatcagaat caagaaacga acaagaacct 240
 tccttctgaa gaagagtatc tcgctctttg tctcctcatg ctcgctcgtg gctccgccgt 300
 acaatctcct cctcttcctc ctctaccgtc acgtgcgtca ccgtccgatc accgagatta 360
 caagtgtacg gtctgtggga agtccttttc gtcataccaa gccttaggtg gacacaagac 420

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gagtcaccgg aaaccgacga acactagtat cacttccggt aaccaagaac tgtctaataa 480
cagtcacagt aacagcggtt ccgttggtat taacggtacc gtgaacactg gtaacggtgt 540
tagtcaaagc ggaaagattc acacttgtc aatctgtttc aagtcgtttg cgtctggtca 600
agccttaggt ggacacaaac ggtgtcacta tgacggtggc aacaacggta acggtaacgg 660
aagtagcagc aacagcgtag aactcgtcgc tggtagtgac gtcagcgatg ttgataatga 720
gagatggtcc gaagaaagtg cgatcggtgg ccaccgtgga tttgacctaa acttaccggc 780
tgatcaagtc tcagtgcga cttcttaacg ttgactgagt ttgaggaaaa agtcaactat 840
caagcgaaga aagggttagt ggacggtgaa gattaacggt cgtttctttc cagttgcttc 900
ggtttgagct tgactgggtc tgtaatgaaa atgattggag tggacttggc attattatta 960
ttatttttaa aaagaaatgt taatttggtt ttggatttgt ttatagatag aggaaacaat 1020
tgggatacac aaatatTTTT tttttttaca aagaaaataa taatgcagag atggatgatt 1080
ggatcgtaga cgttattata tagtggacca ttctgtaatc gtgaattatt attatttggt 1140
agaaatttaa ttttcgt 1157

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<210> 35
 <211> 245
 <212> PRT
 <213> Arabidopsis thaliana

<400> 35
 Met Ala Leu Glu Thr Leu Asn Ser Pro Thr Ala Thr Thr Thr Ala Arg
 1 5 10 15
 Pro Leu Leu Arg Tyr Arg Glu Glu Met Glu Pro Glu Asn Leu Glu Gln
 20 25 30
 Trp Ala Lys Arg Lys Arg Thr Lys Arg Gln Arg Phe Asp His Gly His
 35 40 45
 Gln Asn Gln Glu Thr Asn Lys Asn Leu Pro Ser Glu Glu Glu Tyr Leu
 50 55 60
 Ala Leu Cys Leu Leu Met Leu Ala Arg Gly Ser Ala Val Gln Ser Pro
 65 70 75 80
 Pro Leu Pro Pro Leu Pro Ser Arg Ala Ser Pro Ser Asp His Arg Asp
 85 90 95
 Tyr Lys Cys Thr Val Cys Gly Lys Ser Phe Ser Ser Tyr Gln Ala Leu
 100 105 110
 Gly Gly His Lys Thr Ser His Arg Lys Pro Thr Asn Thr Ser Ile Thr
 115 120 125
 Ser Gly Asn Gln Glu Leu Ser Asn Asn Ser His Ser Asn Ser Gly Ser
 130 135 140
 Val Val Ile Asn Val Thr Val Asn Thr Gly Asn Gly Val Ser Gln Ser
 145 150 155 160
 Gly Lys Ile His Thr Cys Ser Ile Cys Phe Lys Ser Phe Ala Ser Gly
 165 170 175
 Gln Ala Leu Gly Gly His Lys Arg Cys His Tyr Asp Gly Gly Asn Asn
 180 185 190
 Gly Asn Gly Asn Gly Ser Ser Ser Asn Ser Val Glu Leu Val Ala Gly
 195 200 205

Ser Asp Val Ser Asp Val Asp Asn Glu Arg Trp Ser Glu Glu Ser Ala
 210 215 220

Ile Gly Gly His Arg Gly Phe Asp Leu Asn Leu Pro Ala Asp Gln Val
 225 230 235 240

Ser Val Thr Thr Ser
 245

<210> 36
 <211> 1213
 <212> DNA
 <213> Oryza sativa

<400> 36
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 gtggaagcat gtcgagcgcg tcgtccatgg aagcgctcca cgccgcggtg ctcaaggagg 180
 agcagcagca gcacgaggtg gaggaggcga cggtcgtgac gagcagcagc gccacgagcg 240
 gggaggaggg cggacacctg ccccaggggt gggcgaagcg gaagcggtcg cgccgccagc 300
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 gcgtccaggc gccgcctccg ctctcggtt cggcgcccc gccggcaggt gcggagttca 420
 agtgctccgt ctgcggcaag tccttcagct cctaccaggc gtcggcggc cacaagacga 480
 gccaccgggt caagctgccg actccgccc cagctcccgt cttggtccc gccccgctcg 540
 ccgccttgct gccttccgcc gaggaccgcg agccagccac gtcattccacc gccgcgtcct 600
 ccgacggcat gaccaacaga gtccacaggt gttccatctg ccagaaggag ttccccaccg 660
 ggcaggcgct cggcgggcac aagaggaagc actacgacgg tggcgtaggc gccggcgccg 720
 gcgcattctc aaccgagctc ctggccacgg tggcgccga gtccgaggtg ggaagctccg 780
 gcaacggcca gtccgccacc cgggcgttcg acctcaacct cccggcgtg ccggagttcg 840
 tgtggcggcc gtgctccaag ggcaagaaga tgtgggacga ggaggaggag gtccagagcc 900
 ccctcgctt caagaagccc cggcttctca ccgcgtaatt cagcagctgc acggatccga 960
 tccgtcagag tttttgtcta gggagtgaat ttcagtcgaa acacactatt cgttgattcg 1020
 ttttgtgccg ctattgttta atttggtcct gcttttgtac agagcaagcg agtgatacat 1080
 agccatacat acagtcatac agatataggt ctagctcttc cttggttctt tgtaaacactg 1140
 gaactgtacc tgtatctttt acactttgtt ctttgacagt catatattgt agaccaaaaa 1200
 aaaaaaaaaaaa aaa 1213

<210> 37
 <211> 269
 <212> PRT
 <213> Oryza sativa

<400> 37
 Met Ser Ser Ala Ser Ser Met Glu Ala Leu His Ala Ala Val Leu Lys
 1 5 10 15
 Glu Glu Gln Gln Gln His Glu Val Glu Glu Ala Thr Val Val Thr Ser
 20 25 30
 Ser Ser Ala Thr Ser Gly Glu Glu Gly Gly His Leu Pro Gln Gly Trp
 35 40 45
 Ala Lys Arg Lys Arg Ser Arg Arg Gln Arg Ser Glu Glu Glu Asn Leu
 50 55 60
 Ala Leu Cys Leu Leu Met Leu Ala Arg Gly Gly His His Arg Val Gln
 65 70 75 80

Ala Pro Pro Pro Leu Ser Ala Ser Ala Pro Pro Pro Ala Gly Ala Glu
85 90 95

Phe Lys Cys Ser Val Cys Gly Lys Ser Phe Ser Ser Tyr Gln Ala Leu
100 105 110

Gly Gly His Lys Thr Ser His Arg Val Lys Leu Pro Thr Pro Pro Ala
115 120 125

Ala Pro Val Leu Ala Pro Ala Pro Val Ala Ala Leu Leu Pro Ser Ala
130 135 140

Glu Asp Arg Glu Pro Ala Thr Ser Ser Thr Ala Ala Ser Ser Asp Gly
145 150 155 160

Met Thr Asn Arg Val His Arg Cys Ser Ile Cys Gln Lys Glu Phe Pro
165 170 175

Thr Gly Gln Ala Leu Gly Gly His Lys Arg Lys His Tyr Asp Gly Gly
180 185 190

Val Gly Ala Gly Ala Gly Ala Ser Ser Thr Glu Leu Leu Ala Thr Val
195 200 205

Ala Ala Glu Ser Glu Val Gly Ser Ser Gly Asn Gly Gln Ser Ala Thr
210 215 220

Arg Ala Phe Asp Leu Asn Leu Pro Ala Val Pro Glu Phe Val Trp Arg
225 230 235 240

Pro Cys Ser Lys Gly Lys Lys Met Trp Asp Glu Glu Glu Glu Val Gln
245 250 255

Ser Pro Leu Ala Phe Lys Lys Pro Arg Leu Leu Thr Ala
260 265

<210> 38
<211> 528
<212> DNA
<213> Arabidopsis thaliana

<400> 38
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agcaaaacga accataataa ccaacttcgaa tgcaaaacgt gtaaccggaa atttgattcc 180
ttccaagctc ttggaggtca tagagctagc cacaagaaac ctaagctgat cgttgaccaa 240
gaacaggtga agcatcgtaa caaagagaat gatatgcata agtgtacaat ttgcgatcaa 300
atgtttggga ccggtcaagc tctaggcggc cacatgagaa agcataggac gagcatgata 360
accgagcaat cgattgtccc ttctgtgggt tattccagac cggtttttaa tcgttgacgt 420
agcagcaagg agatcttgga cttaaattcta actccattgg aaaatgatct tgtgttaatc 480
tttgggaaga atttggttcc acaaattgat ttgaagtttg tgaattag 528

<210> 39
<211> 175
<212> PRT
<213> Arabidopsis thaliana

<400> 39

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Met Lys Arg Asp Arg Ser Asp Tyr Glu Glu Ser Met Lys His Ile Asp
1          5          10          15

Ile Val Glu Ser Leu Met Met Leu Ser Arg Ser Phe Val Val Lys Gln
          20          25          30

Ile Asp Val Lys Gln Ser Thr Gly Ser Lys Thr Asn His Asn Asn His
          35          40          45

Phe Glu Cys Lys Thr Cys Asn Arg Lys Phe Asp Ser Phe Gln Ala Leu
          50          55          60

Gly Gly His Arg Ala Ser His Lys Lys Pro Lys Leu Ile Val Asp Gln
65          70          75          80

Glu Gln Val Lys His Arg Asn Lys Glu Asn Asp Met His Lys Cys Thr
          85          90          95

Ile Cys Asp Gln Met Phe Gly Thr Gly Gln Ala Leu Gly Gly His Met
          100          105          110

Arg Lys His Arg Thr Ser Met Ile Thr Glu Gln Ser Ile Val Pro Ser
          115          120          125

Val Val Tyr Ser Arg Pro Val Phe Asn Arg Cys Ser Ser Ser Lys Glu
          130          135          140

Ile Leu Asp Leu Asn Leu Thr Pro Leu Glu Asn Asp Leu Val Leu Ile
145          150          155          160

Phe Gly Lys Asn Leu Val Pro Gln Ile Asp Leu Lys Phe Val Asn
          165          170          175

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<210> 40

<211> 820

<212> DNA

<213> Saccharum officinarum

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<221> misc_feature

<222> (406)..(406)

<223> n can be any nucleotide

<220>

<221> misc_feature

<222> (581)..(582)

<223> n can be any nucleotide

<220>

<221> misc_feature

<222> (589)..(589)

<223> n can be any nucleotide

<400> 40

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cccacgacga ctacgtctcc ctctgcctca tggcgctcgc agccgcggga ggcggaggcc      120

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aagctgggttt aacaacgcag tacgctctga acacggctgc ctggacagcg acggcgcaag 180
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tgggcgggca caaggccagc caccgcaage cgacgctcgt acaggcacat gcgtcgtcct 300
cagccggagg cgcggcgtcg tcgtcggtaa caatgacctc ggccgtaggc agcagtgggc 360
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cgatggccgc caacgctgcg acaagggtgg gagaggagaa nnaagtcana aacccttggc 600
ggtcaagaga aggcggcttg ccggtccgct ttggacccta atttaacgat ttagaagtec 660
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ttttttatatt ttacaccct tttttttttt tagaagaaga 820

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<210> 41
 <211> 1509
 <212> DNA
 <213> Arabidopsis thaliana

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<400> 41
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ctcatcctct tctcctgtt actcctccct cttccttctt cttcttccct caatccggag 180
acctccgcgc tccaccgcgc ccaccaactc ctctctcttc tctcctctc cgagaagccc 240
tccctctcct cagcctcagc ccgcaccaaa aacaacaaga ccaccatcac aaccatgacc 300
accttattca agaaccacct tcaacctcca tggatgtcga ctacgatcat caccatcaag 360
atgatcatca taacctcgat gacgatgacc atgacgtcac cgttgctctt cacataggcc 420
ttccaagccc tagtgctcaa gagatggcct ctttgctcat gatgtcttct tcttctctt 480
cctcgaggac cactcatcat cagaggaca tgaatcaca gaaagacctc gaccatgagt 540
acagccacgg agctgtcggg ggaggagaag atgacgatga agattcagtc ggccggagacg 600
gcggtgtgag aatcagcaga ctcaacaagg gtcaatatgt gatccctaca ctttctcaga 660
ttctcattgg ccctactcag ttctcatgtc ctgtttgctt caaaaccttc aacagataca 720
ataacatgca gatgcataat tggggacatg gatcacaata cagaaaagga cctgaatctc 780
taaggggaac acaaccaaca ggaatgctaa ggcttccgtg ctattgctgc gcccaggct 840
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tattgcaaga caatgtagca gtctaacc aaacgggttat ttctatttgt 1440
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taaattatg 1509

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<210> 42
 <211> 383
 <212> PRT
 <213> Arabidopsis thaliana

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<400> 42
Met Thr Asp Pro Tyr Ser Asn Phe Phe Thr Asp Trp Phe Lys Ser Asn
1          5          10          15

Pro Phe His His Tyr Pro Asn Ser Ser Thr Asn Pro Ser Pro His Pro
20          25          30

