

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
12 July 2007 (12.07.2007)

PCT

(10) International Publication Number
WO 2007/078286 A2

(51) International Patent Classification:

C12N 15/82 (2006.01) A01H 5/00 (2006.01)
C12N 15/79 (2006.01) C12N 5/14 (2006.01)[US/US]; 3658 Valencia Ave., Simi Valley, California 93063 (US). **NADZAN, Gregory** [US/US]; 633 Canoga Ave., Apt. 148, Woodland Hills, California 91367 (US).

(21) International Application Number:

PCT/US2005/047423

(74) Agent: **SVENSSON, Leonard, R.; BIRCH, STEWART, KOLASCH & BIRCH, LLP**, P.O. Box 747, Falls Church, Virginia 22040-0747 (US).

(22) International Filing Date:

29 December 2005 (29.12.2005)

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(25) Filing Language:

English

(26) Publication Language:

English

(71) Applicant (for all designated States except US): **CERES, INC.** [US/US]; 1535 Rancho Conejo Boulevard, Thousand Oaks, California 91320-1440 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **ALEXANDROV, Nickolai** [US/US]; 1404 Oak Trail Street, Thousand Oaks, California 91320 (US). **BROVER, Vyacheslav** [RU/US]; 1741 N. Warfield Circle, Simi Valley, California 93063 (US). **MASCIA, Peter** [US/US]; 1800 Cannes Drive, Thousand Oaks, California 91362 (US). **FLEDMANN, Kenneth, A.** [US/US]; 3806 Calle Mazatlan, Newbury Park, California 91320 (US). **CHRISTENSEN, Cory**

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: NUCLEOTIDE SEQUENCES AND CORRESPONDING POLYPEPTIDES CONFERRING MODULATED PLANT GROWTH RATE AND BIOMASS IN PLANTS

CeresGdna:1460991	-----MVA	ALKNVVGSTA	SMDFSRFMNS	23
Lead-clone123905-Taxonomy:3702	-----MVA	ALKNVVGSTA	SMDFSRFMNS	30
gi151536200	-----MVA	ALKNVVGSTA	SMDFSRFMNS	43
CeresClone:1494990	-----MVA	ALKNVVGSTA	SMDFSRFMNS	41
CeresClone:634402	-----MVA	ALKNVVGSTA	SMDFSRFMNS	50
Consensus	-----MVA	ALKNVVGSTA	SMDFSRFMNS	50
CeresGdna:1460991	I N P I L T S P	Q F S A S N N G	-----N G F C N	67
Lead-clone123905-Taxonomy:3702	I N P I L T S P	Q F S A S N N G	-----N G F C N	80
gi151536200	I N P I L T S P	Q F S A S N N G	-----N G F C N	81
CeresClone:1494990	I N P I L T S P	Q F S A S N N G	-----N G F C N	79
CeresClone:634402	I N P I L T S P	Q F S A S N N G	-----N G F C N	88
Consensus	I N P I L T S P	Q F S A S N N G	-----N G F C N	100
CeresGdna:1460991	L G C N F F	Q R I E K N H Q E	-----P P N Q E D	89
Lead-clone123905-Taxonomy:3702	L G C N F F	Q R I E K N H Q E	-----P P N Q E D	130
gi151536200	L G C N F F	Q R I E K N H Q E	-----P P N Q E D	124
CeresClone:1494990	L G C N F F	Q R I E K N H Q E	-----P P N Q E D	112
CeresClone:634402	L G C N F F	Q R I E K N H Q E	-----P P N Q E D	121
Consensus	L G C N F F	Q R I E K N H Q E	-----P P N Q E D	150
CeresGdna:1460991	R V K K N Y R G V R	Q R P W G K W A E	I R D P R K A A R V	139
Lead-clone123905-Taxonomy:3702	R V K K N Y R G V R	Q R P W G K W A E	I R D P R K A A R V	180
gi151536200	R V K K N Y R G V R	Q R P W G K W A E	I R D P R K A A R V	174
CeresClone:1494990	R V K K N Y R G V R	Q R P W G K W A E	I R D P R K A A R V	162
CeresClone:634402	R V K K N Y R G V R	Q R P W G K W A E	I R D P R K A A R V	171
Consensus	R V K K N Y R G V R	Q R P W G K W A E	I R D P R K A A R V	200

(57) Abstract: The present invention relates to isolated nucleic acid molecules and their corresponding encoded polypeptides able confer the trait of modulated plant size, vegetative growth, organ number, plant architecture, growth rate, seedling vigor, growth rate, fruit and seed yield, tillering and/or biomass in plants. The present invention further relates to the use of these nucleic acid molecules and polypeptides in making transgenic plants, plant cells, plant materials or seeds of a plant having plant size, vegetative growth, organ number, plant architecture, growth rate, seedling vigor and/or biomass that are altered with respect to wild type plants grown under similar conditions



Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

**NUCLEOTIDE SEQUENCES AND CORRESPONDING
POLYPEPTIDES CONFERRING MODULATED PLANT GROWTH RATE AND
BIOMASS IN PLANTS**

FIELD OF THE INVENTION

[0001] The present invention relates to isolated nucleic acid molecules and their corresponding encoded polypeptides able to modulate plant growth rate, vegetative growth, organ size, architecture seedling vigor and/or biomass in plants. The present invention further relates to using the nucleic acid molecules and polypeptides to make transgenic plants, plant cells, plant materials or seeds of a plant having modulated growth rate, vegetative growth, organ number, architecture, seedling vigor and/or biomass as compared to wild-type plants grown under similar conditions.

BACKGROUND OF THE INVENTION

[0002] Plants specifically improved for agriculture, horticulture, biomass conversion, and other industries (e.g. paper industry, plants as production factories for proteins or other compounds) can be obtained using molecular technologies. As an example, great agronomic value can result from modulating the size of a plant as a whole or of any of its organs or the number of any of its organs.

[0003] Similarly, modulation of the size and stature of an entire plant, or a particular portion of a plant, or growth rate, or seedling vigor allows production of plants better suited for a particular industry. For example, reductions in the height of specific crops and tree species can be beneficial by allowing easier harvesting. Alternatively, increasing height, thickness or organ size, organ number may be beneficial by providing more biomass useful for processing into food, feed, fuels and/or chemicals (see the US Department of Energy website for Energy Efficiency and Renewable Energy). Other examples of commercially desirable traits include increasing the length of the floral stems of cut flowers,

increasing or altering leaf size and shape or enhancing the size of seeds and/or fruits. Changes in organ size, organ number and biomass also result in changes in the mass of constituent molecules such as secondary products and convert the plants into factories for these compounds.

[0004] Availability and maintenance of a reproducible stream of food and animal feed to feed animals and people has been a high priority throughout the history of human civilization and lies at the origin of agriculture. Specialists and researchers in the fields of agronomy science, agriculture, crop science, horticulture, and forest science are even today constantly striving to find and produce plants with an increased growth potential to feed an increasing world population and to guarantee a supply of reproducible raw materials. The robust level of research in these fields of science indicates the level of importance leaders in every geographic environment and climate around the world place on providing sustainable sources of food, feed, chemicals and energy for the population.

[0005] Manipulation of crop performance has been accomplished conventionally for centuries through plant breeding. The breeding process is, however, both time-consuming and labor-intensive. Furthermore, appropriate breeding programs must be specially designed for each relevant plant species.

[0006] On the other hand, great progress has been made in using molecular genetics approaches to manipulate plants to provide better crops. Through introduction and expression of recombinant nucleic acid molecules in plants, researchers are now poised to provide the community with plant species tailored to grow more efficiently and produce more product despite unique geographic and/or climatic environments. These new approaches have the additional advantage of not being limited to one plant species, but instead being applicable to multiple different plant species (Zhang et al. (2004) *Plant Physiol.* 135:615).

[0007] Despite this progress, today there continues to be a great need for generally applicable processes that improve forest or agricultural plant growth to suit particular needs depending on specific environmental conditions. To this end, the present invention is directed to advantageously manipulating plant size, organ number, plant growth rate, plant architecture and/or biomass to maximize the benefits of various crops depending on the benefit sought and the particular environment in which the crop must grow, characterized by expression of recombinant DNA molecules in plants. These molecules may be from the plant itself, and simply expressed at a higher or lower level, or the molecules may be from different plant species.

SUMMARY OF THE INVENTION

[0008] The present invention, therefore, relates to isolated nucleic acid molecules and polypeptides and their use in making transgenic plants, plant cells, plant materials or seeds of plants having life cycles, particularly plant size, vegetative growth, plant growth rate, organ number, plant architecture and/or biomass, that are altered with respect to wild-type plants grown under similar or identical conditions.

[0009] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

BRIEF DESCRIPTION OF THE FIGURES

[0010] **Figure 1.** Amino acid sequence alignment of homologues of Lead 29 (ME04717), SEQ ID NO. 93. Conserved regions are enclosed in a box. A consensus sequence is shown below the alignment.

[0011] **Figure 2.** Amino acid sequence alignment of homologues of Lead 36 (ME03195), SEQ ID NO. 99. Conserved regions are enclosed in a box. A consensus sequence is shown below the alignment.

[0012] **Figure 3.** Amino acid sequence alignment of homologues of Lead 15 (ME04077), SEQ ID NO. 81. Conserved regions are enclosed in a box. A consensus sequence is shown below the alignment.

[0013] **Figure 4.** Amino acid sequence alignment of homologues of Lead ME04012, SEQ ID NO. 110. Conserved regions are enclosed in a box. A consensus sequence is shown below the alignment.

[0014] **Figure 5.** Amino acid sequence alignment of homologues of Lead Clone 691319, SEQ ID NO. 104. Conserved regions are enclosed in a box. A consensus sequence is shown below the alignment.

DETAILED DESCRIPTION OF THE INVENTION

1. THE INVENTION

[0015] The invention of the present application may be described by, but not necessarily limited to, the following exemplary embodiments.

[0016] The present invention discloses novel isolated nucleic acid molecules, nucleic acid molecules that interfere with these nucleic acid molecules, nucleic acid molecules that hybridize to these nucleic acid molecules, and isolated nucleic acid molecules that encode the same protein due to the degeneracy of the DNA code. Additional embodiments of the present application further include the polypeptides encoded by the isolated nucleic acid molecules of the present invention.

[0017] More particularly, the nucleic acid molecules of the present invention comprise: (a) a nucleotide sequence encoding an amino acid sequence that is at least 85%

identical to any one of Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively, (b) a nucleotide sequence that is complementary to any one of the nucleotide sequences according to (a), (c) a nucleotide sequence according to any one of SEQ ID Nos. 80, 90, 92, 98, 109, and 103, (d) a nucleotide sequence that is in reverse order of any one of the nucleotide sequences according to (c) when read in the 5' to 3' direction, (e) a nucleotide sequence able to interfere with any one of the nucleotide sequences according to (a), (f) a nucleotide sequence able to form a hybridized nucleic acid duplex with the nucleic acid according to any one of paragraphs (a) – (e) at a temperature from about 40°C to about 48°C below a melting temperature of the hybridized nucleic acid duplex, and (g) a nucleotide sequence encoding any one of amino acid sequences of Leads 15, 28, 29, 36, ME04012 and Clone 691319 corresponding to SEQ ID Nos. 81, 91, 93, 99, 110, and 104, respectively.

[0018] Additional embodiments of the present invention include those polypeptide and nucleic acid molecule sequences disclosed in SEQ ID Nos. 80, 81, 90, 91, 92, 93, 98, 99, 109, 110, 103 and 104.

[0019] The present invention further embodies a vector comprising a first nucleic acid having a nucleotide sequence encoding a plant transcription and/or translation signal, and a second nucleic acid having a nucleotide sequence according to the isolated nucleic acid molecules of the present invention. More particularly, the first and second nucleic acids may be operably linked. Even more particularly, the second nucleic acid may be endogenous to a first organism, and any other nucleic acid in the vector may be endogenous to a second organism. Most particularly, the first and second organisms may be different species.

[0020] In a further embodiment of the present invention, a host cell may comprise an isolated nucleic acid molecule according to the present invention. More

particularly, the isolated nucleic acid molecule of the present invention found in the host cell of the present invention may be endogenous to a first organism and may be flanked by nucleotide sequences endogenous to a second organism. Further, the first and second organisms may be different species. Even more particularly, the host cell of the present invention may comprise a vector according to the present invention, which itself comprises nucleic acid molecules according to those of the present invention.

[0021] In another embodiment of the present invention, the isolated polypeptides of the present invention may additionally comprise amino acid sequences that are at least 85% identical to any one of Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to SEQ ID Nos. 81, 91, 93, 99, 110, and 104, respectively.

[0022] Other embodiments of the present invention include methods of introducing an isolated nucleic acid of the present invention into a host cell. More particularly, an isolated nucleic acid molecule of the present invention may be contacted to a host cell under conditions allowing transport of the isolated nucleic acid into the host cell. Even more particularly, a vector as described in a previous embodiment of the present invention, may be introduced into a host cell by the same method.

[0023] Methods of detection are also available as embodiments of the present invention. Particularly, methods for detecting a nucleic acid molecule according to the present invention in a sample. More particularly, the isolated nucleic acid molecule according to the present invention may be contacted with a sample under conditions that permit a comparison of the nucleotide sequence of the isolated nucleic acid molecule with a nucleotide sequence of nucleic acid in the sample. The results of such an analysis may then be considered to determine whether the isolated nucleic acid molecule of the present invention is detectable and therefore present within the sample.

[0024] A further embodiment of the present invention comprises a plant, plant cell, plant material or seeds of plants comprising an isolated nucleic acid molecule and/or vector of the present invention. More particularly, the isolated nucleic acid molecule of the present invention may be exogenous to the plant, plant cell, plant material or seed of a plant.

[0025] A further embodiment of the present invention includes a plant regenerated from a plant cell or seed according to the present invention. More particularly, the plant, or plants derived from the plant, plant cell, plant material or seeds of a plant of the present invention preferably has increased size (in whole or in part), increased vegetative growth, increased organ number and/or increased biomass (sometimes hereinafter collectively referred to as increased biomass), lethality, sterility or ornamental characteristics as compared to a wild-type plant cultivated under identical conditions. Furthermore, the transgenic plant may comprise a first isolated nucleic acid molecule of the present invention, which encodes a protein involved in modulating growth and phenotype characteristics, and a second isolated nucleic acid molecule which encodes a promoter capable of driving expression in plants, wherein the growth and phenotype modulating component and the promoter are operably linked. More preferably, the first isolated nucleic acid may be mis-expressed in the transgenic plant of the present invention, and the transgenic plant exhibits modulated characteristics as compared to a progenitor plant devoid of the gene, when the transgenic plant and the progenitor plant are cultivated under identical environmental conditions. In another embodiment of the present invention the modulated growth and phenotype characteristics may be due to the inactivation of a particular sequence, using for example an interfering RNA.

[0026] A further embodiment consists of a plant, plant cell, plant material or seed of a plant according to the present invention which comprises an isolated nucleic acid molecule of the present invention, wherein the plant, or plants derived from the plant, plant cell, plant

material or seed of a plant, has the modulated growth and phenotype characteristics as compared to a wild-type plant cultivated under identical conditions.

[0027] The polynucleotide conferring increased biomass or vigor may be mis-expressed in the transgenic plant of the present invention, and the transgenic plant exhibits an increased biomass or vigor as compared to a progenitor plant devoid of the polynucleotide, when the transgenic plant and the progenitor plant are cultivated under identical environmental conditions. In another embodiment of the present invention increased biomass or vigor phenotype may be due to the inactivation of a particular sequence, using for example an interfering RNA.

[0028] Another embodiment consists of a plant, plant cell, plant material or seed of a plant according to the present invention which comprises an isolated nucleic acid molecule of the present invention, wherein the plant, or plants derived from the plant, plant cell, plant material or seed of a plant, has increased biomass or vigor as compared to a wild-type plant cultivated under identical conditions.

[0029] Another embodiment of the present invention includes methods of enhancing biomass or vigor in plants. More particularly, these methods comprise transforming a plant with an isolated nucleic acid molecule according to the present invention. Preferably, the method is a method of enhancing biomass or vigor in the transformed plant, whereby the plant is transformed with a nucleic acid molecule encoding the polypeptide of the present invention.

[0030] Polypeptides of the present invention include consensus sequences. The consensus sequences are those as shown in Figures 1-5.

2. DEFINITIONS

[0031] The following terms are utilized throughout this application:

[0032] Biomass: As used herein, "biomass" refers to useful biological material including a product of interest, which material is to be collected and is intended for further processing to isolate or concentrate the product of interest. "Biomass" may comprise the fruit or parts of it or seeds, leaves, or stems or roots where these are the parts of the plant that are of particular interest for the industrial purpose. "Biomass", as it refers to plant material, includes any structure or structures of a plant that contain or represent the product of interest.

[0033] Transformation: Examples of means by which this can be accomplished are described below and include *Agrobacterium*-mediated transformation (of dicots (Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443; Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. (USA)* 85: 2444), of monocots (Yamauchi et al. (1996) *Plant Mol Biol.* 30:321-9; Xu et al. (1995) *Plant Mol. Biol.* 27:237; Yamamoto et al. (1991) *Plant Cell* 3:371), and biolistic methods (P. Tijessen, "Hybridization with Nucleic Acid Probes" *In Laboratory Techniques in Biochemistry and Molecular Biology*, P.C. vand der Vliet, ed., c. 1993 by Elsevier, Amsterdam), electroporation, *in planta* techniques, and the like. Such a plant containing the exogenous nucleic acid is referred to here as a T₀ for the primary transgenic plant and T₁ for the first generation.

[0034] Functionally Comparable Proteins or Functional Homologs: This term describes those proteins that have at least one functional characteristic in common. Such characteristics include sequence similarity, biochemical activity, transcriptional pattern similarity and phenotypic activity. Typically, the functionally comparable proteins share some sequence similarity or at least one biochemical. Within this definition, analogs are considered to be functionally comparable. In addition, functionally comparable proteins generally share at least one biochemical and/or phenotypic activity.

[0035] Functionally comparable proteins will give rise to the same characteristic to a similar, but not necessarily the same, degree. Typically, comparable

proteins give the same characteristics where the quantitative measurement due to one of the comparables is at least 20% of the other; more typically, between 30 to 40%; even more typically, between 50-60%; even more typically between 70 to 80%; even more typically between 90 to 100% of the other.

[0036] Heterologous sequences: “Heterologous sequences” are those that are not operatively linked or are not contiguous to each other in nature. For example, a promoter from corn is considered heterologous to an *Arabidopsis* coding region sequence. Also, a promoter from a gene encoding a growth factor from corn is considered heterologous to a sequence encoding the corn receptor for the growth factor. Regulatory element sequences, such as UTRs or 3' end termination sequences that do not originate in nature from the same gene as the coding sequence, are considered heterologous to said coding sequence. Elements operatively linked in nature and contiguous to each other are not heterologous to each other. On the other hand, these same elements remain operatively linked but become heterologous if other filler sequence is placed between them. Thus, the promoter and coding sequences of a corn gene expressing an amino acid transporter are not heterologous to each other, but the promoter and coding sequence of a corn gene operatively linked in a novel manner are heterologous.

[0037] Misexpression: The term “misexpression” refers to an increase or a decrease in the transcription of a coding region into a complementary RNA sequence as compared to the wild-type. This term also encompasses expression and/or translation of a gene or coding region or inhibition of such transcription and/or translation for a different time period as compared to the wild-type and/or from a non-natural location within the plant genome, including a gene or coding region from a different plant species or from a non-plant organism.

[0038] Percentage of sequence identity: As used herein, the term “percent sequence identity” refers to the degree of identity between any given query sequence and a

subject sequence. A query nucleic acid or amino acid sequence is aligned to one or more subject nucleic acid or amino acid sequences using the computer program ClustalW (version 1.83, default parameters), which allows alignments of nucleic acid or protein sequences to be carried out across their entire length (global alignment).

[0039] ClustalW calculates the best match between a query and one or more subject sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a query sequence, a subject sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the following default parameters are used: word size: 2; window size: 4; scoring method: percentage; number of top diagonals: 4; and gap penalty: 5. For multiple alignment of nucleic acid sequences, the following parameters are used: gap opening penalty: 10.0; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of protein sequences, the following parameters are used: word size: 1; window size: 5; scoring method: percentage; number of top diagonals: 5; gap penalty: 3. For multiple alignment of protein sequences, the following parameters are used: weight matrix: blosum; gap opening penalty: 10.0; gap extension penalty: 0.05; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; residue-specific gap penalties: on. The output is a sequence alignment that reflects the relationship between sequences. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher website and at the European Bioinformatics Institute website on the World Wide Web.

[0040] In case of the functional homolog searches, to ensure a subject sequence having the same function as the query sequence, the alignment has to be along at least 80% of the length of the query sequence so that the majority of the query sequence is covered by the subject sequence. To determine a percent identity between a query sequence and a subject sequence, ClustalW divides the number of identities in the best

alignment by the number of residues compared (gap positions are excluded), and multiplies the result by 100. The output is the percent identity of the subject sequence with respect to the query sequence. It is noted that the percent identity value can be rounded to the nearest tenth. For example, 78.11, 78.12, 78.13, and 78.14 are rounded down to 78.1, while 78.15, 78.16, 78.17, 78.18, and 78.19 are rounded up to 78.2.

[0041] Regulatory Regions: The term “regulatory region” refers to nucleotide sequences that, when operably linked to a sequence, influence transcription initiation or translation initiation or transcription termination of said sequence and the rate of said processes, and/or stability and/or mobility of a transcription or translation product. As used herein, the term “operably linked” refers to positioning of a regulatory region and said sequence to enable said influence. Regulatory regions include, without limitation, promoter sequences, enhancer sequences, response elements, protein recognition sites, inducible elements, protein binding sequences, 5’ and 3’ untranslated regions (UTRs), transcriptional start sites, termination sequences, polyadenylation sequences, and introns. Regulatory regions can be classified in two categories, promoters and other regulatory regions.

[0042] Seedling vigor: As used herein, “seedling vigor” refers to the plant characteristic whereby the plant emerges from soil faster, has an increased germination rate (i.e., germinates faster), has faster and larger seedling growth and/or germinates faster under cold conditions as compared to the wild type or control under similar conditions. Seedling vigor has often been defined to comprise the seed properties that determine “the potential for rapid, uniform emergence and development of normal seedlings under a wide range of field conditions”.

[0043] Stringency: “Stringency,” as used herein is a function of nucleic acid molecule probe length, nucleic acid molecule probe composition (G + C content), salt concentration, organic solvent concentration and temperature of hybridization and/or wash

conditions. Stringency is typically measured by the parameter T_m , which is the temperature at which 50% of the complementary nucleic acid molecules in the hybridization assay are hybridized, in terms of a temperature differential from T_m . High stringency conditions are those providing a condition of $T_m - 5^\circ\text{C}$ to $T_m - 10^\circ\text{C}$. Medium or moderate stringency conditions are those providing $T_m - 20^\circ\text{C}$ to $T_m - 29^\circ\text{C}$. Low stringency conditions are those providing a condition of $T_m - 40^\circ\text{C}$ to $T_m - 48^\circ\text{C}$. The relationship between hybridization conditions and T_m (in $^\circ\text{C}$) is expressed in the mathematical equation:

$$T_m = 81.5 - 16.6(\log_{10}[\text{Na}^+]) + 0.41(\%G+C) - (600/N) \quad (\text{I})$$

where N is the number of nucleotides of the nucleic acid molecule probe. This equation works well for probes 14 to 70 nucleotides in length that are identical to the target sequence. The equation below, for T_m of DNA-DNA hybrids, is useful for probes having lengths in the range of 50 to greater than 500 nucleotides, and for conditions that include an organic solvent (formamide):

$$T_m = 81.5 + 16.6 \log \{ [\text{Na}^+] / (1 + 0.7[\text{Na}^+]) \} + 0.41(\%G+C) - 500/L - 0.63(\%\text{formamide}) \quad (\text{II})$$

where L represents the number of nucleotides in the probe in the hybrid (21). The T_m of Equation II is affected by the nature of the hybrid: for DNA-RNA hybrids, T_m is $10\text{-}15^\circ\text{C}$ higher than calculated; for RNA-RNA hybrids, T_m is $20\text{-}25^\circ\text{C}$ higher. Because the T_m decreases about 1°C for each 1% decrease in homology when a long probe is used (Frischauf et al. (1983) *J. Mol Biol*, 170: 827-842), stringency conditions can be adjusted to favor detection of identical genes or related family members.

[0044] Equation II is derived assuming the reaction is at equilibrium. Therefore, hybridizations according to the present invention are most preferably performed under conditions of probe excess and allowing sufficient time to achieve equilibrium. The time required to reach equilibrium can be shortened by using a hybridization buffer that includes a hybridization accelerator such as dextran sulfate or another high volume polymer.

[0045] Stringency can be controlled during the hybridization reaction, or after hybridization has occurred, by altering the salt and temperature conditions of the wash solutions. The formulas shown above are equally valid when used to compute the stringency of a wash solution. Preferred wash solution stringencies lie within the ranges stated above; high stringency is 5-8°C below T_m , medium or moderate stringency is 26-29°C below T_m and low stringency is 45-48°C below T_m .

[0046] T_0 : The term " T_0 " refers to the whole plant, explant or callus tissue, inoculated with the transformation medium.

[0047] T_1 : The term T_1 refers to either the progeny of the T_0 plant, in the case of whole-plant transformation, or the regenerated seedling in the case of explant or callous tissue transformation.

[0048] T_2 : The term T_2 refers to the progeny of the T_1 plant. T_2 progeny are the result of self-fertilization or cross-pollination of a T_1 plant.

[0049] T_3 : The term T_3 refers to second generation progeny of the plant that is the direct result of a transformation experiment. T_3 progeny are the result of self-fertilization or cross-pollination of a T_2 plant.

3. IMPORTANT CHARACTERISTICS OF THE POLYNUCEOTIDES AND POLYPEPTIDES OF THE INVENTION

[0050] The nucleic acid molecules and polypeptides of the present invention are of interest because when the nucleic acid molecules are mis-expressed (*i.e.*, when expressed at a non-natural location or in an increased or decreased amount relative to wild-type) they produce plants that exhibit modulated biomass, growth rate, or seedling vigor as compared to wild-type plants, as evidenced by the results of various experiments disclosed below. This trait can be used to exploit or maximize plant products. For example, the nucleic acid molecules and polypeptides of the present invention are used to increase the expression of genes that cause the plant to have modulated biomass, growth rate or seedling vigor.

[0051] Because the disclosed sequences and methods increase vegetative growth, and growth rate, the disclosed methods can be used to enhance biomass production. For example, plants that grow vegetatively have an increase biomass production, compared to a plant of the same species that is not genetically modified for substantial vegetative growth. Examples of increases in biomass production include increases of at least 5%, at least 20%, or even at least 50%, when compared to an amount of biomass production by a plant of the same species not growing vegetatively.

[0052] The sequence of Lead 36 of the present invention and its functional homologs in particular provide transformed plants with enhanced yield, including fruit yield and yield per acre, somewhat early maturity, and a more compact stature (20%, 30%, 40% or 60% more compact) with shorter stems, but without proportionally reduced biomass. In tomatoes, this results in plants with increased fruit yield on more compact plants. In rice, this results in plants with an increase number of tillers. The sequence of Lead 29 of the present invention and its functional homologs in particular provide transformed plants with enhanced

yield, including fruit yield and yield per acre, somewhat early maturity, and a more compact stature (20%, 30%, 40% or 60% more compact) with shorter stems. In tomatoes, this results in plants with increased fruit yield on more compact plants. In rice, this results in plants with an increase number of tillers. The sequences of Leads 15 and 28 of the present invention and their functional homologs in particular provide transformed plants with enhanced yield, including fruit yield and yield per acre. In tomatoes, this results in plants with increased fruit yield on more compact plants. In rice, this results in plants with an increase number of tillers.

[0053] The life cycle of flowering plants in general can be divided into three growth phases: vegetative, inflorescence, and floral (late inflorescence phase). In the vegetative phase, the shoot apical meristem (SAM) generates leaves that later will ensure the resources necessary to produce fertile offspring. Upon receiving the appropriate environmental and developmental signals the plant switches to floral, or reproductive, growth and the SAM enters the inflorescence phase (I) and gives rise to an inflorescence with flower primordia. During this phase the fate of the SAM and the secondary shoots that arise in the axils of the leaves is determined by a set of meristem identity genes, some of which prevent and some of which promote the development of floral meristems. Once established, the plant enters the late inflorescence phase (Xu et al. (1995) *Plant Mol. Biol.* 27:237) where the floral organs are produced. If the appropriate environmental and developmental signals the plant switches to floral, or reproductive, growth are disrupted, the plant will not be able to enter reproductive growth, therefore maintaining vegetative growth.

[0054] Seed or seedling vigor is an important characteristic that can greatly influence successful growth of a plant, such as crop plants. Adverse environmental conditions, such as dry, wet, cold or hot conditions, can affect a plant growth cycle, and the vigor of seeds (i.e. vitality and strength under such conditions can differentiate between successful and failed crop growth). Seedling vigor has often been defined to comprise the

seed properties that determine “the potential for rapid, uniform emergence and development of normal seedlings under a wide range of field conditions”. Hence, it would be advantageous to develop plant seeds with increased vigor.

[0055] For example, increased seedling vigor would be advantageous for cereal plants such as rice, maize, wheat, etc. production. For these crops, growth can often be slowed or stopped by cool environmental temperatures during the planting season. In addition, rapid emergence and tillering of rice would permit growers to initiate earlier flood irrigation which can save water and suppress weak growth. Genes associated with increased seed vigor and/or cold tolerance in rice, have therefore been sought for producing improve rice varieties. See e.g., Pinson, S., “Molecular Mapping of Seedling Vigor QTLs in Tropical Rice”, USDA Agricultural Research Service, December 16, 2000.

[0056] Seedling vigor has been measured by different tests and assays, including most typically a cold tolerance test and an accelerated aging test.

[0057] Some of the nucleotide sequences of the invention code for basic-helix-loop (bHCH) transcription factors. It is known that transcription factors often control the expression of multiple genes in a pathway. The basic/helix-loop-helix (BHLH) proteins are a superfamily of transcription factors that bind as dimers to specific DNA target sites. The bHLH transcription factors have been well characterized in nonplant eukaryotes and have been identified as important regulatory components in diverse biological processes. Many different functions have been identified for those proteins in animals, including the control of cell proliferation and transcription often involves homo- or hetero-dimerization. Members of the R/B basic helix-loop-helix (bHLH) family of plant transcription factors are involved in a variety of growth and differentiation processes.

[0058] A basic-helix-loop-helix (bHLH) is a protein structural motif that characterizes a family of transcription factors. The motif is characterized by two α helices

connected by a loop. Transcription factors of this type are typically dimeric, each with one helix containing basic amino acid residues that facilitate DNA binding. One helix is typically smaller and due to the flexibility of the loop allows dimerization by folding and packing against another helix. The larger helix typically contains the DNA binding regions. bHLH proteins typically bind to a consensus sequence called an E-box, CANNTG. The canonical E-box is CACGTG, however some bHLH transcription factors bind to different sequences, which are often similar to the E-box. bHLH transcription factors are often important in development or cell activity.

4. THE POLYNUCLEOTIDES/POLYPEPTIDES OF THE INVENTION

[0059] The polynucleotides of the present invention and the proteins expressed via translation of these polynucleotides are set forth in the Sequence Listing, specifically SEQ ID NOS. 80, 81, 90, 91, 92, 93, 98, 99, 109, 110, 103, and 104. The Sequence Listing also consists of functionally comparable proteins. Polypeptides comprised of a sequence within and defined by one of the consensus sequences can be utilized for the purposes of the invention, namely to make transgenic plants with modulated biomass, growth rate and/or seedling vigor.

5. USE OF THE POLYPEPTIDES TO MAKE TRANSGENIC PLANTS

[0060] To use the sequences of the present invention or a combination of them or parts and/or mutants and/or fusions and/or variants of them, recombinant DNA constructs are prepared that comprise the polynucleotide sequences of the invention inserted into a vector and that are suitable for transformation of plant cells. The construct can be made using standard recombinant DNA techniques (*see*, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989, New York.) and can be

introduced into the plant species of interest by, for example, *Agrobacterium*-mediated transformation, or by other means of transformation, for example, as disclosed below.

[0061] The vector backbone may be any of those typically used in the field such as plasmids, viruses, artificial chromosomes, BACs, YACs, PACs and vectors such as, for instance, bacteria-yeast shuttle vectors, lambda phage vectors, T-DNA fusion vectors and plasmid vectors (*see*, Shizuya et al. (1992) *Proc. Natl. Acad. Sci. USA*, 89: 8794-8797; Hamilton et al. (1996) *Proc. Natl. Acad. Sci. USA*, 93: 9975-9979; Burke et al. (1987) *Science*, 236:806-812 ; Sternberg N. et al. (1990) *Proc Natl Acad Sci U S A.*, 87:103-7; Bradshaw et al. (1995) *Nucl Acids Res*, 23: 4850-4856; Frischauf et al. (1983) *J. Mol Biol*, 170: 827-842; Huynh et al., Glover NM (ed) *DNA Cloning: A practical Approach*, Vol.1 Oxford: IRL Press (1985); Walden et al. (1990) *Mol Cell Biol* 1: 175-194).

[0062] Typically, the construct comprises a vector containing a nucleic acid molecule of the present invention with any desired transcriptional and/or translational regulatory sequences such as, for example, promoters, UTRs, and 3' end termination sequences. Vectors may also include, for example, origins of replication, scaffold attachment regions (SARs), markers, homologous sequences, and introns. The vector may also comprise a marker gene that confers a selectable phenotype on plant cells. The marker may preferably encode a biocide resistance trait, particularly antibiotic resistance, such as resistance to, for example, kanamycin, bleomycin, or hygromycin, or herbicide resistance, such as resistance to, for example, glyphosate, chlorosulfuron or phosphinotricin.

[0063] It will be understood that more than one regulatory region may be present in a recombinant polynucleotide, *e.g.*, introns, enhancers, upstream activation regions, transcription terminators, and inducible elements. Thus, more than one regulatory region can be operably linked to said sequence.

[0064] To “operably link” a promoter sequence to a sequence, the translation initiation site of the translational reading frame of said sequence is typically positioned between one and about fifty nucleotides downstream of the promoter. A promoter can, however, be positioned as much as about 5,000 nucleotides upstream of the translation initiation site, or about 2,000 nucleotides upstream of the transcription start site. A promoter typically comprises at least a core (basal) promoter. A promoter also may include at least one control element, such as an enhancer sequence, an upstream element or an upstream activation region (UAR). For example, a suitable enhancer is a cis-regulatory element (-212 to -154) from the upstream region of the octopine synthase (ocs) gene. Fromm *et al.*, *The Plant Cell* 1:977-984 (1989).

[0065] A basal promoter is the minimal sequence necessary for assembly of a transcription complex required for transcription initiation. Basal promoters frequently include a “TATA box” element that may be located between about 15 and about 35 nucleotides upstream from the site of transcription initiation. Basal promoters also may include a “CCAAT box” element (typically the sequence CCAAT) and/or a GGGCG sequence, which can be located between about 40 and about 200 nucleotides, typically about 60 to about 120 nucleotides, upstream from the transcription start site.

[0066] The choice of promoters to be included depends upon several factors, including, but not limited to, efficiency, selectability, inducibility, desired expression level, and cell- or tissue-preferential expression. It is a routine matter for one of skill in the art to modulate the expression of a sequence by appropriately selecting and positioning promoters and other regulatory regions relative to said sequence.

[0067] Some suitable promoters initiate transcription only, or predominantly, in certain cell types. For example, a promoter that is active predominantly in a reproductive tissue (*e.g.*, fruit, ovule, pollen, pistils, female gametophyte, egg cell, central cell, nucellus,

suspensor, synergid cell, flowers, embryonic tissue, embryo sac, embryo, zygote, endosperm, integument, or seed coat) can be used. Thus, as used herein a cell type- or tissue-preferential promoter is one that drives expression preferentially in the target tissue, but may also lead to some expression in other cell types or tissues as well. Methods for identifying and characterizing promoter regions in plant genomic DNA include, for example, those described in the following references: Jordano, *et al.*, *Plant Cell*, 1:855-866 (1989); Bustos, *et al.*, *Plant Cell*, 1:839-854 (1989); Green, *et al.*, *EMBO J.* 7, 4035-4044 (1988); Meier, *et al.*, *Plant Cell*, 3, 309-316 (1991); and Zhang, *et al.*, *Plant Physiology* 110: 1069-1079 (1996).

[0068] Examples of various classes of promoters are described below. Some of the promoters indicated below are described in more detail in U.S. Patent Application Ser. Nos. 60/505,689; 60/518,075; 60/544,771; 60/558,869; 60/583,691; 60/619,181; 60/637,140; 10/950,321; 10/957,569; 11/058,689; 11/172,703; 11/208,308; and PCT/US05/23639. It will be appreciated that a promoter may meet criteria for one classification based on its activity in one plant species, and yet meet criteria for a different classification based on its activity in another plant species.

[0069] Other Regulatory Regions: A 5' untranslated region (UTR) can be included in nucleic acid constructs described herein. A 5' UTR is transcribed, but is not translated, and lies between the start site of the transcript and the translation initiation codon and may include the +1 nucleotide. A 3' UTR can be positioned between the translation termination codon and the end of the transcript. UTRs can have particular functions such as increasing mRNA stability or attenuating translation. Examples of 3' UTRs include, but are not limited to, polyadenylation signals and transcription termination sequences, *e.g.*, a nopaline synthase termination sequence.

[0070] Various promoters can be used to drive expression of the genes of the present invention. Nucleotide sequences of such promoters are set forth in SEQ ID NOS: 1-79. Some of them can be broadly expressing promoters, others may be more tissue preferential.

[0071] A promoter can be said to be "broadly expressing" when it promotes transcription in many, but not necessarily all, plant tissues or plant cells. For example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the shoot, shoot tip (apex), and leaves, but weakly or not at all in tissues such as roots or stems. As another example, a broadly expressing promoter can promote transcription of an operably linked sequence in one or more of the stem, shoot, shoot tip (apex), and leaves, but can promote transcription weakly or not at all in tissues such as reproductive tissues of flowers and developing seeds. Non-limiting examples of broadly expressing promoters that can be included in the nucleic acid constructs provided herein include the p326 (SEQ ID NO: 76), YP0144 (SEQ ID NO: 55), YP0190 (SEQ ID NO: 59), p13879 (SEQ ID NO: 75), YP0050 (SEQ ID NO: 35), p32449 (SEQ ID NO: 77), 21876 (SEQ ID NO: 1), YP0158 (SEQ ID NO: 57), YP0214 (SEQ ID NO: 61), YP0380 (SEQ ID NO: 70), PT0848 (SEQ ID NO: 26), and PT0633 (SEQ ID NO: 7). Additional examples include the cauliflower mosaic virus (CaMV) 35S promoter, the mannopine synthase (MAS) promoter, the 1' or 2' promoters derived from T-DNA of *Agrobacterium tumefaciens*, the figwort mosaic virus 34S promoter, actin promoters such as the rice actin promoter, and ubiquitin promoters such as the maize ubiquitin-1 promoter. In some cases, the CaMV 35S promoter is excluded from the category of broadly expressing promoters.

[0072] Root-active promoters drive transcription in root tissue, *e.g.*, root endodermis, root epidermis, or root vascular tissues. In some embodiments, root-active promoters are root-preferential promoters, *i.e.*, drive transcription only or predominantly in root tissue. Root-preferential promoters include the YP0128 (SEQ ID NO: 52), YP0275

(SEQ ID NO: 63), PT0625 (SEQ ID NO: 6), PT0660 (SEQ ID NO: 9), PT0683 (SEQ ID NO: 14), and PT0758 (SEQ ID NO: 22). Other root-preferential promoters include the PT0613 (SEQ ID NO: 5), PT0672 (SEQ ID NO: 11), PT0688 (SEQ ID NO: 15), and PT0837 (SEQ ID NO: 24), which drive transcription primarily in root tissue and to a lesser extent in ovules and/or seeds. Other examples of root-preferential promoters include the root-specific subdomains of the CaMV 35S promoter (Lam *et al.*, *Proc. Natl. Acad. Sci. USA* 86:7890-7894 (1989)), root cell specific promoters reported by Conkling *et al.*, *Plant Physiol.* 93:1203-1211 (1990), and the tobacco RD2 gene promoter.

[0073] In some embodiments, promoters that drive transcription in maturing endosperm can be useful. Transcription from a maturing endosperm promoter typically begins after fertilization and occurs primarily in endosperm tissue during seed development and is typically highest during the cellularization phase. Most suitable are promoters that are active predominantly in maturing endosperm, although promoters that are also active in other tissues can sometimes be used. Non-limiting examples of maturing endosperm promoters that can be included in the nucleic acid constructs provided herein include the napin promoter, the Arcelin-5 promoter, the phaseolin gene promoter (Bustos *et al.* (1989) *Plant Cell* 1(9):839-853), the soybean trypsin inhibitor promoter (Riggs *et al.* (1989) *Plant Cell* 1(6):609-621), the ACP promoter (Baerson *et al.* (1993) *Plant Mol Biol*, 22(2):255-267), the stearyl-ACP desaturase gene (Slocumbe *et al.* (1994) *Plant Physiol* 104(4):167-176), the soybean α' subunit of β -conglycinin promoter (Chen *et al.* (1986) *Proc Natl Acad Sci USA* 83:8560-8564), the oleosin promoter (Hong *et al.* (1997) *Plant Mol Biol* 34(3):549-555), and zein promoters, such as the 15 kD zein promoter, the 16 kD zein promoter, 19 kD zein promoter, 22 kD zein promoter and 27 kD zein promoter. Also suitable are the Osgt-1 promoter from the rice glutelin-1 gene (Zheng *et al.* (1993) *Mol. Cell Biol.* 13:5829-5842), the beta-amylase gene promoter, and the barley hordein gene promoter. Other maturing

endosperm promoters include the YP0092 (SEQ ID NO: 38), PT0676 (SEQ ID NO: 12), and PT0708 (SEQ ID NO: 17).

[0074] Promoters that drive transcription in ovary tissues such as the ovule wall and mesocarp can also be useful, *e.g.*, a polygalacturonidase promoter, the banana TRX promoter, and the melon actin promoter. Other such promoters that drive gene expression preferentially in ovules are YP0007 (SEQ ID NO: 30), YP0111 (SEQ ID NO: 46), YP0092 (SEQ ID NO: 38), YP0103 (SEQ ID NO: 43), YP0028 (SEQ ID NO: 33), YP0121 (SEQ ID NO: 51), YP0008 (SEQ ID NO: 31), YP0039 (SEQ ID NO: 34), YP0115 (SEQ ID NO: 47), YP0119 (SEQ ID NO: 49), YP0120 (SEQ ID NO: 50) and YP0374 (SEQ ID NO: 68).

[0075] In some other embodiments of the present invention, embryo sac/early endosperm promoters can be used in order drive transcription of the sequence of interest in polar nuclei and/or the central cell, or in precursors to polar nuclei, but not in egg cells or precursors to egg cells. Most suitable are promoters that drive expression only or predominantly in polar nuclei or precursors thereto and/or the central cell. A pattern of transcription that extends from polar nuclei into early endosperm development can also be found with embryo sac/early endosperm-preferential promoters, although transcription typically decreases significantly in later endosperm development during and after the cellularization phase. Expression in the zygote or developing embryo typically is not present with embryo sac/early endosperm promoters.