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Leu Pro Pro Val Thr Pro Pro Ser Ser Phe Phe Phe Phe Pro Gln Ser
 35 40 45
 Gly Asp Leu Arg Arg Pro Pro Pro Pro Thr Pro Pro Pro Ser Pro
 50 55 60
 Pro Leu Arg Glu Ala Leu Pro Leu Leu Ser Leu Ser Pro Ala Asn Lys
 65 70 75 80
 Gln Gln Asp His His His Asn His Asp His Leu Ile Gln Glu Pro Pro
 85 90 95
 Ser Thr Ser Met Asp Val Asp Tyr Asp His His His Gln Asp Asp His
 100 105 110
 His Asn Leu Asp Asp Asp Asp His Asp Val Thr Val Ala Leu His Ile
 115 120 125
 Gly Leu Pro Ser Pro Ser Ala Gln Glu Met Ala Ser Leu Leu Met Met
 130 135 140
 Ser Ser Ser Ser Ser Ser Ser Arg Thr Thr His His His Glu Asp Met
 145 150 155 160
 Asn His Lys Lys Asp Leu Asp His Glu Tyr Ser His Gly Ala Val Gly
 165 170 175
 Gly Gly Glu Asp Asp Asp Glu Asp Ser Val Gly Gly Asp Gly Gly Cys
 180 185 190
 Arg Ile Ser Arg Leu Asn Lys Gly Gln Tyr Trp Ile Pro Thr Pro Ser
 195 200 205
 Gln Ile Leu Ile Gly Pro Thr Gln Phe Ser Cys Pro Val Cys Phe Lys
 210 215 220
 Thr Phe Asn Arg Tyr Asn Asn Met Gln Met His Met Trp Gly His Gly
 225 230 235 240
 Ser Gln Tyr Arg Lys Gly Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr
 245 250 255
 Gly Met Leu Arg Leu Pro Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn
 260 265 270
 Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu
 275 280 285
 Gln Thr His Tyr Lys Arg Lys His Gly Ile Lys Pro Phe Met Cys Arg
 290 295 300
 Lys Cys Gly Lys Ala Phe Ala Val Arg Gly Asp Trp Arg Thr His Glu
 305 310 315 320
 Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys
 325 330 335
 His Lys Arg Ser Leu Lys Asp His Ile Lys Ala Phe Gly Asn Gly His

340 345 350

Gly Ala Tyr Gly Ile Asp Gly Phe Asp Glu Glu Asp Glu Pro Ala Ser
355 360 365

Glu Val Glu Gln Leu Asp Asn Asp His Glu Ser Met Gln Ser Lys
370 375 380

<210> 43
<211> 1303
<212> DNA
<213> Arabidopsis thaliana

<400> 43

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taatccagct	tgttcgaatc	tcttcaacaa	tggatgtgac	cataatagct	tcaactattc	180
cacttctctc	tcttacattt	acaactctca	cggtagctac	tattactcta	ataccacaaa	240
ccctaattac	attaatcata	ctcataccac	ttccacttcc	cctaactcac	ccccactaag	300
agaagctctt	cctcttctta	gcttaagccc	cataaggcac	caagaacaac	aagaccaaca	360
ctatttcatg	gacacccatc	aaattagctc	ttcaaacttt	cttgatgac	ctcttgtgac	420
tgtggatctt	catctagggt	taccaaacta	cgggtgttgg	gagagcatta	ggagcaatat	480
tgctcctgat	gcaaccacgg	acgagcaaga	tcaagatcat	gaccgaggag	tagaagtcac	540
agttgagtc	caccttgatg	atgatgatga	tcatcatgga	gatctacaca	gaggtcatca	600
ctattggatt	cctactcctt	ctcagatttt	gattgggtcct	acacagttca	cttgtcctct	660
ttgcttcaag	acattcaaca	gatacaacaa	catgcagatg	cacatgtggg	gacacggctc	720
acaatacaga	aagggaccag	aatccttaag	aggaacccaa	ccaacaggaa	tgctaagact	780
accatgtttc	tgctgtgcac	ccggttgcaa	gaacaacatt	gaccaccac	gagccaagcc	840
tcttaaggac	tttcgaaccc	tccaaacaca	ttacaaacgt	aaacatgggt	ctaaaccatt	900
tgcttgtcgt	atgtgtggta	aggcctttgc	agtgaaggga	gattggagaa	cgcatgagaa	960
gaattgtgga	aagctttggg	attgctcttg	tggctcggat	tttaagcaca	agaggtcgct	1020
taaggaccat	gtcaaggcct	ttggaaatgg	tcatgttcct	tgtgggattg	atagttttgg	1080
aggagatcat	gaggactact	atgatgctgc	ttctgatatc	gagcaataag	atgatagcaa	1140
caacaatgag	tgtaatttag	gggttttgtt	tatttttcct	ctcatgcatt	agttgattgt	1200
atgcacgtgt	tcttttagttt	tggtcttcgg	atctttgttt	tattttgttt	tgagctgttt	1260
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<210> 44
<211> 337
<212> PRT
<213> Arabidopsis thaliana

<400> 44

Met	Ser	Asn	Pro	Ala	Cys	Ser	Asn	Leu	Phe	Asn	Asn	Gly	Cys	Asp	His
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Asn	Ser	Phe	Asn	Tyr	Ser	Thr	Ser	Leu	Ser	Tyr	Ile	Tyr	Asn	Ser	His
			20					25					30		
Gly	Ser	Tyr	Tyr	Tyr	Ser	Asn	Thr	Thr	Asn	Pro	Asn	Tyr	Ile	Asn	His
		35					40					45			
Thr	His	Thr	Thr	Ser	Thr	Ser	Pro	Asn	Ser	Pro	Pro	Leu	Arg	Glu	Ala
	50					55					60				
Leu	Pro	Leu	Leu	Ser	Leu	Ser	Pro	Ile	Arg	His	Gln	Glu	Gln	Gln	Asp
65					70				75						80

Gln His Tyr Phe Met Asp Thr His Gln Ile Ser Ser Ser Asn Phe Leu
 85 90 95
 Asp Asp Pro Leu Val Thr Val Asp Leu His Leu Gly Leu Pro Asn Tyr
 100 105 110
 Gly Val Gly Glu Ser Ile Arg Ser Asn Ile Ala Pro Asp Ala Thr Thr
 115 120 125
 Asp Glu Gln Asp Gln Asp His Asp Arg Gly Val Glu Val Thr Val Glu
 130 135 140
 Ser His Leu Asp Asp Asp Asp Asp His His Gly Asp Leu His Arg Gly
 145 150 155 160
 His His Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro Thr
 165 170 175
 Gln Phe Thr Cys Pro Leu Cys Phe Lys Thr Phe Asn Arg Tyr Asn Asn
 180 185 190
 Met Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly Pro
 195 200 205
 Glu Ser Leu Arg Gly Thr Gln Pro Thr Gly Met Leu Arg Leu Pro Cys
 210 215 220
 Phe Cys Cys Ala Pro Gly Cys Lys Asn Asn Ile Asp His Pro Arg Ala
 225 230 235 240
 Lys Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg Lys
 245 250 255
 His Gly Ser Lys Pro Phe Ala Cys Arg Met Cys Gly Lys Ala Phe Ala
 260 265 270
 Val Lys Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Leu Trp
 275 280 285
 Tyr Cys Ser Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys Asp
 290 295 300
 His Val Lys Ala Phe Gly Asn Gly His Val Pro Cys Gly Ile Asp Ser
 305 310 315 320
 Phe Gly Gly Asp His Glu Asp Tyr Tyr Asp Ala Ala Ser Asp Ile Glu
 325 330 335

Gln

<210> 45
 <211> 495
 <212> DNA
 <213> Arabidopsis thaliana

<400> 45
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60

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aaactcatta acagtagcga tccatcactt cttggatcct tgtctaaca gaaaactaaa 240
acggcgacgt ctcatccttg tccgatatgt ggcgtggagt ttccgatggg gcaagctctt 300
ggtggtcaca tgaggagaca taggagtgag aaagcctcac caggcacgtt ggttacacgt 360
tcttttttac cggagacgac gacggtgacg actttgaaaa aatcgagtag tgggaagaga 420
gtggcttggt tggacttaga ttcgatggag agtttagtca attggaagtt ggagttggga 480
agaacgattt cttga 495

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<210> 46
 <211> 164
 <212> PRT
 <213> Arabidopsis thaliana

<400> 46
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 1 5 10 15
 Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Cys Gly Gly Gly Gly
 20 25 30
 Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
 35 40 45
 Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys Leu Ile Asn
 50 55 60
 Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
 65 70 75 80
 Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
 85 90 95
 Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
 100 105 110
 Ser Pro Gly Thr Leu Val Thr Arg Ser Phe Leu Pro Glu Thr Thr Thr
 115 120 125
 Val Thr Thr Leu Lys Lys Ser Ser Ser Gly Lys Arg Val Ala Cys Leu
 130 135 140
 Asp Leu Asp Ser Met Glu Ser Leu Val Asn Trp Lys Leu Glu Leu Gly
 145 150 155 160
 Arg Thr Ile Ser

<210> 47
 <211> 1209
 <212> DNA
 <213> Arabidopsis thaliana

<400> 47
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 tactatgggtc taagggaaga ctcgaagaag aaaacccagg aatctccgga accaatgaag 180
 aagattttgt ttcgatgcga agaattgtga aaagggtttc ggtacgagaa atattttaag 240

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aatcatcgct cgatgatgca tttatcgccg aacgagaagg tttgtgaaga atccttgatg 300
actctgtctc gtagccttgg gtttgtgaag aagaagaaaa gatcaagact tggtaggtct 360
gggaagactt tatttactac gtttcttgaa ccgagttcta tttttgatgc gactgatgaa 420
gaattagaag tggcggattg tttgattcta ttgtctaaga gtgctcccaa ggttgtagac 480
gaattgaaaa gtcttttctga ggcagtacgt gttactcctg aaacacctga aagtagctat 540
gatttggggtt gtttgctcaa caagaaaccg agaaaagggtg gtgaattgga atctgggggtt 600
ttaagtaatg agcaaagact tatggaagaa gggtttagta gttatggaac atcgaaagaa 660
ccagctagct tcttgagaga cgaaaacaga ttggatcagc agaaacggag aaaagatggg 720
gaatttgaat ccggactttt gagtaatgag caaagactgc tagaagaaga gattactact 780
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<210> 48
 <211> 402
 <212> PRT
 <213> Arabidopsis thaliana

<400> 48

Met Glu Asp Glu His Gln Asp Leu His Lys Pro Ile Asn Gly Ala Leu
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Arg Asp Leu Lys Ile Thr Arg Ser Gln Lys Glu Thr Glu Lys Ser Thr
20 25 30

Asn Gln Gln Gln Asp Val Thr Cys Tyr Tyr Gly Leu Arg Glu Asn Ser
35 40 45

Lys Lys Lys Thr Gln Glu Ser Pro Glu Pro Met Lys Lys Ile Leu Phe
50 55 60

Arg Cys Glu Glu Cys Gly Lys Gly Phe Arg Tyr Glu Lys Tyr Phe Lys
65 70 75 80

Asn His Arg Ser Met Met His Leu Ser Pro Asn Glu Lys Val Cys Glu
85 90 95

Glu Ser Leu Met Thr Leu Ser Arg Ser Leu Gly Phe Val Lys Lys Lys
100 105 110

Lys Arg Ser Arg Leu Gly Arg Ser Gly Lys Thr Leu Phe Thr Thr Phe
115 120 125

Leu Glu Pro Ser Ser Ile Phe Asp Ala Thr Asp Glu Glu Leu Glu Val
130 135 140

Ala Asp Cys Leu Ile Leu Leu Ser Lys Ser Ala Pro Lys Val Val Asp
145 150 155 160

Glu Leu Lys Ser Leu Ser Glu Ala Val Arg Val Thr Pro Glu Thr Pro
165 170 175

Glu Ser Ser Tyr Asp Leu Gly Cys Leu Leu Asn Lys Lys Pro Arg Lys

<400>	49						
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atcataaaaag	ggaaacgtac	gaagcgacaa	agatcgtctt	cgacgtttgt	ggtgacggcg		240
gcgacaacag	tgacttcaac	aagttcatcg	gccggtggaa	gtggaggaga	aagagctggt		300
tcagatgaat	acaactcggc	ggtttcgtct	ccggtgacta	ctgattgtac	gcaagaagaa		360
gaagacatgg	cgatttgtct	catcatgtta	gctcgtggga	cagttcttcc	atcgccggat		420
ctcaagaact	cgagaaaaat	tcatcagaag	atttcgtcgg	agaattctag	tttctatgtg		480

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tacgagtgtgta aaacgtgtaa ccggacgttt tcgtcgttcc aagcacttgg tggacacaga 540
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cccaagtcta gtgcatcaga agaagggcaa aacagtcatt tcaaagtttc cggctcagcc 660
ctagcttcac aggcaagtaa catcatcaac aaggcaaaca aagtacacga gtgttccatc 720
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gccgtaacca cgattagccc cgttgcagcc accgcagaag taagcagaaa cagtacagag 840
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ttctcagcaa caccagcgtt aatagattgt cattactagt tgtttttttt actacataat 1020
atgatgaaat atttgtgaat tcttcttact tactactata ttgttgatca aaaaaaaaaa 1080
aaaaaaaaa 1087

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<210> 50
<211> 284
<212> PRT
<213> Arabidopsis thaliana

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<400> 50
Met Gly Gln Asp Glu Val Gly Ser Asp Gln Thr Gln Ile Ile Lys Gly
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Lys Arg Thr Lys Arg Gln Arg Ser Ser Ser Thr Phe Val Val Thr Ala
20 25 30

Ala Thr Thr Val Thr Ser Thr Ser Ser Ala Gly Gly Ser Gly Gly
35 40 45

Glu Arg Ala Val Ser Asp Glu Tyr Asn Ser Ala Val Ser Ser Pro Val
50 55 60

Thr Thr Asp Cys Thr Gln Glu Glu Glu Asp Met Ala Ile Cys Leu Ile
65 70 75 80

Met Leu Ala Arg Gly Thr Val Leu Pro Ser Pro Asp Leu Lys Asn Ser
85 90 95

Arg Lys Ile His Gln Lys Ile Ser Ser Glu Asn Ser Ser Phe Tyr Val
100 105 110

Tyr Glu Cys Lys Thr Cys Asn Arg Thr Phe Ser Ser Phe Gln Ala Leu
115 120 125

Gly Gly His Arg Ala Ser His Lys Lys Pro Arg Thr Ser Thr Glu Glu
130 135 140

Lys Thr Arg Leu Pro Leu Thr Gln Pro Lys Ser Ser Ala Ser Glu Glu
145 150 155 160

Gly Gln Asn Ser His Phe Lys Val Ser Gly Ser Ala Leu Ala Ser Gln
165 170 175

Ala Ser Asn Ile Ile Asn Lys Ala Asn Lys Val His Glu Cys Ser Ile
180 185 190

Cys Gly Ser Glu Phe Thr Ser Gly Gln Ala Leu Gly Gly His Met Arg
195 200 205

Arg His Arg Thr Ala Val Thr Thr Ile Ser Pro Val Ala Ala Thr Ala

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210					215					220									
Glu	Val	Ser	Arg	Asn	Ser	Thr	Glu	Glu	Glu	Ile	Glu	Ile	Asn	Ile	Gly				
225					230					235					240				
Arg	Ser	Met	Glu	Gln	Gln	Arg	Lys	Tyr	Leu	Pro	Leu	Asp	Leu	Asn	Leu				
				245					250					255					
Pro	Ala	Pro	Gly	Asp	Asp	Leu	Arg	Glu	Ser	Lys	Phe	Gln	Gly	Ile	Val				
			260					265					270						
Phe	Ser	Ala	Thr	Pro	Ala	Leu	Ile	Asp	Cys	His	Tyr								
		275					280												

Claims

1. Method for increasing plant yield relative to corresponding wild type plants, comprising any one or more of the following alternatives: (1) modifying through recombinant means expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein; (2) modifying through recombinant means in a plant the level of a 2xC2H2 zinc finger protein; or (3) modifying through recombinant means in a plant the activity of a 2xC2H2 zinc finger protein.
2. Method according to claim 1, wherein said increased yield is an increased seed yield.
3. Method for increasing aboveground biomass of a plant relative to corresponding wild-type plants, comprising any one of the following alternatives: (1) modifying through recombinant means expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein; (2) modifying through recombinant means in a plant the level of a 2xC2H2 zinc finger protein; or (3) modifying through recombinant means in a plant the activity of a 2xC2H2 zinc finger protein.
4. Method according to claim 3, wherein said aboveground biomass is increased leaf surface area.
5. Method for altering the cycle time of a plant relative to corresponding wild-type plants, comprising any one or more of the following alternatives: (1) modifying through recombinant means expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein; (2) modifying through recombinant means in a plant the level of a 2xC2H2 zinc finger protein; or (3) modifying through recombinant means in a plant the activity of a 2xC2H2 zinc finger protein.
6. Method according to claim 5, wherein said altered cycle time is a prolonged vegetative growth.
7. Method for increasing leaf surface area relative to corresponding wild type plants, comprising any one or more of the following alternatives: (1) modifying through recombinant means expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein; (2) modifying through recombinant means in a plant level of a 2xC2H2 zinc finger

protein; or (3) modifying through recombinant means in a plant the activity of a 2xC2H2 zinc finger protein.

8. Method for prolonging vegetative growth phase of a plant relative to corresponding wild type plants, comprising any one or more of the following alternatives: (1) modifying through recombinant means expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein; (2) modifying through recombinant means in a plant level of a 2xC2H2 zinc finger protein; or (3) modifying through recombinant means in a plant the activity of a 2xC2H2 zinc finger protein.
9. Method according to any one of claims 1-8, wherein said modifying expression comprises enhanced or increased expression of a nucleic acid encoding a 2xC2H2 zinc finger protein.
10. Method according to any one of claims 1-8, wherein said modifying expression comprises decreasing expression of a nucleic acid encoding a 2xC2H2 zinc finger protein.
11. Method according to any one of claims 1 to 10, wherein said 2xC2H2 zinc finger protein comprises a QALGGH motif.
12. Method according to any one of claims 1 to 10, wherein said 2xC2H2 zinc finger protein comprises a NNM(W)QMH motif.
13. Method according to any one of claims 1 to 12, wherein said 2xC2H2 zinc finger protein comprises an EAR motif.
14. Method according to any one of claims 1 to 13, wherein said 2xC2H2 zinc finger protein further comprises a B-box.
15. Method according to any one of claims 1 to 14, wherein said 2xC2H2 zinc finger protein further comprises an L-box.
16. Method according to any one of claims 1 to 15, wherein said 2xC2H2 zinc finger protein is obtained from a dicotyledonous plant.
17. Method according to claim 16 wherein said 2xC2H2 zinc finger protein is obtained from the family *Brassicaceae*.

18. Method according to claim 17 wherein said 2xC2H2 zinc finger protein is obtained from *Arabidopsis thaliana*.
19. Method according to any of claims 1 to 15 wherein the nucleic acid is represented by any one or more of: (1) SEQ ID NO 2; (2) SEQ ID NO. 1; or (3) sequences hybridising therewith in hybridization conditions comprising 4-6x SSC / 0.1-0.5% w/v SDS at 37-45°C for 2-3 hours, wherein said sequences hybridizing therewith encode a 2xC2H2 zinc finger protein.
20. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 30% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
21. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 31% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
22. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 32% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
23. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 33% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
24. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 34% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
25. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 35% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.

26. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 36% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
27. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 37% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
28. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 38% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
29. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 39% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
30. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 40% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
31. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 41% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
32. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 42% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.

33. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 43% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
34. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 44% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
35. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 45% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
36. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 46% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
37. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 47% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
38. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 48% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
39. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 49% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
40. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 50% sequence identity with the sequence of SEQ ID NO. 2 when determined by

utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.

41. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 52% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
42. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 54% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
43. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 56% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
44. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 58% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
45. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 60% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
46. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 62% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
47. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 64% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.

48. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 66% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
49. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 68% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
50. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 70% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
51. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 72% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
52. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 74% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
53. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 76% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
54. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 78% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.

55. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 80% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
56. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 82% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
57. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 84% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
58. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 86% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
59. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 88% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
60. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 90% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
61. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 92% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
62. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 94% sequence identity with the sequence of SEQ ID NO. 2 when determined by

utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.

63. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 96% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
64. Method according to any one of claims 1-19, wherein said 2xC2H2 zinc finger protein has at least 98% sequence identity with the sequence of SEQ ID NO. 2 when determined by utilizing a GAP sequence alignment program with default parameters, and has the same biological action as the protein of SEQ ID NO. 2.
65. Method according to any one of claims 1 to 64, wherein said plant is a monocot.
66. Method according to any one of claims 1 to 65, wherein said modifying expression is effected by introducing into a plant a nucleic acid for any one or more of (1) modifying expression of a gene encoding a 2xC2H2 zinc finger protein; (2) modifying level of a 2xC2H2 zinc finger protein; or (3) modifying activity of a 2xC2H2 zinc finger protein.
67. Method according to claim 66, wherein said nucleic acid is a nucleic acid encoding a 2xC2H2 protein.
68. Method according to claim 67, wherein said 2xC2H2 protein is selected from the group consisting of:
- (i) a 2xC2H2 protein comprising a QALGGH motif
 - (ii) a 2xC2H2 protein comprising a NNM(W)QMH motif
 - (iii) a 2xC2H2 protein comprising an EAR motif
 - (iv) a 2xC2H2 protein comprising a B-box motif
 - (v) a 2xC2H2 protein comprising an L-box motif
 - (vi) a 2xC2H2 protein having at least 95% sequence identity with the sequence of SEQ ID NO: 2 when determined by utilizing a GAP sequence alignment program with default parameters, and having the same biological action as the protein of SEQ ID NO: 2
 - (vii) a 2xC2H2 protein having at least 31% sequence identity with the sequence of SEQ ID NO: 2 when determined by utilizing a GAP sequence alignment

program with default parameters, and having the same biological action as the protein of SEQ ID NO: 2.

69. Method according to any one of claims 1 to 68, wherein said modifying expression comprises increased expression.
70. Method according to any one of claims 1 to 69, wherein expression of said nucleic acid is driven by a plant promoter.
71. Method of claim 70 wherein the plant promoter is a constitutive promoter.
72. Method of claim 71 wherein the constitutive promoter is a GOS2 promoter.
73. Method according to claim 70 wherein the plant promoter is a tissue preferred promoter.
74. Method according to claim 73 wherein the tissue preferred promoter is a seed-preferred promoter.
75. Method according to any one of claims 1, 2, 4, 6, and 9-75, wherein said increased yield comprises increased above ground biomass.
76. Method according to any one of claims 1, 4, 6 and 9-75, wherein said increased yield comprises increased seed yield.
77. Method according to any one of claims 1, 2, 4 6 and 9-75, wherein said increased yield comprises increased root yield.
78. Method for the production of a transgenic plant having any one or more of: (1) increased yield; (2) increased leaf surface area; or (3) prolonged vegetative growth, which method comprises
 - (i) introducing into a plant or plant cell a 2xC2H2 zinc finger nucleic acid;
 - (ii) Cultivating the plant or plant cell under conditions promoting plant growth.
79. Use of any one or more of (1) a nucleic acid encoding a 2xC2H2 protein; and (2) a 2xC2H2 protein to increase plant yield.

80. Use of any one or more of (1) a nucleic acid encoding a 2xC2H2 protein; and (2) a 2xC2H2 protein to increase leaf surface area.
81. Use of any one or more of (1) a nucleic acid encoding a 2xC2H2 protein, (2) a 2xC2H2 protein to prolong vegetative growth.

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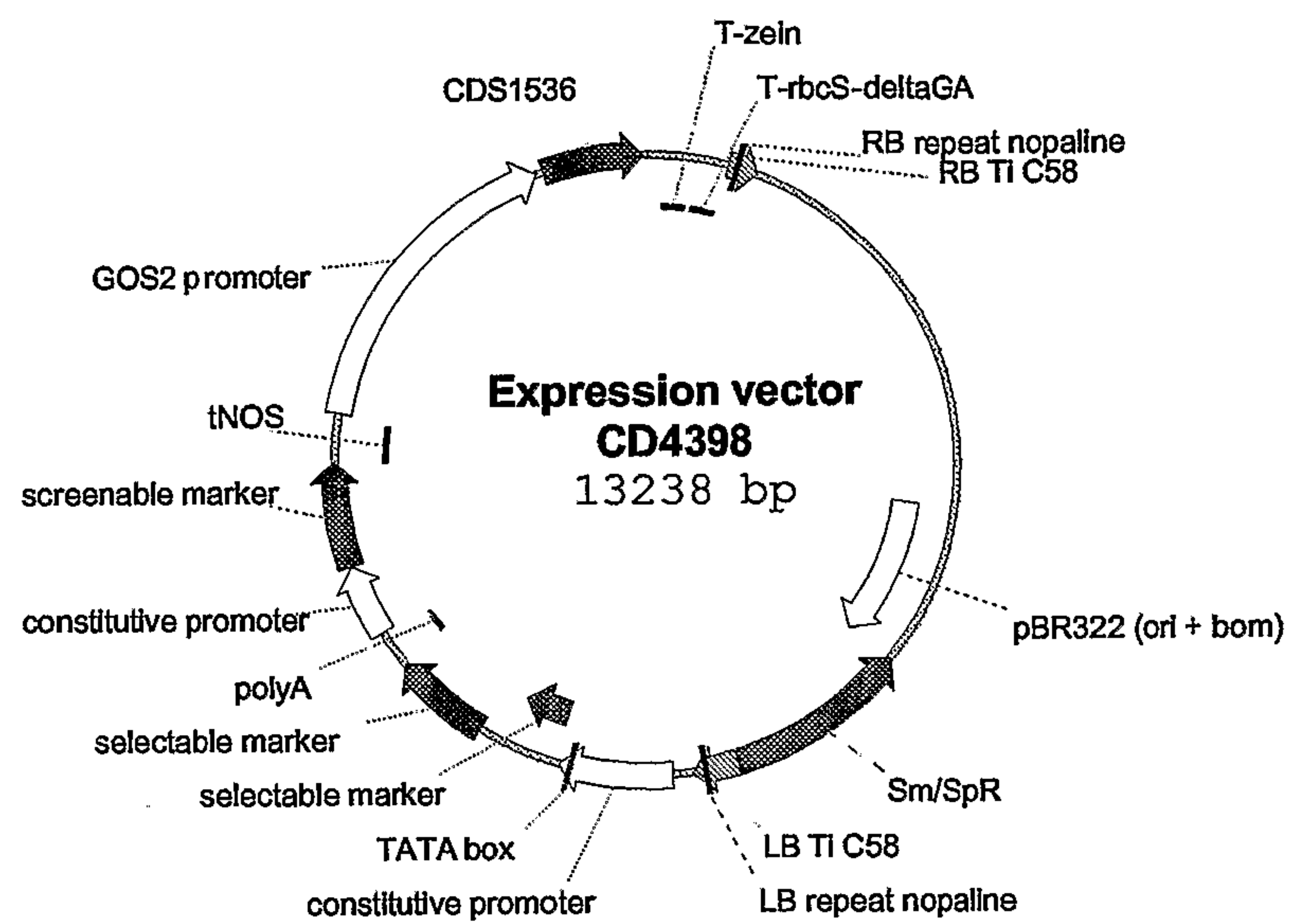
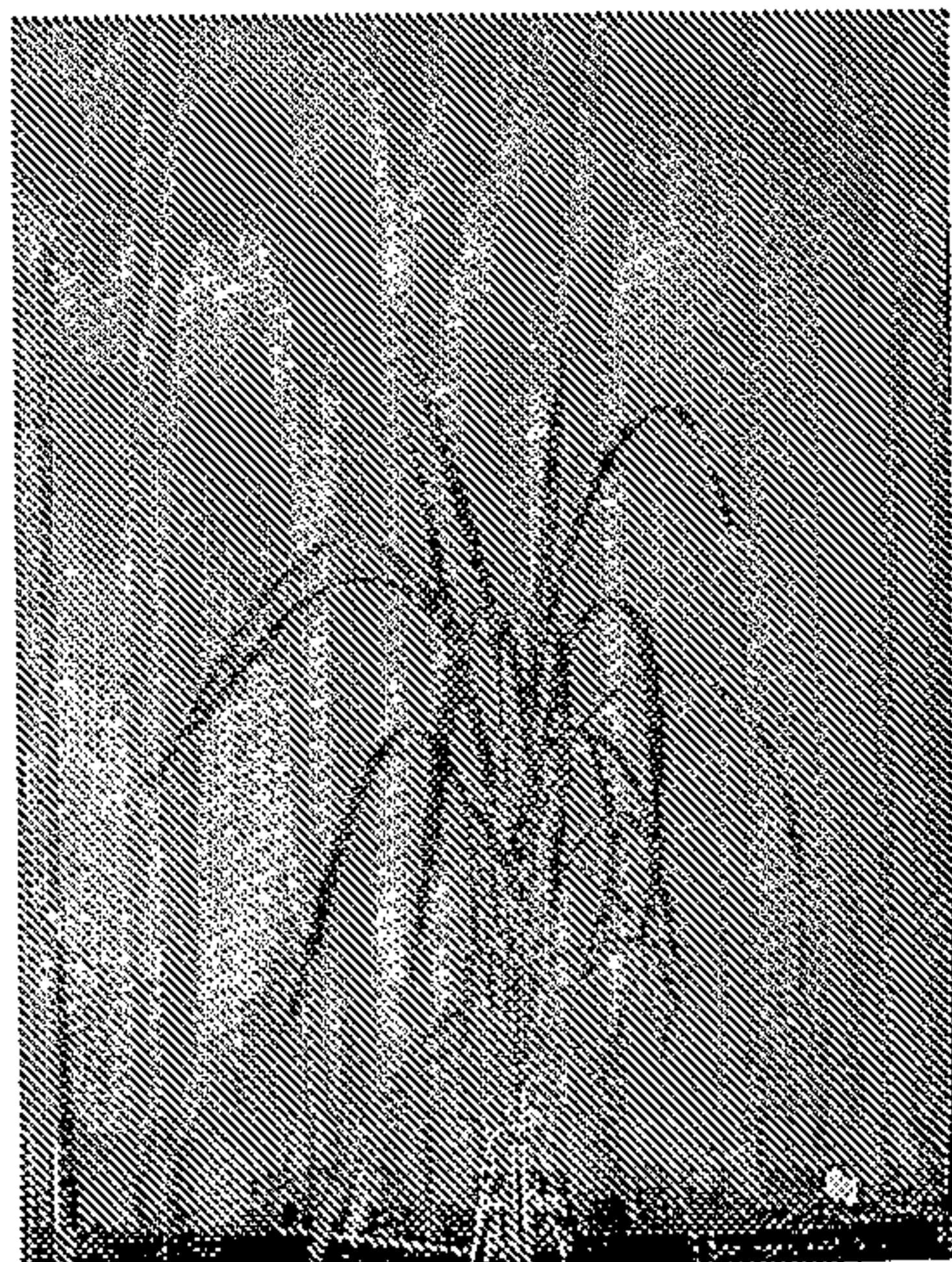
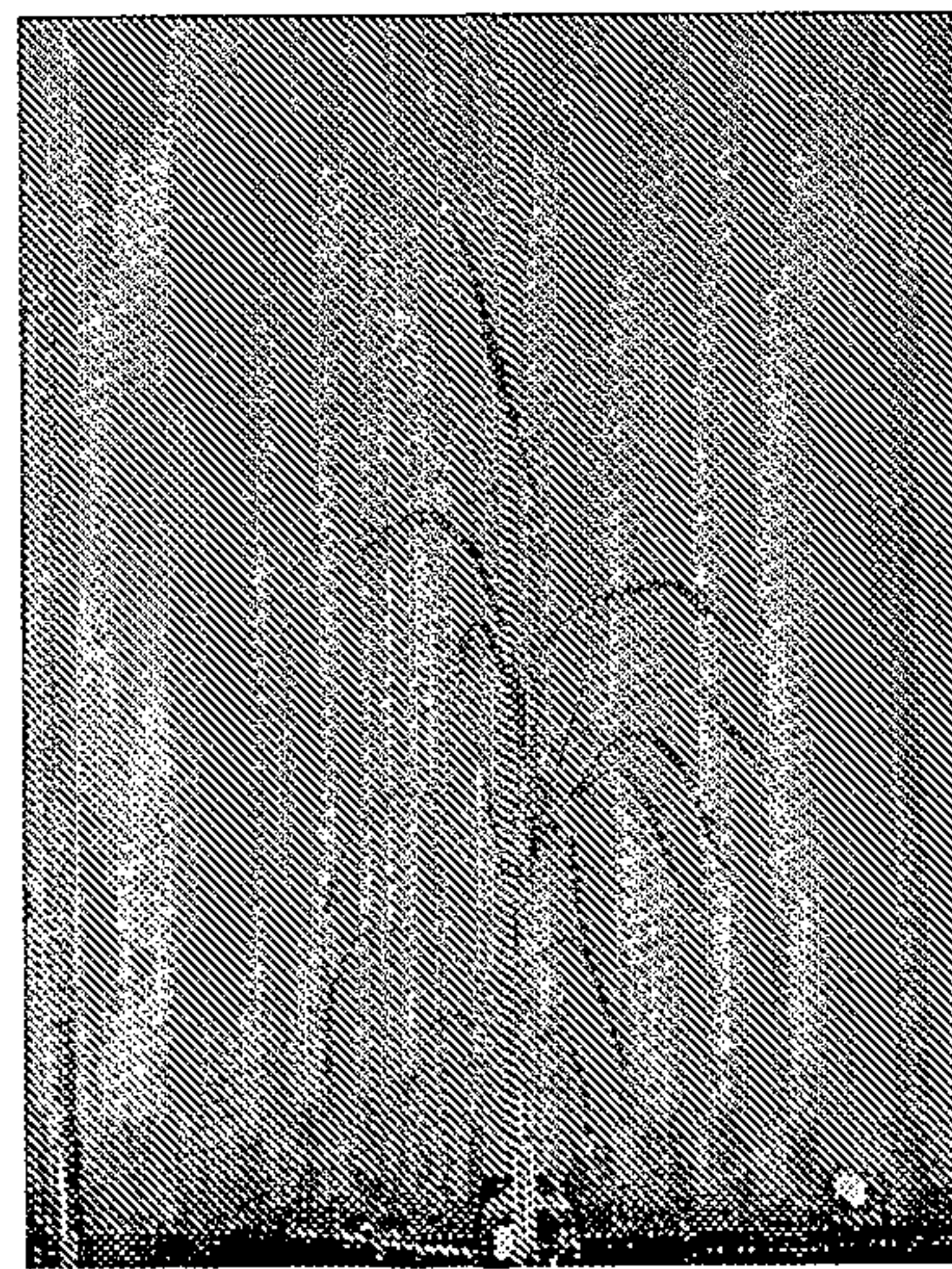
**FIGURE 1****A****B****FIGURE 2**