[0076] Promoters that may be suitable include those derived from the following genes: *Arabidopsis* viviparous-1 (see, GenBank No. U93215); *Arabidopsis* atmycl (see, Urao (1996) *Plant Mol. Biol.*, 32:571-57; Conceicao (1994) *Plant*, 5:493-505); *Arabidopsis* FIE (GenBank No. AF129516); *Arabidopsis* MEA; *Arabidopsis* FIS2 (GenBank No. AF096096); and FIE 1.1 (U.S. Patent 6,906,244). Other promoters that may be suitable include those derived from the following genes: maize MAC1 (see, Sheridan (1996) *Genetics*, 142:1009-

1020); maize Cat3 (see, GenBank No. L05934; Abler (1993) *Plant Mol. Biol.*, 22:10131-1038). Other promoters include the following *Arabidopsis* promoters: YP0039 (SEQ ID NO: 34), YP0101 (SEQ ID NO: 41), YP0102 (SEQ ID NO: 42), YP0110 (SEQ ID NO: 45), YP0117 (SEQ ID NO: 48), YP0119 (SEQ ID NO: 49), YP0137 (SEQ ID NO: 53), DME, YP0285 (SEQ ID NO: 64), and YP0212 (SEQ ID NO: 60). Other promoters that may be useful include the following rice promoters: p530c10, pOsFIE2-2, pOsMEA, pOsYp102, and pOsYp285.

[0077] Promoters that preferentially drive transcription in zygotic cells following fertilization can provide embryo-preferential expression and may be useful for the present invention. Most suitable are promoters that preferentially drive transcription in early stage embryos prior to the heart stage, but expression in late stage and maturing embryos is also suitable. Embryo-preferential promoters include the barley lipid transfer protein (Ltp1) promoter (*Plant Cell Rep* (2001) 20:647-654, YP0097 (SEQ ID NO: 40), YP0107 (SEQ ID NO: 44), YP0088 (SEQ ID NO: 37), YP0143 (SEQ ID NO: 54), YP0156 (SEQ ID NO: 56), PT0650 (SEQ ID NO: 8), PT0695 (SEQ ID NO: 16), PT0723 (SEQ ID NO: 19), PT0838 (SEQ ID NO: 25), PT0879 (SEQ ID NO: 28) and PT0740 (SEQ ID NO: 20).

[0078] Promoters active in photosynthetic tissue in order to drive transcription in green tissues such as leaves and stems are of particular interest for the present invention. Most suitable are promoters that drive expression only or predominantly such tissues. Examples of such promoters include the ribulose-1,5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch (*Larix laricina*), the pine cab6 promoter (Yamamoto *et al.* (1994) *Plant Cell Physiol.* 35:773-778), the Cab-1 gene promoter from wheat (Fejes *et al.* (1990) *Plant Mol. Biol.* 15:921-932), the CAB-1 promoter from spinach (Lubberstedt *et al.* (1994) *Plant Physiol.* 104:997-1006), the cab1R promoter from rice (Luan *et al.* (1992) *Plant Cell* 4:971-981), the pyruvate orthophosphate dikinase (PPDK)

promoter from corn (Matsuoka *et al.* (1993) *Proc Natl Acad. Sci USA* 90:9586-9590), the tobacco Lhcb1*2 promoter (Cerdan *et al.* (1997) *Plant Mol. Biol.* 33:245-255), the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter (Truernit *et al.* (1995) *Planta* 196:564-570), and thylakoid membrane protein promoters from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS. Other promoters that drive transcription in stems, leafs and green tissue are PT0535 (SEQ ID NO: 3), PT0668 (SEQ ID NO: 2), PT0886 (SEQ ID NO: 29), PR0924 (SEQ ID NO: 78), YP0144 (SEQ ID NO: 55), YP0380 (SEQ ID NO: 70) and PT0585 (SEQ ID NO: 4).

[0079] In some other embodiments of the present invention, inducible promoters may be desired. Inducible promoters drive transcription in response to external stimuli such as chemical agents or environmental stimuli. For example, inducible promoters can confer transcription in response to hormones such as gibberellic acid or ethylene, or in response to light or drought. Examples of drought inedible promoters are YP0380 (SEQ ID NO: 70), PT0848 (SEQ ID NO: 26), YP0381 (SEQ ID NO: 71), YP0337 (SEQ ID NO: 66), YP0337 (SEQ ID NO: 66), PT0633 (SEQ ID NO: 7), YP0374 (SEQ ID NO: 68), PT0710 (SEQ ID NO: 18), YP0356 (SEQ ID NO: 67), YP0385 (SEQ ID NO: 73), YP0396 (SEQ ID NO: 74), YP0384 (SEQ ID NO: 72), YP0384 (SEQ ID NO: 72), PT0688 (SEQ ID NO: 15), YP0286 (SEQ ID NO: 65), YP0377 (SEQ ID NO: 69), and PD1367 (SEQ ID NO: 79). Examples of promoters induced by nitrogen are PT0863 (SEQ ID NO: 27), PT0829 (SEQ ID NO: 23), PT0665 (SEQ ID NO: 10) and PT0886 (SEQ ID NO: 29). An example of a shade inducible promoter is PR0924 (SEQ ID NO: 78).

[0080] Other Promoters: Other classes of promoters include, but are not limited to, leaf-preferential, stem/shoot-preferential, callus-preferential, guard cell-preferential, such as PT0678 (SEQ ID NO: 13), and senescence-preferential promoters. Promoters designated YP0086 (SEQ ID NO: 36), YP0188 (SEQ ID NO: 58), YP0263 (SEQ ID NO: 62), PT0758

(SEQ ID NO: 22), PT0743 (SEQ ID NO: 21), PT0829 (SEQ ID NO: 23), YP0119 (SEQ ID NO: 49), and YP0096 (SEQ ID NO: 39), as described in the above-referenced patent applications, may also be useful.

[0081] Alternatively, misexpression can be accomplished using a two component system, whereby the first component consists of a transgenic plant comprising a transcriptional activator operatively linked to a promoter and the second component consists of a transgenic plant that comprise a nucleic acid molecule of the invention operatively linked to the target-binding sequence/region of the transcriptional activator. The two transgenic plants are crossed and the nucleic acid molecule of the invention is expressed in the progeny of the plant. In another alternative embodiment of the present invention, the misexpression can be accomplished by having the sequences of the two component system transformed in one transgenic plant line.

[0082] Another alternative consists in inhibiting expression of a biomass or vigor-modulating polypeptide in a plant species of interest. The term “expression” refers to the process of converting genetic information encoded in a polynucleotide into RNA through transcription of the polynucleotide (*i.e.*, via the enzymatic action of an RNA polymerase), and into protein, through translation of mRNA. “Up-regulation” or “activation” refers to regulation that increases the production of expression products relative to basal or native states, while “down-regulation” or “repression” refers to regulation that decreases production relative to basal or native states.

[0083] A number of nucleic-acid based methods, including anti-sense RNA, ribozyme directed RNA cleavage, and interfering RNA (RNAi) can be used to inhibit protein expression in plants. Antisense technology is one well-known method. In this method, a nucleic acid segment from the endogenous gene is cloned and operably linked to a promoter so that the antisense strand of RNA is transcribed. The recombinant vector is then

transformed into plants, as described above, and the antisense strand of RNA is produced. The nucleic acid segment need not be the entire sequence of the endogenous gene to be repressed, but typically will be substantially identical to at least a portion of the endogenous gene to be repressed. Generally, higher homology can be used to compensate for the use of a shorter sequence. Typically, a sequence of at least 30 nucleotides is used (*e.g.*, at least 40, 50, 80, 100, 200, 500 nucleotides or more).

[0084] Thus, for example, an isolated nucleic acid provided herein can be an antisense nucleic acid to one of the aforementioned nucleic acids encoding a biomass-modulating polypeptide. A nucleic acid that decreases the level of a transcription or translation product of a gene encoding a biomass-modulating polypeptide is transcribed into an antisense nucleic acid similar or identical to the sense coding sequence of the biomass- or growth rate-modulating polypeptide. Alternatively, the transcription product of an isolated nucleic acid can be similar or identical to the sense coding sequence of a biomass growth rate-modulating polypeptide, but is an RNA that is unpolyadenylated, lacks a 5' cap structure, or contains an unsplicable intron.

[0085] In another method, a nucleic acid can be transcribed into a ribozyme, or catalytic RNA, that affects expression of an mRNA. (See, U.S. Patent No. 6,423,885). Ribozymes can be designed to specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. Heterologous nucleic acids can encode ribozymes designed to cleave particular mRNA transcripts, thus preventing expression of a polypeptide. Hammerhead ribozymes are useful for destroying particular mRNAs, although various ribozymes that cleave mRNA at site-specific recognition sequences can be used. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target RNA contain a 5'-UG-3' nucleotide sequence.

The construction and production of hammerhead ribozymes is known in the art. See, for example, U.S. Patent No. 5,254,678 and WO 02/46449 and references cited therein. Hammerhead ribozyme sequences can be embedded in a stable RNA such as a transfer RNA (tRNA) to increase cleavage efficiency *in vivo*. Perriman, *et al.* (1995) *Proc. Natl. Acad. Sci. USA*, 92(13):6175-6179; de Feyter and Gaudron, *Methods in Molecular Biology*, Vol. 74, Chapter 43, "Expressing Ribozymes in Plants", Edited by Turner, P.C, Humana Press Inc., Totowa, NJ. RNA endoribonucleases such as the one that occurs naturally in *Tetrahymena thermophila*, and which have been described extensively by Cech and collaborators can be useful. See, for example, U.S. Patent No. 4,987,071.

[0086] Methods based on RNA interference (RNAi) can be used. RNA interference is a cellular mechanism to regulate the expression of genes and the replication of viruses. This mechanism is thought to be mediated by double-stranded small interfering RNA molecules. A cell responds to such a double-stranded RNA by destroying endogenous mRNA having the same sequence as the double-stranded RNA. Methods for designing and preparing interfering RNAs are known to those of skill in the art; see, *e.g.*, WO 99/32619 and WO 01/75164. For example, a construct can be prepared that includes a sequence that is transcribed into an interfering RNA. Such an RNA can be one that can anneal to itself, *e.g.*, a double stranded RNA having a stem-loop structure. One strand of the stem portion of a double stranded RNA comprises a sequence that is similar or identical to the sense coding sequence of the polypeptide of interest, and that is from about 10 nucleotides to about 2,500 nucleotides in length. The length of the sequence that is similar or identical to the sense coding sequence can be from 10 nucleotides to 500 nucleotides, from 15 nucleotides to 300 nucleotides, from 20 nucleotides to 100 nucleotides, or from 25 nucleotides to 100 nucleotides. The other strand of the stem portion of a double stranded RNA comprises an antisense sequence of the biomass-modulating polypeptide of interest, and can have a length

that is shorter, the same as, or longer than the corresponding length of the sense sequence. The loop portion of a double stranded RNA can be from 10 nucleotides to 5,000 nucleotides, *e.g.*, from 15 nucleotides to 1,000 nucleotides, from 20 nucleotides to 500 nucleotides, or from 25 nucleotides to 200 nucleotides. The loop portion of the RNA can include an intron. See, *e.g.*, WO 99/53050.

[0087] In some nucleic-acid based methods for inhibition of gene expression in plants, a suitable nucleic acid can be a nucleic acid analog. Nucleic acid analogs can be modified at the base moiety, sugar moiety, or phosphate backbone to improve, for example, stability, hybridization, or solubility of the nucleic acid. Modifications at the base moiety include deoxyuridine for deoxythymidine, and 5-methyl-2'-deoxycytidine and 5-bromo-2'-deoxycytidine for deoxycytidine. Modifications of the sugar moiety include modification of the 2' hydroxyl of the ribose sugar to form 2'-O-methyl or 2'-O-allyl sugars. The deoxyribose phosphate backbone can be modified to produce morpholino nucleic acids, in which each base moiety is linked to a six-membered morpholino ring, or peptide nucleic acids, in which the deoxyphosphate backbone is replaced by a pseudopeptide backbone and the four bases are retained. See, for example, Summerton and Weller, 1997, *Antisense Nucleic Acid Drug Dev.*, 7:187-195; Hyrup *et al.*, 1996, *Bioorgan. Med. Chem.*, 4: 5-23. In addition, the deoxyphosphate backbone can be replaced with, for example, a phosphorothioate or phosphorodithioate backbone, a phosphoroamidite, or an alkyl phosphotriester backbone.

Transformation

[0088] Nucleic acid molecules of the present invention may be introduced into the genome or the cell of the appropriate host plant by a variety of techniques. These techniques, able to transform a wide variety of higher plant species, are well known and

described in the technical and scientific literature (*see, e.g.,* Weising et al. (1988) *Ann. Rev. Genet.*, 22:421 and Christou (1995) *Euphytica*, 85:13-27).

[0089] A variety of techniques known in the art are available for the introduction of DNA into a plant host cell. These techniques include transformation of plant cells by injection (Newell (2000)), microinjection (Griesbach (1987) *Plant Sci.* 50:69-77), electroporation of DNA (Fromm et al. (1985) *Proc. Natl. Acad. Sci. USA* 82:5824), PEG (Paszkowski et al. (1984) *EMBO J.* 3:2717), use of biolistics (Klein et al. (1987) *Nature* 327:773), fusion of cells or protoplasts (Willmitzer, L. (1993) *Transgenic Plants*. In: *Iotechnology, A Multi-Volume Comprehensive treatise* (H.J. Rehm, G. Reed, A. Püler, P. Stadler, eds., Vol. 2, 627-659, VCH Weinheim-New York-Basel-Cambridge), and *via* T-DNA using *Agrobacterium tumefaciens* (*Crit. Rev. Plant. Sci.* 4:1-46; Fromm et al. (1990) *Biotechnology* 8:833-844) or *Agrobacterium rhizogenes* (Cho et al. (2000) *Planta* 210:195-204) or other bacterial hosts (Broothaerts et al. (2005) *Nature* 433:629-633), for example.

[0090] In addition, a number of non-stable transformation methods that are well known to those skilled in the art may be desirable for the present invention. Such methods include, but are not limited to, transient expression (Lincoln et al. (1998) *Plant Mol. Biol. Rep.* 16:1-4) and viral transfection (Lacomme et al. (2001), "Genetically Engineered Viruses" (C.J.A. Ring and E.D. Blair, Eds). Pp. 59-99, BIOS Scientific Publishers, Ltd. Oxford, UK).

[0091] Seeds are obtained from the transformed plants and used for testing stability and inheritance. Generally, two or more generations are cultivated to ensure that the phenotypic feature is stably maintained and transmitted.

[0092] A person of ordinary skill in the art recognizes that after the expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be

introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

[0093] The nucleic acid molecules of the present invention may be used to confer the trait of an altered flowering time.

[0094] The nucleic acid molecules of the present invention encode appropriate proteins from any organism, but are preferably found in plants, fungi, bacteria or animals.

[0095] The methods according to the present invention can be applied to any plant, preferably higher plants, pertaining to the classes of *Angiospermae* and *Gymnospermae*. Plants of the subclasses of the *Dicotylodenae* and the *Monocotyledonae* are particularly suitable. Dicotyledonous plants belonging to the orders of the *Magniolales*, *Illiciales*, *Laurales*, *Piperales*, *Aristolochiales*, *Nymphaeales*, *Ranunculales*, *Papaverales*, *Sarraceniales*, *Trochodendrales*, *Hamamelidales*, *Eucomiales*, *Leitneriales*, *Myricales*, *Fagales*, *Casuarinales*, *Caryophyllales*, *Batales*, *Polygonales*, *Plumbaginales*, *Dilleniales*, *Theales*, *Malvales*, *Urticales*, *Lecythidales*, *Violales*, *Salicales*, *Capparales*, *Ericales*, *Diapensales*, *Ebenales*, *Primulales*, *Rosales*, *Fabales*, *Podostemales*, *Haloragales*, *Myrtales*, *Cornales*, *Proteales*, *Santales*, *Rafflesiales*, *Celastrales*, *Euphorbiales*, *Rhamniales*, *Sapindales*, *Juglandales*, *Geraniales*, *Polygalales*, *Umbellales*, *Gentianales*, *Polemoniales*, *Lamiales*, *Plantaginales*, *Scrophulariales*, *Campanulales*, *Rubiales*, *Dipsacales*, and *Asterales*, for example, are also suitable. Monocotyledonous plants belonging to the orders of the *Alismatales*, *Hydrocharitales*, *Najadales*, *Triuridales*, *Commelinales*, *Eriocaulales*, *Restionales*, *Poales*, *Juncals*, *Cyperales*, *Typhales*, *Bromeliales*, *Zingiberales*, *Arecales*, *Cyclanthales*, *Pandanales*, *Arales*, *Lilliales*, and *Orchidales* also may be useful in embodiments of the present invention. Further examples include, but are not limited to, plants belonging to the class of the *Gymnospermae* are *Pinales*, *Ginkgoales*, *Cycadales* and *Gnetales*.

[0096] The methods of the present invention are preferably used in plants that are important or interesting for agriculture, horticulture, biomass for bioconversion and/or forestry. Non-limiting examples include, for instance, tobacco, oilseed rape, sugar beet, potatoes, tomatoes, cucumbers, peppers, beans, peas, citrus fruits, avocados, peaches, apples, pears, berries, plums, melons, eggplants, cotton, soybean, sunflowers, roses, poinsettia, petunia, guayule, cabbages, spinach, alfalfa, artichokes, sugarcane, mimosa, *Servicea lespedera*, corn, wheat, rice, rye, barley, sorghum and grasses such as switch grass, giant reed, Bermuda grass, Johnson grasses or turf grass, millet, hemp, bananas, poplars, eucalyptus trees and conifers. Of interest are plants grown for energy production, so called energy crops, such as broadleaf plants like alfalfa, hemp, Jerusalem artichoke and grasses such as sorghum, switchgrass, Johnson grass and the likes.

Homologues Encompassed by the Invention

[0097] It is known in the art that one or more amino acids in a sequence can be substituted with other amino acid(s), the charge and polarity of which are similar to that of the substituted amino acid, *i.e.* a conservative amino acid substitution, resulting in a biologically/functionally silent change. Conservative substitutes for an amino acid within the polypeptide sequence can be selected from other members of the class to which the amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic (negatively charged) amino acids, such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids, such as arginine, histidine, and lysine; (3) neutral polar amino acids, such as serine, threonine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as glycine, alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, cysteine, and methionine.

[0098] Nucleic acid molecules of the present invention can comprise sequences that differ from those encoding a protein or fragment thereof selected from the group consisting of Leads 15, 28, 29, 36, ME04012 and Clone 691319, SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively, due to the fact that the different nucleic acid sequence encodes a protein having one or more conservative amino acid changes.

[0099] Biologically functional equivalents of the polypeptides, or fragments thereof, of the present invention can have about 10 or fewer conservative amino acid changes, more preferably about 7 or fewer conservative amino acid changes, and most preferably about 5 or fewer conservative amino acid changes. In a preferred embodiment of the present invention, the polypeptide has between about 5 and about 500 conservative changes, more preferably between about 10 and about 300 conservative changes, even more preferably between about 25 and about 150 conservative changes, and most preferably between about 5 and about 25 conservative changes or between 1 and about 5 conservative changes.

Identification of Useful Nucleic Acid Molecules and Their Corresponding Nucleotide Sequences

[00100] The nucleic acid molecules, and nucleotide sequences thereof, of the present invention were identified by use of a variety of screens that are predictive of nucleotide sequences that provide plants with altered size, vegetative growth, growth rate, organ number, plant architecture and/or biomass. One or more of the following screens were, therefore, utilized to identify the nucleotide (and amino acid) sequences of the present invention.

[00101] The present invention is further exemplified by the following examples. The examples are not intended to in any way limit the scope of the present application and its uses.

6. EXPERIMENTS CONFIRMING THE USEFULNESS OF THE POLYNUCLEOTIDES AND POLYPEPTIDES OF THE INVENTION

General Protocols

Agrobacterium-Mediated Transformation of Arabidopsis

[00102] *Wild-type Arabidopsis thaliana Wassilewskija* (WS) plants are transformed with Ti plasmids containing clones in the sense orientation relative to the 35S promoter. A Ti plasmid vector useful for these constructs, CRS 338, contains the Ceres-constructed, plant selectable marker gene phosphinothricin acetyltransferase (*PAT*), which confers herbicide resistance to transformed plants.

[00103] Ten independently transformed events are typically selected and evaluated for their qualitative phenotype in the T₁ generation.

[00104] Preparation of Soil Mixture: 24L SunshineMix #5 soil (Sun Gro Horticulture, Ltd., Bellevue, WA) is mixed with 16L Therm-O-Rock vermiculite (Therm-O-Rock West, Inc., Chandler, AZ) in a cement mixer to make a 60:40 soil mixture. To the soil mixture is added 2 Tbsp Marathon 1% granules (Hummert, Earth City, MO), 3 Tbsp OSMOCOTE® 14-14-14 (Hummert, Earth City, MO) and 1 Tbsp Peters fertilizer 20-20-20 (J.R. Peters, Inc., Allentown, PA), which are first added to 3 gallons of water and then added to the soil and mixed thoroughly. Generally, 4-inch diameter pots are filled with soil mixture. Pots are then covered with 8-inch squares of nylon netting.

[00105] Planting: Using a 60 mL syringe, 35 mL of the seed mixture is aspirated. 25 drops are added to each pot. Clear propagation domes are placed on top of the pots that are then placed under 55% shade cloth and subirrigated by adding 1 inch of water.

[00106] Plant Maintenance: 3 to 4 days after planting, lids and shade cloth are removed. Plants are watered as needed. After 7-10 days, pots are thinned to 20 plants per

pot using forceps. After 2 weeks, all plants are subirrigated with Peters fertilizer at a rate of 1 Tsp per gallon of water. When bolts are about 5-10 cm long, they are clipped between the first node and the base of stem to induce secondary bolts. Dipping infiltration is performed 6 to 7 days after clipping.

[00107] Preparation of *Agrobacterium*: To 150 mL fresh YEB is added 0.1 mL each of carbenicillin, spectinomycin and rifampicin (each at 100 mg/ml stock concentration). *Agrobacterium* starter blocks are obtained (96-well block with *Agrobacterium* cultures grown to an OD₆₀₀ of approximately 1.0) and inoculated one culture vessel per construct by transferring 1 mL from appropriate well in the starter block. Cultures are then incubated with shaking at 27°C. Cultures are spun down after attaining an OD₆₀₀ of approximately 1.0 (about 24 hours). 200 mL infiltration media is added to resuspend *Agrobacterium* pellets. Infiltration media is prepared by adding 2.2 g MS salts, 50 g sucrose, and 5 µl 2 mg/ml benzylaminopurine to 900 ml water.

[00108] Dipping Infiltration: The pots are inverted and submerged for 5 minutes so that the aerial portion of the plant is in the *Agrobacterium* suspension. Plants are allowed to grow normally and seed is collected.

[00109] High-throughput Phenotypic Screening of Misexpression Mutants: Seed is evenly dispersed into water-saturated soil in pots and placed into a dark 4°C cooler for two nights to promote uniform germination. Pots are then removed from the cooler and covered with 55% shade cloth for 4-5 days. Cotyledons are fully expanded at this stage. FINALE[®] (Sanofi Aventis, Paris, France) is sprayed on plants (3 ml FINALE[®] diluted into 48 oz. water) and repeated every 3-4 days until only transformants remain.

[00110] Screening: Screening is routinely performed at four stages: Seedling, Rosette, Flowering, and Senescence.

- Seedling - the time after the cotyledons have emerged, but before the 3rd true leaf begins to form.
- Rosette - the time from the emergence of the 3rd true leaf through just before the primary bolt begins to elongate.
- Flowering - the time from the emergence of the primary bolt to the onset of senescence (with the exception of noting the flowering time itself, most observations should be made at the stage where approximately 50% of the flowers have opened).
- Senescence - the time following the onset of senescence (with the exception of “delayed senescence”, most observations should be made after the plant has completely dried). Seeds are then collected.

[00111] **Screens:** Screening for increased size, vegetative growth and/or biomass is performed by taking measurements, specifically T₂ measurements were taken as follows:

- Days to Bolt = number of days between sowing of seed and emergence of first inflorescence.
- Rosette Leaf Number at Bolt = number of rosette leaves present at time of emergence of first inflorescence.
- Rosette Area = area of rosette at time of initial inflorescence emergence, using formula $((L \times W) \times 3.14) / 4$.
- Height = length of longest inflorescence from base to apex. This measurement was taken at the termination of flowering/onset of senescence.
- Primary Inflorescence Thickness = diameter of primary inflorescence 2.5 cm up from base. This measurement was taken at the termination of flowering/onset of senescence.

- Inflorescence Number = total number of unique inflorescences. This measurement was taken at the termination of flowering/onset of senescence.

[00112] PCR was used to amplify the cDNA insert in one randomly chosen T₂ plant. This PCR product was then sequenced to confirm the sequence in the plants.

RESULTS:

[00113] Plants transformed with the genes of interest were screened as described above for modulated growth and phenotype characteristics. The observations include those with respect to the entire plant, as well as parts of the plant, such as the roots and leaves. The observations for transformants with each polynucleotide sequence are noted in the Sequence listing for each of the tested nucleotide sequences and the corresponding encoded polypeptide. The modulated characteristics (i.e. observed phenotypes) are noted by an entry in the “miscellaneous features” field for each respective sequence. The “Phenotype” noted in the Sequence Listing for each relevant sequence further includes a statement of the useful utility of that sequence based on the observations.

[00114] The observations made for the various transformants can be categorized, depending upon the relevant plant tissue for the observation and the consequent utility/usefulness of the nucleotide sequence/polypeptide used to make that transformant. Table 1 correlates the shorthand notes in the sequence listing to the observations noted for each transformant (the “description” column), the tissue of the observation, the phenotype thereby associated with the transformant, and the consequent utility/usefulness of the inserted nucleotide sequence and encoded polypeptide (the “translation” column).

[00115] For some of the polynucleotides/polypeptides of the invention, the sequence listing further includes (in a “miscellaneous feature” section) an indication of

important identified dominant(s) and the corresponding function of the domain or identified by comparison to the publicly available pfam database.

TABLE 1

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
WHOLE PLANT	Senescence Time	Early Senescence	the plant senesces significantly early (note the approximate number of days early it started to senesce in the comments)	Useful for accelerating crop development and harvest
INFLORESCENCE	Flowering Time	Early Flowering	the plant flowers significantly early (note the approximate number of days early it flowered in the comments)	Useful for accelerating flowering time
INFLORESCENCE	Flowering Time	Late Flowering	the plant flowers significantly late (note the approximate number of days late it flowered in the comments)	Useful for delaying flowering time
INFLORESCENCE	Flowering Time	Dtb	days to bolt	Useful for delaying flowering time
WHOLE PLANT	Senescence Time	Late Senescence	the plant senesces significantly late (note the approximate number of days late it started to senesce in the comments)	Useful for delaying senescence
COTYLEDONS	Silver	Silver	cotyledons have a gray/silver colored surface; This phenotype is often accompanied by a small size mutation, but not always	Useful for drought or stress tolerance
WHOLE SEEDLING	Dark Green	Dark Green	plant is visibly darker green	Useful for increasing chlorophyll and photosynthetic capacity
WHOLE PLANT	Color	Dark Green	the plant is abnormally dark green	Useful for increasing chlorophyll and photosynthetic capacity
WHOLE SEEDLING	High Anthocyanin	High Anthocyanin	the plant is purple in color	Useful for increasing increasing anthocyanin content
WHOLE PLANT	Color	High Anthocyanin	the plant is purple in color	Useful for increasing increasing anthocyanin content
ROOT	No Growth in Soil	No Growth in Soil	roots grow along the soil surface instead of into the soil	Useful for increasing root growth eg to enhance nutrient uptake

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
ROOT	Other	Other	this correlates with any root mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for increasing root growth eg to enhance nutrient uptake
LATERAL ROOTS	Number	Less Lateral Roots	there is an abnormally low number of lateral roots	Useful for increasing root growth eg to enhance nutrient uptake
LATERAL ROOTS	Other	Other	this correlates with any lateral root mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for increasing root growth eg to enhance nutrient uptake
ROOT	Classic	Classic	there is a lack of lateral roots (buds may appear but do not elongate)	Useful for increasing root growth eg to enhance nutrient uptake
ROOT	Dwarf	Dwarf	there is a stunted root system	Useful for increasing root growth eg to enhance nutrient uptake
ROOT	Mid-Section	Mid-Section	there are lateral roots in the top and bottom quarters of the whole root, but none in the middle	Useful for increasing root growth eg to enhance nutrient uptake
ROOT	Split	Split	appears as "classic" but with two primary roots, both originating from the hypocotyl base	Useful for increasing root growth eg to enhance nutrient uptake
ROOT	Other	Other	this correlates with any overall root structure mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for increasing root growth eg to enhance nutrient uptake
PRIMARY ROOT	Other	Other	this correlates with any primary root mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for increasing root growth eg to enhance nutrient uptake
ROOT HAIRS	Length	Longer Root Hair	the root hairs are abnormally long	Useful for increasing root growth eg to enhance nutrient uptake
ROOT HAIRS	Length	Smaller Root Hair	the root hairs are abnormally short	Useful for increasing root growth eg to enhance

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
				nutrient uptake
ROOT HAIRS	Number	Less root hairs	there is an abnormally low number of root hairs	Useful for increasing root growth eg to enhance nutrient uptake
ROOT HAIRS	Other	Other	this correlates with any root hair mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for increasing root growth eg to enhance nutrient uptake
ROOT HAIRS	Bulbous Root Hairs	Bulbous Root Hairs	Bulbous Root Hairs	Useful for increasing root growth eg to enhance nutrient uptake
ROOT	Bearded (Nitrogen)	Bearded (Nitrogen)	the lateral roots are long in high nitrogen, and they are short in low nitrogen	Useful for increasing root growth eg to enhance nutrient uptake
PRIMARY ROOT	Thickness	Thicker Primary Root	the primary root is abnormally thick	Useful for increasing root growth eg to enhance nutrient uptake
WHOLE PLANT	Stress	Root Architecture	Identify plants with increased root mass	Useful for increasing root growth eg to enhance nutrient uptake
PRIMARY ROOT	Thickness	Thinner Primary Root	the primary root is abnormally thin	Useful for increasing root growth eg to enhance nutrient uptake
PRIMARY ROOT	Wavy	Wavy	there is a consistent and gentle wavy appearance	Useful for increasing root growth eg to enhance nutrient uptake
LATERAL ROOTS	Length	Longer Lateral Root	the lateral roots are abnormally long	Useful for increasing root growth eg to enhance nutrient uptake
LATERAL ROOTS	Number	More Lateral Roots	there is an abnormally high number of lateral roots	Useful for increasing root growth eg to enhance nutrient uptake
ROOT HAIRS	Number	More root hairs	there is an abnormally high number of root hairs	Useful for increasing root growth eg to enhance nutrient uptake
				Useful for increasing seed carbon or nitrogen
SEED	Seed Weight	Weight	weight of seed	Useful for increasing seed weight
SILIQUES	Length	Long	siliques are abnormally long (the percent difference in length compared to the control should be noted in the comments)	Useful for increasing seed/fruit yield or modifying fruit content
SILIQUES	Length	Short	siliques are abnormally short (the percent difference in length	Useful for increasing seed/fruit yield or modifying fruit content

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			compared to the control should be noted in the comments)	
SILIQUES	Other	Other	this correlates with any silique mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for increasing seed/fruit yield or modifying fruit content
ROSETTE LEAVES	Size	Large	rosette leaves are abnormally large (the percent difference in size compared to the control should be noted in the comments)	Useful for increasing vegetative growth and enhancing foliage
				Useful for making nutraceuticals/pharmaceuticals in plants
HYPOCOTY L	Other	Other	this correlates with any hypocotyl mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making larger plants
WHOLE SEEDLING	Other	Other	this correlates with any whole plant mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making larger plants
WHOLE PLANT	Other	Other	this correlates with any whole plant mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making larger plants
CAULINE LEAVES	Petiole Length	Long Petioles	the cauline petioles are abnormally long (the percent difference in size compared to the control should be noted in the comments)	Useful for making larger plants
WHOLE SEEDLING	Size	Large	plant is abnormally large (the percent difference in size compared to the	Useful for making larger plants

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			control should be noted in the comments)	
WHOLE PLANT	Size	Large	plant is abnormally large (the percent difference in size compared to the control should be noted in the comments)	Useful for making larger plants
SEED	Lethal	Lethal	the seed is inviable and appears as a small, dark, raisin-like seed in the mature silique	Useful for making lethal plants for genetic confinement systems
WHOLE SEEDLING	Germination	No Germination	none of the seed germinates	Useful for making lethal plants for genetic confinement systems
WHOLE SEEDLING	Germination	Poor Germination	a portion of the seed never germinates	Useful for making lethal plants for genetic confinement systems
WHOLE SEEDLING	Germination	Slow Germination	a portion of the seed germinates significantly later than the rest of the seed in the pot	Useful for making lethal plants for genetic confinement systems
ROSETTE LEAVES	Vitrified	Vitrified	leaves are somewhat translucent or ?water soaked?	Useful for making lethal plants for genetic confinement systems
CAULINE LEAVES	Vitrified	Vitrified	leaves are somewhat translucent or ?water soaked?	Useful for making lethal plants for genetic confinement systems
COTYLEDONS	Albino	Opaque Albino	plant is opaque and devoid of pigment	Useful for making lethal plants for genetic confinement systems
COTYLEDONS	Albino	Translucent Albino	plant is translucent and devoid of pigment	Useful for making lethal plants for genetic confinement systems
WHOLE SEEDLING	Lethal	Seedling Lethal	cotyledons emerge (although they are often small), but then the plant ceases to develop further; No true leaves appear and the plant dies early (These differ from yellow-green lethals in that the cotyledons are wild-type in color and may not look differ	Useful for making lethal plants for genetic confinement systems

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
WHOLE SEEDLING	Lethal	Yellow-Green Lethal	cotyledons are small and pale yellow-green in color, but NOT totally devoid of pigment; In addition to yellow-green cotyledons, these plants produce no or severely reduced size true leaves, which, if present, are also yellow-green; These plants die prem	Useful for making lethal plants for genetic confinement systems
WHOLE SEEDLING	Meristem Mutant	Meristem Mutant	this term encompasses a variety of phenotypes, all of which have one thing in common, i.e., they all have something significantly wrong with how the meristem is producing its leaves; Depending on the severity of the phenotype, the plants in this category	Useful for making lethal plants for genetic confinement systems
WHOLE SEEDLING	Seedling Defective	Seedling Defective	this term encompasses a variety of phenotypes which share similar characteristics, i.e., they are small, have distorted structures, and are prone to early death; For example, patterning mutants would be a class of mutants which fall under this category	Useful for making lethal plants for genetic confinement systems
WHOLE PLANT	Color	Yellow-Green Viable 1	the leaves and cotyledons are yellow-green in color, but this is not a lethal phenotype	Useful for making lethal plants for genetic confinement systems
WHOLE PLANT	Color	Yellow-Green Viable 2	the leaves are yellow-green in color but the cotyledons are a wild-type green in color	Useful for making lethal plants for genetic confinement systems
WHOLE PLANT	Color	Yellow-Green Viable 3	the leaves start out wild-type green and gradually turn yellow-green in color, while the	Useful for making lethal plants for genetic confinement systems

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			cotyledons stay wild-type green	
WHOLE PLANT	Color	Yellow-Green Viable 4	the leaves appear wild-type green, but slowly turn yellow-green over time, while the cotyledons appear and remain yellow-green	Useful for making lethal plants for genetic confinement systems
WHOLE PLANT	Stress	Seed Bleaching	Identify plants whose seed coats do not bleach out under long bleach soaking	Useful for making low fiber seeds with increased digestability
ROSETTE LEAVES	Fused	Leaf Fused to Inflorescence	the leaf is fused to an inflorescence	Useful for making ornamental plants with flowers and leaves fused
ROSETTE LEAVES	Interveinal Chlorosis	Interveinal Chlorosis	the leaf tissue is chlorotic between its veins	Useful for making ornamental plants with modified color
CAULINE LEAVES	Interveinal Chlorosis	Interveinal Chlorosis	the leaf tissue is chlorotic between its veins	Useful for making ornamental plants with modified color
FLOWER	Organ Morphology	Fused Sepals	the sepals are fused together and won't open naturally, but the flower is otherwise wild-type	Useful for making ornamental plants with modified flowers
FLOWER	Organ Morphology	Narrow Petals	the petals are abnormally narrow	Useful for making ornamental plants with modified flowers
FLOWER	Organ Morphology	Narrow Sepals	the sepals are abnormally narrow	Useful for making ornamental plants with modified flowers
FLOWER	Organ Morphology	Short Petals	the petals are abnormally short	Useful for making ornamental plants with modified flowers
FLOWER	Organ Morphology	Short Sepals	the sepals are abnormally short	Useful for making ornamental plants with modified flowers
FLOWER	Size	Large	flower is abnormally large (the percent difference in size compared to the control should be noted in the comments)	Useful for making ornamental plants with modified flowers
FLOWER	Size	Small	flower is abnormally small (the percent difference in size compared to the control should be noted in the comments)	Useful for making ornamental plants with modified flowers

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
FLOWER	Other	Other	this correlates with any flower mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Aerial Rosette	Aerial Fosette	rosette forms at or above the first internode	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Appearance	Corkscrew Appearance	the inflorescence is really twisted, almost like a corkscrew, but somewhat more irregular	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Appearance	Curved Appearance	the inflorescence has a slight, irregular curve upwards, greater than that of the control plants	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Appearance	Multi-Inflorescence Fusion	the inflorescence is fused to another inflorescence, creating a celery-like appearance	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Appearance	Undulate Appearance	the inflorescence is wavy in appearance	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Branching	Acauline Branching	first branching is not subtended by a cauline leaf	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Wax	Glaucous	inflorescence is abnormally dull in appearance	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Wax	Glossy	inflorescence is shiny/glossy in appearance	Useful for making ornamental plants with modified flowers
INFLORESCENCE	Other	Other	this correlates with any inflorescence mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making ornamental plants with modified flowers
COTYLEDONS	Asymmetric	Asymmetric	the shape of the cotyledon is asymmetric in reference to the vertical axis	Useful for making ornamental plants with modified foliage
ROSETTE LEAVES	Other	Other	this correlates with any leaf mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making ornamental plants with modified leaves

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
CAULINE LEAVES	Other	Other	this correlates with any cauline mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making ornamental plants with modified leaves
FLOWER	Homeotic Mutant	Homeotic Mutant	the flower has one or more of its organs converted to another type of organ (specific details should be noted in the comments)	Useful for making plants sterile and for genetic confinement
FLOWER	Organ Morphology	Aberrant Organ Number	there is an abnormal number of some or all of the flowers organs	Useful for making plants sterile and for genetic confinement
FLOWER	Organ Morphology	Short Stamens	the stamens are abnormally short; This often leads to mechanical problems with fertility	Useful for making plants sterile and for genetic confinement
FLOWER	Fertility	Aborted fertility	the ovule is unfertilized and appears as a brown or white speck in the mature silique	Useful for making plants sterile and for genetic confinement
FLOWER	Fertility	Female-sterile	there is a problem with the ovules such that no fertilization is occurring	Useful for making plants sterile and for genetic confinement
FLOWER	Fertility	Male-sterile	there is a problem with the pollen such that no fertilization is occurring	Useful for making plants sterile and for genetic confinement
FLOWER	Fertility	Reduced fertility	a reduced number of successful fertilization events, and therefore seeds, are being produced by the plant	Useful for making plants sterile and for genetic confinement
FLOWER	Fertility	Sterile	no successful fertilization events, and therefore no seed is being produced by the plant; The reason for this sterility is not known at the time of the observation	Useful for making plants sterile and for genetic confinement
FLOWER	Fertility	Other	this correlates with any fertility mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for making plants sterile and for genetic confinement

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
WHOLE PLANT	Stress	Early Flowering	Identify plants that flower early	Useful for making plants that flower early
COTYLEDONS	Petiole Length	Long Petioles	the cotyledon petioles are abnormally long (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants that grow and better in shade
ROSETTE LEAVES	Petiole Length	Varying Petiole Lengths	the leaf petioles vary in length throughout the rosette	Useful for making plants that grow better in shade
ROSETTE LEAVES	Petiole Length	Long Petioles	the leaf petioles are abnormally long (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants that grow better in shade
				Useful for making plants tolerant to biotic stress
WHOLE PLANT	Stress		Identify plants able to tolerate high density and no phosphate and nitrogen, possible lead assay for vigor under population density and low nutrient conditions	Useful for making plants tolerant to density and low fertilizer
WHOLE PLANT	Stress	pH (high)	Identify plants tolerant to high pH, and possibly low phosphate	Useful for making plants tolerant to high pH or low phosphate
WHOLE PLANT	Stress	Low Nitrate	Identify plants tolerant to low nitrogen/nitrate growth media	Useful for making plants tolerant to low nitrogen
WHOLE PLANT	Stress	LNABA	Identify plants tolerant to low nitrogen and high ABA concentrations	Useful for making plants tolerant to low nitrogen
WHOLE PLANT	Stress	No Nitrogen	Identify plants with increased vigor under no nitrogen conditions	Useful for making plants tolerant to low nitrogen
WHOLE PLANT	Stress	MSX	Identify plants tolerant to nitrogen assimilation inhibitor, and possibly low nitrogen tolerance and/or seed nitrogen accumulation	Useful for making plants tolerant to low nitrogen

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
WHOLE PLANT	Stress	No N, No PO4	Identify plants tolerant to no nitrogen and no phosphate growth media	Useful for making plants tolerant to low nitrogen/low phosphate
WHOLE PLANT	Stress	Oxidative	Identify plants tolerant to oxidative stress	Useful for making plants tolerant to oxidative stresses
ROSETTE LEAVES	Trichomes	Few Trichomes	trichomes are sparse but present on the leaves	Useful for making plants with enhanced chemical composition
ROSETTE LEAVES	Trichomes	Glabrous	trichomes are totally absent	Useful for making plants with enhanced chemical composition
ROSETTE LEAVES	Trichomes	Abnormal Trichome Shape	the trichomes are abnormally shaped	Useful for making plants with enhanced chemical composition
CAULINE LEAVES	Trichomes	Few Trichomes	trichomes are sparse but present on the leaves	Useful for making plants with enhanced chemical composition
CAULINE LEAVES	Trichomes	Glabrous	trichomes are totally absent	Useful for making plants with enhanced chemical composition
CAULINE LEAVES	Trichomes	Abnormal Trichome Shape	the trichomes are abnormally shaped	Useful for making plants with enhanced chemical composition
INFLORESCENCE	Trichomes	Glabrous	trichomes are totally absent	Useful for making plants with enhanced chemical composition
INFLORESCENCE	Trichomes	Abnormal Trichome Shape	the trichomes are abnormally shaped	Useful for making plants with enhanced chemical composition
ROSETTE LEAVES	Curled	Corkscrew	leaves appear as "Curled 5", with the additional attribute of twisting like a corkscrew, instead of uniformly curling from both sides of the leaf	Useful for making plants with altered leaf shape eg curled leaves
ROSETTE LEAVES	Curled	Cup-shaped	leaves are curled up at the leaf margins such that they form a cup or bowl-like shape	Useful for making plants with altered leaf shape eg curled leaves
ROSETTE LEAVES	Curled	Curled 1	leaves are abnormally curled slightly up or down at the leaf margins, but do not fall under the "cup-shaped" description (least severe type)	Useful for making plants with altered leaf shape eg curled leaves
ROSETTE LEAVES	Curled	Curled 2	leaves are abnormally curled up or down at the leaf margins, but do not fall under the "cup-shaped"	Useful for making plants with altered leaf shape eg curled leaves