FIGURE 3

3/17**ORTHOLOGS OF STZ in OTHER PLANT SPECIES**

SEQ ID NO 10: Dg_AF119050_1 *Datisca glomerata* zinc-finger protein 1 (zfp1) mRNA, complete cds

GGCACGAGGACAAATTCTCTCTCTATCCTCTGAATATCTTTGGTTTGTGAACTGAGAAGCTA
TTAG**ATGG**CTCTAGAAGCGCTCAACTCTCCGACCACAGCTACGCCGGTGTTCCTACTACGACG
ACCCAGCTTGAATTACCTTGAGCCATGGACCAAGCGTAAGCGTTCCAAGCGTACGCGCTTA
GATAGCCCCATACCGAGGAAGAGTACCTTGCTTTCTGCCTCATCATGCTCGCTCGTGGCCGC
GTTGCCTCTGCAAATCGACGGGATTCTCAGTCTTCCATTCAGATTCAGCCTGAAGCAACGAC
TTCGGCTACCAAAGTCAGTTATAAGTGCTCTGTGTGCGATAAGGCCTTTTCGTCTTATCAGG
CTTTGGGTGGGCACAAGGCCAGCCACAGAAAGCTCGCTGGCGGCGAAGATCAATCGACTTCC
TTTGCCACCACGAATTCAGCCACCGTCACTACCACCACAGCCTCCGGAGGTGGTGGCAGGTC
TCATGAGTGTCTATTTGCCACAAATCGTTCCCGACTGGCCAGGCCTTGGGTGGTCACAAGC
GCTGCCACTACGAAGGCAGTATCGGCGGCAATAGTATTCACCACCACAACAATACCACCAAC
AGCGGAAGCAACGGTGGCATGAGCATGACCTCCGAAGTAGGTTCCACACACACAGTCAGCCA
CAGTCACCGTGACTTCGATCTCAACATCCCGGCCTTGCCGGAGTTTCGGTCTGAATTTCTTCA
TATCCGGGGATGACGAGGTGAGAGTCTCATCCGGCCAAGAAACCCCGTATATTGATGAAA
TAAAACATTTCTCAAGATCACTGAACCAGGCTTTAGTTTCTTTATAGGAGGAGATTTAAAAA
AGTAGTATCTCTCTTTCTTTATCCGTAGGATAATTAATATATTTTCGTGTACATAAATTTGTA
GTTCTTTAACACACTCTGTTTCATTTTCTTGCTTTGCTCAACTTTGTATTGGTTATTTTCATT
ATGAAAATTCAATT

SEQ ID NO 11: Dg_AF119050_1 *Datisca glomerata*, STZ ortholog, protein

MALEALNSPTTATPVFHYDDPSLNYLEPWTKRKRSKRTRLDSPHTEEEYLAFLIMLARGRV
ASANRRDSQSSIIQIQPEATTSATKVSYSKCSVCDKAFSSYQALGGHKASHRKLGGEDQSTSF
ATTNSATVTTTTASGGGGRSHECSICHKSEPTGQALGGHKRCHYECSIGGNSIHNNNTTNS
GSNGGMSMTSEVGSTHTVSHSHRDFDLNIPALPEFRSNFFISGDDEVESPHPAKKPRIIMK

SEQ ID NO 12: Gm_T09602_U68763.1_GMU68763 *Glycine max* (soybean) probable zinc finger protein SCOF-1 mRNA, complete cds

AAAATTCTCACTCTCTCTCTCATCTCGAGATCATAGTATCATATTCAATATCATTTTCATACC
AAACACATGGCTTTGGAAGCTCTCAACTACCAACAACAACCGCTCCATCTTTTCCCTTTGA
CGACCCAATATTCATGGGCGAAACGAAACGTTCAAAGCGTTCTCGCGACCATCCTTCTG
AAGAAGAGTACCTCGCCCTCTGCCTCATC**ATG**CTCGCTCGCGGCGGCACCACCACCGTCAAC
AACCGCCACGTCAGCCCTCCGCGCTACAGCCACAGCCACAGCCGACACCAGATCCTTCCAC
CAAGCTCAGTTACAAATGCTCCGTTTGCGACAAGAGCTTCCCCTCTTACCAAGCGCTCGGTG
GACACAAGGCCAGTCACCGGAAACTCGCCGGCGCCGCGGAAGACCAACCCCCCAGCACCACC
ACTTCTCCGCGCCGCGCCACCAGCTCCGCCTCCGGAGGTAAGGCCCATGAGTGCTCCATTTG
CCACAAATCCTTCCCCACCGGACAGGCCCTTGCGGGACACAAACGTTGTCACTACGAAGGTA
ACGGTAACGGAAATAACAACAACAGTAACAGCGTTGTCAACGTCGCCTCGGAAGGCGTGGGC
TCCACCCACACTGTCAGTCACGGCCACCACCGCGACTTCGATCTCAACATCCCGGCCTTTCC
GGATTTTTCGACCAAGGTGCGGAGAAGACGAGGTTGAGAGCCCTCACCTGTCATGAAGAAGC
CTCGCCTCTTCGTCAATCCCAAGATCGAAATCCCCCAATTTCAAT**TGA**ACTCGTTGAATTTT
AGTTTATTTTTCGACTATATATTTTGGAGAATTTTGAGAGTTACTATAATTTGATTTTGTAC
ATAGTACTTGGAAGTTTTGTTGGACCGTACCGGACCCAGTTCTCTGGTTGAGGTTGTACTTT
CACAACAGTGGCAGATTTGCAATTCAATTCAATTTATTTGTTTATTTTAAAAAAAAAAAAAA
AAAA

FIGURE 3 (continued)

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SEQ ID NO 13: Gm_T09602 Glycine max (soybean) probable zinc finger protein SCOF-1, STZ ortholog, protein
 MALEALNSPTTTAPSFPPFDDPTIPWAKRKRSKRSRDHPSEEEYLALCLIMLARGGTTTVNNR
 HVSPPLQPQPQPTPDPSTKLSYKCSVCDKSFPSYQALGGHKASHRKLAGAAEDQPPSTTTS
 SAAATSSASGGKAHECSICHKSFPTGQALGGHKRCHYEGNGNGNNNSNSVVTVAASEGVGST
 HTVSHGHRDFDLNIPAFPDFSTKVGEDEVESPHPMKKPRLFVIPKIEIPQFQ

SEQ ID NO 14: Ms_CAB77055_Y18788.1_MSY18788 Medicago sativa putative TFIIIA (or kruppel)-like zinc finger protein mRNA
 AATTCGGCAGAGAAATAACCACTTCTCTCTCAAACCTCCTTTTGCCTTTTGCTTCTACTT
 TCACTTGCGTAACGCTAACTAATCTCTCGAGTGTTCTTCTTTTCATCATATGGCTATGGA
 AGCACTTAACCTACCCACCACTGCTACTCCTTTTACACCCCTTTGAGGAACCAAATCTGAGTT
 ATCTTGAAACACCGTGGACGAAAGGTAAACGATCAAAGCGTTCTCGCATGGATCAATCTTCA
 TGCCTGAAGAAGAGTATCTCGCTCTTTGTCTCATCATGCTTGCTCGCAGCGGTAACAACAA
 CGACAAAAGTCTGATTGCGGTGGCGACGCCGCTAACCACCGTTAAACTCAGTCACAAATGCT
 CAGTCTGCAACAAAGCTTTCTCATCTTATCAAGCCCTAGGTGGACACAAAGCCAGTCACCGG
 AAAGCTGTTATGTCCGCAACCACCGCTGAAGATCAGATCACCACCACTTCATCCGCCGTGAC
 TACCAGCTCTGCTTCCAACGGTAAGAACAAGACTCATGAGTGTTCCATCTGTACAAATCCT
 TCCCTACTGGACAGGCTTTGGGAGGACACAAGCGTTGTCACTACGAAGGCAGCGTTGGTGCC
 GGTGCCGGTGCTGGAAGTAACGCTGTAAGTGCCTCTGAAGGAGTTGGATTGTCACACAGCCA
 CCACCGTGATTTTGTATCTTAACCTCCCGGCTTTTCCGGACTTTTCAAAGAAGTTTTTCGTGG
 ATGACGAGGTTTTTAGTCCTTTACCTGCTGCAAGAAGCCCTGTCTTTTCAAGCTGGAAATT
 CCTTCTCATTAATGAATCAATAATAGATCCAATTTTATTGTTATTATTATTAATAATTATTAT
 CGCTTAGGGCATAGTTATTTTCTTTTCTTTTCAATTATTTTCGGATCAATTTGTTCTGTACA
 TACAAATTGGGATTGGTTTTAGAATTTAGGACGGTTGTAGACAATGGAAATTCAATTCAATT
 ATTTAATTTTGTGT

SEQ ID NO 15: Ms_CAB77055_Medicago sativa putative TFIIIA (or kruppel)-like zinc finger protein, STZ ortholog, protein
 MAMEALNSPTTATPFTPFEENLSYLETPWTKGKRKRSRMDQSSCTEEYALCLIMLARS
 GNNNDKKS DSVATPLTTVKLSHKCSVCNKAFFSSYQALGGHKASHRKAVMSATTAEDQITTS
 SAVTTSSASNGKNKTHECSICHKSFPTGQALGGHKRCHYEGSVGAGAGAGSNAVTAASEGVGL
 SHSHHRDFDLNLPAPDFSKKFFVDDEVFSPLPAKKPCLFKLEIPSHY

SEQ ID NO 16: Nt_AAC06243_AF053077 Nicotiana tabacum osmotic stress-induced zinc-finger protein (zfp) mRNA, complete cds
 TTTTCCCTCGAATTTGATAACTAAAGAGAATATTATGACTCTTGAAGCTTTGAAGTCACCTA
 CGGCGGCAACGCCGACTCTACCACCACGCTATGAAGATGATGATGAAATTCATAATTTGGAT
 TCTTGGGCTAAAGGAAAACGATCAAACGGCCCCGTATTGATGCCCCACCGACTGAAGAAGA
 GTATTTAGCCCTCTGTCTCATCATGCTCGCTCGCAGCGGAACCGGAACCAGAACCGGTTTAA
 CTGATGCTACTACTTCCCAACAACCTGCCGATAAAAAAACC GCCGAGTTGCCGCCGGTTCAT
 AAGAAAGAGGTGGCAACAGAGCAAGCAGAGCAATCTTACAAGTG TAGCGTGTGTGACAAGGC
 TTTTCTTCTTATCAAGCACTCGGTGGGCATAAAGCAAGTCACCGTAAACTACTACTACTG
 CTACCGCCGCCTCTGATGATAACAATCCTTCAACTTCAACTTCCACTGGCGCCGTTAATATC
 TCTGCTCTTAATCCAATGGTTCGTTACACGTCTGTTCTATTTGCCACAAGGCTTTTCCTAC
 TGGCCAAGCTTTGGGTGGGCACAAGCGCCGCCACTATGAAGGCAAACCTCGGTGGTAACAGCC
 GCGACTTAGGCGGCGGCGGCGGCGGTCATAGTGGAAGCGTCTTGACTACTTCAGACGGC

FIGURE 3 (continued)

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GGCGCGTCGACTCACACGCTACGTGACTTTGACCTGAACATGCCTGCTTCGCCGGAATTGCA
 ACTGGGTCTGAGTATTGATTGTGGACGGAAAAGTCAACTGTTGCCGATGGTCCAAGAGGTGG
 AAAGTCCTATGCCTGCAAAGAAACCGCGTTTATTGTTTTTCGTTGGGT**TGA**AACTTCTTTAGG
 GGAATTGAATTGATTGTGTTTTAGCCAAATTAGTAAATTGGTTCATGTGATTTTATTTTAG
 GAAAAGGAATTATTGATTGTTTTACCCGTTTATTCTTAGGGTGGTATTATGTACAGGGAGTG
 AATCATTCATTGGTTTTACACTTTCTTAATTATATATTCTTTTTTTTTTACACATAAAAAAA
 AAAAAA

SEQ ID NO 17: Nt_AAC06243_Nicotiana tabacum osmotic stress-
 induced zinc-finger protein, STZ otholog, protein
 MTLEALKSPTAATPTLPPRYEDDDEIHNLD SWAKGKRSKRPRIDAPPTEEEYLALCLIMLAR
 SGTGTRTGLTDATTSQQPADKKTAE LPPVHKKEVATEQAEQSYKCSVCDKAFSSYQALGGHK
 ASHRKTTTTATAASDDNNPSTSTSTGAVNISALNPTGRSHVCSICHKAFPTGQALGGHKRRH
 YEGKLGGNSRDLGGGGGGHSGSVLTTS DGGASTHTLRDFDLNMPASPELQLGLSIDCGRKS
 QLLPMVQEVESPMPAKKPRL LFSLG

SEQ ID NO 18: Os_AF332876 Oryza sativa zinc finger
 transcription factor ZF1 mRNA, complete cds
 AATTCGGCACGAGGCCACACAGCAACCAGCCAGCTGCCACACTAGCTTGAGGCGAGCGAGCG
 AAGCTTAGCTAGCGGATAGAACAAGTCGTCGATCTGCTTGCTGCTTTTGTGAATTGCGGTGG
 AAG**ATG**TCGAGCGCGTCGTC CATGGAAGCGCTCCACGCCGCGGTGCTCAAGGAGGAGCAGC
 AGCAGCACGAGGTGGAGGAGGCGACGGTCGTGACGAGCAGCAGCGCCACGAGCGGGGAGGAG
 GGCGGACACCTGCCCCAGGGGTGGGCGAAGCGGAAGCGGTGCGCGCCGCGAGCGATCGGAGGA
 GGAGAACCTCGCGCTCTGCCTCCTCATGCTCGCCCGCGGGCGGCCACCACCGCGTCCAGGCGC
 CGCCTCCGCTCTCGGCTTCGGCGCCCCCGCCGGCAGGTGCGGAGTTCAAGTGCTCCGTCTGC
 GGCAAGTCCTTCAGCTCCTACCAGGCGCTCGGCGGCCACAAGACGAGCCACCAGGGTCAAGCT
 GCCGACTCCGCCCCGAGCTCCCGTCTTGGCTCCCGCCCCCGTCCGCGCCTTGCTGCCTTCCG
 CCGAGGACCGCGAGCCAGCCACGTCATCCACCGCCGCGTCTCCGACGGCATGACCAACAGA
 GTCCACAGGTGTTCCATCTGCCAGAAGGAGTTCCCCACCGGGCAGGCGCTCGGCGGGCACA
 GAGGAAGCACTACGACGGTGGCGTAGGCGCCGGCGCGCGCATCTTCAACCGAGCTCCTGG
 CCACGGTGGCCGCCGAGTCCGAGGTGGGAAGCTCCGGCAACGGCCAGTCCGCCACCCGGGCG
 TTCGACCTCAACCTCCCGGCCGTGCCGGAGTTCGTGTGGCGGCCGTGCTCCAAGGGCAAGAA
 GATGTGGGACGAGGAGGAGGAGGTCCAGAGCCCCCTCGCCTTCAAGAAGCCCCGGCTTCTCA
 CCGCG**TAA**TTTCAGCAGCTGCACGGATCCGATCCGTCAGAGTTTTTGTCTAGGGAGTGAAATT
 CAGTCGAAACACACTATTCGTTGATTCGTTTTGTGCCGCTATTGTTTAATTTGTTCTGCTT
 TTGTACAGAGCAAGCGAGTGATACATAGCCATACATACAGTCATACAGATATAGGTCTAGCT
 CTTCTTGGTTCTTTGTAACACTGGAAGTGTACCTGTATCTTTTACACTTTGTTCTTTGACA
 GTCATATATTGTAGACCAAAAAAAAAAAAAAAAAA

SEQ ID NO 19: Os_AF332876 Oryza sativa seedling zinc finger
 transcription factor ZF1, STZ otholog, protein
 MSSASSMEALHAAVLKEEQQQHEVEEATVVTSSSATSGEEGGHLPQGWAKRKRSRRQRSEEE
 NLALCLLMLARGGHRVQAPPLSASAPPPAGAEFKCSVCGKSFSSYQALGGHKTS HRVKLP
 TPPAAPVLAPAPVAALLPSAEDREPATSSSTAASSDGMTNRVHRC SICQKEFPTGQALGGHKR
 KHYDGGVGAGAGASSTELLATVAAESEVGSSGNGQSATRAFDLNLPAVPEFVWRPCSKGK
 WDEEEEVQSPLAFKKPRL LTA

FIGURE 3 (continued)

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SEQ ID NO 20: Ph_BAA05079_D26086.1 [Petunia x hybrida].
 PETZFP4 zinc-finger protein gene
 TTCACTCACCAAAACAACCTTCTCTACCTCTTCTACTTGCACATTCAAATTCCTTTCATTACTA
 CTTATCTCTACTAATCTTGATTCGATTTTAGTAAATCAAACAAGAGAATCTTTTCAGTAATA
 CAAACAAGAAAATTTTCTCTCTATACTTGATTGAGTTTAGTAAGGCAAACAAGAAAACCTATC
ATGGCACTTGAAGCATTGAATTCCTCAACTACAACAACACCACCATCATTCCTCAATTTGAGAA
 CAACGGGCTTAAGTACCTTGAGAGTTGGACAAAAGGTAAAAGATCAAAAAGGCAACGCAGCA
 TGGAACGACAGTGTACTGAAGAAGAGTATTTAGCACTTTGTCTTATCATGCTAGCACGTAGC
 GATGGTTCTGTTAATAACTCACGGTCTCTACCACCACCACCCTACCACCATCAGTTCAGT
 AACGTCGCAAATAAACGCGACGTTATTGGAACAGAAGAATTTGTACAAGTGTTCCGTTTGTG
 GTAAAGGGTTTGGGTCTTATCAAGCTTTAGGTGGACATAAAGCAAGTCACCGGAAACTTGTC
 AGCATGGGAGGAGATGAACAATCTACTACTTCCACTACTACTAACGTAACGGGAACTAGTTC
 CGCTAACGTTAACGGTAACGGAAGAAGTACGGAATGTTCAATTTGTCACAAGTGCTTTTCTA
 CTGGACAAGCTTTAGGTGGTCATAAAAGGTGCCACTATGACGGTGGTAACGGTAACGGTAAC
 GGAAGTGTAAGTGTTGGGGTGACGTCATCTGAAGGTGTGGGGTCCACTATTAGTCATCACCG
 TGACTTTGACTTGAATATTCCCGCGTTGCCGGAGTTTGGCCGGGATTTGGTTCCGGCGAGG
 ATGAGGTGGAGAGTCCTCATCCAGCAAAGAAGTCAAGGCTATCTCTTCCACCTAAACTTGAA
 TTATTCAAAGGATTAT**TAG**AGGGAATATTGATTGTGTTACAGGAAGATTTATTAGGATTCACGA
 ATTTTTTGTGACTAGTTTATGTAATAT

SEQ ID NO 21: Ph_BAA05079 [Petunia x hybrida] zinc-finger
 protein, STZ ortholog, protein
 MALEALNSPTTTTPPSFQFENGLKYLESWTKGKRSKRQRSMERQCTEEYLLALCLIMLARS
 DGSVNNSRSLPPPPLPPSVPTSQINATLLEQKNLYKCSVCGKGFSGSYQALGGHKASHRKLV
 SMGGDEQSTTSTTTNVTGTSSANVNGNGRTHECSICHKCFPTGQALGGHKRCHYDGGNGNGN
 GSVSVGVTSSEGVGSTISHHRDFDLNIPALPEFWPGFGSGEDEVESEPHPAKKSRLSLPPKLE
 LFKGL

SEQ ID NO 22: Ta_BAA03901 Triticum aestivum gene for zinc-
 finger protein WZF1, complete cds
ATGTCGTCGTCGGCCATGGAAGCGCTCCACGCCCTGATCCCGGAGCAGCACCAGCTGGACGT
 TGAGGCGGCTGCGGCTGTCAGCAGCGCCACCAGCGGCGAGGAGAGCGGCCACGTGCTGCAGG
 GGTGGGCCAAGAGGAAGCGATCGCGCCGCCAGCGCTCCGAGGAGGAGAACCTCGCGCTCTGC
 CTCCTCATGCTCTCGCGCGGCGGCAAGCAGCGTGTTAGGCGCCGCAGCCGGAGTCGTTTCGC
 TCGCGCCGGTGCTGCGGAGTTCAAGTGCTCCGTCTGCGGCAAGTCCTTCAGCTCCTACCAGG
 CGCTCGGAGGCCACAAGACGAGCCACCGGGTGAAGCAGCCGTCTCCTCCCTCTGATGCCGCT
 GCTGCCCCACTCGTGGCCCTCCCGGCCGTGCGCGCCATCCTGCCGTCCGCCGAGCCGGCCAC
 GTCGTCCACCGCCGCGTCCTCCGACGGCGCGACCAACAGAGTCCACAGGTGCTCCATCTGCC
 AAAAGGAGTTCCCGACTGGGCAGGCGCTCGGCGGGCACAAGAGGAAGCACTACGACGGAGGC
 GTGGGCGCCGCGCCTCGTCGACCGAGCTTCTGGCCGCCGCGGCCGCGGAGTCTGAGGTGGG
 GAGCACCGGCAACGGGAGCTCCGCCGCCGGGCCTTCGACCTGAACATTCCGGCCGTGCCGG
 AGTTCGTGTGAGAGCCGTGCGCCAAGGGCAAGATGATGTGGGAGGACGATGAGGAGGTGCAG
 AGCCCCCTCGCCTTCAAGAAGCCTCGGCTTCTCACCGCT**TGA**

FIGURE 3 (continued)

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SEQ ID NO 23: Ta_BAA03901_WZF1 *Triticum aestivum*, STZ ortholog, protein

MSSSAMEALHALIPEQHQLDVEAAAAVSSATSGEESGHVLQGWAKRKRSRRQRSEEEENLALC
LLMLSRGGKQRVQAPQPESFAAPVPAEFKCSVCGKSFSSYQALGGHKTSHRVKQPSPPSDAA
AAPLVALPAVAAILPSAEPATSSSTAASSDGATNRVHRCSICQKEFPTGQALGGHKRKHVDGG
VGAAASSTELLAAAAAESEVGSTGNGSSAARAFDLNIPAVPEFVWRPCAKGKMMWEDDEEVQ
SPLAFKKPRLTA

SEQ ID NO 24: Ca AF539746 *Capsicum annum* zinc finger protein mRNA, complete cds