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			description (more severe than Curled 1, but less severe than Curled 3)	
ROSETTE LEAVES	Curled	Curled 3	leaves are abnormally curled up or down at the leaf margins, but do not fall under the "cup-shaped" description (more severe than Curled 2, but less severe than Curled 4)	Useful for making plants with altered leaf shape eg curled leaves
ROSETTE LEAVES	Curled	Curled 4	leaves are abnormally curled/rolled up or down at the leaf margins (more severe than Curled 3, but less severe than Curled 5)	Useful for making plants with altered leaf shape eg curled leaves
ROSETTE LEAVES	Curled	Curled 5	leaves are completely curled/rolled up or down at the leaf margins (most severe type)	Useful for making plants with altered leaf shape eg curled leaves
CAULINE LEAVES	Curled	Corkscrew	leaves appear as "Curled 5", with the additional attribute of twisting like a corkscrew, instead of uniformly curling from both sides of the leaf	Useful for making plants with altered leaf shape eg curled leaves
CAULINE LEAVES	Curled	Cup-shaped	the cauline leaves are curled up at the leaf margins such that they form a cup or bowl-like shape	Useful for making plants with altered leaf shape eg curled leaves
CAULINE LEAVES	Curled	Curled 1	the cauline leaves are abnormally curled slightly up or down at the leaf margins, but do not fall under the "cup-shaped" description (least severe type)	Useful for making plants with altered leaf shape eg curled leaves
CAULINE LEAVES	Curled	Curled 2	the cauline leaves are abnormally curled up or down at the leaf margins, but do not fall under the "cup-shaped" description (more severe than Curled 1, but less severe than Curled 3)	Useful for making plants with altered leaf shape eg curled leaves

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
CAULINE LEAVES	Curled	Curled 3	the cauline leaves are abnormally curled up or down at the leaf margins, but do not fall under the "cup-shaped" description (more severe than Curled 2, but less severe than Curled 4)	Useful for making plants with altered leaf shape eg curled leaves
CAULINE LEAVES	Curled	Curled 4	the cauline leaves are abnormally curled/rolled up or down at the leaf margins (more severe than Curled 3, but less severe than Curled 5)	Useful for making plants with altered leaf shape eg curled leaves
CAULINE LEAVES	Curled	Curled 5	the cauline leaves are completely curled/rolled up or down at the leaf margins (most severe type)	Useful for making plants with altered leaf shape eg curled leaves
ROSETTE LEAVES	Size	Small	rosette leaves are abnormally small (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants with decreased vegetative growth
COTYLEDONS	Wilted	Wilted	cotyledons appear wilted, i.e., they look as though they have suffered from drought conditions	Useful for making plants with enhanced abiotic stress tolerance
ROSETTE LEAVES	Wax	Glaucous	leaves are abnormally dull in appearance	Useful for making plants with enhanced abiotic stress tolerance
ROSETTE LEAVES	Wax	Glossy	leaves are shiny/glossy in appearance	Useful for making plants with enhanced abiotic stress tolerance
CAULINE LEAVES	Wax	Glaucous	leaves are abnormally dull in appearance	Useful for making plants with enhanced abiotic stress tolerance
CAULINE LEAVES	Wax	Glossy	leaves are shiny/glossy in appearance	Useful for making plants with enhanced abiotic stress tolerance
WHOLE PLANT	Stress	Metabolic Profiling	Identify plants with altered metabolic profiles as defined in 4a	Useful for making plants with enhanced metabolite accumulation
WHOLE PLANT	Stress	Plant Architecture	Identify plants with improved architecture	Useful for making plants with enhanced plant architecture

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
WHOLE PLANT	Stress	ABA	Identify plants tolerant to ABA, and possibly drought and/or other stresses	Useful for making plants with enhanced tolerance to drought
WHOLE PLANT	Stress	Mannitol	Identify plants tolerant to mannitol, and possibly drought stress	Useful for making plants with enhanced tolerance to drought
WHOLE PLANT	Stress	Dessication	Identify plants tolerant to water loss, possibly drought stress tolerant	Useful for making plants with enhanced tolerance to drought
WHOLE PLANT	Stress	High Sucrose	Identify plants tolerant to high sucrose conditions (possible Lead assay for C/N partitioning)	Useful for making plants with enhanced tolerance to drought
WHOLE PLANT	Stress	Heat	Identify plants with thermotolerance	Useful for making plants with enhanced tolerance to heat
WHOLE PLANT	Stress	High Nitrogen	Identify plants tolerant to high nitrogen conditions	Useful for making plants with enhanced tolerance to high nitrogen
WHOLE PLANT	Stress	Etiolation	Identify plants with increased vigor in the dark	Useful for making plants with enhanced tolerance to light stress
ROSETTE LEAVES	Disorganized Rosette	Disorganized Rosette	rosette leaves do not appear in the normal fashion, i.e., their phyllotaxy may be abnormal or too many leaves may be emerging in comparison to the control	Useful for making plants with increased biomass
INFLORESCENCE	Phyllotaxy	Even Phyllotaxy	a phyllotaxy mutant whose new branches emerge at exactly the same height as each other, i.e., there is no internode between them	Useful for making plants with increased biomass
COTYLEDONS	Shape	Elliptic Shape	cotyledons are quite narrow and pointed, more so than lanceolate	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Fused	Leaf Fused to Petiole	the leaf is fused to its petiole	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Cordate Shaped	similar to ovate, except the leaf is not rounded at its base	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Elliptic Shaped	leaves are quite narrow and pointed, more so than lanceolate	Useful for making plants with increased biomass and foliage

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
ROSETTE LEAVES	Shape	Lanceolate Shaped	leaves are narrow and come to a dull point at the apex	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Lobed Shaped	leaves have very deep and rounded serrations, giving an appearance of many lobes forming the margins of the leaves	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Oval Shaped	leaves are much rounder than wild-type	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Ovate Shaped	leaves are wider at base than at apex, otherwise similar to wild-type	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Serrate Margins	leaf margins have little ?teeth? on them, i.e., they are serrated	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Trident Shaped	leaves look somewhat like a trident, i.e., they have a sharp point at the apex, and a sharp point on each side	Useful for making plants with increased biomass and foliage
ROSETTE LEAVES	Shape	Undulate Shaped	leaves are wavy	Useful for making plants with increased biomass and foliage
WHOLE PLANT	Rosette Shape	Bushy Rosette Shaped	the different petioles have very varied liminal angles, giving the plant a very bushy appearance; This is often accompanied by a "Disorganized Rosette" phenotype	Useful for making plants with increased biomass and foliage
WHOLE PLANT	Rosette Shape	Flat Rosette Shaped	the petioles have a very small liminal angle, i.e., the rosette appears flat instead of having its usual slight vertical angle	Useful for making plants with increased biomass and foliage
WHOLE PLANT	Rosette Shape	Standing Rosette Shaped	the petioles have a very large liminal angle, i.e., it appears as though the leaves are standing up instead of having their usual small vertical angle from the soil	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Fused	Leaf Fused to Inflorescence	the cauline leaf is fused to an inflorescence or branch	Useful for making plants with increased biomass and foliage

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
CAULINE LEAVES	Fused	Leaf Fused to Leaf	the cauline leaf is fused to itself or another cauline leaf	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Cordate Shaped	similar to ovate, except the leaf is not rounded at its base	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Elliptic Shaped	leaves are quite narrow and pointed, more so that lanceolate	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Lanceolate Shaped	leaves are narrow and come to a dull point at the apex	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Lobed Shaped	leaves have very deep and rounded serrations, giving an appearance of many lobes forming the margins of the leaves	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Oval Shaped	leaves are much rounder than wild-type	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Ovate Shaped	leaves are wider at base than at apex, otherwise similar to wild-type	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Serrate Margins	leaf margins have little ?teeth? on them, i.e., they are serrated	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Trident Shaped	leaves look somewhat like a trident, i.e., they have a sharp point at the apex, and a sharp point on each side	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Shape	Undulate Shaped	leaves are wavy	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Size	Large	cauline is abnormally large (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants with increased biomass and foliage
CAULINE LEAVES	Size	Small	cauline is abnormally small (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants with increased biomass and foliage
LATERAL ROOTS	Length	Smaller Lateral Root	the lateral roots are abnormally short	Useful for making plants with increased root growth to prevent lodging or enhance nutrient uptake

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
PRIMARY ROOT	Length	Long Primary Root	the primary root is abnormally long (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants with increased root growth to prevent lodging or enhance nutrient uptake
PRIMARY ROOT	Length	Short Primary Root	the primary root is abnormally short (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants with increased root growth to prevent lodging or enhance nutrient uptake
WHOLE PLANT	Stress	Plant Size	Identify plants of increased size compared to wild type	Useful for making plants with increased size and biomass
WHOLE PLANT	Stress	Starch	Identify plants with increased starch accumulation	Useful for making plants with increased starch content
WHOLE PLANT	Stress	Cold Germination	Identify plants that germinate better at cold temperatures	Useful for making plants with increased tolerance to cold stress
WHOLE PLANT	Stress	Cold Growth	Identify plants that grow faster at cold temperatures	Useful for making plants with increased tolerance to cold stress
WHOLE PLANT	Stress	Soil Drought	Identify plants with increased tolerance to soil drought	Useful for making plants with increased tolerance to drought
WHOLE PLANT	Stress	Soil Drought - Desiccation tolerance	Identify plants that are tolerant to low soil moisture and resist wilting	Useful for making plants with increased tolerance to drought
WHOLE PLANT	Stress	PEG	Identify plants tolerant to PEG, and possibly drought stress	Useful for making plants with increased tolerance to drought
SEED	Size	Large	the seed is abnormally large (the percent difference in size compared to the control should be noted in the comments)	Useful for making plants with larger seeds
INFLORESCENCE	Branching	Asecondary Branching	the plant does not form any secondary inflorescences	Useful for making plants with modified flowers
SEED	Size	Small	the seed is abnormally small (the percent difference in size compared to the	Useful for making plants with smaller seeds or no seeds

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			control should be noted in the comments)	
WHOLE PLANT	Stress	C/N Content	Identify plants/seeds with altered carbon/nitrogen levels	Useful for making seeds with altered carbon/nitrogen levels
INFLORESCENCE	Internode Length	Short Internode	the internode is abnormally short (the percent difference in length compared to the control should be noted in the comments)	Useful for making shorter plants and plants with modified flowers
WHOLE PLANT	Dwarf	Brassino-Steroid Dwarf	these plants are small in stature, dark green, have oval leaves, strong bolts, and are often sterile	Useful for making smaller plants
WHOLE PLANT	Dwarf	Misc. Dwarf	these are dwarf plants the do not fall under the brassino-steroid dwarf category	Useful for making smaller plants
HYPOCOTYL	Length	Short	hypocotyl is visibly shorter than in wild-type (the percent difference in size compared to the control should be noted in the comments)	Useful for making smaller plants
INFLORESCENCE	Height	Short	the inflorescences of the plants are abnormally short (plant height is encompassed under the whole plant size category, but this entry would be used if the height of the plant is abnormal, but is otherwise of normal size) (the percent difference in size	Useful for making smaller plants
WHOLE SEEDLING	Size	Small	plant is abnormally small (the percent difference in size compared to the control should be noted in the comments)	Useful for making smaller plants
ROSETTE LEAVES	Petiole Length	Short Petioles	the leaf petioles are abnormally short (the percent difference in size	Useful for making smaller plants

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			compared to the control should be noted in the comments)	
WHOLE PLANT	Size	Small	plant is abnormally small (the percent difference in size compared to the control should be noted in the comments)	Useful for making smaller plants
CAULINE LEAVES	Petiole Length	Short Petioles	the cauline petioles are abnormally short (the percent difference in size compared to the control should be noted in the comments)	Useful for making smaller plants
INFLORESCENCE	Strength	Strong	the primary inflorescence appears significantly stronger, whether by thickness or rigidity	Useful for making stronger plants
INFLORESCENCE	Strength	Weak	the primary inflorescence appears significantly weaker, whether by thickness or rigidity	Useful for making stronger plants
INFLORESCENCE	Inflorescence	Thickness	thickness of the primary inflorescence	Useful for making stronger plants
HYPOCOTYL	Length	Long	hypocotyl is visibly longer than in wild-type (the percent difference in size compared to the control should be noted in the comments)	Useful for making taller plants
INFLORESCENCE	Internode Length	Long Internode	the internode is abnormally long (the percent difference in length compared to the control should be noted in the comments)	Useful for making taller plants and plants with longer flowers
INFLORESCENCE	Height	Tall	the inflorescences of the plants are abnormally long (plant height is encompassed under the whole plant size category, but this entry would be used if the height of the plant is abnormal, but is otherwise of	Useful for making taller plants and plants with longer inflorescences

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			normal size) (the percent difference in size	
SEED	Color	Dark Color	the seed is abnormally dark	Useful for modifying fiber content in seed
SEED	Color	Light Color	the seed is abnormally light; Transparent Testa is an example of this phenotype	Useful for modifying fiber content in seed
SILIQUES	Shape	Bent	the silique has sharp bend to it part of the way down the length of the silique; this bend can be as much as approaching 90 degrees	Useful for modifying fruit shape, composition and seed yield
SILIQUES	Shape	Bulging	the seeds in the silique appears "shrink-wrapped", giving the silique a bulging appearance	Useful for modifying fruit shape, composition and seed yield
SILIQUES	Shape	Clubbed	the silique is somewhat bulbous at its terminal end	Useful for modifying fruit shape, composition and seed yield
SILIQUES	Shape	Sickle	the silique is curved, much like the blade of a sickle	Useful for modifying fruit shape, composition and seed yield
INFLORESCENCE	Branching	No Branching	there is no branching at all	Useful for modifying plant architecture, ie amount of branching
INFLORESCENCE	Branching	Horizontal Branching	new branches arise at a 90 degree angle from the bolt they are emerging from	Useful for modifying plant architecture, ie branch angle
COTYLEDONS	Horizontally Oblong	Horizontally Oblong	cotyledon is visibly wider than it is long, and it is also symmetrical (or very close to it) when cut along its horizontal axis	Useful for modifying plant architecture, ie leaf structure
INFLORESCENCE	Branching	Two Leaf Branching	two cauline leaves subtend branches instead of one	Useful for modifying plant architecture, ie reducing foliage
INFLORESCENCE	Branching	Reduced Apical Dominance	the dominance of the primary inflorescence is diminished, with the secondaries appearing as dominant or nearly as dominant	Useful for modifying plant structure, ie increased branching

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
SEED	Seed Arrangement	Stacked Arrangement	the seeds/embryos are stacked one on top of the other within the silique, instead of having the usual side-by-side distribution	Useful for modifying seed content
SEED	Other	Other	this correlates with any seed mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for modifying seed content
SEED	Shape	Oval Shape	the seeds are much more rounded on the ends, giving the seed a true oval appearance	Useful for modifying seed structure and composition
SEED	Shape	Ridged Shape	the seeds have small ridges or bumps on them	Useful for modifying seed structure and composition
SEED	Shape	Tapered Shape	the ends of the seeds narrow down to a much sharper point than usual	Useful for modifying seed structure and composition
COTYLEDONS	Cotyledon Number	Single Cotyledon	Only one cotyledon appears after germination; This is simply one cotyledon that had formed instead of two, and is not related to the fused phenotype; With this exception, the plant is often otherwise wild-type in appearance	Useful for modifying seed structure and content
COTYLEDONS	Cotyledon Number	Tricot	three cotyledons emerge instead of two; With this exception, the plant is often otherwise wild-type in appearance	Useful for modifying seed structure and content
COTYLEDONS	Curled	Cup-shaped	cotyledons are curled up at the cotyledon margins such that they form a cup or bowl-like shape	Useful for modifying seed structure and content
COTYLEDONS	Curled	Curled 1	cotyledons are abnormally curled slightly up or down at the cotyledon margins, but do not fall under the "cup-shaped" description (least severe type)	Useful for modifying seed structure and content

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
COTYLEDONS	Curled	Curled 2	cotyledons are abnormally curled up or down at the cotyledon margins, but do not fall under the "cup-shaped" description (more severe than Curled 1, but less severe than Curled 3)	Useful for modifying seed structure and content
COTYLEDONS	Curled	Curled 3	cotyledons are abnormally curled up or down at the cotyledon margins, but do not fall under the "cup-shaped" description (more severe than Curled 2, but less severe than Curled 4)	Useful for modifying seed structure and content
COTYLEDONS	Curled	Curled 4	cotyledons are abnormally curled/rolled up or down at the cotyledon margins (more severe than Curled 3, but less severe than Curled 5)	Useful for modifying seed structure and content
COTYLEDONS	Curled	Curled 5	cotyledons are completely curled/rolled up or down at the cotyledon margins (most severe type)	Useful for modifying seed structure and content
COTYLEDONS	Dimorphic Cotyledons	Dimorphic Cotyledons	one cotyledon is significantly larger than the other	Useful for modifying seed structure and content
COTYLEDONS	Fused	Fused 1	cotyledons are fused to each other, creating one cotyledon structure (least severe type)	Useful for modifying seed structure and content
COTYLEDONS	Fused	Fused 2	cotyledons are fused to each other, creating one cotyledon structure (more severe than Fused 1, but less severe than Fused 3)	Useful for modifying seed structure and content
COTYLEDONS	Fused	Fused 3	cotyledons are fused to each other, creating one cotyledon structure (more severe than Fused 2, but less severe than Fused 4)	Useful for modifying seed structure and content

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
COTYLEDONS	Fused	Fused 4	cotyledons are fused to each other, creating one cotyledon structure (more severe than Fused 3, but less severe than Fused 5)	Useful for modifying seed structure and content
COTYLEDONS	Fused	Fused 5	cotyledons are fused to each other, creating one cotyledon structure (most severe type)	Useful for modifying seed structure and content
COTYLEDONS	Other	Other	this correlates with any cotyledon mutant phenotypes which do not fit into the above categories (a picture should be taken for documentation)	Useful for modifying seed structure and content
ROSETTE LEAVES	Fused	Leaf Fused to Leaf	the leaf is fused to itself or another leaf	Useful for plants with fused leaves eg ornamentals
COTYLEDONS	Petiole Length	Short Petioles	the cotyledon petioles are abnormally short (the percent difference in size compared to the control should be noted in the comments)	Useful for shade avoidance and for making smaller plants
PRIMARY ROOT	Agravitropic	Agravitropic	the primary root does not appear to have a gravitropic response	
PRIMARY ROOT	Kinked	Kinked	there is a sharp bend in the root	
ROSETTE LEAVES	Rosette Diameter	Diameter	diameter of rosette	
WHOLE PLANT	Plant Weight	Plant Weight	weight of whole plant	
WHOLE PLANT	Plant Height	Height	height of whole plant	
WHOLE PLANT	Plant DTH	Dth	days to harvest of plant	
WHOLE PLANT	Plant Harvest Index	Harvest Index	harvest index of plant	
CAULINE LEAVES	Fused	Leaf Fused to Petiole	the cauline leaf is fused to its petiole	
N/A	N/A	N/A	N/A	
WHOLE PLANT	HERBICIDE SEGREGATION	HERBICIDE SEGREGATION	herbicide segregation ratio	
WHOLE PLANT	N/A	No Mutant Phenotype Observed	The plants were screened at all appropriate stages and showed no mutant phenotype, i.e., they looked like normal, wild type	

TISSUE	PHENOTYPE QUALIFIER	PHENOTYPE	DESCRIPTION	TRANSLATION
			Arabidopsis plants	

[00116] From the results reported in Table 1 and the Sequence Listing, it can be seen that the nucleotides/polypeptides of the inventions are useful, depending upon the respective individual sequence, to make plants with modified growth and phenotype characteristics, including:

- a. modulated plant size, including increased and decreased height or length;
- b. modulated vegetative growth (increased or decreased);
- c. modulated organ number;
- d. increased biomass;
- e. sterility;
- f. seedling lethality;
- g. accelerated crop development or harvest;
- h. accelerated flowering time;
- i. delayed flowering time;
- j. delayed senescence;
- k. enhanced drought or stress tolerance;
- l. increased chlorophyll and photosynthetic capacity;
- m. increased anthocyanin content;
- n. increased root growth, and increased nutrient uptake;
- o. increased or decreased seed weight or size, increased seed carbon or nitrogen content;
- p. modified, including increased, seed/fruit yield or modified fruit content;
- q. enhanced foliage;
- r. usefulness for making nutraceuticals/pharmaceuticals in plants;
- s. plant lethality;
- t. decrease seed fiber content to provide increased digestability;
- u. modified ornamental appearance with modified leaves, flowers, color or foliage;

- v. modified sterility in plants;
- w. enhanced ability to grow in shade;
- x. enhanced biotic stress tolerance;
- y. increased tolerance to density and low fertilizer;
- z. enhanced tolerance to high or low pH, to low or high nitrogen or phosphate;
- aa. enhanced tolerance to oxidative stress;
- bb. enhanced chemical composition;
- cc. altered leaf shape;
- dd. enhanced abiotic stress tolerance;
- ee. increased tolerance to cold stress;
- ff. increased starch content;
- gg. reduced number or no seeds;
- hh. enhanced plant strength;
- ii. modified flower length;
- jj. longer inflorescences;
- kk. modified seed fiber content;
- ll. modified fruit shape;
- mm. modified fruit composition;
- nn. modified seed yield;
- oo. modified plant architecture, such as modified amount or angle of branching, modified leaf structure, or modified seed structure; and
- pp. enhanced shade avoidance.

Example 1: Lead 28 – ME04701 – Clone 1952 – cDNA 13499809 (SEQ ID NO: 90)

Qualitative analysis of the T₁ plants:

All 10 of the events produced rosettes with more leaves and more inflorescences than the control. The plants were also slightly smaller than the control (Table 1-1). The transgenic “control” was a set of plants expressing a different 35S::cDNA but which were indistinguishable from the untransformed WS wildtype. This method of scoring phenotypes is typical for our large-scale morphological phenotyping project.

Table 1-1. Qualitative phenotypes observed in 35S::cDNA 13499809 T₁ events

Event	Increased Rosette Leaf Number, Increased Inflorescence Number, & Slightly Smaller
ME04701-01	x
ME04701-02	x
ME04701-03	x
ME04701-04	x
ME04701-05	x
ME04701-06	x
ME04701-07	x
ME04701-08	x
ME04701-09	x
ME04701-10	x

Quantitative analysis of the T₂ plants:

Events ME04701-08 and ME04701-09 were evaluated in greater detail in the T₂ generation.

These two events were selected because they had the most advantageous phenotypes.

Eighteen individuals were sown and observed for both events. The transgenic plants showed an increased number of inflorescences to a 0.05 level of statistical significance (Table 1-2).

The T₂ plants did not have significantly more leaves than the controls, unlike in the T₁.

ME04701-08 was slightly later flowering than the control. ME04701-09 had significantly larger rosettes than the control. All plants noted in the table as ME04701-08 and ME04701-09 were segregating progeny of the T₁ which exhibited the phenotype of interest. All plants noted in the table as -08 or -09 Control were T₂ segregating progeny which did not exhibit the phenotype and did not contain the transgene (internal controls; Table 1-2).

Segregation frequencies of the plants under test suggest that each event contains a single insert, as calculated by a Chi-square test (Table 1-2 and data not shown).

The increase in the inflorescence number for the two events was much less than the increase observed when the 35S promoter was used to express this cDNA (data not shown).

This evidence further supports our hypothesis that the degree of expression/dosage of the

gene product is highly relevant to the strength of the observed phenotype. By using a promoter with a different expression pattern, we were able to keep the positive phenotype of the previously observed 35S phenotype, while removing the negative aspects of infertility previously observed. Of course, the trade-off is to lessen the positive phenotype, although keeping it significant.

Table 1-2. Quantitative phenotypes observed in p326F::cDNA 13499809 T₂ events (PIT = Primary Inflorescence Thickness)

Event/Control	Number of Observations	Rosette Area (mm ²)	Number of Leaves	Height (cm)	PIT (mm)	Days to Bolt	Number of Inflorescences
ME04701-08	14	1241.8	6.0	42.1	0.99	17.8*	4.3*
-08 Control	4	1419.1	5.8	38.8	1.02	16.5	2.8
ME04701-09	14	1620.0*	5.9	40.1	1.01	16.8	4.8*
-09 Control	4	996.5	6.0	40.4	0.93	16.6	2.8
*significantly different from control at 0.05 level, via t-test							
Although all of the plants in this experiment had fewer inflorescences than the general greenhouse population, the plants were healthy. The transgenics had significantly greater number of inflorescences than the control, so the overall decrease – which was due to greenhouse conditions prevailing at the time of the experiment - in the number of inflorescences did not affect the conclusions of the experiment.							

LEAD SUMMARY/DISCUSSION:

- Over-expression of Lead 28/cDNA 13499809 with an appropriate promoter results in an increase in the number of inflorescences. As this is a glycine-rich protein (GRP) there is a likely effect on cell wall structure affecting cell expansion or adhesion, different positioning of cell planes, and/or different opportunities for inflorescence initiation. It would be interesting to combine this gene with the gene encoding an unknown protein with an AP2 which also affects plant growth and development.
- This polynucleotide/protein can be an especially useful one for controlling the number/rate of cell division in meristems without disturbing overall plant morphology. It can be developed in crops with an appropriate promoter to regulate size and growth rate of many individual organs.

		Event 1	Event 4	Event 5	Event 7	Event Average	Percent Increase
Plant weight	1952 Transgenic	1888	1423	1682	1523	1629	110%
	1952 Control	1516	1471	1383	1559	1482	
Fruit weight per plant	1952 Transgenic	5892	3704	5131	5814	5135	105%
	1952 Control	4746	4826	4601	5343	4879	
Percent red fruit	1952 Transgenic	40.1	42.4	36.5	47.2	42	107%
	1952 Control	42.4	46.7	28.7	37.8	39	
Harvest index	1952 Transgenic	75.7%	72.2%	75.3%	79.2%	76%	99%
	1952 Control	75.8%	76.6%	76.9%	77.4%	77%	

- Increased vegetative biomass can give an improved source:sink ratio and improved fixation of carbon to sucrose and starch, leading to improved yield.
- More inflorescences gives the opportunity for more flowers and therefore more seeds. The combination of improved biomass and inflorescence number can give a significant improvement in yield.

Tomato Field Trial Results

Clone 1952 was transformed into tomato under the control of the plasmid p326. 4 independent transgenic events were selected for field testing. Results are shown in the following Table 1-3. On the average, there is an increase in total plant weight, fruit weight and percent red fruit per plant. Event 4 did not show an improvement in performance. If event 4 is not considered in the analysis the average plant weight, fruit weight and percent red fruit each increase to approximately 115% of control.

Table 1-3 – Results from Tomato Field Trials

Example 2: Lead 29 – ME04717 – Clone 123905 - cDNA 12562634 (SEQ ID NO: 92)

- Ectopic expression of Ceres cDNA 12562634 under the control of the 326D promoter induces a number of phenotypes including:
 - Increased number of inflorescences
 - Continuation of rosette leaf initiation after flowering to generate an overall increased number of leaves.
- Misexpression of Ceres cDNA 12562634 can be useful to increase branching and the number of inflorescences. This can have a significant impact on seed number.

Qualitative analysis of the T₁ plants:

Using the 326D promoter, 9 of the 10 events produced rosettes with more leaves and more inflorescences than the control (Table 1). One of the 9 events also had fertility defects, much like what was seen using 35S::cDNA 12562634. The transgenic “control” was a set of plants expressing different 35S::cDNA constructs and which were indistinguishable from the untransformed WS wildtype. This method of scoring phenotypes is typical for our large-scale morphological phenotyping project.

Table 2-1. Qualitative phenotypes observed in p326D::cDNA 12562634 T₁ events (2 events with the most advantageous phenotypes were chosen for T₂ evaluation)

Event	Increased Rosette Leaf Number & Increased Inflorescence Number	Fertility Defects
ME04717-02	x	x
ME04717-03	x	
ME04717-04	x	
ME04717-05	x	
ME04717-06	x	
ME04717-07	x	
ME04717-08	x	
ME04717-09	x	
ME04717-10	x	

Quantitative analysis of the T₂ plants:

Events ME04717-03 and ME04717-05 were evaluated in greater detail in the T₂ generation. Eighteen individuals were sown and observed for both events. The transgenic plants showed an increased number of inflorescences to a 0.05 level of statistical significance. ME04717-03 also had significantly larger rosettes than the control. All plants noted in Table 2-2 as ME04717-03 and ME04717-05 were segregating progeny of the T₁ which exhibited the phenotype of interest. All plants noted in the Table 2-2 as -03 or -05 Control were T₂ segregating progeny which did not exhibit the phenotype and did not contain the transgene (internal controls; Table 2-2).

Segregation frequencies of the plants under test suggest that each event contains a single insert, as calculated by a chi-square test (data not shown).

It should be noted that the increase in the inflorescence number for the events documented below was less than the increase observed in the 35S::cDNA 12532634 events (data not shown). Other p326D::cDNA 12532634 T₂ events, not shown in this report, contained multiple inserts. Some of the T₂ progeny of these multiple insert-containing events exhibited some negative effects (fertility defects and dwarfing) similar to the T₂ progeny of the 35S::cDNA 12532634 events. This evidence further supports our hypothesis that the degree of expression/dosage of the gene product is highly relevant to the strength of the observed phenotype. By using a new promoter, and creating transgenics with a single insert, we were able to keep the positive phenotype of the previously observed 35S phenotype, while removing the negative aspects previously seen. A consequence of accomplishing this goal is a lessening of the degree of the positive phenotype, although keeping it at a very significant level.

Table 2-2. Quantitative phenotypes observed in p326D::cDNA 12562634 T₂ events (PIT = Primary Inflorescence Thickness)

	Number of	Rosette Area	Number of	Height	PIT	Days	Number of
--	-----------	--------------	-----------	--------	-----	------	-----------

Event/Control	Observations	(mm ²)	Leaves	(cm)	(mm)	to Bolt	Inflorescences
ME04717-03	13	2701.5*	7.7*	35.2	0.94	18.0	8.4*
-03 Control	5	1086.9	6.6	32.7	0.99	18.6	3.8
ME04717-05	14	1057.6	5.7	35.0	0.91	16.1	7.3*
-05 Control	4	504.6	5.0	29.3	0.71	16.0	4.0
*significantly different from control at 0.05 level, via t-test							
The decrease in stature and flowering time is accurate. The plants were healthy, but may have been flowering earlier than other plants grown in the greenhouse at that time. This is especially the case for the flat containing ME04717-05 and its controls. All plants were treated equally within the flat Our goal was only to assay for inflorescence number.							

LEAD SUMMARY/DISCUSSION:

- Ectopic expression of Ceres cDNA 12562634 under the control of the 326D promoter induces a number of phenotypes including increased number of inflorescences and more leaves.
- Misexpression of Ceres cDNA 12562634 can be useful to increase branching and the number of inflorescences. This can have a significant impact on seed number.
- There is also likely to be a positive impact on harvest index although it has not yet been measured.
- This gene/protein can be an especially useful one for controlling the rate of cell division in the meristems without disturbing overall plant morphology. It can be developed in crops with an appropriate promoter to regulate size and growth rate of many individual organs.
- Increased vegetative biomass can give an improved source:sink ratio and improved fixation of carbon to sucrose and starch, leading to improved yield.
- More inflorescences gives the opportunity for more flowers and therefore more seeds. The combination of improved biomass and inflorescence number can give a significant improvement in yield.

Tomato Yield Trial Results

Gene 123905 was also transformed into tomato under the control of the promoter p326. 4 independent transgenic events were characterized in the field. A number of independent events were originally evaluated and 4 were selected for further analysis based

on expression of the gene, presence of a simple insert and the phenotype of the plants observed in the greenhouse. Homozygous T2 seeds were planted in the field in a randomized complete block design. Each event had a corresponding control line. Results of plant weight, the total weight of individual plants, total fruit weight per plant, percent red fruit per plant and harvest index are shown in the Table 2-3 below. The results indicate that events 1 and 21 had substantially reduced leaf mass while retaining yields comparable to controls. Hence, their harvest index improved. These events also had increases in percent red fruit per plant. Event 14 had increased biomass and yield.

Table 2-3 – Tomato Field Trial Results

Per plant		1	14	21	26	average
Leaf/stem weight	C5	1410.0	1537.1	1294.4	1564.1	1451.4
	C5 control	1866.4	1215.9	1738.8	1766.0	1646.8
fruit weight	C5	4300.5	4936.5	4122.5	4159.0	4379.6
	C5-control	4293.5	4608.5	4098.0	4877.0	4469.3
Percent red fruit	C5	35.3	33.2	56.2	36.9	40.4
	C5-control	16.7	33.0	45.8	34.8	32.6
Harvest index	C5	75%	76%	76%	73%	75%
	C5-control	70%	79%	70%	73%	73%

In summary, tomato plants transformed with gene 123905 tended to have more branches and leaves, and more fruit as compared to control.

Rice Field Trial Results:

Gene 123905 was transformed into rice cultivar Kitaake under the control of p326. Five (5) independent transgenic events were evaluated in the field in a randomized complete block design. The traits evaluated were tillers per plant, days to flowering, leaf angle, plant height, biomass in grams per plant, yield in grams per plant and total plot yield in grams, the results for which are shown below in Tables 2-4, 2-5 and 2-6. Each event resulted in an increase in the number of tillers per plant.

Table 2 –4 – Results from Rice Field Trials

	Number of plants Plants	Tillers per plant	Days to first flower	Days to mid flower	Approx. leaf angle
123905-1	1060	7.1	22	32	33.1
123905-4-6	200	8.2	19	28	45
123905-8-3	650	7.4	28	33	32.1
123905-12-3	300	8.9	22	33	38.6
Kitaake control	1200	5.4	22	31	31.2

Several events showed significant reductions in height. Event 8-3 showed an increase in height, biomass and yield relative to control. While generally lower in yield, and significantly reduced in stature, event 1 and event 12 produce biomass similar to controls indicating an increase in biomass density relative to controls.

Table 2 –5 – Results from Rice Field Trials

	Plant Height (cm)	Biomass (grams per plant)	Yield (grams per plant)	Total Yield per plot (gms)
123905-1	54.0	25.3	12.52	417.0
123905-4-6	37.0	19.6	7.82	116.5
123905-8-3	65.5	30.6	14.9	668.8
123905-12-3	48.8	23.3	10.02	312.3
Kitaake	61.2	26.7	13.59	537.5

Observations on reduced stature in rice

Gene 123905 was transformed into rice cultivar Kitaake under the control of p326. Measurements were conducted to determine which internodes were reduced in length, where internode I is the uppermost internode and internode V is the lowermost internode. In events 1, 4 and 12 which have significantly reduced stature relative to control, internodes III and IV are significantly reduced in length, while internodes I and II are reduced only slightly or not at all.

Table 2 –6 – Results from Rice Field Trials

	Plant height (cm)	No. panicle	Internode I	Internode II	Internode III	Internode IV	Internode V
123905-1	89.0	8.8	35.2	20.0	7.9	3.0	0.1
123905-4-6	68.2	18.3	30.4	16.4	4.6	1.7	0.1
123905-8-3	111.6	9.8	38.4	24.8	19.8	10.6	0.8
123905-12-3	82.6	12.2	32.4	21.4	7.0	4.1	0.3

Kitaake Control	110.6	10.0	36.6	24.5	19.8	11.6	0.4
--------------------	-------	------	------	------	------	------	-----

Observations on germination in rice

Transgenic lines 123905-1 and 123905-12-3 germinate 1 to 2 days faster than Kitaake control seed.

Example 3: Lead 36 – ME03195 – Clone 679923 - cDNA 13594332 (SEQ ID NO:98)

Clone 679923 in the Ceres soy cDNA library, contains cDNA 13594332, encoding a transcription factor similar to the Arabidopsis LEAFY PETIOLE (LEP) gene. This protein sequence contains an AP2 domain. The cDNA was placed into the Ceres Misexpression Pipeline because it was determined to be a putative ortholog of a known Arabidopsis gene (LEP).

Qualitative analysis of the T₁ plants:

All 5 events produced larger rosettes with slightly curled leaves with little to no petiole elongation, and very short inflorescences compared to the controls. These plants were also delayed in flowering time by several days and had no fertility defects (Table 3-1). The transgenic “control” was a set of plants expressing a different 35S::cDNA fusion and which were indistinguishable from the untransformed WS wildtype. This method of scoring phenotypes is typical for our large-scale morphological phenotyping project. After seed collection, it was also apparent that these plants produced a significantly higher number of seeds relative to typical mutants of their height.

Table 3-1. Qualitative phenotypes observed in 35S::cDNA 13594332 T₁ events

Event	Large rosettes with curled leaves with short/no petioles, short inflorescences, delayed flowering time
ME03195-01	X
ME03195-02	X
ME03195-03	X

ME03195-04	x
ME03195-05	x

Quantitative analysis of the T₂ plants:

The original hypothesis formulated from the T₁ observations was that the 35S::cDNA 13594332 plants may have a significantly increased harvest index. Events ME03195-02 and ME03195-04 were evaluated in greater detail in the T₂ generation to test this hypothesis. Eighteen individuals were sown and observed for both events. Segregation frequencies of the plants under test suggest that each event contains a single insert, as calculated by a chi-square test (data not shown).

After detailed T₂ analyses, we determined the following regarding the transgenics (results below are statistically significant to a 0.05 level or better via t-test unless otherwise noted):

- Flowering time (days to bolt) was 5-8 days later than controls.
- Rosette leaf number at bolt was increased by approximately 2.5 leaves.
- Rosette area was 2-3 times larger than controls.
- Height was approximately ½ that of controls.
- Total seed weight was not significantly different than controls.
- Total plant dry weight was slightly greater for event -04, and no different than the controls for event -02.
- Harvest index was slightly lower than the controls.
- Twice as much seed was produced per unit height of plant than in controls.

Details can be found in Tables 3-2 and 3-3.

Table 3-2. Quantitative phenotypes observed in p35S::cDNA 13594332 T₂ events

Event/Control	Number of Observations	Day to Bolt	Number of Leaves	Rosette Area (mm ²)	Height (cm)
ME03195-02	12	26*	9.6*	6735.43*	18.63*
-02 Control	3	18	7	1802.62	42.33

ME03195-04	8	24.9*	10.3*	7758.16*	25.06*
-04 Control	7	19	7.7	2884.43	44.71
*significantly different from control at 0.05 level, via t-test					

Table 3-3. Quantitative phenotypes observed in p35S::cDNA 13594332 T₂ events

Event/Control	Number of Observations	Seed Weight (g)	Plant Weight (g)	Harvest Index	Seed Weight (g) per Unit Height (cm)
ME03195-02	12	0.375	0.73	53.25*	0.0204*
-02 Control	3	0.376	0.58	64.47	0.0090
ME03195-04	8	0.431	0.8258*	53.26*	0.0171*
-04 Control	7	0.397	0.6119	64.90	0.0089
*significantly different from control at 0.05 level, via t-test					

Events -02 and -04 each had three T₂ plants which exhibited a much more severe form of the above-described phenotype. These plants were severely late bolting, had little inflorescence elongation, and were nearly sterile. From other experiments using these plant lines (data not shown), we determined that the detrimental phenotype is due to a dosage/homozygous insert effect, suggesting that hemi/heterozygous plants gave a beneficial trait of increased seed production per unit height, but that the homozygous lines gave the negative phenotype. Our statistical analyses compared the internal controls to the plants which contained the transgene and beneficial phenotype. All transgene-containing plants with the detrimental phenotype were omitted from the statistical analyses in Tables 3-2 and 3-3.

Example 4: ME04012 - Gemini ID 5000F6 (SEQ ID NO: 109)

ME04012 contains a genomic clone which encodes a putative Cytochrome P450. Plant line ME04012 was being assayed for drought tolerance when it was observed that 15/20 plants in event -03 showed a plant architecture phenotype. 6/15 were a weaker version showing only a wavy stem. 9/15 were strong and showed a wavy stem, decreased height and decreased branch and pedicel angles.

Example5: Lead 15 – ME04077 – Clone 92459 - cDNA 12561537 (SEQ ID NO: 80)

Clone 92459 in the Ceres Arabidopsis cDNA library, contains cDNA 12561537, encoding Arabidopsis MADS Affecting Flowering 1 (MAF1). The cDNA was placed into the Ceres Misexpression Pipeline because it is a transcription factor. Transcription factors are of particular interest because they can affect many genes simultaneously, and they therefore have an increased likelihood of producing an altered phenotype in Arabidopsis when overexpressed.

- Ectopic expression of Ceres cDNA 12561537 under the control of the 35S promoter induces a number of phenotypes including:
 - Taller plants
 - Thicker inflorescences
 - Larger rosettes
 - Increased rosette leaf number
 - Delayed flowering
- Misexpression of Ceres cDNA 12561537 can be useful to increase overall plant size/biomass.

Qualitative analysis of the T₁ plants:

All ten events were late flowering, produced larger rosettes with more leaves and tall, thick inflorescences compared to the controls (Table 5-1). The transgenic “control” was a set of different 35S::cDNA expressing plants which were indistinguishable from the untransformed WS wild type. This method of scoring phenotypes is typical for our large-scale morphological phenotyping project.

Table 5- 1. Qualitative phenotypes observed in 35S::cDNA 12561537 T₁ events

Event	Increased Rosette Size Increased Rosette Leaf Number	Late Flowering	Tall & Thick
ME04077-01	X	X	X
ME04077-02	X	X	X
ME04077-03	X	X	X
ME04077-04	X	X	X

ME04077-05	X	X	X
ME04077-06	X	X	X
ME04077-07	X	X	X
ME04077-08	X	X	X
ME04077-09	X	X	X
ME04077-10	X	X	X

Quantitative analysis of the T₂ plants:

Events ME04077-06 and ME04077-10 were evaluated in greater detail in the T₂ generation. Eighteen individuals were sown and observed for event 06, whereas 17 individuals were sown and observed for event 10. The transgenic plants for both events showed increased primary inflorescence thickness, increased number of rosette leaves, a larger rosette, and delay of flowering time to a 0.05 level of statistical significance (Table 5-2). The plants of both events were visibly much taller than the controls, but only event -10 was quantitatively taller to a 0.05 level of statistical significance via t-test. If a greater number of internal controls were available for event -06, this event would very likely fall under the same degree of significance via the same test. Both events had normal fertility. All plants noted in the table as ME04077-06 and ME04077-10 were segregating progeny of the T₁ event which we had confirmed to contain the transgene under test. All plants noted in the table as -06 Control or -10 Control were T₂ segregating progeny which did not contain the transgene under test (internal controls).

Both events produce significantly more seeds than the control, as would be expected for a typical, fertile, late flowering plant.

Event ME04077-06 had 12 transgene-containing plants which exhibited the beneficial phenotype and 3 transgene-containing plants which appeared wild-type (these three were omitted from statistical analyses in Table 5-2). Event ME04077-10 had 9 transgene-containing plants which exhibited the beneficial phenotype and 1 transgene-containing plant which appeared wild-type. Our statistical analyses compared the internal controls to those plants with the beneficial phenotype which contained the transgene.

Segregation frequencies of the transgene under test suggest that each event contains a single insert, as calculated by a Chi-square test. The T₂ seeds segregate 3R:1S for both events (data not shown).

Table 5-2. Quantitative phenotypes observed in 35S::cDNA 12561537 T₂ events

Event/Control	Number of Observations	Rosette Area (mm ²)	Number of Leaves	Height (cm)	Primary Inflorescence Thickness (inches)	Days to Bolt
ME04077-06	12	7302.7*	15.6*	72.8	0.068*	23.9
-06 Control	3	1666.3	6.7	55.9	0.046	18.3
ME04077-10	9	9343.9*	19.6*	73.0*	0.086*	24.4*
-10 Control	7	2696.1	8.9	52.3	0.053	18.6
*significantly different from control at 0.05 level, via t-test						

LEAD SUMMARY/DISCUSSION:

- The ectopic expression of cDNA 12561537 with a strong constitutive promoter (35S) results in taller plants, with thicker inflorescences, a larger rosette, and more rosette leaves.
- The increase in plant size seen by this expression is accompanied by a delay in flowering time, but no reduction in fertility.
- It can also be a useful gene to increase root growth, given the similar expression pattern in shoot meristems and root tip cells.
- Increased vegetative biomass can give an improved source:sink ratio and improved fixation of carbon to sucrose and starch, leading to improved yield.
- Taller inflorescences give the opportunity for more flowers and therefore more seeds. The combination of improved biomass and inflorescence stature can give a significant improvement in yield.
- Thicker inflorescences may prevent against “snap” against wind, rain or drought.
- Biomass advantage and presumed photosynthesis advantage should be useful in corn and soybean.

- This gene/protein can be an especially useful one for controlling the number/rate of cell division in meristems without disturbing overall plant morphology. It can be developed in crops with an appropriate promoter to regulate size and growth rate of many individual organs. The protein can be useful for creating sturdier stems in corn and preventing against “snap”.

Tomato Field Trial Results

This Lead 15 (clone 92459) was transformed into tomato under the control of plasmid p13879. 1 transgenic event was selected for field testing. This event shows an increase in biomass, as shown below in the results of Table 5-3.

Table 5-3: Tomato Field Trial Results

		Event-13	Percent Increase
Plant weight	92459 Transgenic	2042.54	120%
	92459 Control	1707.50	
Fruit weight per plant	92459 Transgenic	4932	100%
	92459 Control	4956	
Percent red fruit	92459 Transgenic	28.9	93%
	92459 Control	31.0	
Harvest index	92459 Transgenic	71%	95%
	92459 Control	74%	

Example 6 – Determination of Functional Homolog Sequences

The “Lead” sequences described above in Examples 1 - 5 are utilized to identify functional homologs of the lead sequences and, together with those sequences, are utilized to determine a consensus sequence for a given group of lead and functional homolog sequences.

A subject sequence is considered a functional homolog of a query sequence if the subject and query sequences encode proteins having a similar function and/or activity. A process known as Reciprocal BLAST (Rivera et al, *Proc.Natl Acad. Sci. USA*, 1998, 95:6239-6244) is used to identify potential functional homolog sequences from databases consisting of all available public and proprietary peptide sequences, including NR from NCBI and peptide translations from Ceres clones.

Before starting a Reciprocal BLAST process, a specific query polypeptide is searched against all peptides from its source species using BLAST in order to identify polypeptides having sequence identity of 80% or greater to the query polypeptide and an alignment length of 85% or greater along the shorter sequence in the alignment. The query polypeptide and any of the aforementioned identified polypeptides are designated as a cluster.

The main Reciprocal BLAST process consists of two rounds of BLAST searches; forward search and reverse search. In the forward search step, a query polypeptide sequence, "polypeptide A," from source species S^A is BLASTed against all protein sequences from a species of interest. Top hits are determined using an E-value cutoff of 10^{-5} and an identity cutoff of 35%. Among the top hits, the sequence having the lowest E-value is designated as the best hit, and considered a potential functional homolog. Any other top hit that had a sequence identity of 80% or greater to the best hit or to the original query polypeptide is considered a potential functional homolog as well. This process is repeated for all species of interest.

In the reverse search round, the top hits identified in the forward search from all species are used to perform a BLAST search against all protein or polypeptide sequences from the source species S^A . A top hit from the forward search that returned a polypeptide from the aforementioned cluster as its best hit is also considered as a potential functional homolog.

Functional homologs are identified by manual inspection of potential functional homolog sequences. Representative functional homologs are shown in Figures 1 - 5. Each Figure represents a grouping of a lead/query sequence aligned with the corresponding identified functional homolog subject sequences. Lead sequences and their corresponding functional homolog sequences are aligned to identify conserved amino acids and to determine a consensus sequence that contains a frequently occurring amino acid residue at particular positions in the aligned sequences, as shown in Figures 1-5.

Each consensus sequence then is comprised of the identified and numbered conserved regions or domains, with some of the conserved regions being separated by one or more amino acid residues, represented by a dash (-), between conserved regions.

Useful polypeptides of the inventions, therefore, include each of the lead and functional homolog sequences shown in Figures 1-5, as well as the consensus sequences shown in those Figures. The invention also encompasses other useful polypeptides constructed based upon the consensus sequence and the identified conserved regions. Thus, useful polypeptides include those which comprise one or more of the numbered conserved regions in each alignment table in an individual Figure depicted in Figures 1-5, wherein the conserved regions may be separated by dashes. Useful polypeptides also include those which comprise all of the numbered conserved regions in an individual alignment table selected from Figures 1-5, alternatively comprising all of the numbered conserved regions in an individual alignment table and in the order as depicted in an individual alignment table selected from Figures 1-5. Useful polypeptides also include those which comprise all of the numbered conserved regions in an individual alignment table and in the order as depicted in an individual alignment table selected from Figures 1-5, wherein the conserved regions are separated by dashes, wherein each dash between two adjacent conserved regions is comprised of the amino acids depicted in the alignment table for lead and/or functional homolog

sequences at the positions which define the particular dash. Such dashes in the consensus sequence can be of a length ranging from length of the smallest number of dashes in one of the aligned sequences up to the length of the highest number of dashes in one of the aligned sequences.

Such useful polypeptides can also have a length (a total number of amino acid residues) equal to the length identified for a consensus sequence or of a length ranging from the shortest to the longest sequence in any given family of lead and functional homolog sequences identified in an individual alignment table selected from Figures 1-5.

The present invention further encompasses nucleotides that encode the above described polypeptides, as well as the complements thereof, and including alternatives thereof based upon the degeneracy of the genetic code.

The invention being thus described, it will be apparent to one of ordinary skill in the art that various modifications of the materials and methods for practicing the invention can be made. Such modifications are to be considered within the scope of the invention as defined by the following claims.

Each of the references from the patent and periodical literature cited herein is hereby expressly incorporated in its entirety by such citation.

REFERENCES

- (1) Zhang et al. (2004) *Plant Physiol.* 135:615.
- (2) Salomon et al. (1984) *EMBO J.* 3:141.
- (3) Herrera-Estrella et al. (1983) *EMBO J.* 2:987.
- (4) Escudero et al. (1996) *Plant J.* 10:355.
- (5) Ishida et al. (1996) *Nature Biotechnology* 14:745.
- (6) May et al. (1995) *Bio/Technology* 13:486
- (7) Armaleo et al. (1990) *Current Genetics* 17:97.
- (8) Smith. T.F. and Waterman, M.S. (1981) *Adv. App. Math.* 2:482.
- (9) Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443.
- (10) Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. (USA)* 85: 2444.
- (11) Yamauchi et al. (1996) *Plant Mol Biol.* 30:321-9.
- (12) Xu et al. (1995) *Plant Mol. Biol.* 27:237.
- (13) Yamamoto et al. (1991) *Plant Cell* 3:371.
- (14) P. Tijessen, "Hybridization with Nucleic Acid Probes" *In* Laboratory Techniques in Biochemistry and Molecular Biology, P.C. vand der Vliet, ed., c. 1993 by Elsevier, Amsterdam.
- (15) Bonner et al., (1973) *J. Mol. Biol.* 81:123.
- (16) Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, 1989, New York.
- (17) Shizuya et al. (1992) *Proc. Natl. Acad. Sci. USA*, 89: 8794-8797.
- (18) Hamilton et al. (1996) *Proc. Natl. Acad. Sci. USA*, 93: 9975-9979.
- (19) Burke et al. (1987) *Science*, 236:806-812.
- (20) Sternberg N. et al. (1990) *Proc Natl Acad Sci U S A.*, 87:103-7.
- (21) Bradshaw et al. (1995) *Nucl Acids Res*, 23: 4850-4856.

- (22) Frischauf et al. (1983) *J. Mol Biol*, 170: 827-842.
- (23) Huynh et al., Glover NM (ed) *DNA Cloning: A practical Approach*, Vol.1 Oxford: IRL Press (1985).
- (24) Walden et al. (1990) *Mol Cell Biol* 1: 175-194.
- (25) Vissenberg et al. (2005) *Plant Cell Physiol* 46:192.
- (26) Husebye et al. (2002) *Plant Physiol* 128:1180.
- (27) Plesch et al. (2001) *Plant J* 28:455.
- (28) Weising et al. (1988) *Ann. Rev. Genet.*, 22:421.
- (29) Christou (1995) *Euphytica*, v. 85, n.1-3:13-27.
- (30) Newell (2000)
- (31) Griesbach (1987) *Plant Sci.* 50:69-77.
- (32) Fromm et al. (1985) *Proc. Natl. Acad. Sci. USA* 82:5824.
- (33) Paszkowski et al. (1984) *EMBO J.* 3:2717.
- (34) Klein et al. (1987) *Nature* 327:773.
- (35) Willmitzer, L. (1993) Transgenic Plants. In: *Biotechnology, A Multi-Volume Comprehensive treatise* (H.J. Rehm, G. Reed, A. Püler, P. Stadler, eds., Vol. 2, 627-659, VCH Weinheim-New York-Basel-Cambridge).
- (36) *Crit. Rev. Plant. Sci.* 4:1-46.
- (37) Fromm et al. (1990) *Biotechnology* 8:833-844.
- (38) Cho et al. (2000) *Planta* 210:195-204.
- (39) Broothaerts et al. (2005) *Nature* 433:629-633.
- (40) Lincoln et al. (1998) *Plant Mol. Biol. Rep.* 16:1-4.
- (41) Lacomme et al. (2001), "Genetically Engineered Viruses" (C.J.A. Ring and E.D. Blair, Eds). Pp. 59-99, BIOS Scientific Publishers, Ltd. Oxford, UK.

CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule comprising:
 - (a) a nucleotide sequence encoding an amino acid sequence that is at least 85% identical to any one of Leads 15, 28, 29, 36, ME04012 and Clone 691319, SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively ;
 - (b) a nucleotide sequence that is complementary to any one of the nucleotide sequences according to paragraph (a);
 - (c) a nucleotide sequence according to any one of SEQ ID Nos. 80, 90, 92, 98, 109, and 103;
 - (d) a nucleotide sequence that is in reverse order of any one of the nucleotide sequences according to (c) when read in the 5' to 3' direction;
 - (e) a nucleotide sequence that is an interfering RNA to the nucleotide sequence according to paragraph (a);
 - (f) a nucleotide sequence able to form a hybridized nucleic acid duplex with the nucleic acid according to any one of paragraphs (a) – (d) at a temperature from about 40°C to about 48°C below a melting temperature of the hybridized nucleic acid duplex;
 - (f) a nucleotide sequence encoding any one of the amino acid sequences identified as Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to, SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively;or
 - (g) a nucleotide sequence encoding any one of the lead, functional homolog or consensus sequences in Figures 1 – 5.

2. A vector, comprising:
 - a) a first nucleic acid having a regulatory region encoding a plant transcription and/or translation signal; and
a second nucleic acid having a nucleotide sequence according to any one the nucleotide sequences of claim 1, wherein said first and second nucleic acids are operably linked.
3. A method of modulating plant size, modulating vegetative growth, modulating plant architecture, seedling vigor, growth rate, fruit and seed yield, tillering and/or modulating the plant biomass, said method comprising introducing into a plant cell an isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of :
 - (a) a nucleotide sequence encoding an amino acid sequence that is at least 85% identical to any one of Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to SEQ ID NOs. 80, 90, 92, 98, 109, and 103, respectively;
 - (b) a nucleotide sequence that is complementary to any one of the nucleotide sequences according to paragraph (a);
 - (c) a nucleotide sequence according to any one of SEQ ID NOs. 80, 90, 92, 98, 109, and 103.
 - (d) a nucleotide sequence that is in reverse order of any one of the nucleotide sequences according to (c) when read in the 5' to 3' direction;
 - (e) a nucleotide sequence that is an interfering RNA to the nucleotide sequence according to paragraph (a);

- (f) a nucleotide sequence able to form a hybridized nucleic acid duplex with the nucleic acid according to any one of paragraphs (a) – (d) at a temperature from about 40°C to about 48°C below a melting temperature of the hybridized nucleic acid duplex;
 - (f) a nucleotide sequence encoding any one of the amino acid sequences identified as Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively; or
 - (g) a nucleotide sequence encoding any one of the lead, functional homolog or consensus sequences in Figures 1 – 5, wherein said plant produced from said plant cell has modulated plant size, modulated vegetative growth, modulated plant architecture, modulated seeding vigor and/or modulated biomass as compared to the corresponding level in tissue of a control plant that does not comprise said nucleic acid.
4. The method according to claim 3, wherein said consensus sequence comprises one or more of the conserved regions identified in any one of the alignment tables in Figures 1-5.
5. The method according to claim 4, wherein said consensus sequence comprises all of the conserved regions identified in any one of the alignment tables in Figures 1- 5.
6. The method according to claim 5, wherein said consensus sequence comprises all of the conserved regions and in the order identified in any one of the alignment tables in Figures 1- 5

7. The method according to claim 6, wherein said conserved regions are separated by one or more amino acid residues.

8. The method according to claim 7, wherein each of said of one or more amino acids consisting in number and kind of the amino acids depicted in the alignment table for the lead and/or functional homolog sequences at the corresponding positions that.

9. The method according to claim 8, wherein said consensus sequence has a length in terms of total number of amino acids that is equal to the length identified for a consensus sequence in one of Figures 1- 5, or equal to a length ranging from the shortest to the longest sequence in any individual alignment table in any one of Figures 1- 5.

10. The method of claim 3, wherein said difference is an increase in the level of plant size, vegetative growth, organ number, seedling vigor, growth rate, fruit and seed yield, tillering and/or biomass.

11. The method of claim 3, wherein said isolated nucleic acid is operably linked to a regulatory region.

12. The method of claim 11, wherein said regulatory region is a promoter selected from the group consisting of YP0092 (SEQ ID NO: 38), PT0676 (SEQ ID NO: 12), PT0708 (SEQ ID NO: 17), PT0613 (SEQ ID NO: 5), PT0672 (SEQ ID NO: 11), PT0678 (SEQ ID NO: 13), PT0688 (SEQ ID NO: 15), PT0837 (SEQ ID NO: 24), the napin promoter, the Arcelin-5 promoter, the phaseolin gene promoter, the soybean trypsin inhibitor promoter, the ACP promoter, the stearyl-ACP desaturase gene, the soybean α' subunit of β -conglycinin promoter, the oleosin promoter, the 15 kD zein promoter, the 16 kD zein promoter, the 19 kD zein promoter, the 22 kD zein promoter, the 27 kD zein promoter, the Osgt-1 promoter, the beta-amylase gene promoter, and the barley hordein gene promoter

13. The method of claim 11, wherein said regulatory region is a promoter selected from the group consisting of p326 (SEQ ID NO: 76), YP0144 (SEQ ID NO: 55), YP0190 (SEQ ID NO: 59), p13879 (SEQ ID NO: 75), YP0050 (SEQ ID NO: 35),

p32449 (SEQ ID NO: 77), 21876 (SEQ ID NO: 1), YP0158 (SEQ ID NO: 57), YP0214 (SEQ ID NO: 61), YP0380 (SEQ ID NO: 70), PT0848 (SEQ ID NO: 26), and PT633 (SEQ ID NO: 7), the cauliflower mosaic virus (CaMV) 35S promoter, the mannopine synthase (MAS) promoter, the 1' or 2' promoters derived from T-DNA of *Agrobacterium tumefaciens*, the figwort mosaic virus 34S promoter, actin promoters such as the rice actin promoter, and ubiquitin promoters such as the maize ubiquitin-1 promoter.

14. The method of claim 11, wherein said regulatory region is a promoter selected from the group consisting of ribulose-1,5-bisphosphate carboxylase (RbcS) promoters such as the RbcS promoter from eastern larch (*Larix laricina*), the pine cab6 promoter, the Cab-1 gene promoter from wheat, the CAB-1 promoter from spinach, the cab1R promoter from rice, the pyruvate orthophosphate dikinase (PPDK) promoter from corn, the tobacco Lhcb1*2 promoter, the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter, and thylakoid membrane protein promoters from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS, PT0535 (SEQ ID NO: 3), PT0668 (SEQ ID NO: 2), PT0886 (SEQ ID NO: 29), PR0924 (SEQ ID NO: 78), YP0144 (SEQ ID NO: 55), YP0380 (SEQ ID NO: 70) and PT0585 (SEQ ID NO: 4).

15. A plant cell comprising an isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding an amino acid sequence that is at least 85% identical to any one of Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively;
- (b) a nucleotide sequence that is complementary to any one of the nucleotide sequences according to paragraph (a);
- (c) a nucleotide sequence according to any one of SEQ ID Nos. 80, 90, 92, 98, 109, and 103;
- (d) a nucleotide sequence that is in reverse order of any one of the nucleotide sequences according to (c) when read in the 5' to 3' direction;

- (e) a nucleotide sequence that is an interfering RNA to the nucleotide sequence according to paragraph (a);
 - (f) a nucleotide sequence able to form a hybridized nucleic acid duplex with the nucleic acid according to any one of paragraphs (a) – (d) at a temperature from about 40°C to about 48°C below a melting temperature of the hybridized nucleic acid duplex;
 - (f) a nucleotide sequence encoding any one of the amino acid sequences identified as Leads 15, 28, 29, 36, ME04012 and Clone 691319, corresponding to SEQ ID Nos. 80, 90, 92, 98, 109, and 103, respectively; or
 - (g) a nucleotide sequence encoding any one of the lead, functional homolog or consensus sequences in Figures 1 – 5.
16. A transgenic plant comprising the plant cell of claim 15.
17. Progeny of the plant of claim 16, wherein said progeny has modulated plant size, modulated vegetative growth, modulated plant architecture, modulated seedling vigor, growth rate, fruit and seed yield, tillering and/or modulated biomass as compared to the corresponding level in tissue of a control plant that does not comprise said nucleic acid.
18. Seed from a transgenic plant according to claim 16.
19. Vegetative tissue from a transgenic plant according to claim 16.
20. A food product comprising vegetative tissue from a transgenic plant according to claim 16.
21. A feed product comprising vegetative tissue from a transgenic plant according to claim 16.

22. A product comprising vegetative tissue from a transgenic plant according to claim 16 used for the conversion into fuel or chemical feedstocks.
23. A method for detecting a nucleic acid in a sample, comprising:
providing an isolated nucleic acid according to claim 1;
contacting said isolated nucleic acid with a sample under conditions that permit a comparison of the nucleotide sequence of the isolated nucleic acid with a nucleotide sequence of nucleic acid in the sample; and
analyzing the comparison.
24. A method for promoting increased biomass in a plant, comprising:
(a) transforming a plant with a nucleic acid molecule comprising a nucleotide sequence encoding any one of the lead, functional homolog or consensus sequences in any one of Figures 1-5 and
(b) expressing said nucleotide sequence in said transformed plant, whereby said transformed plant has an increased biomass or enhance seedling vigor as compared to a plant that has not been transformed with said nucleotide sequence.
25. A method for modulating the biomass of a plant, said method comprising altering the level of expression in said plant of a nucleic acid molecule according to claim 1.

[illegible]

Fig. 1

CeresGdna:1460991	183	SEKRSEFETE
Lead:clone123905.Taxonomy:3702	219	GANAASASV
gil51536200	224	MTPTLSPCSA
CeresClone:1494990	203	CSPSPSPRSA
CeresClone:634402	214	CSPSPSPRSA
Consensus	250	---SPS-SP-SA
CeresGdna:1460991	217	---
Lead:clone123905.Taxonomy:3702	258	---
gil51536200	262	---
CeresClone:1494990	239	---
CeresClone:634402	249	---
Consensus	300	---
CeresGdna:1460991	229	---
Lead:clone123905.Taxonomy:3702	267	---
gil51536200	274	---
CeresClone:1494990	256	---
CeresClone:634402	266	---
Consensus	318	---

Fig. 1

gi 50941583 Lead-clone679923-Taxonomy-3847 CeresGdna:1479788 CeresGdna:1533259	MAIDAAEQHHR MENLSPITYK MENFPPLLYR MENFPPLLYR	QEETAAATT NP NP NP	PQMMMR RRR RRR RRR	ARRSSEYLG V V V	RRRPWGRYAA RRRPWGRYAA RRRPWGRYAA RRRPWGRYAA	50 36 35 35
Consensus	MENF-PLLYR	NP	RS	SRQSSRYLG	RRRPWGRYAA	50
gi 50941583 Lead-clone679923-Taxonomy-3847 CeresGdna:1479788 CeresGdna:1533259	EIRNPYTKER EIRNPYTKER EIRNPYTKER EIRNPYTKER	HWLGTFTAE HWLGTFTAE HWLGTFTAE HWLGTFTAE	EAAVAYDL SA SA SA	ISISGAAAR KIGINAR SFSGIERAR SFSGIERAR	TNFLYP DMHH TNFHY TNFHY TNFHY TNFHY	100 83 83 83
Consensus	EIRNPYTKER	HWLGTFTAE	EAAVAYDLSS	IS-SGIERAR	TNFPY-FF	100
gi 50941583 Lead-clone679923-Taxonomy-3847 CeresGdna:1479788 CeresGdna:1533259	HHPSPPPQH AL SLPPLPMS SL AHPSPSQEA AHPSPSQEA	SPAVPP PPPP PPPP PPPP PPPP	PPPSPL YDD PELD PSV EME KGD EME KGD	YLSPAAAE EE EVCLEMM NAA QLG MEDV MEDV	VEAGDDE SLT SYDGDDE SLV DGNNA GTTQDDE SLV	150 128 118 123
Consensus	AHPSP-QEAL	PPPP	PPP-E-EKGD	QLG	---GDDESLV	150
gi 50941583 Lead-clone679923-Taxonomy-3847 CeresGdna:1479788 CeresGdna:1533259	ATILQSFQY ASI LQSF LEIL LK ASI LQSF	QSVPP ASSG SNSG AGNG CQST	SMFY NCST K SYST HPQI	175 144 129 143		
Consensus	IASILQSF	---A-SG	S-SF	---		178

Fig. 2

gi 31580813	MGRKKLEI KR	I ENKSSRQVT	FSKRRNGLI E	KARQLSVLCD	ASVALLVVSA	50
gi 34591565	MGRKKLEI KR	I ENKSSRQVT	FSKRRNGLI E	KARQLSVLCD	ASVALLVVSA	50
gi 71834745	MGRRKVEI KL	I ENKSSRQVT	FSKRRNGLI E	KARQLSVLCE	SSVAVLVVSA	50
Lead·Peptide·Clone·CeresClone·	MGRRKI EI KR	I ENKSSRQVT	FSKRRNGLI D	KARQLSI LCE	SSVAVVVVSA	50
Consensus	MGR-KLEI KR	I ENKSSRQVT	FSKRRNGLI E	KARQLSVLC-	-SVA-LVVSA	50
gi 31580813	SGKLYNFSAG	DNLVKI LDY	GKQHA-DDLK	ALDLQSKAPK	YGSHHELLEL	99
gi 34591565	SGKLYNFSAG	DDLVKVI DRY	GEQHA-DDDK	ALDLQSEAPK	YGSHHELLEL	100
gi 71834745	SGKLYNSSSG	DNMTNI VDRY	EIQHA-GELR	SLDLAEKTRN	YLPHKELLEL	99
Lead·Peptide·Clone·CeresClone·	SGKLYDSSSG	DDISKI I DRY	EIQHA-DELR	ALDLEEKI QN	YLPHKELLEL	99
Consensus	SGKLYN-S-G	D-L-KI I DRY	--QHA-D-L-	ALDLQ-KA--	Y--H-ELLE-	100
gi 31580813	VESKLVESNS	D-VSVDSLVSQ	LEDHLETALS	VTARKTELM	LKLVDSLKEK	148
gi 34591565	VESKLVESNS	D-VSVDSLVSQ	LENHLETALS	VTARKTELL	LKLVDSLKEK	149
gi 71834745	VKSNEEPPNV	DSVSVDSLIS	LEDQLETALS	ATRARKTELT	MEFVKMLQEK	149
Lead·Peptide·Clone·CeresClone·	VQSKLEEPPNV	DNVSVDSLIS	LEEQLETALS	VSARKAEELM	MEYI ESKKEK	149
Consensus	VESKL-E-N-	D-VSVDSL--	LED-LETALS	VTARKTELM	---VDSLKEK	150
gi 31580813	EKLLKEENQG	LASQMEKNNL	AGAEADKMEM	SPGQI SDI NR	PVTLRLLY--	196
gi 34591565	EKLLKEENQG	LASQMEKNNL	AGAEADKMEV	SPGQI SDI NC	PVTLPLLY--	197
gi 71834745	EELLREENLV	LVSQI GITNG	R-RENNSS---	PVNSSGI NIP	PETLPLLKVT	194
Lead·Peptide·Clone·CeresClone·	EKLLREENQV	LASQMGKNTL	L-ATDDERGM	FPGSSSGNKI	PETLPLLNPP	198
Consensus	EKLL-EENQ-	LASQM-KNNL	AGAE-DKMEM	SPG--S-I N-	P-TLPLLY--	200
gi 31580813	-----	196				
gi 34591565	-----	197				
gi 71834745	SVI QRLS-	201				
Lead·Peptide·Clone·CeresClone·	SSTAEFSp	206				
Consensus	S-----S-	208				

Fig. 3

Lead-ME04012	MSNI QEMEMI	LMVSLC LTT L	LTFL KQFL	KRTANK	-VNLPSP	PW	44
gi 3582021	---MVSLSY	FLIALLCITLP	FLLFLNKW	RRSYSG	-KITPPSP	PP	38
gi 46947673	---MKMLEQNP	QYLYFFSLFL	VTI FLN KWL T	LKKTPL	-KNLPPSP	PP	42
gi 25282608	---MAI LV	SLFLAI ALI	FFL LKLN	EKREKK	-PNLPPSP	PP	36
gi 34904242	MAVSLV VVV	VVI AIV PLL	YLV L PAMKP	ARRDDGDGGM	RRRLPPSP	PPW	50
CeresClone:703961	MAVSPILALVL	LLLAFAVSL	YILRRPAPLR	SGSDGG	RRHLPPSP	PR	45
Consensus	MAV-M-ALMV	LLIAL-I-LL	-LLFL-KW--	-R-D-G	--NLPPSP	PP	50
Lead-ME04012	RLPLI GNLHQ	LSLHPRSLH	SLSLRYGPLM	LLHFGRPVPL	VVSSGEAAQE		94
gi 3582021	KLPVI GNLHQ	LGYPHRYLQ	SLSRRYGPLM	QLHFGSMPVL	VASSPEAARE		88
gi 46947673	QYPII GNLHQ	I GPDPPQASLR	DLAQKYGPLM	FLKFGTMPVL	VVSSADAAARE		92
gi 25282608	NLPII GNLHQ	LGNLPHRSLR	SLANELGPLI	LLHLGHJ PTL	VSTAETAE		86
gi 34904242	GLPLLGHHL	L GALPHRALR	SLAAAHGPVL	LLRLGRVPV	VVSSAAAAEE		100
CeresClone:703961	GLPLLGHHL	LGSLPHRALR	SLAAAHGPVL	LLRLGRVPAM	VVSSPAAAEE		95
Consensus	-LPLI GNLHQ	LG-LPHRSLR	SLA--YGPLM	LL--GRVPVL	VVSSAEAAEE		100
Lead-ME04012	VLKTHDLKFA	NRPRSKAVHG	LMNGGRDVVF	GPYGEYWRQM	KSVCI LNL	LT	144
gi 3582021	LMKNQDI VFS	NRPKMSI ANR	LFNNRDVAF	TQYGEYWRQI	RSI CVLQLLS		138
gi 46947673	ALKTHDLVFA	DRPYSSVANK	I FYNGKDMVF	ARYTEYWRQV	KSI CVTQLLS		142
gi 25282608	ILKTHDLIFA	SRPSTTAARR	I FYDCTDVAF	SPYGEYWRQV	RKI CVLELLS		136
gi 34904242	VMRTDL EFA	SRPRVAMAEER	LLYGGRDVAF	APYGEYWRQT	RRI CVVHLLS		150
CeresClone:703961	VMRARDLAFA	SRPRSAMADR	LLY-GRDVAF	APYGEYWRQA	RRV CVVHLLS		144
Consensus	V-KT-DLVFA	SRPRS-MANR	L-YNGRDVAF	APYGEYWRQV	R-I CVL-LLS		150
Lead-ME04012	NKMWASFEKI	REEELNEMI K	KLEK-ASSSS	SSENLSSELFW	TLPSDVT SRI		193
gi 3582021	NKRVQSFRRV	REEETSI MVE	KIMQLGSSSS	TPVNLSELL	SLTNDVVCRV		188
gi 46947673	NKRVNSFHYV	REEEVDLLVQ	NL---ENSHS	KVANL TELL	EVTGNVVCRV		189
gi 25282608	IKRVNSYRSI	REEEVGLMME	RI SQ-SCSTG	EAVNLSELL	LLSSGTI TRV		185
gi 34904242	ARRVLSFRRV	REEEAAALVA	RVR---AAG	GAVDLVEHL	AYSNTV SRA		196
CeresClone:703961	PLRI LSFRGV	REEEAAALVE	RVRG-AAAGG	AAVDLCELLV	AYANTV SRA		193
Consensus	NKRV-SFRRV	REEEV-L-VE	R--Q-ASSS-	-AVNLSELL-	-L-NDVVSRV		200

Fig. 4

Lead-ME04012	ALGRKHS	--EDETARDL	KKRVQRQIMEL	LG-EFFPGDY	VPALAWIDRI	237
gi 3582021	TLGKKYGG	-NGSEEVDKL	KEMLTEIQNL	MG-ISPVMWF	LPWLNMTRRF	235
gi 46947673	SMG	--SGDKVDSY	KJLLEIMDM	LGYSRSIEDF	FPLLGWVDM	230
gi 25282608	AFGKKYEG	-EEERKNKF	ADLATEITL	MG-AFFVGDY	FPSFAWVNL	230
gi 34904242	VFGDESARGL	YGDVDRGRVL	RKLAFDFVEL	LG-QEPMGEL	LPWLGWVDA	245
CeresClone:703961	AFGDDSARGL	YEEGNKEREL	RKVFNDFQEL	LG-TAPLGEL	LPWLGWLDV	242
Consensus	A-GKKYA-G-	--E-E----	KKL--EI MEL	LG---P-G--	I PWLGWVD-L	250
Lead-ME04012	NGFNARIKEV	SQGFSDLMDKI	VVQEHLF	DKDG	GNHKEDFVDI	275
gi 3582021	DGVDDQVRDRI	VKAFDGFLES	VIQEHEKRDG	---	GDGALDFVDI	280
gi 46947673	TGLRGKVAEA	AKGVDTFLEG	VLKEHLS---	---	GSKYNDFFVSI	269
gi 25282608	TGMDARLKRNI	HGELDAFVDH	VIDDHLLSRK	ANGS	GVEQKDLVDV	275
gi 34904242	NGMEVKVQRT	FEALDGTLEK	VIDDHRRRRR	EVGRQMDDGG	GCDHRDFVDV	295
CeresClone:703961	RGMEGKIRRT	FKALDGMLEK	VIDGHRRRRQ	AGQQTGD---	GCDHRDFVDV	290
Consensus	NGM---IKR-	-KALDG-LEK	VIQ-H--RR-	-----D	G---H-DFVD-	300
Lead-ME04012	LLSL-ESEKS	I GFQAQRDDI	KFMI LDMFI G	GTSTTSSTLE	WLMIELIRNP	324
gi 3582021	LLQF-QRENK	NRSPVEDDTV	KALI LDMFVA	GTDTTATALE	WAVAEIKNP	329
gi 46947673	LLEI--QEA	AGSSMDNECI	KSLI WDM LGA	GTETSTALE	WTLALIKNP	317
gi 25282608	LLHL-QKDS	LGVHLNRNLI	KAVI LDMFSG	GTDTTAVTLE	WMAELIKHP	324
gi 34904242	LLDVNETDMD	AGVQLGTIEI	KAI I LDMFAA	GTDTTTTVE	WMAELI THP	345
CeresClone:703961	LLDVSDTDDE	AGMRLSTTEI	KAI I LDMFAA	GTDTTSTAME	WMAEVI THP	340
Consensus	LL-----	AGMQL--D-I	KA-I LDMFAA	GTDTTSTALE	WMAELI K-P	350
Lead-ME04012	NVMKKLQDEI	RSTIRPHGSY	KEKDVENMK	YLKAVI KEVF	RVHPPLPLIL	374
gi 3582021	RAMKRLQNEV	REMAKSKAE-	IEEEDLEKMP	YLKASIKESL	RLHVPVLLV	378
gi 46947673	DAMFKLQNEV	REIKGKSK-	ISEADLVKMN	YLQAVMKESM	RLYFTAPLLV	366
gi 25282608	DVMEKAKQEV	RRVVGKKAK-	VEEEDLHQLH	YLKELIKETL	RLHPVAPLLV	373
gi 34904242	DAMRNAQDEI	KAVVGITSH-	ITEDHLDRLP	YLKAVLKETL	RLHPPLPLLV	394
CeresClone:703961	DSMRKLQDEL	RAAVGGSGHV	ITEDHIDKLH	YLKAVVKETL	RLHPPI PLLV	390
Consensus	DAM-KLQDEI	RAVVG-K-K-	I -E-DL-K-H	YLKAVI KETL	RLHPPLPLLV	400

Fig. 4

[illegible]

Fig. 4

Lead-clone691319	MSLLTVAHQH	-GSGEFIRFT	ESHGCGGDDV	SGDGEHGGCH	DDGSGAGGSL	49
CeresGdna:1443093	MGYSSSTIEMS	-MVSELTTHVV	SGQRGSTDW	GSYGAVGLG	-----	38
CeresGdna:1452324	MGYSSSAEEMS	AMVSALTTHVV	SGHRGSTDW	GSYGASGLG	-----	39
Consensus	MGYSSSAEEMS	-MVSELTTHVV	SGHRGSTDW	GSYGA-GLG-	-----	50
Lead-clone691319	GLNFNQVMQQ	GEVTMQGGSL	VSGYNRQDPE	LREI VSAL TH	VVSSCSGQRS	99
CeresGdna:1443093	-----	-----GATI	TSNFGQAAP-	-----	-----GSNT	55
CeresGdna:1452324	-----	-----GATI	TSTVQAAP-	-----	-----GSNT	56
Consensus	-----	-----GATI	TS---QAAP-	-----	-----GSNT	100
Lead-clone691319	TELTQQSGFP	MMSASLSRL	SAFSSSSPSIP	SSGASWVGHK	RGREEEENST	149
CeresGdna:1443093	-----	---STPASPL	SAYSSTSGS-	---GLWI GQK	RGREEEA GAA	89
CeresGdna:1452324	-----	---SPASPSL	SAYSSTSGS-	---GSWI GQK	RGREKEA GAA	89
Consensus	-----	---S-PASP-L	SAYSSTSGS-	---GSWI GQK	RGREEEA GAA	150
Lead-clone691319	SHNLMQQQQQ	SAPRLFRNIG	DFMVPSSQGS	SS-----VITEE	APTST-----T	191
CeresGdna:1443093	A-----QLME	SLPRVYRGFN	DFR-SSQGS	SSSGATATEE	VSASTIVIP	133
CeresGdna:1452324	A-----QLKE	SLPRVHRGFD	DFR-SSQGS	SSSGATATEE	VSASTLVFST	133
Consensus	A-----QL-E	SLPRV-RGF-	DFR-SSQGS	SSSGATATEE	VSAST-V--T	200
Lead-clone691319	TTTAVTENTP	PGG-----	GERRRYRGV	RQRPWGKWAA	EIRDPHKAAR	234
CeresGdna:1443093	TTTPSTTATP	SSEIASLEET	GEQRRYRGV	RQRPWGKWAA	EIRDPHKAAR	183
CeresGdna:1452324	TATPSTTATP	SSETASLGET	GERKRRYRGV	RQRPWGKWAA	EIRDPHKAAR	183
Consensus	TTTPSTTATP	SSE-ASL-ET	GERRRRYRGV	RQRPWGKWAA	EIRDPHKAAR	250
Lead-clone691319	VWLGTFDTIE	AAARAYDEAA	LRFRGNRAKL	NFPENVRAMP	PIQPFQATIR	284
CeresGdna:1443093	VWLGTFDTAE	AAARAYDDAA	LRFRGNRAKL	NFPENVRLLP	AQTQNVTA SQ	233
CeresGdna:1452324	VWLGTFETAE	AAARAYDEAA	LRFRGSRAKL	NFPENARLLP	AQMNVTA SQ	233
Consensus	VWLGTFDTAE	AAARAYDEAA	LRFRGNRAKL	NFPENVRLLP	AQ-QNVTA SQ	300

Fig. 5

Lead-clone691319	LIIVSDITISQ	FRPLSAVAPP	--FIQQPQI--	-----QGSSD	LI RDYLQYSQ	326
CeresGdna:1443093	VPI SHSQLSS	HLQLQPI SSP	RQQAQRPPQAP	APALFQSQAD	II RDYWEYSQ	283
CeresGdna:1452324	VPI SRSQLPS	HHQLQSI SSP	RQQAQRPPQVP	APALFQSQPD	II RDYWEYSQ	283
Consensus	VPI S-SQLSS	H-QLQ-I SSP	RQQAQRPPQ-P	APALFQSQ-D	II RDYWEYSQ	350
Lead-clone691319	LLQSDFFQQQ	I QQQQQQQRQ	QQRQRQQRQ	QQQQQQQQQPS	SLLQQLYYNA	376
CeresGdna:1443093	LLQSS-----	-----	---GEFH---	QQQQQQQQQPS	SLLQPMFYNP	315
CeresGdna:1452324	LLQSS-----	-----	---GDFH---	--GQQQPPPS	NLLEQMFYNP	310
Consensus	LLQSS-----	-----	---G-FH--Q	QQQQQQQQQPS	SLLQQMFYNP	400
Lead-clone691319	QIFASLQSPISM	--LSSSPISFS	S-----SVSPA	PFPLFTFSAS	FPL-LFSSQQM	419
CeresGdna:1443093	QVASLQSSAL	TSLSSSTSVS	SLAAI SSGSS	PSTFSPSASS	FPLLFAGQQL	365
CeresGdna:1452324	QLASLQSSTL	SSLFSSSTSGS	SFAAI PSGS	SSTLSPSASS	FPLLFAGQQL	360
Consensus	Q-ASLQSS-L	-SLSSSTS-S	S-AAI SSGS-	PSTLSPSASS	FPLLFAGQQL	450
Lead-clone691319	GYFQPPESRN	PAGGVPEFPT	STWSDTSSQP	PPSG		453
CeresGdna:1443093	GYFRPPQNQN	PASG-SDFPV	PPWTDSSHNP	SSSG		398
CeresGdna:1452324	GYFRPPENQN	PAAG-SDFPV	PPWTDGSRRP	SSTG		393
Consensus	GYFRPPENQN	PA-G-SDFPV	PPWTD-S--P	SSSG		484

Fig. 5

SEQUENCE LISTING

<110> Nickolai ALEXANDROV
 Vyacheslav BROVER
 Peter MASCIA
 Kenneth A. FELDMANN
 Cory CHRISTENSEN
 Greg NADZAN

<120> NUCLEOTIDE SEQUENCES AND CORRESPONDING POLYPEPTIDES
 CONFERRING MODULATED PLANT GROWTH RATE AND BIOMASS IN
 PLANTS

<130> 2750-1669PW01

<140>

<141> 2005-12-29

<160> 121

<210> 1

<211> 1823

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1823)

<223> Ceres Promoter 21876

<400> 1

gtctcttaaa aaggatgaac aaacacgaaa ctggtggatt atacaaatgt cgccttatac 60
 atatatcggg tattggccaa aagagctatt ttaccttatg gataatgggt ctactatggg 120
 tggagttgga ggtgtagttc aggcttcacc ttctggttta agccctccaa tgggtaatgg 180
 taaatttccg gcaaaaggtc ctttgagatc agccatgttt tccaatgttg aggtcttata 240
 ttccaagtat gagaaaggta aaataaatgc gtttcctata gtggagttgc tagatagtag 300
 tagatgttat gggctacgaa ttggtaagag agttcgattt tggactagtc cactcggata 360
 ctttttcaat tatgggtggc ctggaggaat ctcttggtga gtttgatatt tgcgagtata 420
 atctttgaac ttgtgtagat tgtacccaaa accgaaaaca tctctatat aaatttcatt 480
 atgagagtaa aattgtttgt tttatgtatc atttctcaac tgtgattgag ttgactattg 540
 aaaacatatc ttagataagt ttcgttatga gagttaatga tgattgatga catacacact 600
 cctttatgat ggtgattcaa cgttttggag aaaatttatt tataatctct cataaattct 660
 ccgttattag ttgaataaaa tcttaaatgt ctcctttaac catagcaaac caacttaaaa 720
 atttagattt taaagttaag atggatattg tgattcaacg attaattatc gtaatgcata 780
 ttgattatgt aaaataaaat ctaactaccg gaatttatc aataactcca ttgtgtgact 840

gcattttaa ataatgtttta tgtcccattha attaggctgt aatttcgatt tatcaattta 900
tataactagta ttaattta at tccatagatt tatcaaagcc aactcatgac ggctagggtt 960
ttcogtcacc ttttcgatca tcaagagagt ttttttataa aaaaatttat acaattatac 1020
aatttcttaa ccaaacaaca cataattata agctatttaa catttcaa at tgaaaaaaaa 1080
aatgtatgag aattttgtgg atccattttt gtaattcttt gttgggtaaa ttcacaacca 1140
aaaaaataga aaggcccaaa acgcgtaagg gcaaattagt aaaagtagaa ccacaaagag 1200
aaagcgaaaa ccctagacac ctgtagcta taagtaccct cgagtcgacc aggattaggg 1260
tgogctctca tttttctcac attttcgtag ccgcaagact cttttcagat tcttacttgc 1320
aggttagata ttttctctct ttagtgtctc cgatcttcat cttcttatga ttattgtagc 1380
tgtttagggg ttagattctt agtttttagct ctatattgac tgtgattatc gcttattctt 1440
tgctgttggt atactgcttt tgattctcta gcttttagatc cgtttactcg tcgatcaata 1500
ttgttctat tgagtctgat gtataatcct ctgattaatt gatagcgttt agttttgata 1560
tcgtcttcgc atgtttttta tcatgtcgat ctgtatctgc tctggttata gttgattctg 1620
atgtatttgg ttggtgatgt tccttagatt tgatatacct gttgtctcgt ggtttgatat 1680
gatagctcaa ctggtgatat gtggttttgt ttcagtggat ctgtgtttga ttatattgtt 1740
gaogttttgg ttgttgtatg gttgatgggt gatgtatttt tgttgattct gatgtttcga 1800
tttttgtttt tgttttgaca gct 1823

<210> 2
<211> 1000
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter PT0668

<400> 2
atagagtttt actatgcttt tggaatcttt cttcta atgt gccaaactaca gagaaataca 60
tgtattacca ctaggaatcg gaccatatca tagatatcag gattagataa ctagttctcg 120
tcgctatcac ttcgcattaa gttctagtaa ttgttaaaga ttctaatttt ttactaaaca 180
aaaactaa at caacatcaaa tatgcaaagt gtgtgttgtc cacacaagtg actcaaagta 240
tacgcagggt ggattggacc atattattgc aaatcgtttc cgaaccactc atatttcttt 300
ttttctctcc tttttttatc cggagaatta tggaaccact tcatttcaac ttcaaaacta 360
attttttgggt tcagtgatca aatacaaaaa aaaaaaaaaa gttatagata ttaa atagaa 420

```

aactattcca atcttaaaaa tacaaatgaa accataatTT taatttatac aaaactatTT 480
aattagctaa gggttgtctt aacgtttaga aaataaaaaa ttatgattgt ctgtttaaaa 540
ttacaatgaa tgaataaaaa aaatatgcaa tgaatgaaag aataaatttt gtacatccga 600
tagaatgaga aaatgaattt tgtacaaacc actcaagaat tcaaaacaat tgtcaaagtt 660
ttcttctcag ccgtgtgtcc tctctccta gccgccacat ctcacacact aatgctaacc 720
acgcgatgta accgtaagcg ctgagttttt gcatttcaga tttcacttcc accaaacaaa 780
actgccacg tcatcaatac gaatcattcc gtataaacgt ctagattctt tacagcctac 840
aatgttctct tctttggtcg gccattatTT aacgctttga acctaaatct agcccagcca 900
acgaagaaga cgaagcaaat ccaaaccaaa gttctccatt ttcgtagctt ctttaagctt 960
tttcagtatc atagagacac tttttttttt ttgattagaa 1000