AAAATCTTCGCTACTTACTTACATCTTCTAGAATAGTCACTAGAACCAGTAACTTTATACAA
CGGATATCGATATGGCACTTGAAGCTTTGAATTCTCCAACCTGGTACACCAACTCCGCCACCG
TTTCAATTTGAGAGCGACGGCCAACAGCTTCGATATATCGAAACTGGAGGAAGGGAAAGAG
ATCTAAAAGGTCACGCAGCATGGAGCACCAGCCTACTGAGGAAGAATACTTAGCGCTTTGTT
TGATCATGCTTGACGTAGCGGTGGCTCCGTTAATCATCAACGATCTCTACCACCGCCGGCT
CCGGTGATGAAACTGCACGCGCCGTCGTCATCATCGGCGGCGGAGGAGGAGAAGGAGAAGAT
GGTGATAAGTGTTCCGTTTGTGGTAAGGGATTTGGGTCTTATCAAGCTTTAGGTGGACACA
AAGCTAGTCACCGGAAACTCGTACCCGGCGGAGATGATCAGTCAACTACCTCCACAACCACT
AACGCAACCGGAACAACAACCTCCGTTAACGGCAACGGCAACAGAAGTGGAAGGACTCACGA
GTGTTTCGATTTGTCACAAGTGTTTTCCCACTGGACAAGCTTTAGGTGGACACAAAAGGTGTC
ACTACGACGGCGGTATCGGTAACGGAAACGCTAACAGTGGCGTTAGTGCTAGCGTTGGAGTG
ACGTCATCGGAGGGTGTTGGGTCCACAGTCAGTCACCGGGATTTGACTTGAACATTCGGG
GTTGCCGGAATTCTGGCTGGGATTTGGTTCGGCGAAGATGAGGTGGAGAGTCCACATCCGG
CGAAGAAATCGCGGTTATGTTTGCTCCAAAATATGAATTATTTCAACATTAATGGGAATTT
GATTGTTAGGATTTACTATTTTGGTAGACAAAATTATACTATGTAAGTTTTAATTTTCATTG
TGGGTGGGAGCAAAATTTTTAATTTTTTGTCTATAGACCTAGCTAGTTACTAATAGCAAAAA
TTCAATTGATTGATTTAAAAA

SEQ ID NO 25: Ca AF539746-capsicum annum, STZ ortholog, protein
MALEALNSPTGTPTPPPFQFESDQQLRYIENWRKGRSKRSRSMEHQPTEEYLLALCLIML
ARSGGSVNHQRLPPPAPVMKLHAPSSSSAAEEKEKMKVYKCSVCGKGFGSYQALGGHKASH
RKLVPGGDDQSTTSTTTNATGTTTSVNGNGNRSGRTHECSICHKCFPTGQALGGHKRCHYDG
GIGNGNANSVGSASVGVTSSEGVGSTVSHRDFDLNIPALPEFWLGFSGEDEVESPHPAKKS
RLCLPPKYELFQH

PARALOGS OF STZ IN ARABIDOPSIS THALIANA

SEQ ID NO 26: gi_18402298_ref_NM_112848.1 mRNA

ACTTCACTCTCTAATTTCTTCTCTCTATCTCTCACCATATTCGCGATTAAAACTCTCAAC
TTTTCTCTCAAATTTCTGATCCTTTGATCCAACAGTTAGAAGAAGATTCATCTGATCATGGC
CCTCGAAGCGATGAACACTCCAACCTTCTTCTTACCAGAATCGAAACGAAAGAAGATTTGA
TGAACGACGCCGTTTTTCATTGAGCCGTGGCTTAAACGCAAACGCTCCAAACGTCAGCGTTCT
CACAGCCCTTCTTCGTCTTCTTCTCCTCACCGCCTCGATCTCGACCCAAATCCCAGAATCAAGA
TCTTACGGAAGAAGAGTATCTCGCTCTTTGTCTCCTCATGCTCGCTAAAGATCAACCGTCGC
AAACGCGATTTTCATCAACAGTCGCAATCGTTAACGCCGCCGCGCAGAATCAAAGAACCTTCGG
TACAAGTGTAACGTCTGTGAAAAAGCGTTTCCTTCTATCAGGCTTTAGGCGGTACAAAGC
AAGTCACCGAATCAAACCAACCGTAATCTCAACAACCGCCGATGATTCAACAGCTCCGA

FIGURE 3 (continued)

FIGURE 3 (continued)

9/17**SEQ ID NO 30:** gi_30693252_ref_NM_114853.2_mRNA

ATGGCTCTCGACACTCTCAATTCTCCACCTCCACCACCACAACCACCGCTCCTCCTCCTTT
CCTCCGTTGCCTCGACGAAACCGAGCCCGAAAACCTCGAATCATGGACCAAAGAAAACGTA
CAAAACGTCACCGTATAGATCAACCAAACCTCCTCCTTCTGAAGAAGAGTATCTCGCTCTT
TGCTCCTTATGCTCGCTCGTGGCTCCTCCGATCATCACTCTCCACCGTCGGATCATCACTC
TCTTTCTCCACTGTCCGATCATCAGAAAGATTACAAGTGTTCCGTCTGTGGCAAATCTTTCC
CGTCTTACCAAGCGTTAGGTGGACACAAAACAAGTCACCGGAAACCGGTTAGTGTGATGTT
AATAATAGTAACGGAACCGTTACTAATAACGGAATATTAGTAACGGTTTAGTTGGTCAAAG
TGGAAGACTCATAACTGCTCTATATGTTTTAAGTCGTTTCCCTCTGGTCAAGCATTGGGTG
GTCACAAACGTTGTCCTATGATGGTGGTAACGGTAACAGTAACGGTGACAATAGCCACAAG
TTTGACCTAAATTTACCGGCTGATCAAGTTAGTGATGAGACAATTGGAAAAAGTCAACTCTC
CGGTGAAGAAACAAAGTCGGTGTTGTGATTATTATTATTTTACCGATCGGGATTAGCTAG
TGTTGATCATTAGCTGAGTCTGTAATGAAAATGAT

SEQ ID NO 31: Translation of gi_30693252_ref_NM_114853.2

MALDTLNSPTSTTTTTAPPPFLRCLDETEPENLESWTKRKRTRHRIDQPNPPPSEEEYLAL
CLLMLARGSSDHHSPPSDHHSLSPLSDHQDYKCSVCGKSFPSYQALGGHKTSRKPVSVDV
NNSNGTVTNNGNISNGLVGQSGKTHNCISCFKSFPSGQALGGHKRCHYDGGNGNSNGDNSHK
FDLNLPADQVSDETIGKSQLSGEETKSVL

SEQ ID NO 32: gi_30694224_ref_NM_123683.2_mRNA

AAATTTTCTATAGCAATGGCGCTTGAAGCTCTTAATTCACCAAGATTGGTCGAGGATCCCTT
AAGATTCAATGGCGTTGAGCAGTGGACCAAATGTAAGAAACGATCCAAACGTTTCGAGATCTG
ATCTTCATCATAACCACCGTCTCACTGAGGAAGAGTATCTAGCTTTCTGTCTCATGCTTCTT
GCTCGGGATGGCGGCGATCTTGACTCTGTGACGGTTGCGGAGAAGCCGAGTTATAAGTGTGG
CGTTTGTTACAAGACGTTTTTCGTCTTACCAAGCTCTCGGCGGTCATAAAGCGAGCCACCGGA
GCTTATACGGTGGTGGAGAGAATGATAAATCGACACCATCCACCGCCGTGAAATCTCACGTT
TGTTCCGTTTGCGGGAAATCTTTCGCCACCGGTCAAGCTCTCGGCGGCCACAAGCGGTGCCA
CTACGATGGTGGCGTTTTCGAACTCGGAAGGTGTGGGGTCTACTAGCCACGTCAGCAGTAGTA
GCCACCGTGGATTTGACCTTAATATTATACCGGTGCAGGGATTTTCGCCGGACGACGAAGTG
ATGAGTCCGATGGCGACTAAGAAGCCTCGCCTGAAGTAAGTCTTTGTTGAAGACCTGGAAGT
TTATCAAATGTAAATATCAAATTTCAATTTCAAGGAACAGTTTTGTTGATTCTATTACCAAT
ACACAATACGATTCAATTCC

SEQ ID NO 33: Translation of gi_30694224_ref_NM_123683.2_

MALEALNSPRLVEDPLRFNGVEQWTKCKKRSKRSRSDLHHNHRLTEEEYLAFCLMLLARDGG
DLDSVTVAEKPSYKCGVCYKTFSSYQALGGHKASHRSLYGGGENDKSTPSTAVKSHVCSVCG
KSFATGQALGGHKRCHYDGGVSNSEGVGSTSHVSSSSHRGFDLNIIPVQGFSPDDEVMSMA
TKKPRLK

FIGURE 3 (continued)

10/17**SEQ ID NO 34:** gi_30698307_ref_NM_126145.2_mRNA

CACACTTCACTCTTTCTTCATCTTCTTCTTCTTAAATAGCTCGAAATCACATCTCACAGAAT
TAAATCTTATGGCTCTCGAGACTCTCAATTCTCCAACAGCTACCACCACCGCTCGGCCTCTT
CTCCGGTATCGTGAAGAAATGGAGCCTGAGAATCTCGAGCAATGGGCTAAAAGAAAACGAAC
AAAACGTCAACGTTTTTGATCACGGTCATCAGAATCAAGAAACGAACAAGAACCTTCCTTCTG
AAGAAGAGTATCTCGCTCTTTGTCTCCTCATGCTCGCTCGTGGCTCCGCCGTACAATCTCCT
CCTCTTCCTCCTCTACCGTCACGTGCGTCACCGTCCGATCACCGAGATTACAAGTGTACGGT
CTGTGGGAAGTCCTTTTCGTCATACCAAGCCTTAGGTGGACACAAGACGAGTCACCGGAAAC
CGACGAACACTAGTATCACTTCCGGTAACCAAGAACTGTCTAATAACAGTCACAGTAACAGC
GGTTCCGTTGTTATTAACGTTACCGTGAACACTGGTAACGGTGTAGTCAAAGCGGAAAGAT
TCACACTTGCTCAATCTGTTTCAAGTCGTTTTCGCTCTGGTCAAGCCTTAGGTGGACACAAAC
GGTGTCACTATGACGGTGGCAACAACGGTAACGGTAACGGAAGTAGCAGCAACAGCGTAGAA
CTCGTCGCTGGTAGTGACGTCAGCGATGTTGATAATGAGAGATGGTCCGAAGAAAGTGCGAT
CGGTGGCCACCGTGGATTTGACCTAACTTACCGGCTGATCAAGTCTCAGTGACGACTTCTT
AACGTTGACTGAGTTTGAGGAAAAAGTCAACTATCAAGCGAAGAAAGGGTTAGTGGACGGTG
AAGATTAACGGTCGTTTCTTTCCAGTTGCTTCGGTTTGAGCTTGACTGGGTCTGTAATGAAA
ATGATTGGAGTGGACTTGGCATTATTATTATTATTTTAAAAAGAAATGTTAATTTGTTGTT
GGATTTGTTTATAGATAGAGGAAACAATTGGGATACACAAATATTTTTTTTTTTTACAAAGA
AAATAATAATGCAGAGATGGATGATTGGATCGTACACGTTATTATATAGTGGACCATTTCTGT
AATCGTGAATTATTATTATTGTTAGAAATTTAATTTTCGT

SEQ ID NO 35: Translation of gi_30698307_ref_NM_126145.2_
MALETILNSPTATTTARPLLRYREEMEPENLEQWAKRKRTKRQRFDHGHQONQETNKNLPSEEE
YLALCLLMLARGSAVQSPPLPPLPSRASPSDHRDYKCTVCGKSFSSYQALGGHKTSHRKPTN
TSITSGNQELSNNSHSNSGVSVINVTVNTGNVGSQSGKIHTCSICFKSFASGQALGGHKRCH
YDGGNNGNGNGSSSNSVELVAGSDVSDVDNERWSEESAIGGHRGFDLNLPADQVSVTTS

OTHER GENES IN EVALUATION

SEQ ID NO 36: gi_12698881_ref_AF_332876.1_mRNA, 2xC2H2,
Oryza sativa

AATTCGGCACGAGGCCACACAGCAACCAGCCAGCTGCCACACTAGCTTGAGGCGAGCGAGCG
AAGCTTAGCTAGCGGATAGAACAAGTCGTCGATCTGCTTGCTGCTTTTGTGAATTGCGGTGG
AAGCATGTGAGCGCGTCGTCATGGAAGCGCTCCACGCCGCGGTGCTCAAGGAGGAGCAGC
AGCAGCACGAGGTGGAGGAGGCGACGGTCGTGACGAGCAGCAGCGCCACGAGCGGGGAGGAG
GGCGGACACCTGCCCCAGGGGTGGGCGAAGCGGAAGCGGTGCGCGCCGCCAGCGATCGGAGGA
GGAGAACCTCGCGCTCTGCCTCCTCATGCTCGCCCGCGGCGGCCACCACCGCGTCCAGGCGC
CGCCTCCGCTCTCGGCTTCGGCGCCCCCGCCGGCAGGTGCGGAGTTCAAGTGCTCCGTCTGC
GGCAAGTCCTTCAGCTCCTACCAGGCGCTCGGCGGCCACAAGACGAGCCACCGGGTCAAGCT
GCCGACTCCGCCCGCAGCTCCCGTCTTGGCTCCCGCCCCCGTCGCCGCTTGCTGCCTTCCG
CCGAGGACCGCGAGCCAGCCACGTCATCCACCGCCGCGTCTCCGACGGCATGACCAACAGA
GTCCACAGGTGTTCCATCTGCCAGAAGGAGTTCCCCACCGGGCAGGCGCTCGGCGGGCACAA
GAGGAAGCACTACGACGGTGGCGTAGGCGCCGGCGCGCGCATCTTCAACCGAGCTCCTGG
CCACGGTGGCCGCCGAGTCCGAGGTGGGAAGCTCCGGCAACGGCCAGTCCGCCACCCGGGCG
TTCGACCTCAACCTCCCGGCCGTGCCGGAGTTGCTGTGGCGGCCGTGCTCCAAGGGCAAGAA
GATGTGGGACGAGGAGGAGGAGGTCCAGAGCCCCCTCGCCTTCAAGAAGCCCCGGCTTCTCA
CCGCGTAATTCAGCAGCTGCACGGATCCGATCCGTCAGAGTTTTTGTCTAGGGAGTGAAATT
CAGTCGAAACACACTATTCGTTGATTCGTTTTGTGCCGCTATTGTTTAATTTGTTCTGCTT

FIGURE 3 (continued)

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TTGTACAGAGCAAGCGAGTGATACATAGCCATACATACAGTCATACAGATATAGGTCTAGCT
CTTCCTTGGTTCTTTGTAACACTGGAAGTGTACCTGTATCTTTTACACTTTGTTCTTTGACA
GTCATATATTGTAGACCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO 37: gi_12698882_ref_AAK01713.1, 2xC2H2, *Oryza sativa*
MSSASSMEALHAAVLKEEQQHEVEEATVVTSSSATS GEEGGHLPQGWAKRKRSRRQRSEEE
NLALCLLMLARGGHRVQAPPPLSASAPPPAGAEFKCSVCGKSFSSYQALGGHKTSHRVKLP
TPPAAPVLAPAPVAALLPSAEDREPATSSTAASSDGMTNRVHRC SICQKEFPTGQALGGHKR
KHYDGGVGAGAGASSTELLATVAAESEVGSSGNGQSATRAFDLNLPAVPEFVWRPCSKGKKM
WDEEEEVQSPLAFKKPRLTA