```

<210> 3

<211> 1000

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter PT0535

<400> 3

```

ttagtgaat tatgacatta agtaaggTTt tcttagttag ctaatgtatg gctattcaat 60
tgttatgtta ggctatTTta gttagtatat gaatttaggc agtctatgca aatgatttcg 120
ttttcatttt ttcatatgta aacatcaaga tcaagtaacg ccattcgagt tgatattttt 180
tttttaaatt agtgtgtgta aattttggac cgcttatttg agtttgctaa tgaagttgca 240
tatatattac gttaaaccat aggcaacta atttgaaaca tccgattcga tttcctgtaa 300
tttttcttgg ttaattgacc aaaatcaaga tcttcagaaa taaaataaaa gacgaaagaa 360
agctgtcgca aagcagattg tgttaaaaaa aagtggattg ggctcaaacg caacttgtcc 420
agcccgtgac aattacccta tacgcaagta agagtaacgt atcactggca aaagttggta 480
ttagttacga tatctttgtc atggggggcat gcatgggcat ggcttaagag ttaagcctta 540
agaagagtc cactctgtg actctcatga tcaattgttg tttcttacgg gcaaatacat 600
ttaactttat tcttcattta ttcacctata ttcttttgga taataacttt tctctatata 660
aaataacaaa catcgtacgt ttcatttatt tacaacaagc gatgagaatt aaaaggagac 720
cttaattgat gatactcttc ttttctctcg gttacaacgg gattattaca gataatgata 780
atctatatgg atgctgacgt ggaaaaacaa aatttggtga aacacgtcaa ttaagcacga 840
cttttccatg gctagtggct aagatcgTTt catcacatgg ctataTcata taatacttgg 900

```

atgaattcaa aataaacgac tgagaaaatg tccacgtcac ggcgcaccgc tttggactta 960
agtctcctat aataaataca acaccaaaca ttgcattcca 1000

<210> 4
<211> 999
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(999)
<223> Ceres Promoter PT0585

<400> 4
tgaagtcatt taatatgagt ttgacattag gtaaacctaa tctatgagat tatagaatgt 60
agcaaaacta tcaatgtttc ttttccaaaa tttttgtggt tttttctttt tggttcatta 120
tgttttgtta tttgtgaatt attttaatat gaagtaatta tattgatttt atatgatata 180
catattatth tgaataaaaa tttaacactt atccattaaa atagcatggg cataatcaaa 240
atcgggacta ttacgatgaa aaagatagtt aaattgtatg ataaaataaa atgtgtaaga 300
ttaaaattht gggttttaga aaattactaa acaaaatata gacaaagtat gttgactatt 360
atthaaaatt taaatatcat caataagata tagthaaagt cattaagtgt atagcaaat 420
gaaaattcta agattaaaat tcgattaaaa ttttttttac taaattaaat atthaaaaat 480
agggattatc atthactatt tacaattcta atatcatggg taaaattga taactthttt 540
taaaccgcgc tatctaggtg ggcctaacct agthtactaa ttactatatg atthacttat 600
taccacttht acttcttctt ttttgggtcaa atthacttat tgttttttat aaagtcaa 660
tactctttgc attgtaaata atagtagtaa ctaaaatctt aaaacaaaat atthaacctt 720
tccattattt ggaatggtaa tgtcttcaac accattgacc aacgttaagg aatgtctttt 780
aataatthttg gaacctaat gctaatactg tataccacaa tcacttatga gtattgaagt 840
tgagatagag gaggtacaag gagaccttat ctgcagaaga caaaaagcca tttttagcaa 900
aactaaagaa agaaaaaaga ttgaaacaca aatatgcgcc actcgtagtc caccctatc 960
tctttggcaa aagccacttc actctthttt cctthttat 999

<210> 5
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter PT0613

<400> 5

```

ttaataactaa cattgtagaa agccacaaaa aagaaattga aatgtgagta gatgctgagt 60
cagagggtttg gtcaatacac aacagctaata tgagataata ttatacacgt cacgatgact 120
tggttttttct cctcccaact tggttaatttc tttatttctta aaattaaacc atcgcaaaaa 180
cagaagaaca cagctgtttt tctcgactcc caatttctat tttgctgcta aggacatttc 240
atttcattat ttcccaattc aggactcctt agattttcct aaatttgttt tcctaacttg 300
ctctctctca ttctaacatt ttctcatttt tttagattat ctgtgacttt ttagtagatt 360
attttatcag gttttacaaa catacattga cattctaata agggtctcta aaaattcagt 420
gtggaatgct gatatactaa aaaaagggtca tgcaaaatta tctacgattt atctaaaatt 480
agataatttg ccatatataa ctattaacta ataatcgatc ctttgatttt ttgttttagat 540
aaaacgaaac agctatatct tttttttttg ttatcggatt ttaatcgaat aaaagctgaa 600
aaataacagt tatactcttct tcttttttaa ctaatgaaac agttatatct taaacaaaca 660
acagaaacag taaaatatta atgcaaatac gcgtcaagag ataaatttta acaaactaat 720
aacaattgag ataagattag cgcaaaagaa actctaattt tagagcgtgt aaacacaaac 780
acgtcttgaa agtaaacgtg aattacacgc ttctaaaacg agcgtgagtt ttggttataa 840
cgaagatacg gtgaagtgtg acacctttct acgttaattt cagtttgagg acacaactca 900
agttatgttt gatatactaa gacttgcact gtctccaaat ctgcaggaag gactttttga 960
ttggatcaat ataaatacca tctccattct cgtctccttc 1000

```

<210> 6

<211> 351

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(351)

<223> Ceres Promoter PT0625

<400> 6

```

gatcatgac agtttcaact cgctgtgcc acgtgtcgag agatcggcac gtgcctgagc 60
tctcagccgc tcataaatac acttgtttag tagcaacagt atactatagt agtcctctcc 120
tggttggtt ttagcttgca tcgatggatg gatggatgga tcgcatgaga gggcttcgcy 180
aagggtacgga accttacaca acgcgtgtcc tttctacgtg gccatcgtgt aggcgtctcy 240
ccatgctacg tgtcccgag gatgtctcga tgccaaccct tataaatact gttccattcc 300
aatcccatcg ccacagccag tgcaaactcg atcgatcaag ataatcgagc a 351

```

<210> 7

<211> 1022
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(1022)
 <223> Ceres Promoter PT0633

<400> 7
 cccgatcggc cttaatctga gtcctaaaaa ctggtatact taacagttaa cgcatgattt 60
 gatggaggag ccatagatgc aattcaatca aactgaaatt tctgcaagaa tctcaaacac 120
 ggagatctca aagtttgaaa gaaaatttat ttcttcgact caaaacaaac ttacgaaatt 180
 taggtagaac ttatatacat tatattgtaa ttttttgtaa caaatgttt ttattattat 240
 tatagaattt tactggttaa attaaaaatg aatagaaaag gtgaattaag aggagagagg 300
 aggtaaacat tttcttctat ttttcatat tttcaggata aattattgta aaagtttaca 360
 agatttccat ttgactagtg taaatgagga atattctcta gtaagatcat tatttcatct 420
 acttctttta tcttctacca gtagaggaat aaacaatatt tagctccttt gtaaatacaa 480
 attaattttc gttcttgaca tcattcaatt ttaattttac gtataaaata aaagatcata 540
 cctattagaa cgattaagga gaaatacaat tcgaatgaga aggatgtgcc gtttggtata 600
 ataaacagcc acacgacgta aacgtaaaat gaccacatga tgggccaata gacatggacc 660
 gactactaat aatagtaagt tacatttttag gatggaataa atatcatacc gacatcagtt 720
 tgaaagaaaa gggaaaaaaa gaaaaataa ataaaagata tactaccgac atgagttcca 780
 aaaagcaaaa aaaaagatca agccgacaca gacacgcgta gagagcaaaa tgactttgac 840
 gtcacaccac gaaaacagac gtttcatacg tgtcccttta tctctctcag tctctctata 900
 aacttagtga gaccctcttc tgttttactc acaaatatgc aaactagaaa acaatcatca 960
 ggaataaagg gtttgattac ttctattgga aagaaaaaaa tctttggaaa aggcctgcag 1020
 gg 1022

<210> 8
 <211> 1000
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(1000)
 <223> Ceres Promoter PT0650

<400> 8
 cataacttaat tctaaaaaaa caacacttat agtttataag cagctcttat gataaaaatc 60
 tttctgagtt atagctctgt taaacttgta ttcaccccaa aaacggatgt ttcatttctt 120

atTTTTtact tggagtatTT tattgtaatt tgtaaaaaaa aatgtaaagt gggggatatc 180
atgaaaaaca acgtcacttt gtttggtcac aatatacatt tgataaaata atggtcgctcg 240
cgtgatttag ttgatttttg ttttatcaac cacgtgtttc acttgatgag tagttttatat 300
agttaacatg attcggccac ttcagatttg ggtttgccca catatgacat accgacatag 360
aaggTTaaat ccacgtggga aatgccaaata ttcaatgttt ggTTTTcaaa agagaatcat 420
ttcttttatat gatctcaaaa gtatggaatt gaaatgacta atgagcacat gcaattggtg 480
ctatctttaa aaccgaacgt ctttgaattt aatttgTTTT tcaccaaagg tacctaataga 540
aaccctttca ttaaaaaata aaggtaacaa acaaaatttt gtattggaaa aaacattttt 600
tggaatatat aatttggtaa tagaattatg agcaaaaaag aaaaagaaaa gaaagaataa 660
tgagcataat aaagccttta cagtattact aattgggccg agcagttttg ggctcttgat 720
catgtctagt aatctttaa acagcataaa gttaactgca atttagttgg ttcaggtgag 780
ctaccaaata caaaaatacg cagattaggt tcaccgtacc ggaacaaacc ggatttatca 840
aaatccttaa gttatacgaa atcacgcttt tccttcgatt tctccgctct tctccactct 900
tcttctctgt tctatcgag acatttttgt ttatatgcat acataataat aatacactct 960
tgtcaggatt tttgattctc tctttggttt tctcggaaaa 1000

<210> 9

<211> 998

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(998)

<223> Ceres Promoter PT0660

<400> 9

caagtcaagt tccaatatc taaggagaaa taatagtata ctaaacatac attagagagg 60
ttaaacttct ttttggtttt aagtgtgtat gcataggcta tttattctta agtataacta 120
ttaactgtag ctgattttat acaagaaata cataaaactt tatgcatgtg aggtagccat 180
gaatatacgt acatgttgca atcgattata catgttgtat ttggatttct ctatacatgt 240
tttaacttgt cattctctaa gtatatacat accattaata ctgtgggcat gagtttatga 300
taagactttt cttttggaga ccagttttgt tttcctttcc acctatattt gtctataggc 360
ttcacggtac actagtttac aagtgttttt atatgttcta aataaaattg agattttccg 420
gaacggtatg atctgtttgc aaataaggac gtatatataa cagtatcaaa tatatttggt 480
gttataaggc aataatatat tttctgagat attgcgtgtt acaaaaaaga aatatttggt 540

```

aagaaaaaaa aagatggctg aaaaagggga gtaggtgggg gcggtcggct tttgattagt 600
aataaaagaa accacacgag tgacctaccg attcgactca acgagtctac cgagctaaca 660
cagattcaac tcgctcgagc ttcgttttat gacaagttgg tttttttttt tttttttaat 720
tttttcatct tcttggggtt ggttgggtca ctcttcaggt caggtgtgta aaaaagaaag 780
aaagaaaaga gagattgttg tgttgtaacc cctttgacta aaatctaata aactttttta 840
acacaacaaa actccttcag atctgaaagg gttcttcttc tctcttagtc tcttcgtcct 900
tttattctcc gtcgtcggtt catgatctga ctctctggtc ttctcttctt ctcttcttc 960
ttctattttt tcttacttcg tcaactgttg gtctgaac 998

```

```

<210> 10
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter PT0665

```

```

<400> 10
aaaaaggatg ggtaatggga cctattttcc ccaacatccc acatgcacac ttccctctcc 60
attctctcac atttatttct ttcatcttaa tttatccatt ccgtgtgtaa catattcact 120
aataatctca tctcactaac tcattcattg attgtgatat gtttatctag aattagtgtt 180
ttaacactgt gtctacatat gatttccttt tcattgtatg tgaacatgtt aactcactaa 240
tcattttgta ttttcgagtt aacatgagtc tccacttcgg tagactaaag taaagatagg 300
tttgagtata ataaagttta aaatttgctt taaaatcaat atttataaat aagtttttat 360
cataagtgat ttttgtatgt tatattggac cttgtataaa cagactacag aagaaaatta 420
tttatgagaa cttgtaatgt tagagtggac ctctgtataaa ctaattatgt gggcttttac 480
cataaactat ttatgaaaat tattatggcc cacaccacta taactaaagc ccacatattt 540
agcagcccag tttcattgta agagacatgt tcgctctgga actagaattt tctgggtttt 600
gggtatttgt tttcttatgt gtagagaaat gatggtaacg attaaatgtt gtgtattaca 660
atttacaatg gtaagacgat taatatattt acacacaatt ttgttggtgc tgtaacacgt 720
tagtgtgtgt gatgatagaa tttcataaag ctttaactac gaggggcaaa atgttaattc 780
taaatagttg acagcagaaa aagatatgta tacataatat aaggattaaa acgtaaataa 840
taataaataa ggcgagttaa attaaaaccc tgttaaaacc ctagcttgaa acacatgtat 900
aaaaacactt gcgagcgcag cttcatcgcc atcgccattc tctctctcat caaaagcttt 960
tctccttgat tttcgcattc tttagagtct taacgcaaag 1000

```

<210> 11
<211> 999
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(999)
<223> Ceres Promoter PT0672

<400> 11
cagccgtaaa tcctccataa atttattttg caagttttgc tcattatata atgagcggaa 60
tttatgatat aatcgtttgt aataatgtta tgttttgatc aaaatttgaa attaaaagta 120
ggtgagaact tgttatacag tgtagataag gtggatcttg aatataaaaa taaaatttat 180
aagatgtatt taaagcagaa aagcataaaa ctttagataa aataatgtaa aaatgtgtta 240
gcatcaatgt tgggatattg gccgaccga acttaatcaa tgcggaagc cattacttct 300
ctccaaaag acctttttcc ttcggagaac taggaacttc ctactacct ttcgcttaac 360
gtgaaagcca taaatttcat atattcataa aaatcagaaa atctaaaact gtttagtata 420
acctgttttt ggtatagact attggttttg tgttacttcc taaactatat gatttcgtac 480
ttcattggat cttatagaga tgaatattcg taaaaagata agttatctgg tgaaacgtta 540
cttcagtcac gttgggtcta gatttacata ctactatgaa acattttaag ataataatta 600
tcctagccaa ctatatgttc tatattatgg gccagaaga tatagaacta aaagttcaga 660
atttaacgat ataaattact agtatattct aatacttgaa tgattactgt tttagttggt 720
tagaataaat agtagcgtgt tggttaagat accatctatc cacatctata tttgtgtggg 780
ttacataaaa tgtacataat attatataca tatatatgta ttttttgat aaagccatat 840
attactcctt gacctctgcc ccatttccct ttactataa ataggaatac tcatgaccc 900
ctaattcagc aatcaacacc aacgaacaca acctttcca aagccaataa taaaagaaca 960
aaagctttta gtttcatcaa agacgaagct gccttagaa 999

<210> 12
<211> 1000
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter PT0676

<400> 12
aagatagtac agtttcagtg ttttgagaaa aaaagctgaa ctaaaactaa aatgtttaag 60

gacacaatat ttagtttcaa ttagataatt caacagtttg aacaatTTTT tttttttttt 120
tttgaagtca tttatttata caatgtttta aaacgcatta agcatttagg cagccgacaa 180
acgcctattg tctaactgta aataggcgct tccacttagg ttcattattgc atatttacta 240
tatgtgtata gtgacaaaaa ccaatatttc tcttattttg gatgaaggta tagtagttgt 300
taaagtgtca atataattaa gcattaatga caaataaaat aaaattaatt tagttgataa 360
aaagataatc ttataaaaag atcgatgaat agatataatg gtttactgaa ttctatagct 420
cttaccttgc acgactatgt cccaaggaga ggaagtacct taactataat tctgaacata 480
atTTTgtcta tcttggtgag tattatatga cctaaaccct ttaataagaa aaagtataat 540
actggcgtaa cgtaataaat taacacaatc ataagttgtt gacaagcaaa aaaacataca 600
taatttgttt aatgagatat attagttata gttcttatgt caaagtacaa ttatgcctac 660
caaaattaat taatgatttc aacaggaagt ctgagatgat gggccgacgt gtagttacgt 720
ttcttgaatt gtgagagatg gtatttatta tactgaagaa aacattattt actaaataaa 780
ttttcatttc acatcttctg taatcaatgc gggtagatga agaagttgtt aatacgatgg 840
ccaaccatat ggatctcttt tttggcgttt ctatatatag taacctcgac tccaaaggca 900
ttacgtgact caataaaatc aagtcttttg tttcctttta tccaaaaaaa aaaaaaagtc 960
ttgtgtttct cttaggtttg ttgagaatca tttcatttca 1000

<210> 13

<211> 998

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(998)

<223> Ceres Promoter PT0678

<400> 13

aattaaatga aaccgcccct aaattaggag ggatttgggt aagtggtaac acattcactg 60
gaaacatgtg aagaaaggag gatgtcaagt agctgaaaac tcagtatagt aaccaacggc 120
ttctcaccaa cttttcatta ataatttgggt catccctata tttttattca acattttgtt 180
tttcaatagc ttagagcacc ttaatacctt tcagtgtttt tttataaaaa aaacaaaaat 240
tgggattaat catcaatccc caaatgtaac gtttacttag attatgttca tttttctata 300
cacacaaatc atattctttt gttttaatct tcgaaaaacg agaggacatt aaatacccct 360
aaaaaaggag gggacattac taccaacgta cattaacatg tttgatagca aacgatttat 420
tttgttcgtt ttgaaaaggg gaaagtaatg tgtaaattat gtaaagatta ataaactttt 480
atgggtatagt aacatttttcg aataataaga gagggaaaac actcgccatt gtcggcaatt 540

tagaaccaat attagaaggg tttttttaga gaaaaaggac ttaaaagttt agagacctta 600
 acaacaactt atttagaaat agacatgctt aagttgacaa cagcgagttt attttctata 660
 tcgaagaaaa atacgaactt tttcttaatt agatttcgaa tgcattgcact atcgagaatc 720
 gaccgtcaca agaaaaaact aatatacata ctgtacatat ctatattcaa tattggtggg 780
 gatgggttta atgtgtatatt ataattcatg gataaattca cacaataagg tccatgaaac 840
 tagaagggtac caaaaataag cattaatgac tctttgccac ttatatatat gattctctca 900
 tagtaccatt ttattctccc aaacctatct tcttcttctt ctcttgctct tctcgctctc 960
 tctcttctac attgtttctt gaggtcaatc tattaata 998

<210> 14

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter PT0683

<400> 14

gattgaatga tgagtgtgca cccttgtatt actaataaaa aatttagcaa cagttataag 60
 ctaacgtcat ccatgagtca ttcattagat tcaactatttg cgttctcaaa aatcgaattg 120
 ttaaaatttg agaagctcta atatacgagt caatgagatg tggcaaaagc atgtccttga 180
 ccataaaatt tcgaggggtc aactcattag ataaggacaa gaatcaacca attgaaggcg 240
 tcttctataa caagtttctt tattactaat attaaagtcc aatgggggtga gggggagaag 300
 aacttaaata aaaggaaata attggtaagt gaataaaatc taaatacgat actagatgat 360
 tgatttgtgc tagtgcatgg tattagatca gatatgtgtt actattcgaa ttcaaattgg 420
 catattccat gttgttgata agaaaattgt agaagtgtaa aagctgagtt actatattca 480
 aactagtggg ttacataaag tgagacaaca actgtttcac aaaaatgact ataaaatagt 540
 aagtagtatt aggtcaattg attttaaaat tttaatcaaa ttcaaatttg tgatataatc 600
 aaatttgttt atagaaaatg ttaagaaatc aattttggca gaactaattc agtgagaaac 660
 aatcattttac aaaaacaatt ttaacattat ttaacagtaa gatttgacat ttaacccgtt 720
 cgtgtgaacc catcatatct aacatggctc taccatgac gcctccatgc catggacaat 780
 ttgacagat cagaagttct gaacgtggac gaggttaagaa caccatgatg atacgattgg 840
 agttagttat gtcgccaccg acatcactgc caatctcatt aataaaagtg gtactaaatc 900
 tctaattctt attaactata aatataacaa agaaccaaaa gaaagtttct tatctctctt 960

atcttttcata atttccaaga aacacaaacc ttttctacta

1000

<210> 15

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter PT0688

<400> 15

acgttcagag gcatcgcttt tgtacaaatt gaagcgggtt tgttcaatat ttaaaataac 60
acaggaaaca ttcaaagtga ttattgatgt tgcttaggtt tgtgaaatga tatgaaccat 120
atcgtatata ttactagatt tttcttatat gttttaaggg tagtggggct gacctatcat 180
tctgtttggc attaccaatc agactatcag agtattcacc attcaggatt ccataactag 240
aaaaagaagg ggtttacatt ttctcatact gtataatfff ctactatcag agattttatc 300
gattacatta atctcatagt gattattctg atttataaaa aagttgacaa aataattaaa 360
accagtatff tataacaaga ttgtctctct cccatggcca ttattttgac ctctgactta 420
tttaaattctt aattaacagc ataatactgt attaagcgta tttaaatgaa acaaaataaa 480
agaaaaaaag aacaaaacga aagagtggac cacatgcgtg tcaagaaagg ccggtcgtta 540
ccgttaaggt gtgtcgaact gtgattgggc cacgttaacg gcgtatccaa aagaaagaaa 600
gggcacgtgt atagatctag gaaaaagaa agaatggacg gtttagattg tatctaggta 660
ccaggaaatg gaacgtcaca ccaaacggta cgtgtcggat cctgcccgtt gatgctgacg 720
gtcagcaact tccccttatt catgcccccc tgcccgttaa ttacgtgtaa cccttccatg 780
cgaaaatcaa accctttfff ttttttgcgt tcttcttcaa cttttctfff taaatcaaac 840
cttttctfff taaaatcaca ttgcatttcc taacgctcaa caaatctct ctctactaat 900
atctctctct ctctctctct attggtgaag aagactcata atcggagatt gtttgttttt 960
ggtttgctct gtaaattgga gaagttttgt tagagatcaa 1000

<210> 16

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter PT0695

<400> 16

aacattttct ttaacttact cttaaatttt aatagtaagt tgatgcatgt tatgttgatc 60

```

cgtcttgatc acaaattttg ttttatggac gaattctttg acagtaaagtg gctatagtga 120
ctcagcttgg agcatcccgga tatgaaaaca aagtgcagta ttgtgtcgtg gtcataccta 180
acgcactttc ctagaactat cgcgcgtggt tgacctatgc aacacaccag atgtcatgaa 240
cgtatactta aatagaaaca atgatataga caattggcta tattctgtca tggaacgcaa 300
accggataac atgtctatta gattcatcgg acttgatcat ggttatgtct taatagacga 360
attcttttgtt aacgattgggt taaaacggct cacgtagag catcctacta tgacttcaaa 420
attgataaat attacatgga aatcacttta attttagtta gaaggtagtt aatttagata 480
ttcttattta ataaattaaa aaatagaaga aaaaaagatg agaagagttt ttgtttataa 540
aataagaaat atcttttatt gtaattttta aattaaacaa atttaattta tattaataat 600
atctttgttt tattgttaag gcaataatta ttttttttgtt gggaattgtt aaaacaataa 660
ttagtatact gttaagtgggt cttttaataa taagataacg tgatttaaaa aagaacgaga 720
caggctaata tagtagagag gaaaaaatac aatttaggcc caataaagcc caatatagag 780
ttgtgtctca acacaggtct tcgccagatt tcctatgacg ccgtgtgtca atcatgacgc 840
caagtgtcat tcaagaccgt cacgtggcgt tgtttctaca cataggcgat ccatacaaat 900
cagtaacaaa cacgaaaaga gcattcatat gtacgaaagt agaaaagaag agactctttg 960
tgataaaaact aagtaagaaa tagcataaaa gtaaaaggga 1000

```

<210> 17

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter PT0708

<400> 17

```

gtttccaaaa ctagtattct ttatttgctc tattcattat atttttatat ttgtaacgtc 60
ccgaccgtct ttattaggtt tcgacaatca cttctcggaa ggtcgtccat cctgaaatta 120
ctctatccta aacatgttta actataaaat tctctcgaaa cttttgtaac gtatataacc 180
acataaatcc tcttaaactt atttgcatat accattatat ttctgaaatc gatatgttac 240
aatattatct aatatttaga ttacttttac tgaatcgaat taaatatcaa atcgaaacaa 300
atctaatact ccaaaaataa ttttggtata aacatttctt gcctagttct acctcatata 360
catttttagtt aaagaaagaa atcacaacaa ttcccataat tcaataatta aatccacaaa 420
atcttggagt aagtaagaga aataaaaaga tagtatctta acataaacia ttcaaagatg 480

```

```

ctctctcaca caattcacac acacttaca aacaaaagac agaaacaatg ttttcattca 540
aatcaaaaga agttataaca ctagtacaaa aaaagctcaa attctaatag taactctttt 600
tattttcccaa ttacccaaag attctctctc acttcacaaa actagctttg agagtcgtgt 660
tccacaaaat ccattaaagc tgaaacgggt ttgctcacca ttcaaacaaa tacaaaattg 720
caaaacccca aattataaca aaataatata aaaattaaac cgctaaaaag agtgaaccaa 780
caaaaatcgc cgaatgtgtg tgtaatgaga aaaccgaccc atcatcccaa tcatctcttc 840
ccgtgtcact ctcttctctc cccacgtttc ttctctcttc cctttatggg ttttaacttc 900
tccttcttct tcttcttcaa tcttcagttt tcaaattcaa caacaattca ctttttgatt 960
tcttcatcat ctctctctct ctcgcttctc tctcaaatcg 1000

```

```

<210> 18
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter PT0710

```

```

<400> 18
tagtgcgcggt ggggagaggg aatggtgaaa ccttagtggt taagttatga ggaaaatgat 60
aaaaggataa aacaatcaaa tgcagcttga aacggccata acataaagta ccttatgggtg 120
gtgcgaatat ttttgtgttt ctttcactct tttattgctg aaagctacga cacttgtctt 180
aatatatattgt ttccgcaagt cacatgatct actttttatt taacgtctag aaacgccgag 240
atatatgatg attagtatat cacgtctatg caaattgtta gttcgtgttt ggccaaaaga 300
tatcgagaca tgtctgaaga accgagtctg gttttgagat atttcttcaa gcattactat 360
acaatagaaa aaggagacac gcgaatatga taatagcaaa aggcataaaa aggcgaaaat 420
taaagaaaaa cgtaaagtga tttggcctca atcaacggga acgtatctta attttagagg 480
ttcttctttt acttttgaga cgagagaggt tgcgctcttg cgagctgctt tgggtgacta 540
aacattatca tattgaaaac caaaatacaa cggaggaata tttgtcacag tttcactttc 600
acattgtttc cttaacgttt aatcaacctt gttcaaaatt tctatagttg taatcatcat 660
tgttttacaaa attttcgttc aaagatgatt ttaaataaaa ttgtgaaaga aaaccttttc 720
tgaaataagg attggatgat agtggttaaaa gaaaaatatg aactgaggca aaaagaggag 780
tggtccccgg aagattgtga aatgtgtcat ctaaaccagc cagacgtagt cacgtgttct 840
ctctagcttt atgaacttcc ttagccagca ccatcattgt gattgtagta tatatgtaac 900
cctaccttca tctctcccat tttccattct ccatatagac tcctttacaa tatacaaac 960

```

ctatccaaaa gcgaagaagc caagcaaaca tattataaaa

1000

<210> 19
<211> 1002
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1002)
<223> Ceres Promoter PT0723

<400> 19
gtcatatcctt atcaacacgt caacgatcaa aaccttttagc ctattaaatt caacggctta 60
gatcaaaacg aaactaggtg ggtcccaactt ttaatatcgt ggctgcataa ctttcctctg 120
ataactgaag ccgttggtggc ctttctcaga atctgggtgct taaacactct ggtgagttct 180
agtacttctg ctatgatcga tctcattacc atttcttaaa tttctctccc taaatattcc 240
gagttcttga tttttgataa cttcagggtt tctctttttg ataaatctgg tctttccatt 300
tttttttttt tgtgggttaat ttagtttctt atgttcttcg attgtattat gcatgatctg 360
tgtttggaatt ctgttagatt atgttattgg tgaatatgta tgtgtttttg catgtctggc 420
tttggcttta aaaatgttca aatctgatga tttgattgaa gcttttttag tgttggtttg 480
attcttctca aaactactgt taatttacta tcatgttttc caactttgat tcatgatgac 540
acttttgttc tgctttgtta taaaattttg gttgggtttga ttttgtaatt atagtgtaat 600
tttgttagga atgaacatgt ttttaacttc tgttttrcga tttgtcacac attcgaatta 660
ttaatcgata atttaactga aaattcatgg ttctagatct tgttgtcatc agattatttg 720
tttcgataat tcatcaaata tgtagtcctt ttgctgattt gcgactgttt ctttttttct 780
caaaattggt ttttggttaag tttatctaac agttatcggt gtcaaaagtc tctttcattt 840
tgcaaaatct tctttttttt tttggttgta actttgtttt ttaagctaca ctttagtct 900
gtaaaatagc atcgaggaac agttgtctta gtagacttgc atgttcttgt aacttctatt 960
tgtttcagtt tgttgatgac tgctttgatt ttgtaggtca aa 1002

<210> 20
<211> 1001
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1001)
<223> Ceres Promoter PT0740

<400> 20

```

tgtggccact aaagatttac ccttaaccgg gcccatataa gccacgtca agtggcgctt 60
atacgtctctc cgtaagagag ccaacatttg gtatgtaatg ttgcaaatta ttcttcaaga 120
caataaattc aaatataatt caatattgtc caaatatagt gatgtacttc agttgtgcac 180
atagaaaactc cactaaacca acttttagat agatgcattc acaaattttc aacaatgtcg 240
cgaaagtcta atccatcacc agattctaac attttaatta ttatatatta ctatacatatc 300
tctaatacagc atgagtcaaa cgtgtacaat agcccaagca tataataaga ccaaagtcaa 360
actcaataaa atgtctccaa actcaaaact tgaaaaagac ctaattatta catggtagat 420
atgactttgt cgacaagtaa accaactaat cctcgaagct accttctctt ccagttatt 480
atgtgtgatc gatttataaa tctcttcttc taataacacc tatatttttc ttatgatgtg 540
aataaatata aaacttttaa ctttaaaaca ttttatccg aaatattgca cttagatttc 600
aaatagataa ataatagtagc tatctaactg atattgaaaa gacctaacac ggaaaacagt 660
tttataaaaa atcccaaagtg tgggtaatta tcttgatttc ttgggggaaa cagaaaatgg 720
attaagatta atcggagtcg tgtcaagcag ctcgtaata actgtagcaa gttgactgag 780
taagcatcaa cgtgtcatct ccgtaaagcc cattatttct agtctcgccg cgtcttctct 840
tccacgtagc acttcacttt ttctctctt ttgtttctt tggaacacaa acgtttctat 900
ttataggaat aattacgtcg tccgtatctg tgtcggaaca tagatccaaa ttaaagcgga 960
cttacttaat tacatatcgt tcgtgttttt ttcttcaaaa a 1001

```

<210> 21

<211> 1024

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(1024)

<223> Ceres Promoter PT0743

<400> 21

```

tcgattggcc cgatcggccc caaatcaag ctgagccgct tcaaacttca gcttttgaaa 60
tcacccccaa actcatgtcc tcttatcatt ataactaaag gatctttcat tttatttaac 120
tcatcgtctt gcactacca acccaaagg tccaactata cccgaagctt tctaaaggtc 180
caaagacttt ttttttcgag ccagactatt caagccaaga aaagccaaac ccacaagcc 240
agtacttttc aattccatat tataaactta tctgtcttgt tttagtccca ctaaaaacaa 300
cagaatttaa tttagggtga gctaaaacc ttgacaaaag tgtatagtcg tcgattcagt 360
agcacactca tcaactcatca gatttgatag ttgacctaaa gtatgactac tccatttcaa 420
ctaacaaatg aaaataaaag agacctagg gttagaggat tgaaactata ctctcaagtc 480

```

```

ttttatcact aggctactac cagctagtta acttgatgga ttttaagcaag aaaacgtaga 540
at ttatattc gagcagattg ttttagctaaa aaagcttggg tttgaaattg ccttttctcc 600
catataagca cgtcggttcc taaataactc tttctagcgg agagtgtctt tccaataatt 660
taataaaaat ggtgtttgta tatcaaaaaa aaaagaaaaa agaaactgat cgagatagaa 720
cgtttgcagt ttataaaca atttaaaaaa caaaaaaat taaactcaat gtatttttta 780
ttaattcaca aacaataata aatcatagga tcgaatattt acacggtatc aaaacctact 840
cgccgctact atataaaaat tgaagtcaaa tatcaaccgc aattattaaa ccagcaagac 900
aataattcat aaacttaata taaacataaa taaattaatg ttacacaacg atatatggtg 960
agggttatta ctatcttctt cctctcaaaa cacatctcct aaccttaagc ttttagacggc 1020
ctgc 1024

```

```

<210> 22
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter PT0758

```

```

<400> 22
agctagccac atcagtgacc aaaaaagata attaacaaac caaataaaaat aacaaatttt 60
gatcatttgg aataaaattt ataaaaggaa cgaaagcgcc ttctcacggg tcccatccat 120
tgaaatatat tctctctttt tgctctatat aataataacg cgtactaatt tgtagtatat 180
attattacaa agtcgatatt tgattgtttt gtgaacggtg atatattaat tttcttggat 240
gatgacaaaa aaagtcatag aaagtaacgt gtgaacatag cattaacaaa atacaaacat 300
aatatataac caaatatatg aaaataggat aaaatctcat tgaatagatc ttcttctatt 360
caaatatata aatatttggt tgtctataaa attaacagag cattcacatt atctaaaata 420
atagtaaaat caaaataaaa ctaaataaaa ataactctgg ttttataacg attgatttta 480
aatattagtt tttgttgtaa agagatcatt atatatgtct gtaatatttt tatactgagt 540
tacatgatat ttagttatta tagcgtaatt aactaagata agaaattaac taaagtgata 600
ttctgattat tattattttt gttaggacac gtacgtggaa aaactaaaca ctataggtta 660
caaacggta taataaactc accattactg gaaaatgttt gcatttgact caataagtaa 720
cttattataa gttactgata taatgcatag ttttgaaatt cttaaataaa ttattttggt 780
ttcgcagtaa aatatgaaag gagagaaatt tattattgtc acttatatat atatacatcg 840

```

taatcatttt ttcgtgaata attctctctc ccattccatt atttctcagt atctctcttt 900
ctttccotta ctttattgtt gcttttaaac cttcaatttg ctcataaacc aaatatataa 960
tatcaaaaca aacaaacaaa aaatcagaat, tcccctaata 1000

<210> 23
<211> 921
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(921)
<223> Ceres Promoter PT0829

<400> 23
aaagttttga attattggga atcaatttcg aagttttgta attctttggg ggctaataagg 60
atattttatt ttcttgggtt cgtctattgt tgtttttcta tttatgggtg ggcttttaga 120
actctggaca ggcccatgtc atatgttttc ccttctcctt atatttttca tttttcattt 180
tgttaaatta atgcataata tccaaaaaca atttaaattt ttgaaggaa cctttagtta 240
cggctccgaa gctttcacaa gtgagaatgt gagatcaaag aaggcaaag gaggatttta 300
aaagttaaaa tcatctttta tctgcaaaag ttgacaattt ttttgtatca aatctaaatc 360
atcaaactct cttaaaactac aagagcataa caacctctat gtaatccatg aaataatctg 420
cttgaaggac ataacataaa tcattatggc tagagtgcact aacttcaatc aaatcctctt 480
aactctagct cccttacaat ggtatcgtaa aacattatgc attagggatt gttgtcctag 540
gaaaataaaa taaaaatccc cacagaccaa ctaccatttt aacttaaaaa taagcttcgt 600
ccgcgacgaa ttgttttcca tcctaaaaat agaatgggtg aatctgctaa tggtttagtt 660
ccattaactt gcaagttcta ttgaaagcct aaatgtcaat aaagatatta aaattcggag 720
tcaaaagaca aatgaatcaa aagcaacaag acaagtcagc tccattcttc actaccatc 780
ttttacaata aatcatctct cttttcacaa atttcaaact actctcattg ccctttagct 840
ttgttataga gccaacacta cagagagact cacacacttg tttcaataat taaatctgaa 900
tttggtctct cttataaact a 921

<210> 24
<211> 763
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(763)
<223> Ceres Promoter PT0837

<400> 24
aactacaagg gagacataat. atcaccatct ggttcctggt atcatctgaa gatttcttgt 60
tttaccttcc agtgataaaa tgatccttat aatacatata gatataattaa attgctgtat 120
tttaagatta tagatatata aggtacatga gagtggttat ttaaaaaaat tcacttggaa 180
ttcatgtttt gtgatacgtt agattggaat ccatttggga aaagaagaat catctgttct. 240
tatgtctcaa attttgactt cattcacttt tcttcttgtc ttttaagaaa gcttccacaa 300
tctaactggt cgatgtgaaa actgagattc gagtaagaaa atgtgaactg tgttatactg 360
ttttttaatt agataattta gattgcactc agataaatta ataacattcc tcgaatactt 420
ttatgtgatt ggatatatta ggtatatctg ccaaccaacc aataaactgc tatgtttaaa 480
caaattaaat aaattagtat atgtttactc aagaataaag aagatagaaa agaaaattct 540
atatgagcta aatttgctgg aggaggcatc ggacgtgggt accagacctt tccaagcaca 600
cgagtagtgc ttagccatgt catgctaaca tacaccattt ggttcataca aaatccaaat 660
caaaatctat ttttaaaatc ttttgcacac gtctttgaaa aacacctctc atactatagc 720
tacggaagct tcaatttcaa ggtttgtcta aaagctaacg att 763

<210> 25
<211> 751
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(751)
<223> Ceres Promoter PT0838

<400> 25
atactggtat gcttaagggt gaagccaaga tctctgtctt acccaagtaa ccactttcta 60
ttagaaggga tcaacactaa gaatatggag atttaagcct aagggctaag gcggttctca 120
acaatacatg atgtgaatac aatcacagac gatttactga ggtttgttga taagatcttg 180
atcagtctct gcatcatctg ttcaacaatc tcaatctttg actgtttgct ttcgagacca 240
taaacagagg aatcccttat tccctgttat aggagcaata caccaagtat tatttccatg 300
gotgaaattc tcttatggaa acctaattgt tccattgaag ctgtaaaatc gaatctggtg 360
aatattctcg agcaaagccg catgctaatt atgtcaattc agaagagttt gattaggaga 420
ctogaagcga gtttgatgat ctttcttgat gttcaactcc gattgtaagg gtataattga 480
cttttcatgt attacggctc caccacctga cactaaggca ctctttgtcc atctcgttgg 540
tatcatcgga ttcggatggt aaaaataaaa agagcagagg aaacttgta ctcatgcaag 600
cttctcaggt gccacgtcac tccattacgt gtcattctca cacaccatct cgctcaaaac 660

cgatctcatt tttcaaacct taaaggcaga agcaactgat taagttaaca ctcttgagaa 720
gctctcgatt aagcttgaac ttggaggatc a 751

<210> 26
<211> 669
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(669)
<223> Ceres Promoter PT0848

<400> 26
tctcttttaa tcagttaact aaccgtttat atatttacga taaggtttga agagattatt 60
gataaaataa tacatttcat aatcccgcggt tcaaccgttt aaagtaacat ttaagttgac 120
tatatctaata tttttttcca ttaaataatgg agctggtaaa ctttatcaac ttctaaaaag 180
tgtaacaaca aaaattaggt caatcacaat tctgtttttt ttattatttt ggattgactt 240
ccaattgcaa atagtcttag tgatcaccat tatcatacat atatacatca agtaggtttc 300
atcatgatat accacaaagt atttgacaag ccatatgggt ttggatcaaa aagtcgggtcc 360
aaaattaatg ttttatgtgc aagaaccgac ccattgtaca cacgtgttaa catcttcaag 420
actttcatct ctatttttct tttggtcatt aagataccca ttgatccgaa tctgttacat 480
tcccacctac ttttttaatt tttactatcc actccaaatt aaacacaacc gatgatttta 540
ataattggaa gcttttaaaa atatttcaaa acaagcctct ttgtgtttgt ctatatatat 600
acacgtaata agaaggtgaa tgaatctcac agcttacttg ttctaaggct tccaataacg 660
aaaacagta 669

<210> 27
<211> 702
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(702)
<223> Ceres Promoter PT0863

<400> 27
cgggaaacga caatctgatc tctagtccag tcgattggcc cgatcggccg attataaact 60
tacatgagac aagtataaat aattattata aacttattaa gtttaagatc aaggcttttg 120
tgcaatgtat caatgaatgt tagatgtgat atgatgaaag caatgtttta aacacatata 180
tagtcattga tcggaatgtg tgttattaga aatgcatgcc taagccgata gggttatcta 240
tgtttggctc tggacattat agccaaattt cgaatctaata tcttccaata tatatttttt 300

tttttttgct tagggccact actagtattg cttatcaatt ttaagagctc atgaaaatgc 360
aacaatatag tagttgcaaa tccttgtttc aagagaaatc aaagggccac ttgtgaattg 420
aataataata atatttgcaa ataacctttc actaaaccat accaacaaaa ccacacagat 480
ttggcaaaga cataaccttt gggagacgtg aaaaggctca aaatttgaca attgtcctta 540
caaattcgct cattagtgc aattgtgagat ttgtttgcat ccaaattcaa ttcataactc 600
acactcgtct caaattcgaa aaggcctgca gggccagtgc actgggatcc aacaatgtcc 660
tcögactcgt ccaagatcaa gaggaagcgg aaccgcaccg cg 702

<210> 28
<211> 435
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(435)
<223> Ceres Promoter PT0879

<400> 28
ttctaggaag actggtcaag ctaagctggt tctgtttttt gtttttgtac ttactttttt 60
gtttgctagt ggggaactggg tttattgggc cttgaagttg ataaaagatg aataaaagac 120
atatcgccta aagcccatat gagaagcaga agacaaaaac ctccaacttt gggcataaat 180
tttgattata gttaaaagtc cagacccaat ttggcacctg gcttagttac gattctaagg 240
catgacacct gcctaatatg tttattacag aaaataaaga gaatcagcta ggtgtccctt 300
attgaacaca ttaacaaact ccaacgacac tacgtgtctt cgtgactctt actatatcca 360
aaaacctata gctaaagctg aattttccat gattagtata gtcccaacca aaaaaatact 420
gaagaaggca taagc 435

<210> 29
<211> 397
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(397)
<223> Ceres Promoter PT0886

<400> 29
agtgtatttg aaaacgacat tgaagaatta atatattttt ttttaatttt agttttttat 60
agtacaaata ttaaaacaaa caatcctacc atatcataac atttgtaa ataacattttta 120
gttttggttt gagttttaat taattttcta tgacaaaaaa atgaagtcaa tagactaagt 180

```

gaatcatata gtataaataa acacaattta aatagtttca aataaattta gaaagaataa 240
aaciaataga aatcagaagg tgtctgtttc ctctctgcaa catacgatca aagagaaaca 300
acttgaccct ttacattgct caagagctca tctcttcct ctacaaaaat ggccgcacgt 360
ctccaacctt ctccaactc cttcttcgc catcatc 397

```

```

<210> 30
<211> 1024
<212> DNA
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0007

```

```

<400> 30
agcagaacaa ctatatatat tgtgtcacat aaatctgaga tcatttataa ccaccaaaga 60
acctatacac agtaaatgac aaatgtatct ccctctatct ctattgccca tatgtagatg 120
ctaaagtaag atttctcttt tttttaatgt actttttttt gtataaagta tattccataa 180
gaaaaaggaa aagcttggtt atggatcaat tgaccccaaa aaaagttttt agatcaaagc 240
ccaatataaa aaaaaaacac agtagtgaca caaaggaact taaataaacc atgaattgat 300
ctataaacag tagagatcga taaggcgaac attttccatg tgaagtgtct tctttcatct 360
ataatatttt tgacatccaa taatttcctc tataatatca ttcacataat tgatagaaac 420
attatgttag aattgtccac atcatttgag ctgtaatata ttctgtttta acaaattata 480
tggttagttgc ttaatcttat gtccatcttc ttctatgcat cgttttcgcg cctagttgtc 540
cagtccattt caactacctt cctctaattc ttatcttaaa acaacatttt ttaatttaag 600
tattatgctc aaagactaac tagatagaaa accgttatta aacattaaac gaattaaaag 660
tcttacatgg aaaatgtagg tttataaacc acgagttatg attgacaata aaaaaaatgc 720
aatcatcaa tcaaaagaga cttgagtgcg actctatatc aaccattgca attaaaatta 780
tctatcacia aaattttaga cagattaagt taatttagtc taaattcact aattttattt 840
ctataattag taattaacta tattttattt tttacacatt ttctgataat ttagaaattt 900
gcatgaataa caaatataag attttggaat ttagtagcaa atttaattaa taattatttt 960
tgccataaat aaccaaacta taaaacctcc acatacacca gtcacaaat ttacagagac 1020
aaca 1024

```

```

<210> 31
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

```

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter YP0008

<400> 31
ctcgagagat gaagtotttag taatgtttga acaaacaata atcacgtttt ccatcaaatt 60
cgagcattta aagtttatat tactacatgc cccaagatga taccgtccat ctcatccgaa 120
aatattttctg aaattgcgct aagacaacaa tgtttgctca aattcgatca tttaaagttt 180
acaaatctct catcaatctt acaaacttct cacactaaac agaggtacat attttcttat 240
aaagacaaaa ggttcgaaca gctggcttct caactcgagt tgtttgtcag ggcctctctt 300
cactaactac aagttggtac ttcaaataatt ggtggctagc ttcacgtgat attgtctaca 360
aattaaaccc atgaaaaagc tgcattaatt gttccaagtg aaccctgagg agtgtcaata 420
gtctttgctt tagtgtgatc attaaaccaa atctctaaat tcctaatttg tactaacatt 480
tggaacgtat ttcctactct tctccctgct ccaactccca aaaataagat tagttagatt 540
tctataacta atatacatgt atactcccaa aaacagtaaa accatattaa taaagctaatt 600
tttgcataga tttatttcgg taaaccggcg gttcaagttg gggaaaaaaaa agacaaacgg 660
tctaaagtca tccaaagaca aaaaaccaa gacaagttga gagagacgag accaatcaca 720
acattgcttc gtagattgcg tgacatcatc cttgacggct actttcattt gtgtcttatt 780
tggaataaac gcacgtgttt aattcacgaa ccttcatagc aataagaaat ttccattact 840
ttcatatttt caactttttt tattacccat tacatgctta aaatattaat tcacaagtct 900
ttgtcaaaat tcaatatatt ccagggtcat gaaccctttt tatctcaatc tactctataa 960
tatctcccta taaattacaa caaacctct ttatttttca 1000

<210> 32
<211> 999
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(999)
<223> Ceres Promoter YP0019

<400> 32
gatataagta gaatcatttt ttgccgccgt ttctcgctaa cacaccgaaa actgaatcaa 60
atctcctagc tcttctacgc aaaatcgagt gcatcgacaa tggcggaacg tgggtgtcgaa 120
cgtgggtggag atcgcggcga tttcggacgt ggattcgggtg gtcgcggcgg tggaagaggt 180
ggtccgagag gtcgtgggtc ccgtgcaggt cgtgctccag aggaggagaa atgggtgcca 240

gtgactaagc ttggtcgtct cgtaaaggaa ggtaagatca caaagattga gcagatctac 300
 ctccattctc tcccagtcaa ggagtaccag atcatagatt tactcgtcgg tccttcattg 360
 aaagaogaag tgatgaaaat catgccggtt caaaaacaaa ccagagccgg tcagagaacg 420
 agattcaagg ccttcacgtc cgtcggagat agtaacggtc acgtcggatt aggagtcaaa 480
 tgctccaagg aagttgcgac ggcgatcaga ggcgcgatca ttctcgcgaa attgtctgtg 540
 gttccgatac gaagagggtta ttggggtaac aagattggaa aaccacatac ggttccgtgt 600
 aaggtaaccg ggaaatgtgg atctgttact gtacgtatgg ttccagctcc gagaggttct 660
 ggtattgtgg cggctagagt tcctaagaag gttcttcaat tcgctggaat tgatgatgtc 720
 tttacttctt ctagaggatc caccaaaact cttggaaact tcgtcaagggt atgtactttc 780
 acaatggctg ttttggtttg atgaactctg aattaggcag tgaaaaagta atcattacca 840
 gttaagtga tttatattga agattaggat ttagctgatt gtattggttt gagcatgtga 900
 gtttgtgttt aagattgctt gaattgaaat gctttagggt gtttgattac gctaaattct 960
 gactaatgta attcaaattg ttgttggttt tttttggtc 999

<210> 33

<211> 1024

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1024)

<223> Ceres Promoter YP0028

<400> 33

gtcagtgaag tcgattggta gtacttgaaa cacttggttg gtttcatgta tttggcctat 60
 atataaacia acatcgtaat tatatacgga tttttttcgg aattttacgc catatctgta 120
 agtatatata acatgcatgt cgttttcaaa ttcatatgat gaacgatcca cgtaagtgct 180
 actactccta caatattgca tgagagagat atgtatttat aaattttatt ttgaagaaga 240
 aataagaggg aaggttactt gggtaggatc atgtgaaaac aaaagaaga aaagcgaac 300
 ccactaagcc attacatgat atcgaccttc ttatcttttt cctctttatt ttatttttct 360
 catcttcttt ttgtcaggac ttttttctac ttaatgaaac ctccaaacta tctaactaat 420
 aactcccat gtagaataaa gaaaattata taagatattg ttgatatttt gtaactagaa 480
 aatatatttg ctctgtaatt tttcgtaagt taaatcaaca ttttaaagta gaaacaaata 540
 ttactgcaaa aagtaggatc attatttttg tccaaaatct cagtttagcta tagggttgta 600
 gtaaaaacia aacacattct tgatttgccc caaaaaataa agagagagaa gaatattgtt 660
 caaagtggt ctcttctctc tctaattatg ttttactaa acccaattag attcaaacag 720

```

tctacaaagt ccaaaagata aacatgggac aacaattcga tgcaaaaaat cctcttttca 780
tgctcttttt ttattctcta gtctttttaa ttactaataa aaactcacia atccacccaaa 840
cccattctct acaactcacc ttcattctaga tttaccctact cccaccgaga aacacaagaa 900
aaaaaatata catatataaa tatacaagac aacacatgat gctgatgcaa tatacacaaac 960
aaagtattaa atcttagata ttgtgggtct ccctttcttc ttttcatttt cttattcatt 1020
aaaa 1024

```

```

<210> 34
<211> 1024
<212> DNA
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0039

```

```

<400> 34
ccgttcgagt atttgaaaat ttcggttaca cccgcctaaa taggcggacc ttatctagta 60
tatatataca ttggaactat attgtttact ttttagttga tttaggctat gtcattgacat 120
tgacataaat ctacctgtta tttatcacgt gtaattcgtg taaagtgtaa actagaaagt 180
tcaaatacgt atttgttttt gttctgttat ataggattgt catagttgta aatctacaat 240
ttattacaac atgaataagt acacaagcaa tgtaattgga ttttaattgct aaactcttta 300
catggtcaat ctaaatttga taagaaatac gtcacatatt actaagactg atagtttttt 360
tgttgtcacc aattattttt gttaaattga cgaaaacaat tccaaaaact caaatgtaca 420
aaatcataca gtctcaciaa catctcatag agaaagatat aaatctccca tatgggaacg 480
ataacacgag gtcgaaatac tattcgtaaa actaaaacgc cttagttata aatcgttagt 540
tgtaaccgcg gtcgagaata catacagatc cacgaaacta ctactacaca tgctgctgaa 600
ttggaatttg gaaaagacca tcttcttttag gaagagctca cccaatgagt gacaaagggtg 660
tcggtggctt gttttctacc catatgtata catcaaatgg tagtttcatt aacgtttggt 720
tttgagaaaa gtaagacttt ggctagtagc taggttcgta tataataaac tcttttgaga 780
aagttcatca ctggtggaaa atgttaaacc ggttttttct cattttttcc gccatgttaa 840
ccaccggttt aaaaagaccg taacacattg aaagattaat aagggtatat ttgtaattac 900
ggtttgctgg caatttttaa ttattatttt aattagagaa aatagagaag ccctatcaat 960
gtacatggta tatatataaa aggcaaaacc ctagaaaacg atactattcg actcagccgt 1020
cctt 1024

```

<210> 35
<211> 1024
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0050

<400> 35
aatctgatct ctagtccagt cgattggtac ttgagggaaa catcatatTT ttaaaccTTg 60
tctcagtaag ctaacacaca ccccttgtga ttacttatcc atgtttatcc acaagaatgc 120
agttggattg agatattttc ttctttgttg aaatcaggcc tcaagggtgtt catgtggtct 180
gcaaaaaaat tcccaaaaat aaagatagtg acatctgaaa tcgataatgg attagacgaa 240
gagtttctgt ttattccttg gtatgggcgg gtttggggac agatattttg gcacagacga 300
ggactaggcc actgtggtcc tgcagcatta ggtgtccctt ccatgtcctg cattacattt 360
tattgatgga ttcatcacc tatctactac aacggctaca caaactatga agagttttgt 420
ttactaataa atgcccaagt gaggggtcga tcgaaccggg gacacgtttt tcagtttacc 480
atatagaatt atccttgga ccttgatac tccatagaac atcaccacct ctgttgtcat 540
ctcaggaatc caggttcaaa cctagtctct ctctccctag tgggaggtat atggccactg 600
ggccaatgat gacaaaatgc aaaaaaata aaatacattt gggttcatta tctaaaatat 660
ctcttggtgt tgtaagtttt ggttgcacac tcgtgtggtt gaagtgtgtg tgagaggtag 720
tatacaatac actctgcttt tgttttgtac ctatctcttt ctcttctcca catatccaag 780
actttgggga taaagctgag atcattgggt gccatttggt tgtgtagaag caatcaccca 840
tttgctttat ccgaggttga taaatttctt cgggttctcc ttctgacacg tatgacaaat 900
tctaatagta tattcctcgt agatattacc tataattctt caatagttgc aggtacttaa 960
ggctttgtct tggcatcctc gtcctcttca gcaaaactcg tctctcttgc actccaaaaa 1020
gcaa 1024

<210> 36
<211> 999
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(999)
<223> Ceres Promoter YP0086

<400> 36
cttatccttt aacaatgaac aggttttttag aggtagcttg atgattcctg cacatgtgat 60

cttggcttca ggcttaattt tccaggtaaa gcattatgag atactcttat atctcttaca 120
tacttttigag ataatgcaca agaacttcat aactatatgc tttagtttct gcatttgaca 180
ctgocaaatt cattaatctc taatatcttt gttgttgatc tttggtagac atgggtacta 240
gaaaaagcaa actacaccaa ggtaaaatac ttttgtacaa acataaactc gttatcacgg 300
aacatcaatg gagtgtatat ctaacggagt gtagaaacat ttgattattg caggaagcta 360
tctcaggata ttatcgggtt atatggaatc tcttctacgc agagtatctg ttattcccct 420
tctctagct ttcaatttca tggtgaggat atgcagtttt ctttgtatat cattcttctt 480
cttctttgta gcttggagtc aaaatcgggt ccttcatgta catacatcaa ggatatgtcc 540
ttctgaattt ttatatcttg caataaaaaat gcttgtacca attgaaacac cagctttttg 600
agttctatga tcaactgactt ggttctaacc aaaaaaaaaa aaatgtttaa tttacatatc 660
taaaagtagg tttagggaaa cctaaacagt aaaatatattg tatattattc gaatttcact 720
catcataaaa acttaaatg caccataaaa ttttgtttta ctattaatga tgtaatttgt 780
gtaacttaag ataaaaataa tattccgtaa gttaaccggc taaaaccacg tataaaccag 840
ggaacctgtt aaaccggttc tttactggat aaagaaatga aagcccatgt agacagctcc 900
attagagccc aaaccctaaa tttctcatct atataaaagg agtgacatta gggtttttgt 960
tcgtcctctt aaagcttctc gttttctctg ccgtctctc 999

<210> 37

<211> 1024

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1024)

<223> Ceres Promoter YP0088

<400> 37

tcgattggga ttactacttc atctagtaag gttctgaaaa cgtttggtgt tgataaggaa 60
gattcgtctc aggttattac tgttgatctt caagggttgt gattgtgacg cttatacatg 120
tgctgaaact gtggtgttta tttattgaaa acaaaaaaaaa agtctctctt gtagtttcat 180
tgtactaaat agaaaacaag aaacgttttt ttctttaatc ttctacattg ataatttgg 240
atcaaaggat tgtttctgca agacacaaca caaacatact tatactagtt tacttctact 300
aagtactaac tacataccca tacacacact tgcacctaga ctttacttct agacatcatt 360
accctaagggt agaaccaagc ttacaagcaa gttttaccga caactcttac attacaactc 420
tagtctgtag tctttaacgt agacttacta actagtcatt agtggtttta ttttttaaat 480

```

tttcatccat atgtttttgt tgtagatata aactaaagtc ggtcacattt aataattgtc 540
attatgtccg cgtaaaagtc aattcagcta ttggacattt atgaaatgta agattttctc 600
tctcatttcc ccgtgcggtga agacatgcat tggtttttct gtaataatca acaaatccaa 660
accccttttc gatctttatt tggacattgt tagagacaaa atttctctat agtctttttc 720
ctaatttgat accatgtttt tgtttctgca caaatttact cactggttta actaactatc 780
cacttattta tgattttacc attagggctc agctagccct agtcaaattt gtaaacaagc 840
caagctatct acataaatcg agatgtcatt aacgttaatc gtcgttaatt cgaatttgaa 900
aacatagata gctttagcag tacaatgggc aatggtaaga agaatagcaa aaggcccaat 960
atttggtttg cagaaattaa agccttaaaa aaaagcccac agatatttgt caaagaacct 1020
taat 1024

```

```

<210> 38
<211> 1024
<212> DNA
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0092

```

```

<400> 38
aaagattgag ttgagagaga tggtagagac gcagaacaga caaaggaggt ttaccatata 60
gtgctctaaa gggcaatgag attgcagtga tgtggctatc cggggaatca tcgcagggtta 120
ttccttccca tgagcaacaa tcaatggatg ggttccaatt cagaggagaa acagaagaag 180
aaacgtttcc agagaaccac agtagggatt ctcgatcttg cgagttgcag agagcctctg 240
aaactgcaat agaaaggaca ctgatgaaaa gaacacactg aaggagtatg ccaatcatgt 300
gaaaactcag agcttgtatt ggtcttgtgg ttgatgaagt tctcacaaaa cctttggctt 360
tgaatctccc ctcattagtc atggtgagaa caagaacaag acgagaaaca gacaaagaag 420
atgaaaaaac ttgttggcca gtgttgacta agggggaata gcccagaca taacaaaatt 480
agacttgtcg tacatcttta atatTTTTTT atctgtttct ttgtcctgac gctttcatta 540
ttcctgtgat caattttctc ataccattgg tccatcgtta atcctttctt aatttcattt 600
tctacgtaac atgagaggag accaagtcct atgagaacag ttgacgtaac agtgggttgtt 660
aagttaagtt aaaaagagga agctagttag agtgaccgtt aggtagagaa gtgagatctt 720
taaccactct tctttctctc tctctctgct tttttcgtcg tctttcacat ctactgttcg 780
caaactctct tatgttcca ataatggtga taccaattga gacttgcagg agaatctcct 840
cttctccaca ctctatcaac tggtagacca tggaatgggc gtttcagttt caatattcct 900

```

ggattctttt taaggattcc tgtttctctt ctgttcctgg tatattctta acgacgaaat 960
tagtatcgga tcctggtaat acattttgaa gcttttaagt accattgcac tgggatccaa 1020
caat 1024

<210> 39
<211> 1020
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1020)
<223> Ceres Promoter YP0096

<400> 39
gaggtcagtg agtcgattgg tgcaaaattg aaaaattgaa gggtgaaaca aatttaaaga 60
taatatctat taaatcctct aattttaaaa atttagcaaa aattgtatct tcttatggat 120
ctgttagttc acacgtatct taattagtac caaatcatat ctaatgatta gtgataaaac 180
tagttagata tctatatgtg tctttaccat ttaacttgaa tccttcttct tttttttacg 240
taaacaactt gaatccttcg ttaatacata aatttaaagc attttttctt taattctatt 300
gatcgggtata tatttactat aagtttttagc tcataatgcaa tttcaaataga tatgctttta 360
aattttgtct aggtgtgata gttgtatctt taacataaat cttatagcaa aattatactt 420
gatattctaa atttatctat ttgctcttgt gaacctcata ttagtctaga gaaactttga 480
aatcctttca attagttgta tgtccaatac atttttacta acatttatta gtctttttta 540
ttaagattat tgttagaaaa aaaaagattt tttaaaaata aataatatgt tttagataca 600
atgtgagtta ggcttcttat attttaaaaa ataaatttat ttcatactta aaaatagttt 660
ggaatttcaa tttatttggc tgaataccat aaaatatgtc aatttgaacc ttatacccat 720
tgactatttg gtgttagaaa ccctttaaca aaaaaaaact atttggtgtt agatatcaaa 780
ataaaaaaag ttttaaccatt ggtttcttat attgaattgg atattgttac atgtattaaa 840
gttttttttg ttttaattttg aaacgttgat agaaactatt aagtttaagt ttggtagtat 900
atttatttgt ggaaaattta attgccatta aatataacgt caactttttt tgggtttttt 960
tgagaagtta cgttgtgatt ttgatttctt atataaaagt tagattacgt ctttttttaa 1020
1020

<210> 40
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(1000)
 <223> Ceres Promoter YP0097

<400> 40
 ttcatcttta tattaagag tttaaaaact gcaacttttg tttttctttc actaagtctt 60
 atggccacag ttaattaaaa gcagatgaaa ggtggtccaa tggaaaagga gaatgtgatt 120
 gggctagtgt ggagagttct gatgtctagt gttgggtaca cgtgtccgtc agttacacat 180
 agcattaaat cagacggcat gtcattattc aaatctagtt cacatagtac gactaatagc 240
 tgataaatta atgattatac agcatatgaa ttatgaattc aaaaaaaaaa aaaaattgaa 300
 aatgttaagg agatgctata ttttacaaaa ttcacgcaa tgctttctac taatttgcta 360
 agtggctctc tccagttagt cttgtcgatt ccaagcgata ttattaaatc ttgaagcatc 420
 gctcaaagca ttatagctta agataaccaa attgttatta aaaacaccta gtgaaatttt 480
 taaattaaaa caattttgat atctttgtaa tatctaatac tactctttct gtgtctaaaa 540
 ggattaattt tcaaaaattht cacacatatt aaaaaaaaaa aaaaattact agctaaacaa 600
 ttttcaataa tcataaaaca atagtaactt aataatthtt ttttattttc aaaatagtcc 660
 ttcaagttta caattcattt tagtattata atcaacaaaa tttgtattaa aaagttggaa 720
 aattaatctt tgtggaacaa aaaaatctag aaatcatttt ttagaattag agagaggtht 780
 gataaaaaaa aataaaaaaa aatagagaga ggtagtacat actaaacgat gtgatactac 840
 tattgacaaa atcttaattc tcagtttagt agaataaact agaaggaatg aatgaagtaa 900
 atgcgaatcc aactactaac aaaccctact tagtcatcat attttcccat atgaaatccc 960
 tatataaacc catcatcatc tcccacttht ttcatatcca 1000

<210> 41
 <211> 1004
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(1004)
 <223> Ceres Promoter YP0101

<400> 41
 ttctcgtht ctagaatatt gctggaccgg attaggtcaa tattattggg ccagattaga 60
 tattgaattg tcgacgttgc ttacgttacg ttatatcttg tttagaatt aaacctatcg 120
 acttagtctt aattaagaaa acattgcctt aaattctctg gtctgcgacc gtttttttga 180
 ccgttaaccc ctaattaaag aaacaaaata attatagaaa gagcactgaa atgtgattat 240
 tttaacagta ctcttatgag aaaattcgta ctttttagtt ttttttttgt acaaattctc 300

aagaaaaaca ctactactaa ttaagaaacg tttcaaacaa ttttattttc gttgggtcat 360
aatcttttctt tctcggtccg ggactaaccg ttggcaaaaa aaaaaaaaaa gttgacaata 420
attattaaag cgtaaatacat acctctcaaa taaaaacttg aatttggaac caaagacaac 480
taaaaaactc gaatttaaga gaattcctaa aatcaagtga agtatcatca cttggtaaaa 540
tttcataacc gttgggttct atttctatgt gtgccttggg ttgcaggaga taatatttca 600
tttccaacca atgatattcg tacacatagt caaacaaatg tttgtctttg ttattatatt 660
gagaaagaaa caagaaagag agagagagat agataagacg aaggaagtga agcttccaag 720
cgccacccgt taaaaatctc gtgtgcaagt ttcaaataca agtggccggg ggtctccata 780
atttgatcgt catccaatta aaaaggaaga aaaagcgtgt tttatacaag aaaactcatt 840
aaaatagcaa gtctagaaat atctcaacac taatctacca cgtctattac acacacacac 900
acacacactt gatcttaatt tattttcaag attcaagaaa ataccattc cattaccaca 960
acttgaccac acgcctatat ataaaacata aaagcccttt cccc 1004

<210> 42
<211> 1000
<212> DNA
<213> Arabidopsis thaliana
<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter YP0102

<400> 42
atttggttga taacgttttc actcgactaa ttatatactt cagaaggata gtaatagaat 60
acccaaataa ttaaatgatt ggtagtgcc tttagtgaga ctttttaacc gattctaata 120
gactaatgat gtagctaagc atttatttgg gatcatcact gtttgaaaac gtgaaatgtg 180
ataaaagtta tgaaacgatt aaaatataaa ataaccgtac aaacattat gtaccgtttt 240
tttctctgtt cttttggcga tttggtttag ttcgttacac tctaaatgtt attgcagata 300
tatatataat gatgcatttg catctgagga acatataatt ccggttaaca cttccaaatc 360
ttatatccgt ctaggtaggg attttataaa tcatttgtgt catcatgcgt tatgcttgtc 420
ggctttgacc ataacgcaga gatatagaac tagcttttac ttaactttta gatttattat 480
ttgatctaga gttaagtgga gatatatagt gtttttggtta gattattggg ggatgtgaga 540
gtttgtcttt agtttcaagt tgagaatata aggcaagagg agactctgag gcaatcagag 600
gttttgattg gcaaaatatc caaaaggccc aaaccaagtc gaagcccatc tcgtacaaaa 660
aaagaaagag atctgtaaga aaaaatatctc ttgatattc ttacaaaaat aagtgtaaaa 720

cttttatttag tcaaaatcctt caatctttta aaactctcat cactcctacg aaagcgcggtg 780
agagttatga gacattcctt aatagcatta ctcaagaagtc acaagttcaa aacgtctgac 840
tgaacagaa acaagccttt gttgaagtct tgaagaagag acattagtagc tcgtcggtata 900
gccataaaag gtaatatagc aaattttcttc gctaattctct tcaccttcct ctacgcgttt 960
cactttcact ttataaatcc aaatctccct tcgaaaacat 1000

<210> 43
<211> 1004
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1004)
<223> Ceres Promoter YP0103

<400> 43
gttttgaaga acaatctgga tcgaaatcta acataaggtc atcgtattca agttacgcag 60
tcaaggactt gacatcatcc tactctgggc tgaggttacc acttccaaag atgggatttt 120
tcgactcggg atgcttccta agaaattcgt tttattgaac ctagcaaata tcttgtaatg 180
taagattcct gagatgatga agaaaaaaca aacttttggt acagcaggag aacggagaga 240
aagaaaacag agaaccaaat gctcttgaag caaacagaag aagaagacac aaatccaaac 300
ttgagacttc ttctacacca gaaaaccgca gcattctggg acaacgcaaa acacgaaagt 360
gaaacgggca atgatataata tgtcttgggt gcgttacaag gcatcgtttg caactgttga 420
gttgataag tcaactgtct tcttttcctt tggtttagt agctgccttt tttttccttt 480
gttgctttta gaaatagccc gaaaaaaga atgttctaca tttcggagca gaaaactaac 540
cgaatgagtt tttggctgga tcatcggatc gatcagatat attttgagtt acgaactggt 600
ataaaaaaag ccataatttt gtgttgagtt tgcaaaatac cttataactt gttatttgag 660
attgcacctc catatatatt aattcgtaag agtatttatt aagtaagctt tagtataaat 720
ccttttttcc tttaaagtaa gttaatgttc tactaaataa tagtaaagtt gaagaaccgc 780
tcggttttta caccatgcac gtgttatcta acaaagaaaa tatggtacac ctaatggcta 840
atgcaaagga caacacaatg aaactaactt gactctgtgt tatagaaacc catagacatc 900
tgcatacatc ctagtatttg tataaattgg actcaaattc ctgaggacaa tcatagcaaa 960
caatcacatc atcgcaatat acataaacia aagaggaaga aaaa 1004

<210> 44
<211> 1003
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1003)
<223> Ceres Promoter YP0107

<400> 44
taacaatcct tgggaacatt gcatccatag atatccggtt aagatcgatc tttgaactca 60
taaaaactag tagattgggtt ggttgggttc catgtaccag aaggcttacc ctattagttg 120
aaagttgaaa ctttgttccc tactcaattc ctagttgtgt aaatgtatgt atatgtaatg 180
tgtataaaac gtagtactta aatgactagg agtggttctt gagaccgatg agagatggga 240
gcagaactaa agatgatgac ataattaaga acgaatttga aaggctctta ggtttgaatc 300
ctattcgaga atgtttttgt caaagatagt ggcgattttg aaccaaagaa aacattttaa 360
aaatcagtat ccggttacgt tcatgcaaat agaaagtggg ctaggatctg attgtaattt 420
tagacttaaa gagtctctta agattcaatc ctggctgtgt aaaaaactac aaataatcta 480
ttttagacta tttgggcctt aactaaactt ccactccatt atttactgag gttagagaat 540
agacttgcca ataaacacat tccccgagaa atactcatga tcccataatt agtcggaggg 600
tatgccaatc agatctaaga acacacattc cctcaaattt taatgcacat gtaatcatag 660
tttagcacia ttcaaaaata atgtagtatt aaagacagaa atttgtagac ttttttttgg 720
cgttaaaaga agactaagtt tatacgtaca ttttatttta agtggaaaac cgaaattttc 780
catcgaaata tatgaattta gtatatatat ttctgcaatg tactattttg ctattttggc 840
aacittcagt ggactactac tttattacaa tgtgtatgga tgcatgagtt tgagtataca 900
catgtctaaa tgcatgcttt gtaaaacgta acggaccaca aaagaggatc catacaaata 960
catctcatag cttcctccat tattttccga cacaacaga gca 1003

<210> 45
<211> 1024
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0110

<400> 45
gggatgcggg tccgcttcct cttgatcttg gacgagtcgg aggacattgt tggatcccag 60
tgcaatggta atataaaaca agaaaacaag agattttata ggacaatcac taaatgacat 120
ttaattgatt aaacatttat tcattaataa ttgtatgta ctaacttcaa catttaataa 180
ttttgtttta gatacgttta catcagagac tattaatatt tttacagggt gtaactttta 240

actttgtctt gaatcgaaca tgactataga ttttgggcaa acttaaagat aacaacattt 300
 cogttttttt tcaaattatt acaaatcaaa ctgatataatt agacacaaca cgattacacg 360
 taatgaaaaa agaaaaagat aaaaagataa aagaagggat cgattctgtt tgggtctggtt 420
 tagtgagatt caaagttaag ctcttccttt caagacatgc cttcttaaac cggaatgtg 480
 aacgtttgta atgtagtccg tccagttaat gcttccaaca tcaaatccaa attctctctt 540
 ctogtctctt gacatattct ccattaatct ctgggggtatt gctgttatca aatctgtaaa 600
 agaaacaaaa aaaaaaagat gaaaactttg cgggtaccgg ttttgtctgc tctaagaatt 660
 agaatgttaa tgagttctgt cttaccttcc accatagaaa gtgtatggct cataaatagt 720
 agcaagggtgt ttggcttgtt caacagattt cttgcatata aactttagct tctgcatcat 780
 cttactatcc actgaactca taccactcat caaccactc cgttcttgag catctctcca 840
 caaatgatcc gagaaatcat caacggaatt gaaaagtttc atcaaacgca ccataatagg 900
 atcaccttta gagtccatgc atggagatgt tttgtagtgg ttataaagaa gctccgctaa 960
 gtcttcgaaa accagcgggt ttatcgccga agaagcgatc tgatacacgt ttatttcagg 1020
 ttcc 1024

<210> 46

<211> 1024

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1024)

<223> Ceres Promoter YP0111

<400> 46

cgattggatt tagtctatac attatagggc gcaagtttgt ggatttaaga attatataaa 60
 aacttgaaat atatagtttt tatgcattct cctcttgtgt aatacataaa ccaaatatga 120
 gataggttaa tctgtatttc agataatatt aaattccaaa caatattttt acttgttata 180
 agaaggcaat taatatctct ctgttaatgg caagtggtag caagtagtat taaactatta 240
 atgcaatgga agagtactgt tggaaattat aatcctctat cacacattca aacagatctc 300
 ctgaaatctt ctcttccaaa cttgtacttc tctgatccaa atgtaggctc caaaatatag 360
 acatttacca ttactaagt ccacaactcc tttcttgtct ccttcaaaaa tgactcttgt 420
 gtaaccacca tatgactccg acagttcggc attgccatga tgagagctta aaaattcacc 480
 ttcttgagca tttcaagtct tcaactccct agcttgacct gaaccaagat aaaatgcctt 540
 tgtcgtcccg taatatccat cctgctttgg acggcatcat agttacattc gatccatcct 600
 atttacaatg ttatttttagt attaaaaaca tgacaataaa tttgttggtta aacatattca 660

aatacaatat gatttgatttt ataagtaatt gtaatatgaa atgtccttag taatatgtta 720
aaaaatacat agatacacac acgtactaaa agaggcaacg cgggagatgt cattagagga 780
agaactagga agcagagcgt tcatgcaaaa tgctaccaa aacgttaatg caatatctca 840
actaatcagc acagtccatt tcatactgag aatgtaaaaa ccaatcagca tcgtccattt 900
tttcatctaa ttatttggtta actcttaatt ggccacaact tccaaccaca tgacgctctt 960
tctattccct ttatatattc ccatctcaaa tgttcttggg gacacaaaat atcataaaca 1020
tata 1024

<210> 47
<211> 996
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(996)
<223> Ceres Promoter YP0115

<400> 47
gtcgattgga tgatgaacat tctacatata taattattat gttaaagcac ttagacagca 60
taaattcttt ctaattatat aaatctaacc ttgttacatt gtacatctat aaattacttg 120
aagaaataac gagttctatt tctttttaaa aattaaaaat actataccat atctcagtga 180
ttaagttgaa ccaaaaggta cggaggagaa acaagcattt gattcttcct tattttattt 240
tattcatctc tcactaatga tgggtggagaa aaaaagaaaa tacctaacaa acaaatatat 300
attgtcatac aaaaatattt ctatatTTTT agttaattag tttatatcco tcacttttca 360
gggcttatat agaaaagtga gcaaacacaa atcaaaatgc agcagcaaat actatcatca 420
cccatctcct tagttctatt ttataattcc tcttcttttt gtccatagct ttgtaattat 480
agtcttattt ctctttaagg ctcaataaga ggaggacta ttactacact tctctctact 540
tttacttgta ttttagcatt aaaatcctaa aatccgtttt aaattcaaaa ataaacttag 600
agatgtttta tctcgattcg gtttttcggc tttaggagaa taattatatg aaattagtat 660
ggatatcttt actagtttcc attcaaatga ttctgatttc aatctaatac tctcactctt 720
taattaaact atatgtagtg taatttcaca ctgttaaatt tctaccatgt catgtatatt 780
agagttgcat agaaaattgt aaaacatcca tttgaattcg aatgaaacaa aatgttttaa 840
aataaaattt tggtttttaa aagaaaaatc taaaactgaa ttatatcggt taaccaagtt 900
gtaaaagtca taaaacgtag tatcttgtaa atcgctcttc cacgggtcaa atagacttct 960
agtaataaac aagtaaaact aattttggtt tcttac 996

<210> 48
<211> 1024
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0117

<400> 48
gtcagtgagt cgattggatc acagtccttt atgataaaac aaactcataa ttattccacc 60
gacaacatgc gtttttaaatt attttttctt aaatttatatt atattatatt gatatcaacc 120
tagctaaaat aattcggatg gcgaaatcgg acaattttta atagaaaaaa tgggtatgaa 180
gatagtctat gattccgttc ttagcgacta gagggacctg ctcaaattct cggggtgata 240
cgcgatgtca agctcaatag aaccccacaa ccgacgagac cgagaaatcc ttgatttggg 300
ctagaagatt ttgaaataaa tttaatatat tctaagtaac ttgcttaaat tttttttcaa 360
actctaaaga cataactaac ataaagtaaa aaaaaaaaaag ttaatacatg ggaagaaaaa 420
aattaaacta atgatttagct ctctaacgtg tttaatctcg tatcaagttt ttttttaaaa 480
attatattgc tattaaaaca ttgtactatt gtttctatth tgttttagcta ttattcttgt 540
gaaatgaaaa gttgtgttta ttcaattact aaatggcaat atttatcttg gaaaactata 600
cctctaattg gattaggccc tagacatcct ctttagctta ttgacgttaa aattattccc 660
aaaactatta aagtttagta gtttgaaaga tgcatacaaga cctactcaga taggtaaaag 720
tagaaaacta cagtttagtgt gatttatattt taaaatatat aaaacaatct tattaaacta 780
aatattcaag atatatactc aaatggaaga taaaaacatt tagtctgtta ccactaccag 840
cctagctagt cactaatagt cactttggaa ctgagtagat atttgcatct tgagttacca 900
tggaactcaa agtccaaaaa gagaccccgga gtgaaaatgc taccaactta ataacaaga 960
agcatttaca gcggtcaaaa agtatctata aatgtttaca caacagtagt cataagcacc 1020
attg 1024

<210> 49
<211> 1000
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter YP0119

<400> 49
taccaaaaat aaggagtttc caaaagatgg ttctgatgag aaacagagcc catccctctc 60

cttttcccoct tcccatgaaa gaaatcggat ggtcctcctt caatgtcctc cacctactct 120
tctctttcttt cttttttttct ttottattat taaccattta attaatttcc ccttcaattt 180
cagtttctag ttctgtaaaa agaaaataca catctcactt atagatatcc atatctattt 240
atatgcatgt atagagaata aaaaagtgtg agtttctagg tatgttgagt atgtgctgtt 300
tggacaattg ttagatgata tgtccatttt tttctttttt cttctgtgta taaatatatt 360
tgagcacaaa gaaaaactaa taaccttctg ttttcagcaa gtagggctctt ataaccttca 420
aagaaatatt ccttcaattg aaaaccata aaccaaata gatattaca aaggaaagag 480
agatattttc aagaacaaca taattagaaa agcagaagca gcagttaagt ggtactgaga 540
taaagatata agtttctctt caagaacagt ttctcattac ccaccttctc ctttttgctg 600
atctatcgta atcttgagaa ctgaggaag gttgtgaata ttatgcacca ttcattaacc 660
ctaaaaataa gagatttaaa ataaatgttt cttcttttctc tgattcttgt gtaaccaatt 720
catgggtttg atatgtttct tggttattgc ttatcaacaa agagatttga tcattataaa 780
gtagattaat aactcttaaa cacacaaagt ttctttattt tttagttaca tccctaattc 840
tagaccagaa catggatttg atctatttct tggttatgta ttcttgatca ggaaaaggga 900
tttgatcatc aagattagcc ttctctctct ctctctagat atctttcttg aatttagaaa 960
tctttattta attatttggg gatgtcatat ataggatcaa 1000

<210> 50

<211> 999

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(999)

<223> Ceres Promoter YP0120

<400> 50

tagtttttga tttaatctac gtttttctta atcataaatg ggtaattatt agtttttgca 60
aaatcaaaat ccaaaaattg ttctaaacac tgcaaccatt taaggcctat atcactcaga 120
aaatttctgg tgggagaact aatcgtttgt cttttctaaa tctcacatat tagaatttag 180
aattagtgtg ctacataaga atattagttc agctcggaac aactattttt tggtaaaaca 240
gagaacttaa acaaatgcat tattttatca acatgcattt tgaattgaat ataaaatttc 300
ataattgtaa agacataaat tacataaaat ttacatgaa aaaatagata tagaaagaaa 360
atgaaactaa ctgatgatat gctctctaaa ttttttaatc tcataacaag aattcaaatt 420
aattagttca tatttttggg taatataaca ttacctgtc taagttggaa ctttcatttt 480

```

tttctgtttt gtttagtcag tattcttaat gtgaaacgga aagttgaatt tattcaaact 540
taaattcaat agcattaatt aaaggcgaaa gctattatct ctacatgtgg ttcaaactag 600
acatocaatt taattagott attgacgttg aaatgttttc caaaactact atagtttggc 660
aatttgaaag atgcatcaga actactcaga caggtaaaag tagaacctct agctgtgtga 720
attgtatgtt agtcataaa gaacatcttg taaacttcat acttaagata tatattacaa 780
tatatacttg aatggtagat aaaaacgatt agtctgattg ctagcatact cacaactatt 840
tggaatgag taagatattg gcattctaga gttactacta tggagacaaa agtcgaataa 900
aagagacctc acgtgaaaat gttacgagct agtaaaaaaa gcatttacac taacggtaaa 960
aaaagtatct ataaatgttt acacaaggta gtagtcatt 999

```

```

<210> 51
<211> 999
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(999)
<223> Ceres Promoter YP0121

```

```

<400> 51
ttggattttt tttttgttga gtcagcagac catctaactt ctctttttcc accacagcct 60
gctttctatg aagcatttgg gcttacgggt gtggaatcaa tgacttgtgc actcccaacg 120
tttgctacct gtcattggtg acccgagag attatcgaaa acggagtttc tgggttccac 180
attgacccat atcatccaga ccagggttga gctaccttgg tcagcttctt tgagacctgt 240
aacaccaatc caaatcattg ggttaaaatc tctgaaggag ggctcaagcg aatctatgaa 300
aggttggccc attctccttg acaggcttaa caatacaact tgtatcgctt caacaagatg 360
atggcttaat aaggattttt gcatttatag gtacacatgg aagaagtact cagagagact 420
gcttaccctg gctggagtct atgcattctg gaaacatgtg tctaagctcg aaaggagaga 480
aacacgacgt tacctagaga tgttttactc attgaaattt cgtgatttgg ttagtgtaac 540
ccactgttat tcttttgatg tctacatcta ctttacttac attattcttt tcttcggttt 600
gcaggccaat tcaatccgcg tggcaacaga tgagaactga tcatgacagg gtaggatttt 660
atttcctgca ctttcttttag atcttttgtt tgtgttatct tgaataaaaa ttgttgggtt 720
ttgtttcctt cagtgggttg attttggact tatttgtgtt aatgttgttt tggctgttct 780
cttaatatca ataacaata aatttactgg ttggatatcta agatctaaca atagttacta 840
tttttagagg taaagacacc aaccttgta tattggtcag agagctaaaa ccttgacttg 900
ttgggaaaac aaaactctaa tgacagaaaa tctgacatga tgccttataa ttcacagcct 960

```

catgtttctac ataaatccta acaatagcac ttigtittct

999

<210> 52
<211> 1004
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1004)
<223> Ceres Promoter YP0128

<400> 52
gataaactga taatggaaaa gaacaaagaa accagttttt aactatttgc atatgtaatt 60
tatttgtttgc aaatttatatt tagttaaaat gtttcctcta tttatatata tatatatcag 120
tcaagcacta tgtataagaa atgtcaattt ataaatTTTT acatgtcctt taacagaaag 180
aaaatgaatt ttacatgtc attcatagag agtcactcgt ttatttctta tatagagaat 240
aacacactca catgcatatg catgcaatat gatacatTTT atgacaaaga taatcaacgg 300
aaacgggtcaa gacataattt gataaacaac ttgcacgatg cacagatctg atcaaatata 360
taactcttta acatatccaa aatattcaaa aagaaaaact cgatccaaac tagcaacatc 420
acgctcacgc ggtaggctaa aaattttatta atctccaaaa gtctttctta tgaacactgc 480
aaacacaaca acttgaaaag tcatataggt ttagatgatg acgcgtattg gctatcgctt 540
accggagtgg ctcataaata caataaaca tacgtaaaag tcaaagtcaa atatatTTtag 600
tcaactataa ccattaatcg ggcaaaacct ttagctgtca aaacaacgtg aaaacgatat 660
ttgtatatat catcaagaat cagtagataa gagaatgatt taatcccctg actattacaa 720
ttttggtgta ataaacagtc tctattgggt tttattcttt gttttaattt ctcatgacct 780
atagagagaa ttaggtagtt tcgaaaattg gctaataaac ttttgaaaac tactgtctac 840
tttgcttaaa ttctctacac ttagtttcgg ataagataat tgtcggacta atagttaatc 900
ccttgacaat ctttgatatt ataaaagggt tagttaatct cttctctata taaatattca 960
tacaccagct ttcaaaaata tataatccaa acaccaaaaa caaa 1004

<210> 53
<211> 1001
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1001)
<223> Ceres Promoter YP0137

<400> 53

```

gtggcacatg ctgaaacccc gagcatctct cgggaagaca cgcgtcgttc gctccaaaga 60
aaacagtcac agctgccgga gaatctccgc cgtcttcttc tgccaccgga aaaactctct 120
ccaccacttt cagtgcccac ctcgtgttat atccactgta tctctgtagc accatatcag 180
cctaataaaa ttttatgtat caaatTTTaa gacatagcgc aaactacact atactagaca 240
ataataatat gatttgtttc ctgaaaaatt atggtttcat gagaaacatt aatcatctat 300
aaaacaaatt agctatggca tcgaagagtt atcaatcaaa actgatgaat ctttacttaa 360
tatatacaac atatctttac cttgcggcgg agaagatcgg cgagagaagc accccagcca 420
ccgtcactaa aggattcttc agtgatggaa tcaccaaaga gaaaaacctt cgtctctatc 480
atcttccaca caatcttctt gagaaaatct gagagataag aaagggtgtag tggttttgct 540
gaagtgatcg tgtttgattt agtaaagaaa tgctttattt attgttgggg gaaacataaa 600
taaataaagt aaaagtggat gcaactaatg ctttcacca ctaatcacgc acctttcatg 660
gtttattgtg aaatacactc atagatagac atacaatacc ttatgtacgt aaataacatt 720
ttatttgtcg acacttatgt aagtaacgca tagattattt tctatgtgat tgccactctc 780
agactctcag tttcaaccaa taataacaat aactacaaca acattaatca taaacatatg 840
ctctggttta caattaaagc ttagattaag aaactgtaac aacgttacag aaaaaaaatg 900
ttatttacgt tttgtaagat tagtctctag aatcatcacc gttttttata tattaatgat 960
tctttcttat atataaaacc tttctcgaaa taccatgaa a 1001