SEQ ID NO 38: gi_6434215_ref_AL132966.1_region 116202 ...
116729, 2xC2H2, *Arabidopsis thaliana*

ATGAAGAGAGACCGGTCCGATTACGAAGAATCCATGAAGCATATAGACATAGTAGAAAGTCT
AATGATGTTATCTCGAAGTTTCGTGGTCAAACAAATCGATGTAAAGCAATCTACCGGAAGCA
AAACGAACCATAATAACCACTTCGAATGCAAACGTGTAACCGGAAATTTGATTCCCTCCAA
GCTCTTGGAGGTCATAGAGCTAGCCACAAGAAACCTAAGCTGATCGTTGACCAAGAACAGGT
GAAGCATCGTAACAAAGAGAATGATATGCATAAGTGTACAATTTGCGATCAAATGTTTGGGA
CCGGTCAAGCTCTAGGCGGTACATGAGAAAGCATAGGACGAGCATGATAACCGAGCAATCG
ATTGTCCCTTCTGTGGTTTATTCAGACCGGTTTTTAATCGTTGCAGTAGCAGCAAGGAGAT
CTTGGACTTAAATCTAACTCCATTGGAAAATGATCTTGTGTTAATCTTTGGGAAGAATTG
TTCCACAAATTGATTTGAAGTTTGTGAATTAG

SEQ ID NO 39: gi_6729511_ref_CAB67667.1, 2xC2H2, *Arabidopsis thaliana*
MKRDRSDYEE SMK HIDIVESLMMLSRSFVVKQIDVKQSTGSKTNHNNHFECKTCNRKFDSFQ
ALGGHRASHKKPKLIVDQEQVKHRNKENDMHKCTICDQMFGTGQALGGHMRKHRTSMITEQS
IVPSVVYSRPVFNRCSSSKEILDNLTPLENDLVLI FGKNLVPQIDLKFN

SEQ ID NO 40: ref_CA279020, 2xC2H2, sugar cane
CCTAACCGAGCATTAGCTTTTCAAATCAACAAGCCTCGCCGTGACCGATCGATGGCCATCACC
CACGACGACTACGTCTCCCTCTGCCTCATGGCGCTCGCAGCCGCGGGAGGCGGAGGCCAAGC
TGGTTTAACAACGCAGTACGCTCTGAACACGGCTGCCTGGACAGCGACGGCGCAAGAGTCCG
AGCTCCGCTTCCGGTGCTCCGTCTGTGGCAAGGCCTTCGCGTGCACACGAGGCACTGGGCGGG
CACAAGGCCAGCCACCGCAAGCCGACGCTCGTACAGGCACATGCGTCGTCTCAGCCGGAGG
CGCGGCGTCTGTCGTTAACAATGACCTCGGCCGTAGGCAGCAGTGGGCAGGGGAGGCACA
GGTGCACGGTGTGCCATCGGAGCTTCGCGACGGNGCAAGCGCTCGGCGGGCACAAGAGGTGC
CATTACTGGGACGGGCTCTCGGTGTGCTCACC GCGTCGTGCGGCCATCGGGGTCCGGGTC
GACCGTCAAGGGCTTTGATCTGAATTTGGTGCCGGTGCCGCCCGCGATGGCCGCCAACGCTG
CGACAAGGTGGGGAGAGGAGAANNAAGTCANAAACCCTTGCGGTCAAGAGAAGGCGGCTTG
CCGGTCCGTCTTGGACCCTAATTTAACGATTTAGAAGTCCTTTTTTTTAATAATTAAGAGTTC
TTTTGAAGAAGGTTGTAAAGTTTTCGAACCTTGTTCTTTTAATGGATTTGGGTGCTGGCGAA
ATTTTAAACTGGATTTAAATTTGCGCTCACTCTTTTTTTTTTATTTTTTACACCCTTTTTTT
TTTTTAGAAGAAGA

FIGURE 3 (continued)

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SEQ ID NO 41: gi_18027011_ref_AF254447.1, 2xC2H2, *Arabidopsis thaliana*
TTCCTTTCTCTTCCTCTCTCTCTCTCTTCACCATGACTGATCCTTATTCCAATTTCTTCACA
GACTGGTTCAAGTCTAATCCTTTTCACCATTACCCTAATTCCTCCACTAACCCCTCTCCTCA
TCCTCTTCCTCCTGTTACTCCTCCCTCTTCCTTCTTCTTCTTCCCTCAATCCGGAGACCTCC
GCCGTCCACCGCCGCCACCAACTCCTCCTCCTTCTCCTCCTCTCCGAGAAGCCCTCCCTCTC
CTCAGCCTCAGCCCCGCCAACAAACAACAAGACCACCATCACAAACCATGACCACCTTATTCA
AGAACCACCTTCAACCTCCATGGATGTGCGACTACGATCATCACCATCAAGATGATCATCATA
ACCTCGATGACGATGACCATGACGTCACCGTTGCTCTTCACATAGGCCTTCCAAGCCCTAGT
GCTCAAGAGATGGCCTCTTTGCTCATGATGTCTTCTTCTTCTCCTCTTCTCCTCGAGGACCACTCA
TCATCACGAGGACATGAATCACAAAGAAAGACCTCGACCATGAGTACAGCCACGGAGCTGTCTG
GAGGAGGAGAAGATGACGATGAAGATTGAGTCGGCGGAGACGGCGGGCTGTAGAATCAGCAGA
CTCAACAAGGGTCAATATTGGATCCCTACACCTTCTCAGATTCTCATTTGGCCCTACTCAGTT
CTCATGTCTGTTTGCTTCAAAACCTTCAACAGATACAATAACATGCAGATGCATATGTGGG
GACATGGATCACAAATACAGAAAAGGACCTGAATCTCTAAGGGGAACACAACCAACAGGAATG
CTAAGGCTTCCGTGCTATTGCTGCGCCCCAGGCTGTCTGCAACAACATTGACCATCCAAGGGC
AAAGCCTCTCAAAGACTTCAGAACCTTCAAACACATTACAAGAGAAAACATGGGATCAAAC
CTTTCATGTGTAGGAAATGTGGAAAGGCTTTCGCGAGTCCGAGGGGACTGGAGAACACATGAG
AAGAATTGTGGCAAACCTTTGGTATTGCATATGTGGATCTGATTTCAAGCACAAGAGATCTCT
CAAAGATCACATCAAGGCTTTTGGGAATGGTCATGGAGCCTACGGAATTGATGGGTTTGATG
AAGAAGATGAGCCTGCCTCTGAGGTAGAACAATTAGACAATGATCATGAGTCAATGCAGTCT
AAATAGCTTATATATATTACTATAAGTACTAAGTAATTCGGTATATATATTAATTATAAGAA
ACCTAAATCTATGGACCAAGTTTTGATGGAGGTAGGGCTTTTCAAACCTAAAAGCTATATCAT
CTAATTGATCATAGGAAAAAATGAATCAAGAGCACTTGGAAAAATTTTAAATTGTATCTTTA
GCTTCCTAGTTAAATTTATTGCAAGACAATGTAGCAGTCTAACCAATGAGGTTCCCAACGGT
TTATTTCTATTTGTATATTATTTGTCATTAGCTTCACCTTTCGTTAATTCGAAGGACATAA
CTTATAAATGTTTAAATTATG

SEQ ID NO 42: At3g57670, 2xC2H2, *Arabidopsis thaliana*
MTDPYSNFFTDWFKSNPFHHYPNSSTNPSPHPLPPVTPPSSFFFFPQSGDLRRPPPPPTPPP
SPPLREALPLLSLSPANKQQDHHHNHDHLIQEPPSTSMVDVYDHHHQDDHHNLDDDDHDVTV
ALHIGLPSPSAQEMASLLMMSSSSSSSRTHHHHEDMNHKKDLDEYSHGAVGGGEDDDDEDSV
GGDGGCRISRLNKGQYWIPTPSQILIGPTQFSCPVCFKTFNRYNNMQMHMWGHGSQYRKGP
SLRGTQPTGMLRLPCYCCAPGCRNNIDHPRAKPLKDFRTLQTHYKRKHGIKPFMCRCCKGAF
AVRGDWRTHEKNCGLWYCICGSDFKHKRSCLKDHKAFGNHGHGAYGIDGFDEEDEPASEVEQ
LDNDHESMQSK

SEQ ID NO 43: gi_18676370_ref_AJ311810.2, 2xC2H2, *Arabidopsis thaliana*
ATCTACACACTACTACTCACATCTCATCTCTCTCTAGCACATAACCATCAAACCATATAGAT
ACGGTGCTTTTATTCTTGATCTTCTTCTTCTTCTTGTCTTCTCCTCAGAGTCATGTCTAAT
CCAGCTTGTTTGAATCTCTTCAACAATGGATGTGACCATAATAGCTTCAACTATTCCACTTC
TCTCTTTACATTTACAACCTCTCACGGTAGCTACTATTACTCTAATACCACAAACCCTAATT
ACATTAATCATACTCATACCACTTCCACTTCCCCTAACTCACCCCCACTAAGAGAAGCTCTT
CCTCTTCTTAGCTTAAGCCCCATAAGGCACCAAGAACAACAAGACCAACACTATTTTCATGGA
CACCCATCAAATTAGCTCTTCAAACCTTCTTGATGATCCTCTTGTGACTGTGGATCTTCATC
TAGGGTTACCAAACCTACGGTGTTGGTGAGAGCATTAGGAGCAATATTGCTCCTGATGCAACC

FIGURE 3 (continued)

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ACGGACGAGCAAGATCAAGATCATGACCGAGGAGTAGAAGTCACAGTTGAGTCCCACCTTGA
 TGATGATGATGATCATCATGGAGATCTACACAGAGGTCACTACTATTGGATTCCTACTCCTT
 CTCAGATTTTGGATTGGTCCTACACAGTTCACCTTGTCTCTTTGCTTCAAGACATTCAACAGA
 TACAACAACATGCAGATGCACATGTGGGGACACGGCTCACAATACAGAAAGGGACCAGAATC
 CTTAAGAGGAACCCAACCAACAGGAATGCTAAGACTACCATGTTTCTGCTGTGCACCCGGTT
 GCAAGAACAACATTGACCACCCACGAGCCAAGCCTCTTAAGGACTTTCGAACCCTCCAAACA
 CATTACAAACGTAAACATGGGTCTAAACCATTGCTTGTCTGTGTGGTAAGGCCTTTGC
 AGTGAAAGGAGATTGGAGAACGCATGAGAAGAATTGTGGAAAGCTTTGGTATTGCTCTTGTG
 GCTCGGATTTTAAGCACAAGAGGTCGCTTAAGGACCATGTCAAGGCCTTTGGAAATGGTCAT
 GTTCCTTGTGGGATTGATAGTTTTTGGAGGAGATCATGAGGACTACTATGATGCTGCTTCTGA
 TATCGAGCAATAAGATGATAGCAACAACAATGAGTGTTAATTAGGGGTTTTGTTTATTTTTC
 CTCTCATGCATTAGTTGATTGTATGCACGTGTTCTTTAGTTTTGTTCTTCGGATCTTTGTTT
 TATTTTGTTTTGAGCTGTTTTTTTTTTTAATTACTAAGAAGTTAATTATCATCTAAAGATTTT
 C

SEQ ID NO 44: gi_18376498_ref_CAC86167.1, 2xC2H2, Arabidopsis thaliana

MSNPACSNLFNNGCDHNSFNYSTSLSYIYNHSGSYYYSNNTNPNYINHTHTTSTSPNSPPLR
 EALPLLSLSPIRHQEQDQHYFMDTHQISSSNFLDDPLVTVDLHLGLPNYGVGESIRSNIAP
 DATTDEQDQDHDGRGVEVTVESHLDDDDHGDHLRGHHYWIPTPSQILIGPTQFTCPLCFKT
 FNRYNNMQMHMWHGHSQYRKGPESLRGTQPTGMLRLPCFCCAPGCKNNIDHPRAKPLKDFRT
 LQTHYKRKHGSKPFACRMCGKAFVKGDWRTHEKNCCKLWYCSCGSDFKHKRSCLKDHVKAFC
 NGHVPCGIDSFGGDHEDYYDAASDIEQ

SEQ ID NO 45: gi_7798991_ref_AL355775.1_region 7957 ... 8451, 2xC2H2, Arabidopsis thaliana

ATGGTTGCGAGAAGTGAGGAAGTTGAGATAGTGGAAGATACGGCGGCGAAATGTTTGATGTT
 GTTATCAAGAGTTGGAGAATGCGGCGGAGGAGGAGAGAAACGAGTTTTCCGATGCAAGACTT
 GTCTTAAAGAGTTTTCGTCGTTTTCAAGCTTTGGGAGGTCATCGTGCAAGCCACAAGAACTC
 ATTAACAGTAGCGATCCATCACTTCTTGGATCCTTGTCTAACAAGAAAACCTAAAACGGCGAC
 GTCTCATCCTTGTCCGATATGTGGCGTGGAGTTTCCGATGGGGCAAGCTCTTGGTGGTCACA
 TGAGGAGACATAGGAGTGAGAAAGCCTCACCAGGCACGTTGGTTACACGTTCTTTTTTACCG
 GAGACGACGACGGTGACGACTTTGAAAAAATCGAGTAGTGGAAGAGAGTGGCTTGTTTGGA
 CTTAGATTCGATGGAGAGTTTAGTCAATTGGAAGTTGGAGTTGGGAAGAACGATTTCTTGA

SEQ ID NO 46: gi_7798996_ref_CAB90935.1, 2xC2H2, Arabidopsis thaliana

MVARSEEVEIVEDTAAKCLMLLSRVGECGGGGEKRVFRCKTCLKEFSSFQALGGHRASHKKL
 INSSDPSLLGSLSNKKTKTATSHPCPICGVEFPMGQALGGHMRRHRSEKASPGTLVTRSFPL
 ETTTVTTLKKSSSGKRVACLDLDSMESLVNWKLELGRTIS

SEQ ID NO 47: gi_9755794_ref_AL391143.1_region 31730 ... 32938, 2xC2H2, Arabidopsis thaliana

ATGGAAGACGAACATCAAGATCTCCATAAACCCATTAATGGAGCTTTGCGAGACCTCAAGAT
 TACTCGGTCACAGAAAGAAACAGAAAAGTCTACGAACCAACAGCAAGATGTTACTTGTACT
 ATGGTCTAAGGGAAAACCTCGAAGAAGAAAACCCAGGAATCTCCGGAACCAATGAAGAAGATT
 TTGTTTCGATGCGAAGAATGTGGAAAAGGGTTTCGGTACGAGAAATATTTTAAGAATCATCG