```

<210> 54

<211> 1001

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1001)

<223> Ceres Promoter YP0143

<400> 54

```

atacaacaga tggcagatat cgagttaaatt acgtgaatca gcggttacga tattttaaaa 60
ctagaaaatt atttaaaaat attgcaaaat accatttaat ttcatgttc ataaaaaaaa 120
gaaattcaaa aacttaaaaa ctgattcaaa aatttggatt aattctcatt aacagtcttc 180
aacactacaa caacatgttt ctaatttatt ttatatTTTta ataattaaac aatatatacg 240
tctgcacatt gttgctcoga cataatctag tataaaaata gttgcagcat atgtgaaaag 300
caagcagcat ttatcactca atactTTTaa ttttatctgt tgtatgtatt aaggTTTTgt 360
agctTTaaga aaacgcttat aatataaaat aacttctaaa agatatttca tgcgtataca 420
ataaatattt gtgaaaaaac atttcgaaaa cgtgtacaat atataaacta ttgtgttatc 480

```

```

ttttgacatt caaacaaatg ttgacaatgt aattttatcc atgatatgat tggccaatta 540
gctgcgaggt aaaaatccgt atacgagtaa aagtaagata aaatttcgca agaagatttt 600
tagcaggaaa tctaagacaa gtgtcatgaa cgtgtcaatc aacaaacgaa aaggagaatt 660
atagaatcca gattcgacgt accacattaa taaatatcaa aacattttat gttattttat 720
ttttgctctg gcagttacac tctttttcat tgctccaata aaaaaatcac tcgcatgcat 780
gcataatatat acaccatagt aaactccgcc tcttcttcat tttaaaagta tcagtttaca 840
ctgacacaat ccttaactat tttcctttgt tcttcttcat ctttattaca ctttttttc 900
aaggtaacaa ataatctttt taagtcactt ttatactctt taaatcttag attgatatat 960
gaatgcatgt taatatttca agatttatag gtctaccaa c 1001

```

```

<210> 55
<211> 1003
<212> DNA
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(1003)
<223> Ceres Promoter YP0144

```

```

<400> 55
aaacgttgca agattattga ttgtgagaaa gagtgctcaa ggtagtactg atttctgtaa 60
agctcacggt ggtgggaaac gatgttcttg gggagatggg aaatgtgaga aaatttgcta 120
gaggaaagaa gcggtttatg cgctgcgcat aacactatta tgtctcggga gaacaaagat 180
ggaagcaaga gcggtttgat tggaccggga ctcttttagtg gccttgtttt tggctctact 240
tctgatcatt ctcagtctgg agctagcgct gtctctgatt gtactgattc tgttgaacga 300
atacagtttg agaataggca gaagaacaag aagatgatga taccgatgca ggttctagta 360
ccttcatcaa tgaaatctcc aagtaattca catgaaggag aaacaaacat ctatgacttc 420
atgggttccgg aggagagagt tcacggcggt gggctagtaa tgtctttact tgggtggctcc 480
attgatcgaa actgaaagcc atttatggta aaagtgtcac attctcagca aaaacctgtg 540
taaagctgta aaatgtgtgg gaatctccga atctgtttgt agccggttac gttatgctgg 600
atcaaaaact caagatttgt tggatattgt tatgctggat cgggtggtgaa accacttccc 660
ggttgctaaa taaataaacg tttttgtttt ataatctttt tactaaacg gcagtatggg 720
ccttttagtgg gcttccttta agcgaccaat acaatcgctg caccggaatc tactaccatt 780
tataggttta ttcattgtaa acctcggaat atttgagagc cacaacggtc aagagacaaa 840
aacaacttga agataaaggg ataaggaagg ctctctacat gatggacaac atttctttcc 900

```

acacaaattc tcataataaa aatcttataa tacaaatact tacgtcataa tcattcaatc 960
tagtcccat gttttaaggt cctgtttctt gtctgataca aat 1003

<210> 56
<211> 1004
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1004)
<223> Ceres Promoter YP0156

<400> 56
ttggtttgca ttgtgaagat ttgtattaac tatagaacat tgaattgatg gtgttaagtt 60
cttacacaag cgtgcttctc gggttgaaact gtttcttttg tatgttgaat cagagcttag 120
tttataggaa ccagagtatc tacttagtca ttctctgatg ctaagtgcta aggttctacc 180
tagttgccct ctaggccctt atgttattga taacttatga agctatttga acacttgatt 240
cttaggagac ctaagttggg acagccagat agagtgtatg ttcttgttct ctatgtgaca 300
ggatcaagct gccacacata gttcaagggg atgctctgtg tggggttgct cagattgagg 360
acaaatctat acaaggaagt agagtctttg acattttgat gttgtatgat aagaagaaga 420
aaggagagta ataaagaaag agaaaagga aacagaaaca cgtgggagaa catcccaaag 480
aggaagcaca cgcggatctt catgcaaagc tccccgattc tcccatgtgg tccctttctc 540
cctttgtccc cctcctcttt cttcttttct cattttactc ctttttttac cattatacaa 600
cgaatctttt ttatcataat tttttgggtt tgggtttattt tccaataaca ctttcttggt 660
tacttcccat tctcactttt tcatataaga aactcacttt gggaaactta tgtttgagaa 720
tgacaagtct ttttagagaa agtgatgtaa caaatctaaa gtgattatat aataaccttg 780
cacaatgttt ttgatttttt gtaagattcg aatattaggt ttattattcg tagggaataa 840
acttactttc aaaagcgttc ataagttaat actttcatat atgatacata gtacggacac 900
tattgttttt tgtttgtttg tgtttattct aaaagaaagt agcttttaaat tgaaatgtcc 960
tcggaggcac agtttaaagt tcgagtgtaa cagtttctaa ggca 1004

<210> 57
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter YP0158

<400> 57

```

ttattagatt aatagattgc attgcattgc ttgtgctttc aatttacaaa ttgtctccca 60
actccatoga cacatctctt tttgtgtata taagattcag acttgttata ttttttttat 120
aaatatgtta ttagcatctt aagttaaatt gatttttttat atctgcatta aggattacac 180
gactatatatt gcgatttgtt gttgggttaa atataattta ggattgtctt taactacatt 240
taggattata tgactatatt tgggttaaata taaaatctag ctgtgattat tagtattcaa 300
aaataagtag cctaaccaat taaaacaacg gctattgggg caaattagaa ctttttagtg 360
tgtccaaaat ataatgggtca ttaggtcata ttctctctag cttcatcgca gcataattga 420
atgattgoot tatttagaag agcttttcca ctttcccaaa atctaggtgg gatctttttg 480
ttttgacott cttttttctt gtttaccatt ttttagctaaa ttatttacga ttacaaaaga 540
tatcaaaagt tggatcataa tacaatttat agacttactg tagaaaattc gtatgtacaa 600
gtacaacaaa ttcttcataa taaattttga aaattctatt acaaagtgtg taagaaatag 660
aatttgaaat atatataaac taaggagaaa aaaaaagaga acatgcattg ctctagtcag 720
agtggaccaa catcaacgag ataagataac ataaaaacca actcaccata actaaaaaca 780
toccaagaga tccaacgatt catatcaaac acaaaaacat cgaacgatca gatttaaacc 840
atctctggta tctccaaaac acaaacactt ttttttttct tttgtctgaa tggaacaaaa 900
gcatgcgaca tctctgtgtc tttatcttct ctctctctct cttgaaaaac tgaaccttta 960
attcttttct cacatctctt ttagctttct gaagctgcta 1000

```

<210> 58

<211> 1005

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(1005)

<223> Ceres Promoter YP0188

<400> 58

```

gattgggtatg aaatttcgga gaccaacaaa aaaaacttta ttgagcttgg agtgaagcta 60
tatatatggg gcaagatcat aatatgttta tatcggcctt ttcgttaact gaaaataata 120
gttttgagaa atatatcaaa tggtaaacag acatcatctt tgaaaaatac catcaatgaa 180
gttaatatgg ttattggcat atggtttacc catcttaatt ttaatgcaac caaacaacaa 240
agaaacaaaa actgtataag atacaagggtg ttttacgatt ttccgtctta aaaccgaaat 300
atttttgttc ctacgacttt aaacggactt tgcttaagtt gtgtgcatgt aagctcgtcg 360
tccctcgatt gtcacaaaca ttaccaata tcagcctcta tcacacgagt gaagggtggtg 420

```

attcggctta atgaaaacag agaaatattt caatatgatt cctattaaat tttaaattctt 480
 tttttctaat ctctagattt tcattaaaag catcatgatt tttttccact atgttcatat 540
 atctctatca cagtttttagg tacattgtag aaattggata agatacgtca tacgtctaac 600
 atgaatttgg tctagcaagg aaggtttgag ataataagtg aaaagaaaac acaagataat 660
 aaattataat ttataaatgc tttatagtat tgaaaaataa gatgattttt ttttttttta 720
 ataccggatt ggctgatcca cttatgatga ctcaaatgtt attaagtttc aagacaattt 780
 atgatgacac aaatcacaat gagtcaatag tagccacgaa gccagaaaaa aaaaatgtac 840
 tacaaaaaga taatgatagt acaaaatgat acgtcgtact gccacatgta cgacacaact 900
 cgattaccaa aaagcagagc catccaacca taaaactcaa aacacacaga ttccactggc 960
 gtgtgctctc ctcaattcac tcgtccttga aacttgaggt actga 1005

<210> 59
 <211> 1002
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(1002)
 <223> Ceres Promoter YP0190

<400> 59
 taaatagtga cattggtaag aagaaaaaaaa acactattaa atagtgaaaa aatggtttat 60
 aactctctta attaacatta cttattattg ctagcaccta aaatctccca caaaatattt 120
 gttgtaaaac acaaatttac aaaatgattt tgtttttaaa ttagtaacac atgttcatat 180
 atacgttaat aagaacatac cctatatgat tttatataaa aaaatttctt tgagacgtct 240
 tattcttttt tctttaataa tatgcaattg tgagagtttg gatttgaatg gtagcattag 300
 aagcaaactt gaaccaaaca tatttcatga agtcaaactt gaaccaatgt gatcactaat 360
 cacagtgttc gcagtgtgag gcatcagaaa atagaagaag ggacatagct atgaatcata 420
 taatcttgac acatgtttta taggttttag gtgtgtatgc taacaaaaaa tgagacagct 480
 ttctttctaat agacttaata tttgggctaa atgtaccaca gttgtgaatt tcttacaaaa 540
 atgggccgag ctacaaaaaa ctacaggccc actctcaact cttatcaaac gacagcgttt 600
 tactttttta aaagcacaca ctttttgttt ggtgtcggtg acggtgagtt tcgtccgctc 660
 ttccttttaa ttgaagcaac ggttttgatc cgatcaaata caacggtgct gattacacaa 720
 agcccagagc gaaaacgttg actattaagt taggttttaa tctcagccgt taatctacaa 780
 atcaacggtt ccctgtaaaa cgaatcttcc ttccttcttc acttccgctt cttctctctc 840
 aatcacctca aaaaaatcga tttcatcaaa atattcaccc gcccgattt gactctccga 900

tcatogtctc cgaatctaga tcgacgagat caaaacccta gaaatctaaa tcggaatgag 960
aaattgattt tgatacgaat tagggatctg tgtgttgagg ac 1002

<210> 60
<211> 995
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(995)
<223> Ceres Promoter YP0212

<400> 60
agtogattgg tacactctta atttaattag agtaagagat caacaaaaat atagaatttt 60
ctttatatcg aagtgctacg accttatata tatagaaaaa aaagcatagg tgaatctcta 120
aattgagatt gtgctgtagt aaacatatta agtttttagt ttttttaaga aatgaatctt 180
tttgttgatt aattcaaact agtagtcatt aagattccgg agattccaat ttagaaaagt 240
caaagattca aagaacaagt ccaggccac atgttgaatc cgattcatca tccactcatc 300
cttcatatct tctccaccg tctccgccca aaaaatcaat aacaataaaa aatcctaaaa 360
aaacatattt gattttgaaa aaactttatc atatattata ttaattaaat agttatccga 420
tgactcatcc tatggtcagg gccttgctgt ctctgacgtc cttaattatc attattttta 480
aatttgtctc tctcagaaaa ttacgccaca atcttctctt ttcccttttc cgaaaacagc 540
taatatttgt ggacctaaac taaataacgt agcctctaga ttttatataa ttactaatac 600
tatatgctac tacttgttat tatttactcc aatcatatat gataccaatc aagaatcact 660
acataagtag aaaactttgc aatgagtcca ttaattaaaa ttaagaataa acttaaaatt 720
ttatggtatt ttaagattcc ctttggattg taatgacaag aaatcagcaa attagtcgta 780
actcgtaaga ataaacaaga tcaattttta ctttctttac aaagattccg ttgtaatttt 840
agaaattttt ttttgtcact gtttttttat agattaattt atctgcatca atccgattaa 900
gaagtgtaca catgggcac tatatatata taacaggtaa aacgtgtatg tacatgcata 960
aggttttacg tgcttctata aatatatgtg gcagt 995

<210> 61
<211> 1024
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1024)
<223> Ceres Promoter YP0214

<400> 61
ccagtcgatt ggcgcctcgc atgcctatca tatttaaccg tcaataatgg atttggcgggt 60
tttggttaggc cgggtcaacc ggattaaaag aaaacggttt ggagtccttc cttgcaattg 120
aattttcaca cattcgggtt ttgtgatttc tctgtcataa tgggcccggc acatatgggtt 180
cataacccat gtgggcctat ggtataatit ttccaattaa aactattgtt aggtcgataa 240
aacaacaaac aataaaaacg agtgaatac acataccaaa aagaatgtga tgaacattag 300
taattttatt ttgatgggta atgaaaaaca aaataaatgc atcttggcat cttccgttgg 360
aaagcgcaaa tagggcagat tttcagacag atatcactat gatgggggggt gagagaaaga 420
aaacgaggcg tacctaattg aacactactt aattagtcgt tagttatagg actttttttt 480
tgtttggggc tagttatagg atcataaggt aaaaatgaag aatgaatatt agattagtag 540
gagctaataa tggagttaag tatgcacgtg taagaactgg gaagtgaac ctcctgtatg 600
gtgaagaaac tatacaacaa agccctttgt tgggtgtatac gtattaattt ttattctttt 660
atcacaagcg atacgtatct taagacataa taaatatata tcttactcat aataaatatc 720
ttaagatata tatacagtat acacctgtat atatataata aataggcata tagtagaaat 780
taatatgagt tgttgttgtt gcaaatatat aaatcaatca aaagatttaa aaccacccat 840
tcaatcttgg taagtaacga aaaaaaggg aagcaagaag aaccacagaa aagggggcta 900
acaactagac acgtagatct tcatctgcc gtccatctaa cctaccacac tctcatcttc 960
tttttcccggt gtcagtttgt tatataagct ctcaactctcc ggtatatttc cccattgcac 1020
tgga 1024

<210> 62
<211> 911
<212> DNA
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(911)
<223> Ceres Promoter YP0263

<400> 62
atctagctgt ggattccacc aaaattcttg cagggccatg atctaaaaac tgagactgcg 60
cgtgttgttt tgcagtgatt tgtatttcac atttgcacca tccacacag tccacttgggt 120
atcgtaacca aacataagga gaacctaat acattattgt ttttaatttcg tcaaactgggt 180
ttttaccttt tagttacata gttgattctt catttgtttt agtagttatg gagcacaata 240
atgtgcaaca aagaaagatc atagtggatt aatatgttga gaggtcagaa attcttgggt 300
aacaacaaaa agttacaagg actgagattt tgggtgggag aaagccatag cttttaaaa 360

atgattgaac ttaaaagtga tgttatggtt tgaggggaaa aagggtgatg tcaactaaga 420
tagttgaagt aatgtcttaa actaaagtaa accaccggtc caaccgtggt ccggaagcat 480
ctctgggtatg atttatccta aaaatcaaaa tagtagaaac atactttaaa tatatacatt 540
gatcggacga aaattgtaaa ctagtatagt ttcaaaaact agttgaacag gttatgtacc 600
ttaaacatitt atttcaaact taaacactaa agaacatata tgaatagaag tttatataaa 660
ttactatata tctaccataa atctcttata attatgatgt cacgatgagg aagtgttgaa 720
acgttaaaat gccaaaatat aagcatgcga cggaattttg gcagaagatt gtagagttgt 780
aatctgtcgc aatcattact cgtgctagca tttttcattt tcccttcatt tgtggataac 840
gcacgatata acattctaca caccaacaag attctataaa aacgcaaagg ttgtctccat 900
agaatatcgt c 911

<210> 63
<211> 999
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(999)
<223> Ceres Promoter YP0275

<400> 63
aaacattaat atgtagtaac tatgggcgta tgctttactt tttaaaatgg gcctatgcta 60
taattgaatg acaaggatta aacaactaat aaaattgtag atgggttaag atgacttatt 120
tttttactta ccaatttata aatgggcttc gatgtactga aatatatcgc gcctattaac 180
gaggccattc aacgaatgtt ttaagggccc tatttcgaca ttttaaagaa cacctaggtc 240
atcattccag aaatggatat tataggattt agataatttc ccacgtttgg tttatttatc 300
tattttttga cgttgaccaa cataatcgtg cccaaccgtt tcacgcaacg aatttatata 360
cgaaatatat atatttttca aattaagata ccacaatcaa aacagctgtt gattaacaaa 420
gagatTTTTT ttttttggtt ttgagttaca ataacgttag aggataaggt ttcttgcaac 480
gattaggaaa tcgtataaaa taaaatatgt tataattaag tgTTTTTTT tataatgagt 540
attaatataa ataaaacctg caaaaggata gggatattga ataataaaga gaaacgaaag 600
agcaatttta ctcttttata attgaaatta tgtgaatgtt atgtttacaa tgaatgattc 660
atcgttctat atattgaagt aaagaatgag tttattgtgc ttgcataatg acgttaactt 720
cacatataca cttattacat aacatttatc acatgtgcgt cttttttttt ttttactttg 780
taaaatttcc tcaacttttaa gacttttata acaattacta gtaaaataaa gttgcttggg 840

gctacaccct ttctccctcc aacaactcta tttatagata acattatatac aaaatcaaaa 900
catagtcctt ttcttctata aagggtttttt cacaacaaaa tttccattat aaatcaaaaa 960
ataaaaaactt aattagtttt tacagaagaa aagaaaaca 999

<210> 64
<211> 981
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(981)
<223> Ceres Promoter YP0285

<400> 64
gggattatat atgatagacg attgtatttg cgggacattg agatgtttcc gaaaatagtc 60
atcaaataac aaaccagaat ttgatgtgaa aacactaatt aaaacatata attgacaact 120
agactatatac atttggttaag ttgagcggtg aaagaaaatg aaagagtgtg gactgtagta 180
cgtatgagtt tcccaaaaaga tgggtgcttg atattattgg gaagagactt tgggttggttc 240
ggttgaatga agattttttac ctgccatggt gatagagaaa ggcaaataaa tgtaggggtc 300
gatgtctaac gtaaagactg gatcaaccaa gagtcctcct cctcgtcttc accaaaaaaa 360
aagagtcctc ctcggtgaaa cttatttctt ctccagccaa gatctcatct catctcttca 420
ctctatgaaa tataaaggaa tcttatgggt tttctaaaaa ctatagtacg tctatatacc 480
aaaggaaaca atataaaatc agttaatctg ataaattttg agtaaataat aaagttaact 540
ttgtacttac ctatatcaaa ctaattcaca aaataaagta ataataacaa agaattttta 600
gtagatccac aatatacaca cacactatga gaaatcataa tagagaatth taatgattht 660
gtctaactca tagcaacaag tcgctttggc cgagtgggtta aggcgtgtgc ctgctaagta 720
catgggctct gccgcgaga gttcgaatct ctccggcgac gtttcttttg ttttcggcca 780
taaaggaaaa agcccaatta acacgtctcg cttataagcc cataaagcaa acaatgggct 840
gtctctgtct cactcacaca cgcgttttcc tactttttga ctatttttat aaccggcggg 900
tctgacttaa ttagggtttt ctttaataat cagacactct ctactcgtt tcgtcaacat 960
tgaacacaga caaaaccgcg t 981

<210> 65
<211> 996
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(996)

<223> Ceres Promoter YP0286

<400> 65

```
gaaaacaatc ataggttacg ctattatcat cgaaaggtat gtgatgcata ttcccattga 60
accagatttc catatatattt atttgtaaag tgataatgaa tcacaagatg attcaatatt 120
aaaaatgggt aactcacttt gacgtgtagt acgtggaaga atagtttagct atcacgcata 180
catatatcta tgaataagtg tgtatgacat aagaaactaa aatatttacc taaagtccag 240
ttactcatac tgatttcatg catatatgta ttatttattt atttttaata aagaagcgat 300
tggtgttttc atagaaatca tgatagattg ataggatattt cagttccaca aatctagatc 360
tgtgtgctat acatgcatgt attaatTTTT tccccttaaa tcatttcagt tgataatatt 420
gctctttggt ccaacttttag aaaaggtatg aaccaacctg acgattaaca agtaaacatt 480
aattaatctt tatatgagat aaaaccgagg atatatatga ttgtgttgct gtctattgat 540
gatgtgtcga tattatgctt gttgtaccaa tgctcgagcc gagcgtgatc gatgccttga 600
caaactatat atgtttcccg aattaattaa gttttgtatc ttaattagaa taacattttt 660
atacaatgta atttctcaag cagacaagat atgtatccta tattaattac tatatatgaa 720
ttgccgggca cctaccagga tgtttcaaat acgagagccc attagtttcc acgtaaatca 780
caatgacgcg acaaaatcta gaatcgtgtc aaaactctat caatacaata atatatattt 840
caagggcaat ttcgacttct cctcaactca atgattcaac gccatgaatc tctatataaa 900
ggctacaaca ccacaaagga tcatcagtca tcacaaccac attaaactctt caccactatc 960
tctcaatctc tcgtttcatt tcttgacgcg tgaaaa 996
```

<210> 66

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter YP0337

<400> 66

```
taattttttt atttttggaa ctaacactta ttagtttagg tttccatcac ctatttaatt 60
cgtaattctt atacatgcat ataatagaga tacatatata caaatttatg atcatTTTTTg 120
cacaacatgt gatctcattc attagtatgc attatgCGAA aacctcgacg cgcaaaagac 180
acgtaatagc taataatgtt actcatttat aatgattgaa gcaagacgaa aacaacaaca 240
tatatatcaa attgtaaact agatatttct taaaagtGAA aaaaaacaaa gaaatataaa 300
ggacaatttt gagtcagtct cttaatatta aaacatatat acataaataa gcacaaacgt 360
```

```

ggttacctgt cttcatgcaa tgtggacttt agtttatcta atcaaaatca aaataaaagg 420
tgtaatagtt ctcgtcattt ttcaaatttt aaaaatcaga accaagtgat ttttgtttga 480
gtattgatcc attgttttaa caatttaaca cagtatatac gtctcttgag atgttgacat 540
gatgataaaa tacgagatcg tctcttggtt ttcgaatttt gaactttaat agttttcttt 600
tttagggaaa ctttaatagt tgtttatcat aagattagtc acctaatggt tacgttgacg 660
taccgaacca attttttacc cttttttcta aatgtggtcg tggcataatt tccaaaagag 720
atocaaaacc cggtttgctc aactgataag ccggtcggtt ctggtttgaa aaacaagaaa 780
taatctgaaa gtgtgaaaca gcaacgtgct tcggtgtttc atgagccacc tgccacctca 840
ttcacgtcgg tcattttgtc gtttcacggt tcacgctcta gacacgtgct ctgtccccac 900
catgactttc gctgccgact cgcttcgctt tgcaaactca aacatgtgtg tatatgtaag 960
tttcatccta ataagcatct cttaccacat taattaaaaa 1000

```

<210> 67

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter YP0356

<400> 67

```

ttagttcatt gaaacgtcaa ctttttactt gcaaccactt tgtaggacca ttaactgcaa 60
aataagaatt ctctaagctt cacaaggggt tcgtttggtg ctataaaaac attgttttaa 120
gaactggttt actggttcta taaatctata aatccaaata tgaagtatgg caataataat 180
aacatgttag cacaaaaaat actcattaaa ttcctacca aaaaaaatct ttatatgaaa 240
ctaaaactta tatacacaat aatagtgata caaagtaggt cttgatattc aactattcgg 300
gattttctgg tttcgagtaa ttcgtataaa aggtttaaga tctattatgt tcaactgaaat 360
cttaactttg ttttgtttcc agttttaact agtagaaatt gaaattttta aaaattgtta 420
cttacaataa aatttgaatc aatatcctta atcaaaggat cttaagacta gcacaattaa 480
aacatataac gtagaatatc tgaaataact cgaaaatatc tgaactaagt tagtagtttt 540
aaaatataat cccggtttgg accgggcagt atgtacttca atacttgtgg gttttgacga 600
ttttggatcg gattgggcgg gccagccaga ttgatctatt acaaatttca cctgtcaacg 660
ctaactccga acttaatcaa agattttgag ctaaggaaaa ctaatcagtg atcacccaaa 720
gaaaacattc gtgaataatt gtttgctttc catggcagca aaacaaatag gacccaaata 780
ggaatgtcaa aaaaaagaaa gacacgaaac gaagtagtat aacgtaacac acaaaaaata 840

```

actagagata ttaaaaacac atgtccacac atggatacaa gagcatttaa ggagcagaag 900
gcacgtagtg gttagaaggt atgtgatata attaatcggc ccaaatagat tggtaagtag 960
tagccgtota tatcatccat actcatcata acttcaacct 1000

<210> 68
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter YP0374

<400> 68
aagacacccg taaatgttgt catgtagaag aaactagaaa cgttaaacgc atcaaatcaa 60
gaaattaaat tgaaggtaat ttttaacgcc gcctttcaaa tattcttcct aggagaggct 120
acaagacgcy tattttctttc gaattctcca aaccattacc attttgatat ataataccga 180
catgccgttg ataaagtgtg tatgcaaatac gttcattggg tatgagcaaa tgccatccat 240
tggttcttgt aattaaatgg tccaaaaata gtttgttccc actactagtt actaatttgt 300
atcactctgc aaaataatca tgatataaac gtatgtgcta tttctaatta aaactcaaaa 360
gtaatcaatg tacaatgcag agatgaccat aaaagaacat taaaacacta cttccactaa 420
atctatgggg tgcccttgga aggcaattga ataaggagaa tgcataaga tgatatagaa 480
aatgctattc agtttataac attaatgttt tggcggaaaa tttctatat attagacctt 540
tctgtaaaaa aaaaaaatg atgtagaaaa tgctattatg tttcaaaaat ttcgcactag 600
tataatacgg aacattgtag tttacactgc tcattacat gaaaaccaag gcagtatata 660
ccaacattaa taaactaaat cgcgatttct agcaccacca ttaattaatt ttactattat 720
acattctctt tgcttctoga aataataaac ttctctatat cattctacat aataaataag 780
aaagaaatcg acaagatcta aatttagatc tattcagctt tttcgctga gaagccaaaa 840
ttgtgaatag aagaaagcag tcgtcatctt cccacgtttg gacgaaataa aacataacaa 900
taataaaata ataaatcaaa tatataaatc cctaatttgt ctttattact ccacaatttt 960
ctatgtgtat atatataccc acctctctct tgtgtatttg 1000

<210> 69
<211> 998
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature

<222> (1)..(998)

<223> Ceres Promoter YP0377

<400> 69

```
tataaaccat tcctataaca ccatatTTTaa acataacaat gaattgcttg gatttcaaac 60
tttatttaaT ttggattTTTt aattTTTtatt tgattgaatt ataccccctt aattggataa 120
attcaaatat gtcaactTTTt tTTTtgtaag atTTTtTTTt ggaaaaaaa attgattatt 180
cactaaaaag atgacaggTt acttataatt taatatatgt aaaccctaaa aagaagaaaa 240
tagTTTctgt tTtcactTTt ggtcttatta tctaaacttc tTTaagaaaa tcgcaataaa 300
ttggTTtgag tTctaactTTt aaacacatta atattTgtgt gctattTTaa aaataattTt 360
caaaaaaaa aacaaattga cagaaaatat caggTTTtTgt aataagatat tTcctgataa 420
atatttaggg aatataacat atcaaaagat tcaaattctg aaaatcaaga atggtagaca 480
tgtgaaagTt gtcatcaata tggTccactt tTctTtTctc tataacccaa aattgaccct 540
gacagtcaac ttgtacacgc ggccaaacct tTTtataatc atgctattTt tTtcttTcat 600
TTTTattota tTtgotatct aactgattTTt tcatTaacat gataccagaa atgaatttag 660
atggattaat tctTTTccat ccacgacatc tggaaacact tatctcctaa tTaacctTtac 720
TTTTTTTTtT gTTTgtgtgc tCctTcataa aatctatatt gTTTaaaaca aaggTcaata 780
aatataaata tggataagTa taataaatct tTattggata tTtctTTTTt taaaaaagaa 840
ataaatctTTt tTtggatatt tTcgtggcag catcataatg agagactacg tcgaaaccgc 900
tggcaaccac tTTtgccgcg tTTaatTTct tTctgaggct tatataaata gatcaaaggg 960
gaaagtgaga tataatacag acaaaacaag agaaaaga 998
```

<210> 70

<211> 999

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(999)

<223> Ceres Promoter YP0380

<400> 70

```
acaagtacca tTcactTTTt tactTTTtcaa tgtatacaat catcatgtga taaaaaaaaa 60
aatgtaacca atcaacacac tgagatacgg ccaaaaaatg gtaatacata aatgtTtgta 120
ggTTTtgtaa tTTaaatact ttagTTaagt tatgattTTt tTattTTTgc tTatcactTt 180
tacgaaatca tcaatctatt ggtatctctt aatcccgtt tTTaatTTcc accgcacacg 240
caaatcagca aatggTtcca gccacgtgca tgtgaccaca tattgtggTc acagtactcg 300
tctTTTTTTt tTctTTTtgta atcaataaat tTcaatccta aaactTcaca cattgagcac 360
```

gtcggcaacg ttagctccta aatcataacg agcaaaaaag ttcaaattag ggtatatgat 420
caattgatca tcaactacatg tctacataat taatatgtat tcaaccggtc ggtttgttga 480
tactcatagt taagtatata tgtgctaatt agaattagga tgaatcagtt cttgcaaaca 540
actacggttt catataatat gggagtgtta tgtacaaaat gaaagaggat ggatcattct 600
gagatgttat gggctcccag tcaatcatgt tttgctcgca tatgctatct tttgagtctc 660
ttcctaaact catagaataa gcacgttggg tttttccacc gtcctcctcg tgaacaaaag 720
tacaattaca ttttagcaaa ttgaaaataa ccacgtggat ggaccatatt atatgtgatc 780
atattgottg togtcttctg tttcttttaa atgtttacac cactacttcc tgacacgtgt 840
ccctattcac atcatccttg ttatatcgtt ttacttataa aggatcacga acaccaaacc 900
atcaatgtgt acgtcttttg cataagaaga aacagagagc attatcaatt attaacaatt 960
acacaagaca gcgagattgt aaaagagtaa gagagagag 999

<210> 71

<211> 1000

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1000)

<223> Ceres Promoter YP0381

<400> 71

cacggtcaaa gtattgctaa catgggcatt acattgaaaa agaaaattaa ttgtctttac 60
tcatgtttat tctatacaaa taaaaatatt aaccaaccat cgcactaaca aaatagaaat 120
cttattctaa tcaacttaatt gttgacaatt aaatcattga aaaatacact taaatgtcaa 180
atattcgttt tgcatacttt tcaattttaa tacattttaa gttcgacaag ttgcgtttac 240
tatcatagaa aactaaatct cctaccaaag cgaaatgaaa ctactaaagc gacaggcagg 300
ttacataacc taacaaatct ccacgtgtca attaccaaga gaaaaaaga gaagataagc 360
ggaacacgtg gtagcacaaa aaagataatg tgattttaa taaaaaaca aaacaaagac 420
acgtgacgac ctgacgctgc aacatcccac cttacaacgt aataaccact gaacataaga 480
cacgtgtaog atcttgtctt tgttttctcg atgaaaacca cgtgggtgct caaagtcctt 540
gggtcagagt cttccatgat tccacgtgtc gttaatgcac caaacaaggg tactttcggt 600
attttggctt ccgcaaatta gacaaaacag ctttttgttt gattgatttt tctcttctct 660
ttttccatct aaattctctt tgggctctta atttcttttt gagtgttcgt tcgagatttg 720
tcggagattt tttcggtaaa tgttgaaatt ttgtgggatt tttttttatt tctttattaa 780

acttttttttt attgaatttta taaaaaggga aggtcgtcat taatcgaaga aatggaatct 840
tccaaaatttt gatatttttgc tgttttcttg ggatttgaat tgctctttat catcaagaat 900
ctgttataaat ttctaatacta aaatctaagt tgagaaaaag agagatctct aatttaaccg 960
gaattaatat tctccgaccg aagttattat gttgcaggct 1000

<210> 72

<211> 999

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(999)

<223> Ceres Promoter YP0384

<400> 72

tttaaaaaat tggataaaac accgataaaa attcacattt gcaaatttta ttcagtcgga 60
atatatatatt gaaacaagtt ttgaaatcca ttggacgatt aaaattcatt gttgagagga 120
taaatatgga tttgttcata tgaacatgt cgttgattag tgattgacta ccatgaaaaa 180
tatgttatga aaagtataac aacttttgat aaatcacatt tattaacaat aaatcaagac 240
aaaatatgtc aacaataata gtagtagaag atattaattc aaattcatcc gtaacaacaa 300
aaaatcatat cacaattaag tgtacagaaa aaccttttgg atatatttat tgtcgtcttt 360
caatgatttt cgtgaaaagg atatatttgt gtaaaataag aaggatcttg acgggtgtaa 420
aaacatgcac aattcttaat ttagaccaat cagaagacaa cacgaacact tctttattat 480
aagctattta acaaaatctt gcctattttg cttagaataa tatgaagagt gactcatcag 540
ggagtggaaa atatctcagg atttgctttt agctctaaca tgtcaaacta tctagatgcc 600
aacaacacaa agtgcaaatt cttttaatat gaaaacaaca ataatatttc taatagaaaa 660
ttaaaaaggg aaataaaata tttttttaa atatacaaaa gaagaaggaa tccatcatca 720
aagttttata aaattgtaat ataatacaaa cttgtttgct tccttgtctc tccctctgtc 780
tctctcatct ctcttatctt ctccatatat acttcatctt cacacccaaa actccacaca 840
aaatatctct ccctctatct gcaaattttc caaagttgca tcctttcaat tccactcct 900
ctctaataata attcacattt tccactatt gctgattcat ttttttttgt gaattatttc 960
aaaccacat aaaaaaatct ttgttttaat ttaaaacca 999

<210> 73

<211> 998

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature
<222> (1)..(998)
<223> Ceres Promoter YP0385

<400> 73
actcaacaat aggacaagcc aaaaaaatc caattattgt gttactctat tcttctaaat 60
ttgaacacta atagactatg acatatgagt atataatgtg aagtcttaag atattttcat 120
gtgggagatg aataggccaa gttggagtct gcaaacaaga agctcttgag ccacgacata 180
agccaagttg atgaccgtaa ttaatgaaac taaatgtgtg tggttatata ttagggaccc 240
atggccatat acacaatttt tgtttctgtc gatagcatgc gtttatatat atttctaaaa 300
aaactaacat atttactgga tttagattcg aatattgaca ctaatatata ctacgtacca 360
aactacatat gtttatctat atttgattga tcgaagaatt ctgaactgtt ttagaaaatt 420
tcaatacact taacttcata ttacaacggt aaaagaaatc accactagac aaacaatgcc 480
tcataatgtc tcgaaccctc aaactcaaga gtatacattt tactagatta gagaatttga 540
tactctcaag ttgccaaaga attggaagct ttgtttacca aacttagaaa cagaagaagc 600
cacaaaaaaaa gacaaaggga gttaaagatt gaagtgatgc atttgtctaa gtgtgaaagg 660
tctcaagtct caactttgaa ccataataac attactcaca ctcccttttt ttttcttttt 720
ttttcccaaa gtaccctttt taattccctc tataaccacac tcactccatt ccctctttct 780
gtcactgatt caacacgtgg ccacactgat gggatccacc tttcctctta ccacctccc 840
ggtttatata aacccttcac aacacttcac cgctctcaaa ccaactctct ctctctctct 900
ctctctctct ttctacaaga agaaaaaaaa cagagccttt acacatctca aaatcgaact 960
tactttaacc accaaatact gattgaacac acttgaaa 998

<210> 74
<211> 1000
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(1000)
<223> Ceres Promoter YP0396

<400> 74
catagtaaaa gtgaatttaa tcatactaag taaaataaga taaaacatgt tatttgaatt 60
tgaatatcgt gggatgcgta tttcgggtatt tgattaaagg tctggaaacc ggagctccta 120
taaccggaat aaaaatgcat aacatgtttc tccccaacga ggcgagcggg tcagggcact 180
agggtcattg caggcagctc ataaagtcac gatcatctag gagatcaaat tgtatgtcgg 240
ccttctcaaa attacctcta agaattctca acccaatcat agaacctcta aaaagacaaa 300

gtcgtcgcctt tagaatgggt tcggtttttg gaaccatatt tcacgtcaat ttaatgttta 360
gtataatttc tgaacaacag aattttggat ttatttgcac gtatacaa atctaattaa 420
taaggacgac tcgtgactat ccttacatta agtttactg tcgaaataac atagtacaat 480
acttgtcgtt aatttccacg tctcaagtct ataccgtcat ttacggagaa agaacatctc 540
tgtttttcat ccaaactact attctcactt tgtctatata tttaaaatta agtaaaaaag 600
actcaatagt ccaataaaaat gatgaccaa tgagaagatg gttttgtgcc agattttagg 660
aaaagtgagt caaggtttca catctcaaat ttgactgcat aatcttcgcc attaacaacg 720
gcattatata tgtcaagcca attttccatg ttgcgtactt ttctattgag gtgaaaatat 780
gggtttgttg attaatcaaa gagtttgcct aactaatata actacgactt tttcagtgac 840
cattccatgt aaactctgct tagtgtttca tttgtcaaca atattgtcgt tactcattaa 900
atcaaggaaa aatatacaat tgtataattt tcttatattt taaaattaat tttgatgtat 960
taccoccttta taaataggct atcgctacaa caccaataac 1000

<210> 75

<211> 1514

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1514)

<223> Ceres Promoter p13879

<400> 75

tttcgatcct cttctttttt aggtttcttg atttgatgat cgccgccagt agagccgtcg 60
tcggaagttt cagagattaa aaccatcacc gtgtgagttg gtagcgaatt aacggaaagt 120
ctaagtcaag atttttttaa aagaaattta tgtgtgaaaa gaagccgttg tgtatattta 180
tataatttag aaaatgtttc atcattttta ttaaaaaatt aataatttgt agaagaaaga 240
agcatttttt atacataaat cattttacctt ctttactgtg tttttcttca cttacttcat 300
ttttaacttt ttacaaaaaa gtgaaaagta aattacgtaa ttggtaacat aaattcactt 360
taaatttgca tatgttttgt tttcttcgga aactatatcg aaaagcaaac ggaaagaact 420
tcacaaaaaa ccctagctaa ctaaagacgc atgtgttctt cttattcttc atatatcctc 480
tgtttcttgt gttctgtttt gagtcttaca ttttcaatat ctgactctga ttactatata 540
taaaagggaa catgaagaac ttgagaccat gttaaactgt acaatgcctt caaacatggc 600
taactaaaga tacattagat ggctttacag tgtgtaatgc ttattatctt taggtttttt 660
aaatcccttg tattaagtta ttaccaa atgtgttcttg tactgcttat tggcttggtt 720

gttgtgtgct ttgtaaacaa cacctttggc tttatttcat cctttgtaa cctactggtc 780
 tttgttcagc tcctcttgga agtgagtttg tatgcctgga acgggtttta atggagtgtt 840
 tatcgacaaa aaaaaaatgt agcttttgaa atcacagaga gtagttttat attcaaatta 900
 catgcatgca actaagtagc aacaaagttg atatggccga gttggtctaa ggcgccagat 960
 taaggttctg gtccgaaagg gcgtgggttc aaatcccact gtcaacattc tctttttctc 1020
 aaattaatat ttttctgcct caatggttca ggcccaatta tactagacta ctatcgcgac 1080
 taaaataggg actagccgaa ttgatccggc ccagtatcag ttgtgtatca ccacgttatt 1140
 tcaaatttca aactaaggga taaagatgtc atttgacata tgagatatatt ttttgctcca 1200
 ctgagatatatt tttctttgtc ccaagataaa atatcttttc tcgcatcgtc gtctttccat 1260
 ttgcgcatta aacccaaaag tgtcacgtga tatgtcccca accactacga attttaacta 1320
 cagatttaac catggttaaa ccagaattca cgtaaaccga ctctaaacct agaaaatata 1380
 taaaccttgg ttaatatctc agccccctta taaataacga gacttcgtct acatcgttct 1440
 acacatctca ctgctcacta ctctcactgt aatcccttag atcttctttt caaatttcac 1500
 cattgcactg gatg 1514

<210> 76

<211> 1954

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> misc_feature

<222> (1)..(1954)

<223> Ceres Promoter p326

<400> 76

gtgggtaaaa gtatccttct ttgtgcattt ggtattttta agcatgtaat aagaaaaacc 60
 aaaatagacg gctgggtattt aataaaagga gactaatgta tgtatagtat atgattttgtg 120
 tggaatataa taaagttgta aaatatagat gtgaagcgag tatctatctt ttgactttca 180
 aaggtgatcg atcgtgttct ttgtgatagt tttggctgct ggtctacaag tcaacaacca 240
 ccttgaagtt ttcgcgtctc ggtttcctct tcgcatctgg tatccaatag catacatata 300
 ccagtgcgga aaatggcgaa gactagtggg ctigaaccat aagggttggc cccaatacgg 360
 attccaaaca acaagcctag cgcagtcttt tgggatgcat aagactaaac tgtcgcagtg 420
 atagacgtaa gatatatcga cttgattgga atcgtctaag ctaataagtt taccttgacc 480
 gtttatagtt gcgtcaacgt ccttatggag attgatgcc atcaaataaa cctgaaaatc 540
 catcaccatg accaccataa actcccttgc tgccgtgct ttggcttgag caagggtgtt 600
 ccttgtaaag ctccgatctt tggataaagt gttccacttt ttgcaagtag ctctgacccc 660

tctcagagat gtcaccggaa tcttagacag aacctcctct gccaaatcac ttggaagatc 720
 ggacaatgtc atcatTTTTg caggtaattt ctccttcgtt gctgctttgg cttgagcacg 780
 gtgcttcttt gtaaagctcc gatctttgga taagagcgga tcggaatcct ctaggagggtg 840
 ccagtccctt gacctattaa tttatagaag gtttttagtgt attttgttcc aatttcttct 900
 ctaacttaac aaataacaac tgcctcatag tcatgggctt caaattttat cgcttggtgt 960
 atttoggttat ttgcaaggcc ttggcccatt ttgagcccaa taactaaatc tagccttttc 1020
 agaccggaca tgaacttcgc atattggcgt aactgtgcag ttttaccttt ttcggtacag 1080
 acaagatcag atttagacca cccaacaata gtcagtcata ttgacaacc taagctagcc 1140
 gacactacta aaaagcaaac aaaagaagaa ttctatgttg tcattttacc ggtggcaagt 1200
 ggacccttct ataaaagagt aaagagacag cctgtgtgtg tataatctct aattatgttc 1260
 accgacacaa tcacacaaac ctttctctaa tcacacaact tcttcatgat ttacgacatt 1320
 aattatcatt aactctttta attcacttta catgctcaaa aatatctaatt ttgcagcatt 1380
 aatttgagta ccgataacta ttattataat cgtcgtgatt cgcaatcttc ttcatlagat 1440
 gctgtcaagt tgtactcgca cgcggtggtc cagtgaagca aatccaacgg tttaaaacct 1500
 tcttacattt ctagatctaa tctgaaccgt cagatatcta gatctcattg tctgaacaca 1560
 gtttagatgaa actgggaatg aatctggacg aaattacgat cttacaccaa cccctcgac 1620
 gagctcgtat atataaagct tatacgtcc tccttcacct tcgtactact actaccacca 1680
 catttcttta gctcaacctt cattactaat ctccttttaa ggtatgttca ctttcttcg 1740
 attcatactt tctcaagatt cctgcatttc tgtagaattt gaaccaagtg tcgatttttg 1800
 tttgagagaa gtgttgattt atagatctgg ttattgaatc tagattccaa tttttaattg 1860
 attcgagttt gttatgtgtg tttatactac ttctcattga tcttgtttga tttctctgct 1920
 ctgtattagg tttctttcgt gaatcagatc ggaa 1954