FIGURE 3 (continued)

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CTCGATGATGCATTTATCGCCGAACGAGAAGGTTTGTGAAGAATCCTTGATGACTCTGTCTC
GTAGCCTTGGGTTTGTGAAGAAGAAGAAAAGATCAAGACTTGGTAGGTCTGGGAAGACTTTA
TTTACTACGTTTCTTGAACCGAGTTCTATTTTTTGATGCGACTGATGAAGAATTAGAAGTGGC
GGATTGTTTGATTCTATTGTCTAAGAGTGCTCCCAAGGTTGTAGACGAATTGAAAAGTCTTT
CTGAGGCAGTACGTGTTACTCCTGAAACACCTGAAAGTAGCTATGATTTGGGTTGTTTGCTC
AACAAAGAAACCGAGAAAAGGTGGTGAATTGGAATCTGGGGTTTTAAGTAATGAGCAAAGACT
TATGGAAGAAGGGTTTAGTAGTTATGGAACATCGAAAGAACCAGCTAGCTTCTTGAGAGACG
AAAACAGATTGGATCAGCAGAAACGGAGAAAAGATGGTGAATTTGAATCCGGACTTTTGAGT
AATGAGCAAAGACTGCTAGAAGAAGAGATTACTACTCCTGTGACATTCAAAGGTCCAGCGAG
TTCCTTGAGACACAAGTGTGCTTTGGATCGAAATGGAGGTGAATTTGGTCCTGAGTTTTTGA
GTAATGAGCAAACACTGATGGAAGAAACATGGAAAGAACCAGTGAGTTTCTTAGAAGATAAG
CATGAATTTGATCAGCGGAAAATGCGAGAAGCTGGCGACTTTGAATCTAGGTTTTACAGAAT
TGAGCTTGGAGTAGGAGCTATGGAGTGTACTTCTTCAGATACTGATATGCTCACGCAATCTG
ATAAGAAGAACGTTGAGCATCGATGCAGGTTGTGCAACAAGATATTCTCGTCTTATCAAGCT
CTAGGGGGTCATCAGACGTTTCATCGGATGAGCAAATGTAAGAACAAGAAGAATGGCATAGA
GGAATCAGTTGAACCCAGGATGACTCTGTGA

SEQ ID NO 48: gi_9755803_ref_CAC01747.1, 2xC2H2, *Arabidopsis thaliana*

MEDEHQDLHKPINGALRDLKITRSQKETEKSTNQOQDVTCYYGLRENSKKKTQESPEPMKKI
LFRCEECKGKGFYKYEKYNHRSMMHLSPNEKVCEESLMTLSRSLGFVKKKRSRLGRSGKTL
FTTFLEPSSIIFDATDEELEVADCLILLSKSA PKVVDELKSLSEAVRVTPETPESSYDLGCLL
NKKPRKGGELESGVLSNEQRLMEEGFSSYGTSKEPASFLRDENRLDQKRRKDGEFESGLLS
NEQRLLEEEITTPVTFKGPASSLRHKCALDRNGGEFGPEFLSNEQTLMEETWKEPVSFLEDK
HEFDQRMREAGDFESRFYRIELGVGAMECTSSD TDMLTQSDKKNVEHRCRLCNKIESSYQA
LGGHQTFHRMSKCKNKNKNGIEESVEPRMTL

SEQ ID NO 49: gi_1418338_ref_X98678.1, 2xC2H2, *Arabidopsis thaliana*

CTTGTTAGTTCACCTCCACATAATAAACACCAAAGATTTCAATTCTCTTCTCCATAATTTCGAA
GTTTCTTGAATTGGGTTTGTCTTCTTGATTTGTTTCTTGAATTGGGTTTTGGTCTTCTTTTCT
TACTATATTTGGATATGATGATGGGTCAAGATGAGGTTGGGAGTGATCAGACGCAAATCATA
AAAGGGAAACGTACGAAGCGACAAAGATCGTCTTTCGACGTTTGTGGTGACGGCGGCGACAAC
AGTGACTTCAACAAGTTCATCGGCCGGTGGAAGTGGAGGAGAAAGAGCTGTTTCAGATGAAT
ACAACCTCGGCGGTTTCGTCTCCGGTGACTACTGATTGTACGCAAGAAGAAGAAGACATGGCG
ATTTGTCTCATCATGTTAGCTCGTGGGACAGTTCTTCCATCGCCGGATCTCAAGAACTCGAG
AAAAATTCATCAGAAGATTTTCGTGCGAGAATTCTAGTTTCTATGTGTACGAGTGTAACCGT
GTAACCGGACGTTTTTCGTGCTTCCAAGCACTTGGTGGACACAGAGCGAGCCACAAGAAGCCG
AGGACGTCGACTGAGGAAAAGACTAGACTACCCCTGACGCAACCCAAGTCTAGTGCATCAGA
AGAAGGGCAAAACAGTCATTTCAAAGTTTCCGGCTCAGCCCTAGCTTCACAGGCAAGTAACA
TCATCAACAAGGCAAACAAAGTACACGAGTGTTCCATCTGCGGTTCTGAGTTCACTTCCGGG
CAAGCTCTCGGTGGTCACATGAGGCGGCACAGGACAGCCGTAACCACGATTAGCCCCGTTGC
AGCCACCGCAGAAGTAAGCAGAAACAGTACAGAGGAAGAGATTGAGATCAATATAGGCCGTT
CGATGGAACAGCAGAGGAAATATCTACCGTTGGATCTTAATCTACCAGCACCAGGAGATGAT
CTAAGAGAGTCCAAGTTTCAAAGGATAGTATTCTCAGCAACACCAGCGTTAATAGATTGTCA
TTACTAGTTGTTTTTTTTTACTACATAATATGATGAAATATTTGTGAATTCTTCTTACTTACT
ACTATATTGTTGATCAAAAAAAAAAAAAAAAAA

FIGURE 3 (continued)

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SEQ ID NO 50: gi_1418339_ref_CAA67236.1, 2xC2H2, Arabidopsis
thaliana
MGQDEVGSDQTQIIKGKRTKRQRSSSTFVVTAATTVTSTSSSAGGSGGERAVSDEYN SAVSS
PVTTDCTQEEEDMAICLIMLARGTVLPSPDLKNSRKIHQKISSENSSFYVYECKTCNRTFSS
FQALGGHRASHKKPRTSTEEKTRLPLTQPKSSASEEGQNSHFKVSGSALASQASNIINKANK
VHECSICGSEFTSGQALGGHMRRHRTAVTTISPVAATAEVSRNSTEEIEINIGRSMEQQRK
YLPLDLNLPAPGDDLRESKFQGIVFSATPALIDCHY

FIGURE 3 (continued)

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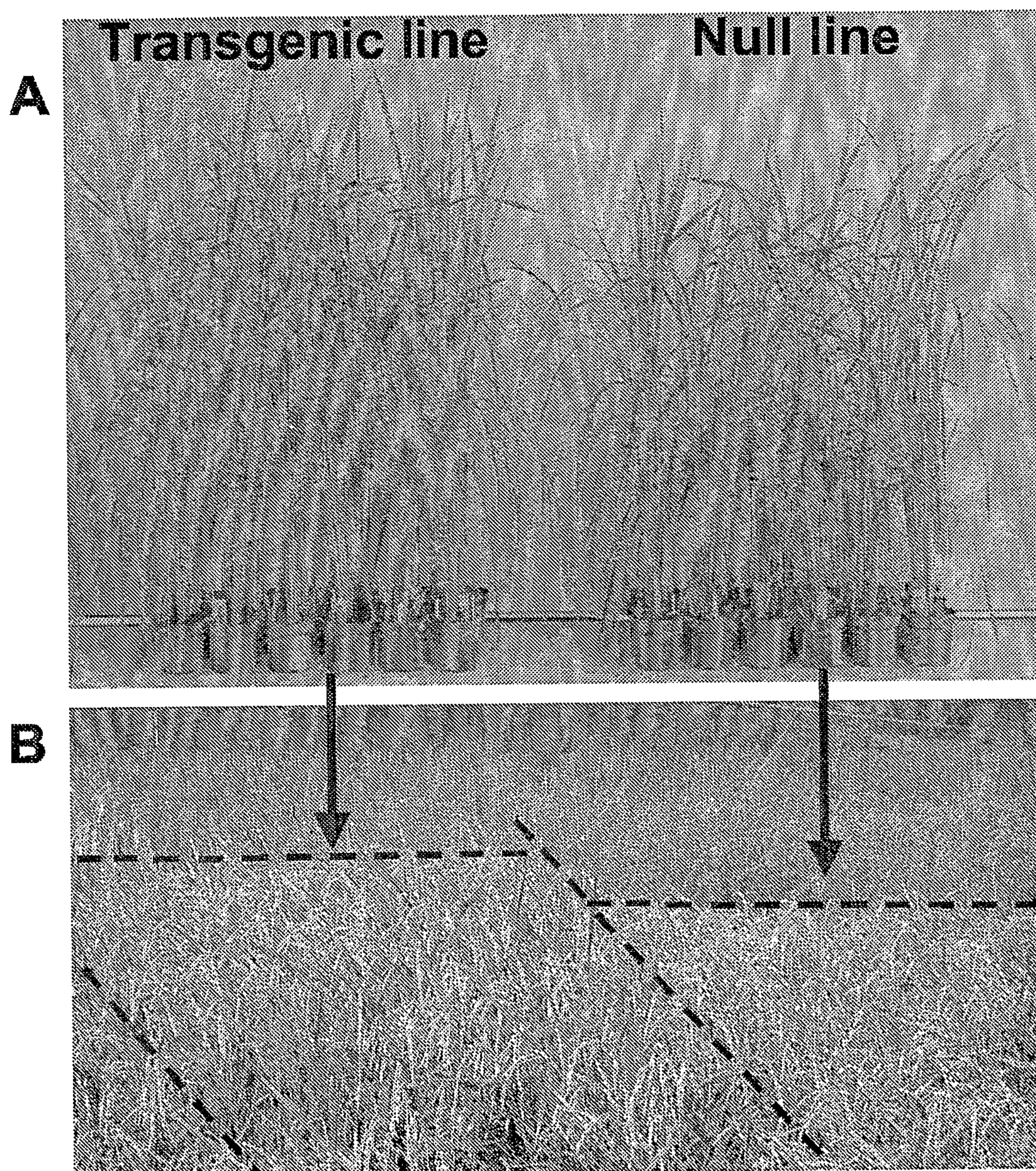


FIGURE 4

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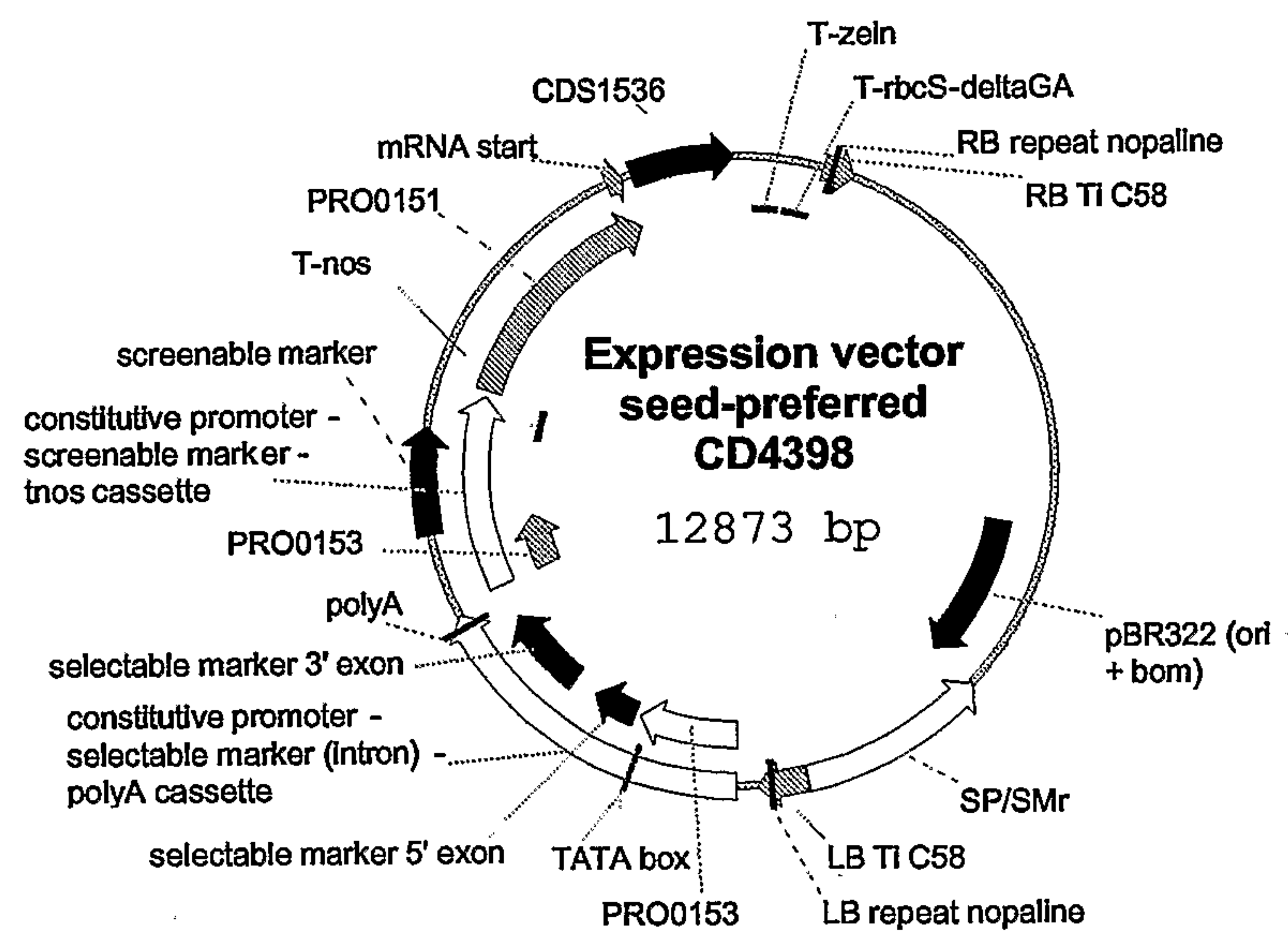


FIGURE 5