<210> 77

<211> 2016

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(2016)

<223> Ceres Promoter p32449

<400> 77

gatcggcctt cttcaggtct tctctgtagc tctgttactt ctatcacagt tatcgggtat 60

ttgagaaaaa agagttagct aaaatgaatt tctccatata atcatggttt actacaggtt 120

tacttgattc gcgttagctt tatctgcac caaagttttt tccatgatgt tatgtcatat 180

gtgataccgt tactatgttt ataactttat acagtctggt tcactggagt ttctgtgatt 240
 atgttgagta catactcatt catcctttgg taactctcaa gtttaggttg tttgaattgc 300
 ctctgtttgtg atacttattg tctattgcat caatcttcta atgcaccacc ctagactatt 360
 tgaacaaaga gctgtttcat tcttaaacct ctgtgtctcc ttgctaaatg gtcattgcttt 420
 aatgtcttca cctgtctttc tcttctatag atatgtagtc ttgctagata gtttagttcta 480
 cagctctctt ttgtagtctt gttagagagt tagttgagat attacctctt aaaagtatcc 540
 ttgaacgctt tccggttatg accaatttgt tgtagctcct tgtaagtaga acttactggg 600
 accagcgaga cagtttatgt gaatgttcat gcttaagtgt cgaacgtatc tatctctact 660
 atagctctgt agtcttggtt gacagttagt ttatatctc catttttttg tagtcttgct 720
 agttgagata ttacctcttc tcttcaaagt atccttgaac gctcaccggg tatgaaatct 780
 ctacactata gctctgtagt cttgctagat agttagttct ttagctctct tttttagacc 840
 tagttcttta gctctccttt tgtagccttg ctacagagta agatgggata ttacctcctt 900
 gaacgctctc cggttatgac caatttggtg tagctccttg taagtagaac ttaggataga 960
 gtgagtcaac ttttaagaaag aacctagtat gtggcataac cagattgcag gctctgtctc 1020
 ggctacagta acgtaactct atagctcttt gttttgttca gaaagaacca gtgattggat 1080
 gattcgtcct tagaaactgg acctaacac agtcattggc tttgaaatca agccacaaca 1140
 atgcctatat gaaccgtcca tttcatttat ccgtttcaaa ccagcccatt acatttcgtc 1200
 ccattgataa ccaaaagcgg ttcaatcaga ttatgtttta attttaccaa attctttatg 1260
 aagttttaat tatactcaca ttaaaaggat tattggataa tgtaaaaatt ctgaacaatt 1320
 actgattttg gaaaattaac aaatatctt tgaaatagaa gaaaaagcct ttttcctttt 1380
 gacaacaaca tataaaatca tactccatt aaaaagattt taatgtaaaa ttctgaatat 1440
 aagatatttt ttacaacaac aaccaaaaat atttattttt ttcctttttt acagcaacaa 1500
 gaaggaaaaa cttttttttt tgtcaagaaa aggggagatt atgtaaacag ataaaacagg 1560
 gaaaataact aaccgaactc tcttaattaa catcttcaaa taaggaaaat tatgatccgc 1620
 atatttagga agatcaatgc attaaaacaa cttgcacgtg gaaagagaga ctatacgctc 1680
 cacacaagtt gcactaatgg tacctctcac aaaccaatca aaatactgaa taatgccaac 1740
 gtgtacaaat tagggtttta cctcacaacc atcgaacatt ctcgaaacat tttaaacagc 1800
 ctggcgccat agatctaaac tctcatcgac caatttttga ccgtccgatg gaaactctag 1860
 cctcaaccca aaactctata taaagaaatc ttttccttcg ttattgctta ccaaatacaa 1920
 accctagccg ccttattcgt cttcttcgtt ctctagtttt ttcctcagtc tctgttctta 1980

gatcccttgt agtttccaaa tcttccgata aggcct

2016

<210> 78

<211> 1024

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1024)

<223> Ceres Promoter PR0924

<400> 78

atctataacg agttaacatg ttgccagttt gaatcaagaa gcttggatga tgaatgaatg 60
gatcgggtttg tgggtacaatt cttaaaattg tagtagagga gacagagaaa aaacatgata 120
agacttttgt atttacaact tgacggagac aagacagtaa gccaaatctg tcacaaaaac 180
actcaaactc ttttctcagt gttttgagtt taaagagaga cttattcact tcccctttcg 240
taacacttat ttgtctccca accaaacagt ttctgtcctt tcccttggtc tcccacgtgc 300
atctttatat ctcatgactt ttcgtttcta gatcttgaat aatgtcttag tggattaggt 360
ttgttgtcgg taaattaggt gaccgttttt ttcttatatt tggaagatcg cgggatgaag 420
cagatactga gtttcagggc atacacacct aatttgaaaa tcattgttag tccaatttca 480
ctttaatctt gtttacaaaa aaattgatct gaaaatgttg atgggataag taaaaatgta 540
agttttgcta gtagtcatga tataataata gcaaaaccag atcaattttg agcaaaagga 600
agaaacaaaa aacagatcga tcccacgagc aagactaagt gtaaagtggg tcccacaaga 660
gccatatgga tatgggtcctt caacttttaa agcccattac ttcagtgggc gacccgacat 720
taogccacga gtagtcacgc acgcacgact ccgttcacgt gacattcacg ttgatatttc 780
ccoctctact ctcttctgct tggttgatct aaaaaacatg aagagaccaa cctaatttca 840
tattaatata tgatatagac ttcatactca acagtcactt tcgtaatcca aatccatatc 900
ttaogaaatt agttcttaat aaaggttgtg gattaagtta taatattgtg ttaagagtta 960
agacacagca tataaccttg taccaacagt gctttattct taaatggaaa caaacatat 1020
gtca 1024

<210> 79

<211> 857

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(857)

<223> Ceres Promoter PD1367

<220>
<221> misc_feature
<222> (116)..(116)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (136)..(136)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (154)..(154)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (159)..(159)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (168)..(168)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (172)..(172)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (175)..(175)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (679)..(679)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (680)..(680)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (686)..(686)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (724)..(724)
<223> n is a, c, t, g, unknown, or other

<220>
<221> misc_feature
<222> (737)..(737)
<223> n is a, c, t, g, unknown, or other

<400> 79
ttggaattaa ttctgcggcc atggggctgc aggaattcga tggcccgatc ggccacagtt 60
ttctttttctc atcttacaac aagtttccag gaggatagag acataaacga agctcnggat 120
tgtatcgttc ttttttnagct tttattcaca tccngaaang tcctgtangt tntangattc 180
tgttatcttg cggttttgag ttaatcagaa acagagtaat caatgtaatg ttgcaggcta 240
gatctttcat ctttggaat ttgttttttt ctcatgcaat ttcttttagct tgaccatgag 300
tgactaaaag atcaatcagt agcaatgatt tgatttggct aagagacatt tgtccacttg 360
gcatcttgat ttggatggtt acaacttgca agaccaatt ggatacttgc tatgacaact 420
ccaactcaag agtgtcgtgt aactaagaac cttgactaat ttgtaatttc aatcccaagt 480
catgttacta tatgtttttt tgtttgtatt attttctctc ctacaattaa gctctttgac 540
gtacgtaatc tccggaacca actcctatat ccaccattta ctccacgttg tctccaatta 600
ttggacgttg aaacttgaca caacgtaaac gtatctacgt ggttgattgt atgtacatat 660
gtacaaacgt acacctttnn ctctncttt cacttcatca cttggcttgt gaattcatta 720
attnctgcg aaggcctgc agggccatca ccactgcagt ggaacaatga agactaatct 780
ttttctcttt ctcatctttt cacttctcct atcattatcc tcggccgaat tcagtaaagg 840
agaagaactt ttcactg 857

<210> 80
<211> 884
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(884)
<223> Ceres CLONE ID no. 92459

<220>
<221> misc_feature
<222> (1)..(884)
<223> Also Known As Ceres ME LINE ME04077

<220>
<221> misc_feature
<222> (1)..(884)
<223> Also Known As Ceres LEAD Number 15

<220>
<221> CDS
<222> (42)..(663)
<223> Referenced by SEQ ID NO: 81

<400> 80
aggattaaat tagggcataa cccttatcgg agatttgaag ccatgggaag aagaaaaatc 60

gagatcaagc gaatcgagaa caaaagcagt cgacaagtca ctttctccaa acgacgcaat 120
ggctctcatcg acaaagctcg acaactttcg attctctgtg aatcctccgt cgctgttgtc 180
gtcgtatctg cctccggaaa actctatgac tcttctccg gtgacgacat ttccaagatc 240
attgatcgtt atgaaataca acatgctgat gaacttagag ccttagatct tgaagaaaaa 300
attcagaatt atcttccaca caaggagtta ctagaaacag tccaaagcaa gcttgaagaa 360
ccaaatgtcg ataatgtaag tgtagattct ctaatttctc tggaggaaca acttgagact 420
gctctgtccg taagtagagc taggaaggca gaactgatga tggagtatat cgagtccctt 480
aaagaaaagg agaaattgct gagagaagag aaccagggtc tggctagcca gatgggaaag 540
aatacgttgc tggcaacaga tgatgagaga ggaatgtttc cggaagtag ctccggcaac 600
aaaataccgg agactctccc gctgctcaat tagccaccat catcaacggc tgagttttca 660
ccttaaactc aaagcctgat tcataattaa gagaataaat ttgtatatta taaaaagctg 720
tgtaatatca aaccttttat ctctctctag tgtggaattt aaggtcaaaa agaaaacgag 780
aaagtatgga tcagtgttgt acctccttcg gagacaagat cagagtttgt gtgttttgtt 840
ctgaatgtac ggattggatt tttaaagttg tgctttcttt cttc 884

<210> 81
<211> 206
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(206)
<223> Ceres CLONE ID no. 92459

<220>
<221> misc_feature
<222> (1)..(206)
<223> Also Known As Ceres CDNA ID no. 23361912

<220>
<221> misc_feature
<222> (1)..(206)
<223> Also Known As Ceres ME LINE ME04077

<220>
<221> misc_feature
<222> (1)..(206)
<223> Also Known As Ceres LEAD Number 15

<220>
<221> misc_feature
<222> (117)..(166)
<223> Pfam Name: K-box; Pfam Description: K-box re.g.ion

<220>
<221> misc_feature

<222> (9)..(59)
<223> Pfam Name: SRF-TF; Pfam Description: SRF-type transcription factor (DNA-binding and dimerisation domain)

<220>
<221> misc_feature
<222>
<223> Phenotype: Late Flowering
Useful for delaying flowering time

<220>
<221> misc_feature
<222>
<223> Phenotype: Dark Green
Useful for increasing chlorophyll and photosynthetic capacity

<220>
<221> misc_feature
<222>
<223> Phenotype: Large
Useful for making larger plants

<220>
<221> misc_feature
<222>
<223> Phenotype: INFLORESCENCE
Useful for making ornamental plants with modified flowers

<220>
<221> misc_feature
<222>
<223> Phenotype: CAULINE LEAVES
Useful for making ornamental plants with modified leaves

<220>
<221> misc_feature
<222>
<223> Phenotype: ROSETTE LEAVES
Useful for making ornamental plants with modified leaves

<220>
<221> misc_feature
<222>
<223> Phenotype: Serrate Margins
Useful for making plants with increased biomass and foliage

<220>
<221> misc_feature
<222>
<223> Phenotype: Serrate Margins
Useful for making plants with increased biomass and foliage

<220>
<221> misc_feature
<222>

<223> Phenotype: Plant Size
Useful for making plants with increased size
and biomass

<220>

<221> misc_feature

<222>

<223> Phenotype: Strong
Useful for making stronger plants

<400> 81

Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala
20 25 30

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Val
35 40 45

Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Asp Ile Ser
50 55 60

Lys Ile Ile Asp Arg Tyr Glu Ile Gln His Ala Asp Glu Leu Arg Ala
65 70 75 80

Leu Asp Leu Glu Glu Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu
85 90 95

Leu Glu Thr Val Gln Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val
100 105 110

Ser Val Asp Ser Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu
115 120 125

Ser Val Ser Arg Ala Arg Lys Ala Glu Leu Met Met Glu Tyr Ile Glu
130 135 140

Ser Leu Lys Glu Lys Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu
145 150 155 160

Ala Ser Gln Met Gly Lys Asn Thr Leu Leu Ala Thr Asp Asp Glu Arg
165 170 175

Gly Met Phe Pro Gly Ser Ser Ser Gly Asn Lys Ile Pro Glu Thr Leu
180 185 190

Pro Leu Leu Asn Pro Pro Ser Ser Thr Ala Glu Phe Ser Pro

<210> 82

<211> 201

<212> PRT

<213> Brassica rapa subsp. pekinensis

<220>

<221> misc_feature

<222> (1)..(201)

<223> Public GI no. 71834745

<220>

<221> misc_feature

<222> (1)..(201)

<223> Functional Homolog of Ceres CLONE ID no. 92459

at SEQ ID NO. 81

with e-value of 6.50E-66 and percent identity of 75.2

<400> 82

Met Gly Arg Arg Lys Val Glu Ile Lys Leu Ile Glu Asn Lys Ser Ser
1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Thr Gly Leu Ile Glu Lys Ala
20 25 30

Arg Gln Leu Ser Val Leu Cys Glu Ser Ser Val Ala Val Leu Val Val
35 40 45

Ser Ala Ser Gly Lys Leu Tyr Asn Ser Ser Ser Gly Asp Asn Met Thr
50 55 60

Asn Ile Val Asp Arg Tyr Glu Ile Gln His Ala Gly Glu Leu Arg Ser
65 70 75 80

Leu Asp Leu Ala Glu Lys Thr Arg Asn Tyr Leu Pro His Lys Glu Leu
85 90 95

Leu Glu Ser Val Lys Ser Asn Leu Glu Glu Pro Asn Val Asp Ser Val
100 105 110

Ser Val Asp Ser Leu Ile Ser Leu Glu Asp Gln Leu Glu Thr Ala Leu
115 120 125

Ser Ala Thr Arg Ala Arg Lys Thr Glu Leu Thr Met Glu Phe Val Lys
130 135 140

Met Leu Gln Glu Lys Glu Glu Leu Leu Arg Glu Glu Asn Leu Val Leu
145 150 155 160

Val Ser Gln Ile Gly Thr Thr Asn Gly Arg Arg Glu Asn Asn Ser Pro
165 170 175

Val Asn Ser Ser Gly Ile Asn Pro Pro Glu Thr Leu Pro Leu Leu Lys
180 185 190

Val Thr Ser Val Ile Gln Arg Leu Ser
195 200

<210> 83

<211> 196

<212> PRT

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(196)

<223> Public GI no. 31580813

<220>

<221> misc_feature

<222> (1)..(196)

<223> Functional Homolog of Ceres CLONE ID no. 92459
 at SEQ ID NO. 81
 with e-value of 3.09E-59 and percent identity of 67.5

<400> 83

```

Met Gly Arg Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1           5           10           15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
          20           25           30

Arg Gln Leu Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val
          35           40           45

Ser Ala Ser Gly Lys Leu Tyr Asn Phe Ser Ala Gly Asp Asn Leu Val
          50           55           60

Lys Ile Leu Asp Arg Tyr Gly Lys Gln His Ala Asp Asp Leu Lys Ala
65           70           75           80

Leu Asp Leu Gln Ser Lys Ala Pro Lys Tyr Gly Ser His His Glu Leu
          85           90           95

Leu Glu Leu Val Glu Ser Lys Leu Val Glu Ser Asn Ser Asp Val Ser
          100          105          110

Val Asp Ser Leu Val Gln Leu Glu Asp His Leu Glu Thr Ala Leu Ser
          115          120          125

Val Thr Arg Ala Arg Lys Thr Glu Leu Met Leu Lys Leu Val Asp Ser
          130          135          140

Leu Lys Glu Lys Glu Lys Leu Leu Lys Glu Glu Asn Gln Gly Leu Ala
145          150          155          160

Ser Gln Met Glu Lys Asn Asn Leu Ala Gly Ala Glu Ala Asp Lys Met
          165          170          175

Glu Met Ser Pro Gly Gln Ile Ser Asp Ile Asn Arg Pro Val Thr Leu
          180          185          190

Arg Leu Leu Tyr
          195
  
```

<210> 84

<211> 197

<212> PRT

<213> Brassica oleracea var. capitata

<220>

<221> misc_feature

<222> (1)..(197)

<223> Public GI no. 34591565

<220>

<221> misc_feature

<222> (1)..(197)

<223> Functional Homolog of Ceres CLONE ID no. 92459

at SEQ ID NO. 81

with e-value of 3.50E-58 and percent identity of 67.0

<400> 84

Met Gly Arg Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
20 25 30

Arg Gln Leu Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val
35 40 45

Ser Ala Ser Gly Lys Leu Tyr Asn Phe Ser Ala Gly Asp Asp Leu Val
50 55 60

Lys Val Ile Asp Arg Tyr Gly Glu Gln His Ala Asp Asp Asp Arg Lys
65 70 75 80

Ala Leu Asp Leu Gln Ser Glu Ala Pro Lys Tyr Gly Ser His His Glu
85 90 95

Leu Leu Glu Leu Val Glu Ser Lys Leu Val Glu Ser Asn Ser Asp Val
100 105 110

Ser Val Asp Ser Leu Val Gln Leu Glu Asn His Leu Glu Thr Ala Leu
115 120 125

Ser Val Thr Arg Ala Arg Lys Thr Glu Leu Leu Leu Lys Leu Val Asp
130 135 140

Ser Leu Lys Glu Lys Glu Lys Leu Leu Lys Glu Glu Asn Gln Gly Leu
145 150 155 160

Ala Ser Gln Met Glu Lys Asn Asn Leu Ala Gly Ala Glu Ala Asp Lys
165 170 175

Met Glu Val Ser Pro Gly Gln Ile Ser Asp Ile Asn Cys Pro Val Thr
180 185 190

Leu Pro Leu Leu Tyr
195

<210> 85

<211> 197

<212> PRT

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(197)

<223> Ceres CLONE ID no. 1065387

<220>

<221> misc_feature

<222> (1)..(197)

<223> Functional Homolog of Ceres CLONE ID no. 92459
at SEQ ID NO. 81

with e-value of 1.30E-60 and percent identity of 67.0

<400> 85

```

Met Gly Arg Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1           5           10           15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
          20           25           30

Arg Gln Leu Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val
          35           40           45

Ser Ala Ser Gly Lys Leu Tyr Ser Phe Ser Ser Gly Asp Asn Leu Val
          50           55           60

Lys Ile Leu Asp Arg Tyr Gly Lys Gln His Asp Asp Asp Leu Lys Ala
65           70           75           80

Leu Asp Arg Gln Ser Lys Ala Leu Asp Cys Gly Ser His His Glu Leu
          85           90           95

Leu Glu Leu Val Glu Ser Lys Leu Glu Glu Ser Asn Val Asp Asn Val
          100          105          110

Ser Val Gly Ser Leu Val Gln Leu Glu Glu His Leu Glu Asn Ala Leu
          115          120          125

Ser Val Thr Arg Ala Arg Lys Thr Glu Leu Met Leu Lys Leu Val Glu
          130          135          140

Asn Leu Lys Glu Lys Glu Lys Leu Leu Glu Glu Glu Asn His Val Leu
145          150          155          160

Ala Ser Gln Met Glu Lys Ser Asn Leu Val Arg Ala Glu Ala Asp Asn
          165          170          175

Met Asp Val Ser Pro Gly Gln Ile Ser Asp Ile Asn Leu Pro Val Thr
          180          185          190

Leu Pro Leu Leu Asn
          195

```

<210> 86

<211> 197

<212> PRT

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(197)

<223> Public GI no. 17933450

<220>

<221> misc_feature

<222> (1)..(197)

<223> Functional Homolog of Ceres CLONE ID no. 92459

at SEQ ID NO. 81

with e-value of 1.59E-60 and percent identity of 66.8

<400> 86

```

Met Gly Arg Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
.1          5          10          15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
          20          25          30

Arg Gln Leu Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val
          35          40          45

Ser Ala Ser Gly Lys Leu Tyr Ser Phe Ser Ser Gly Asp Asn Leu Val
          50          55          60

Lys Ile Leu Asp Arg Tyr Gly Lys Gln His Asp Asp Asp Leu Lys Ala
65          70          75          80

Leu Asp Arg Gln Ser Lys Ala Leu Asp Cys Gly Ser His His Glu Leu
          85          90          95

Leu Glu Leu Val Glu Ser Lys Leu Glu Glu Ser Asn Val Asp Asn Val
          100          105          110

Ser Val Gly Ser Leu Val Gln Leu Glu Glu His Leu Glu Asn Ala Leu
          115          120          125

Ser Val Thr Arg Ala Arg Lys Thr Glu Leu Met Leu Lys Leu Val Glu
          130          135          140

Asn Leu Lys Glu Lys Glu Lys Leu Leu Glu Glu Glu Asn His Val Leu
145          150          155          160

Ala Ser Gln Met Glu Lys Ser Asn Leu Val Arg Ala Glu Ala Asp Asn
          165          170          175

Met Asp Val Ser Pro Gly Gln Ile Ser Asp Ile Asn Leu Pro Val Thr
          180          185          190

Leu Pro Leu Leu Asn
          195

```

<210> 87

<211> 196

<212> PRT

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(196)

<223> Public GI no. 17933456

<220>

<221> misc_feature

<222> (1)..(196)

<223> Functional Homolog of Ceres CLONE ID no. 92459

at SEQ ID NO. 81

with e-value of 4.99E-59 and percent identity of 66.4

<400> 87

Met Gly Arg Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val
 35 40 45

Ser Ala Ser Gly Lys Leu Tyr Asn Phe Ser Ala Gly Asp Asp Leu Val
 50 55 60

Lys Ile Val Asp Arg Tyr Gly Lys Gln His Ala Asp Asp Arg Lys Ala
 65 70 75 80

Leu Asp Leu Gln Ser Glu Ala Pro Lys Tyr Gly Ser His His Glu Leu
 85 90 95

Leu Glu Leu Val Glu Ser Lys Leu Val Glu Ser Asn Ser Asp Val Ser
 100 105 110

Val Asp Ser Leu Val Gln Leu Glu Asn His Leu Glu Thr Ala Leu Ser
 115 120 125

Val Thr Arg Ala Arg Lys Thr Glu Leu Leu Leu Lys Leu Val Asp Ser
 130 135 140

Leu Lys Glu Lys Glu Lys Leu Leu Lys Glu Glu Asn Gln Gly Leu Ala
 145 150 155 160

Ser Gln Met Glu Lys Asn Asn Leu Ala Gly Ala Glu Ala Asp Lys Met
 165 170 175

Glu Val Ser Pro Gly Gln Ile Ser Asp Ile Asn Cys Pro Val Thr Leu
 180 185 190

Pro Leu Leu Tyr
 195

<210> 88

<211> 196

<212> PRT

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(196)

<223> Ceres CLONE ID no. 1091989

<220>

<221> misc_feature

<222> (1)..(196)

<223> Functional Homolog of Ceres CLONE ID no. 92459

at SEQ ID NO. 81

with e-value of 4.99E-59 and percent identity of 66.4

<400> 88

Met Gly Arg Lys Lys Leu Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
 1 5 10 15

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Glu Lys Ala
 20 25 30

Arg Gln Leu Ser Val Leu Cys Asp Ala Ser Val Ala Leu Leu Val Val
 35 40 45

Ser Ala Ser Gly Lys Leu Tyr Asn Phe Ser Ala Gly Asp Asp Leu Val
 50 55 60

Lys Ile Val Asp Arg Tyr Gly Lys Gln His Ala Asp Asp Arg Lys Ala
 65 70 75 80

Leu Asp Leu Gln Ser Glu Ala Pro Lys Tyr Gly Ser His His Glu Leu
 85 90 95

Leu Glu Leu Val Glu Ser Lys Leu Val Glu Ser Asn Ser Asp Val Ser
 100 105 110

Val Asp Ser Leu Val Gln Leu Glu Asn His Leu Glu Thr Ala Leu Ser
 115 120 125

Val Thr Arg Ala Arg Lys Thr Glu Leu Leu Leu Lys Leu Val Asp Ser
 130 135 140

Leu Lys Glu Lys Glu Lys Leu Leu Lys Glu Glu Asn Gln Gly Leu Ala
 145 150 155 160

Ser Gln Met Glu Lys Asn Asn Leu Ala Gly Ala Glu Ala Asp Lys Met
 165 170 175

Glu Val Ser Pro Gly Gln Ile Ser Asp Ile Asn Cys Pro Val Thr Leu
 180 185 190

Pro Leu Leu Tyr
 195

<210> 89

<211> 196

<212> PRT

<213> Brassica napus

<220>

<221> misc_feature

<222> (1)..(196)

<223> Public GI no. 17933458

<220>

<221> misc_feature

<222> (1)..(196)

<223> Functional Homolog of Ceres CLONE ID no. 92459

at SEQ ID NO. 81

with e-value of 1.19E-57 and percent identity of 65.6

<400> 89

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

<210> 90
 <211> 614
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(614)
 <223> Ceres CLONE ID no. 1952

<220>
 <221> misc_feature
 <222> (1)..(614)
 <223> Also Known As Ceres ME LINE ME04701

<220>
 <221> misc_feature
 <222> (1)..(614)
 <223> Also Known As Ceres LEAD Number 28

<220>
<221> CDS
<222> (30)..(429)
<223> Referenced by SEQ ID NO: 91

<400> 90
ggaagtgaag gaggtatatc cggaggtggt atgtctgggg gcagtggaag taaacacaaa 60
attggaggag gtaaacacgg aggtcttgga ggtaaattcg gaaagaaaag aggcattgtcc 120
ggaagtggag gaggcattgtc aggaagtga ggaggtgtgt ctggaagtga aggaagtatg 180
tcgggaggtg gtatgtctgg gggtagcgga agtaaacaca aaattggagg aggtaaacac 240
ggaggtctta gaggtaaatt cggaaagaaa agaggtatgt caggaagtga aggaggtatg 300
tctggaagtg aaggaggtgt gtcggaaagt ggtatgtccg ggagtggagg gggtaaacac 360
aaaatcggag gaggtaaaca caaatttgga ggaggtaaac acggaggtgg aggtggccac 420
atggcggagt aaagaacaat ggtcaagttg ttccaacatt aagcagatca ttgtgcatta 480
gttcaagatt gtatgattgg gaaagtaaaa gaaagaaaaa atattttcta ataagtttta 540
tgtttatatg taatgttgaa tctgattatt atgataaaaa gacataaatg tgatacaatg 600
tttattttta gagc 614

<210> 91
<211> 133
<212> PRT
<213> *Arabidopsis thaliana*

<220>
<221> misc_feature
<222> (1)..(133)
<223> Ceres CLONE ID no. 1952

<220>
<221> misc_feature
<222> (1)..(133)
<223> Also Known As Ceres ME LINE ME04701

<220>
<221> misc_feature
<222> (1)..(133)
<223> Also Known As Ceres LEAD Number 28

<220>
<221> misc_feature
<222>
<223> Phenotype: INFLORESCENCE
Useful for making ornamental plants
with modified flowers

<220>
<221> misc_feature
<222>
<223> Phenotype: ROSETTE LEAVES

Useful for making ornamental plants
with modified leaves

<220>

<221> misc_feature

<222>

<223> Phenotype: Plant Architecture

Useful for making plants
with enhanced plant architecture

<220>

<221> misc_feature

<222>

<223> Phenotype: Disorganized Rosette

Useful for making plants
with increased biomass

<220>

<221> misc_feature

<222>

<223> Phenotype: Lanceolate Shaped

Useful for making plants with increased biomass
and foliage

<400> 91

Met Ser Gly Gly Ser Gly Ser Lys His Lys Ile Gly Gly Gly Lys His
1 5 10 15

Gly Gly Leu Gly Gly Lys Phe Gly Lys Lys Arg Gly Met Ser Gly Ser
20 25 30

Gly Gly Gly Met Ser Gly Ser Glu Gly Gly Val Ser Gly Ser Glu Gly
35 40 45

Ser Met Ser Gly Gly Gly Met Ser Gly Gly Ser Gly Ser Lys His Lys
50 55 60

Ile Gly Gly Gly Lys His Gly Gly Leu Arg Gly Lys Phe Gly Lys Lys
65 70 75 80

Arg Gly Met Ser Gly Ser Glu Gly Gly Met Ser Gly Ser Glu Gly Gly
85 90 95

Val Ser Glu Ser Gly Met Ser Gly Ser Gly Gly Gly Lys His Lys Ile
100 105 110

Gly Gly Gly Lys His Lys Phe Gly Gly Gly Lys His Gly Gly Gly Gly
115 120 125

Gly His Met Ala Glu

<210> 92

<211> 1383

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1383)

<223> Ceres CLONE ID no. 123905

<220>
<221> misc_feature
<222> (1)..(1383)
<223> Also Known As Ceres ME LINE ME04717

<220>
<221> misc_feature
<222> (1)..(1383)
<223> Also Known As Ceres LEAD Number 29

<220>
<221> CDS
<222> (119)..(920)
<223> Referenced by SEQ ID NO: 93

<400> 92
caaaaacaca aacaaaactc atatitttcaa tctccaggtg ctttacacca acagagtcgc 60
aagaaaacaa aaaccaaact cggatttagt ttgacagaag aaggaatcga gagtcgggta 120
tgcattatcc taacaacaga accgaattcg toggagctcc agccccaacc cggatatcaa 180
aggagcagtt gtcaccggag caagagcttt cagttattgt ctctgctttg caacacgtga 240
tctcagggga aaacgaaacg gcgcctgtgc agggtttttc cagtgcacgc acagtgataa 300
gcgcgggaat gcctcgggtg gattcagaca cttgtcaagt ctgtaggatc gaaggatgtc 360
tcggctgtaa ctactttttc gcgcctaatc agagaattga aaagaatcat caacaagaag 420
aagagattac tagtagtagt aacagaagaa gagagagctc tcccgtagcg aagaaagcgg 480
aaggtggcgg gaaaatcagg aagaggaaga acaagaagaa tggttacaga ggagttaggc 540
aaagaccttg gggaaaattt gcagctgaga tcagagatcc taaaagagcc acacgtgttt 600
ggcttggtac ttctgaaacc gcogaagatg cggctcgagc ttatgatoga gccgcgattg 660
gattccgtgg gccaaagggt aaactcaact tcccctttgt ggattacacg tottcagttt 720
catctcctgt tgctgctgat gatataggag caaatgcaag tgcaagcgcc agtgtgagcg 780
ccacagattc agttgaagca gagcaatgga acggaggagg aggggattgc aatatggagt 840
ggatgaatat gatgatgatg atggattttg ggaatggaga ttcttcagat tcaggaaata 900
caattgctga tatgttccag tgataaatga gctctttctt gttggcgttt tttggagtta 960
agtgcagaa gagattgaca ctgtggcttg tttaaagtga acaagaacaa gaaagcatgt 1020
aattagtagt ctcatctttt tgtttgttgt caattctatg tttatctcat ataaaatctg 1080
agttaaacct atctgaggag agagtaaata aagaggttaa gaaacccaac attggtctga 1140
attataaacg taagtgtcaa cgttgtttat aaaggagaaa actataattg gtgacaaaag 1200
acataaagaa aagatgtcta ctctacaaa gcctcgctg cagctattcg acaacaatg 1260
gcctctcca gagaggaaat tccgagctct tggctagtta tcttgtaatg ctgaaaacat 1320

gaatgtatatt gagtttatatt ctgtaacatt ggaagcgaaa taaaagggtt atcaactgtt 1380
acc 1383

<210> 93
<211> 267
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<222> (1)..(267)
<223> Ceres CLONE ID no. 123905

<220>
<221> misc_feature
<222> (1)..(267)
<223> Also Known As Ceres ME LINE ME04717

<220>
<221> misc_feature
<222> (1)..(267)
<223> Also Known As Ceres LEAD Number 29

<220>
<221> misc_feature
<222> (134)..(197)
<223> Pfam Name: AP2; Pfam Description: AP2 domain

<220>
<221> misc_feature
<222>
<223> Phenotype: INFLORESCENCE
Useful for making ornamental plants
with modified flowers

<220>
<221> misc_feature
<222>
<223> Phenotype: ROSETTE LEAVES
Useful for making ornamental plants
with modified leaves

<220>
<221> misc_feature
<222>
<223> Phenotype: Plant Architecture
Useful for making plants
with enhanced plant architecture

<220>
<221> misc_feature
<222>
<223> Phenotype: Disorganized Rosette
Useful for making plants
with increased biomass

<220>
<221> misc_feature
<222>

<223> Phenotype: Lanceolate Shaped
Useful for making plants with increased biomass
and foliage

 $\langle 220 \rangle$

<221> misc feature

 $\langle 222 \rangle$

<223> Phenotype: Short
Useful for making shorter plants

 $\langle 220 \rangle$

<221> misc feature

 $\langle 222 \rangle$

<223> Phenotype: Reduced Apical Dominance
Useful for modifying plant structure, i.e. increased branching

<2.2.0>

<221> misc feature

 $\langle 222 \rangle$

<223> Phenotype: Reduced fertility
Useful for sterility, genetic confinement systems

<400> 93

Met His Tyr Pro Asn Asn Arg Thr Glu Phe Val Gly Ala Pro Ala Pro
1 5 10 15

Thr Arg Tyr Gln Lys Glu Gln Leu Ser Pro Glu Gln Glu Leu Ser Val
20 25 30

Ile Val Ser Ala Leu Gln His Val Ile Ser Gly Glu Asn Glu Thr Ala
35 40 45

Pro Cys Gln Gly Phe Ser Ser Asp Ser Thr Val Ile Ser Ala Gly Met
50 55 60

Pro Arg Leu Asp Ser Asp Thr Cys Gln Val Cys Arg Ile Glu Gly Cys
65 70 75 80

Leu Gly Cys Asn Tyr Phe Phe Ala Pro Asn Gln Arg Ile Glu Lys Asn
85 90 95

His Gln Gln Glu Glu Glu Ile Thr Ser Ser Ser Asn Arg Arg Arg Glu
100 105 110

Ser Ser Pro Val Ala Lys Lys Ala Glu Gly Gly Gly Lys Ile Arg Lys
115 120 125

Arg Lys Asn Lys Lys Asn Gly Tyr Arg Gly Val Arg Gln Arg Pro Trp
130 135 140

Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Arg Ala Thr Arg Val
145 150 155 160

Trp Leu Gly Thr Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp
165 170 175

Arg Ala Ala Ile Gly Phe Arg Gly Pro Arg Ala Lys Leu Asn Phe Pro
180 185 190

Phe Val Asp Tyr Thr Ser Ser Val Ser Ser Pro Val Ala Ala Asp Asp

195 200 205
 Ile Gly Ala Asn Ala Ser Ala Ser Ala Ser Val Ser Ala Thr Asp Ser
 210 215 220
 Val Glu Ala Glu Gln Trp Asn Gly Gly Gly Gly Asp Cys Asn Met Glu
 225 230 235 240
 Trp Met Asn Met Met Met Met Met Asp Phe Gly Asn Gly Asp Ser Ser
 245 250 255
 Asp Ser Gly Asn Thr Ile Ala Asp Met Phe Gln
 <210> 94
 <211> 229
 <212> PRT
 <213> Populus balsamifera subsp. trichocarpa

 <220>
 <221> misc_feature
 <222> (1)..(229)
 <223> 1460991

 <220>
 <221> misc_feature
 <222> (1)..(229)
 <223> Functional Homolog of Ceres CLONE ID no. 123905
 at SEQ ID NO. 93 with e-value of 2.10E-35 and percent
 identity of 59.8

 <400> 94
 Met Val Ala Ala Leu Lys Asn Val Val Ser Gly Thr Ala Ser Met Asp
 1 5 10 15
 Phe Ser Arg Glu Met Asn Ser Ile Asn Met Pro Ile Ile Thr Ser His
 20 25 30
 Pro Gln Phe Gly Ser Ala Ser Asn Asn Gly Asn Gly Phe Cys Asn Ser
 35 40 45
 Ile Leu Pro Pro Ser Ser Asp Leu Asp Thr Cys Gly Val Cys Lys Ile
 50 55 60
 Lys Gly Cys Leu Gly Cys Asn Phe Phe Pro Pro Asn Gln Glu Asp Lys
 65 70 75 80
 Lys Asp Asp Lys Lys Gly Lys Arg Lys Arg Val Lys Lys Asn Tyr Arg
 85 90 95
 Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
 100 105 110
 Pro Arg Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
 115 120 125
 Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile Asp Phe Arg Gly Pro
 130 135 140
 Arg Ala Lys Leu Asn Phe Pro Phe Pro Asp Ser Gly Ile Ala Ser Phe
 145 150 155 160

Glu Glu Ser Lys Glu Lys Gln Glu Lys Gln Gln Glu Ile Ser Glu Lys
 165 170 175
 Arg Ser Glu Phe Glu Thr Glu Thr Gly Lys Asp Asn Glu Phe Leu Asp
 180 185 190
 Asn Ile Val Asp Glu Glu Leu Gln Glu Trp Met Ala Met Ile Met Asp
 195 200 205
 Phe Gly Asn Gly Gly Ser Ser Asn Ser Ser Gly Thr Ala Ser Ala Ala
 210 215 220
 Ala Thr Ile Gly Phe
 225

<210> 95
 <211> 256
 <212> PRT
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (1)..(256)
 <223> Ceres CLONE ID no. 1494990

<220>
 <221> misc_feature
 <222> (1)..(256)
 <223> Functional Homolog of Ceres CLONE ID no. 123905
 at SEQ ID NO. 93 with e-value of 4.19E-37 and percent
 identity of 49.2

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

Trp Ala Ala Glu Ile Arg Asp Pro Arg Arg Ala Val Arg Val Trp Leu
 130 135 140
 Gly Thr Phe Asp Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Arg Ala
 145 150 155 160
 Ala Val Lys Phe Arg Gly Pro Arg Ala Lys Leu Asn Phe Ser Phe Pro
 165 170 175
 Glu Gln His Leu Arg Asp Asp Ser Gly Asn Ala Ala Ala Lys Ser Asp
 180 185 190
 Ala Cys Ser Pro Ser Pro Ser Pro Arg Ser Ala Glu Glu Glu Glu Thr
 195 200 205
 Gly Asp Leu Leu Trp Asp Gly Leu Val Asp Leu Met Lys Leu Asp Glu
 210 215 220
 Ser Asp Leu Cys Leu Leu Leu Pro Val Asp Asn Thr Leu Asp Lys Phe
 225 230 235 240
 His Ala Pro Gly Gln Arg Arg Ser Gly Ser Gly Val Pro Leu Cys Tyr
 245 250 255

<210> 96
 <211> 266
 <212> PRT
 <213> Triticum aestivum

<220>
 <221> misc_feature
 <222> (1)..(266)
 <223> Ceres CLONE ID no. 634402

<220>
 <221> misc_feature
 <222> (1)..(266)
 <223> Functional Homolog of Ceres CLONE ID no. 123905
 at SEQ ID NO. 93 with e-value of 1.80E-36 and percent
 identity of 45.0

<400> 96
 Met Thr Phe Ser Val Ser Pro Ala Thr Gly Ala Ser Gln Glu Tyr Met
 1 5 10 15
 Ile Arg Phe Asp Gly His Phe Glu Asp Pro Ser Ser Ala Ala Ala Ser
 20 25 30
 Ala Glu Pro Pro Leu Pro Phe Ala Gly Arg Ala Phe Ser Pro Gln Gln
 35 40 45
 Glu Gln Ser Ala Met Val Ala Ala Leu Leu His Val Val Ser Gly Tyr
 50 55 60
 Thr Thr Pro Ala Pro Asp Leu Phe Phe Pro Ala Arg Lys Glu Ala Cys

65		70		75		80									
Thr	Ala	Cys	Gly	Met	Asp	Gly	Cys	Leu	Gly	Cys	Glu	Phe	Phe	Gly	Ala
				85					90					95	
Glu	Ala	Gly	Arg	Ala	Val	Ala	Ala	Ser	Asp	Ala	Pro	Arg	Ala	Pro	Ala
			100					105					110		
Ala	Gly	Gly	Pro	Gln	Arg	Arg	Arg	Arg	Asn	Lys	Lys	Asn	Gln	Tyr	Arg
			115				120					125			
Gly	Val	Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp
	130					135				140					
Pro	Arg	Arg	Ala	Val	Arg	Val	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu
145					150					155					160
Asp	Ala	Ala	Arg	Ala	Tyr	Asp	Arg	Ala	Ala	Val	Glu	Phe	Arg	Gly	Pro
			165					170						175	
Arg	Ala	Lys	Leu	Asn	Phe	Ser	Phe	Pro	Glu	Gln	Gln	Gln	Gln	Gln	Leu
			180					185					190		
Gly	Gly	Ser	Gly	Asn	Ala	Ala	Ala	Lys	Ser	Asp	Ala	Cys	Ser	Pro	Ser
		195					200					205			
Pro	Ser	Pro	Arg	Ser	Ala	Asp	Glu	Asp	Glu	Thr	Gly	Asp	Leu	Leu	Trp
	210					215					220				
Asp	Gly	Leu	Val	Asp	Leu	Met	Lys	Leu	Asp	Glu	Ser	Asp	Leu	Cys	Leu
225					230					235					240
Leu	Leu	Pro	Val	Asp	Asn	Thr	Asp	Lys	Phe	His	Ile	Glu	Gly	Lys	Arg
			245					250						255	
Arg	Ser	Gly	Ser	Gly	Val	Pro	Leu	Cys	Tyr						
			260					265							

<210> 97

<211> 274

<212> PRT

<213> *Oryza sativa* subsp. *japonica*

<220>

<221> misc_feature

<222> (1)..(274)

<223> Public GI no. 51536200

<220>

<221> misc_feature

<222> (1)..(274)

<223> Functional Homolog of Ceres CLONE ID no. 123905
 at SEQ ID NO. 93 with e-value of 3.09E-34 and percent
 identity of 43.4

<400> 97

Met	Thr	Lys	Lys	Val	Ile	Pro	Ala	Met	Ala	Ala	Ala	Arg	Gln	Asp	Ser
1				5				10					15		

Cys Lys Thr Lys Leu Asp Glu Arg Gly Gly Ser His Gln Ala Pro Ser
 20 25 30
 Ser Ala Arg Trp Ile Ser Ser Glu Gln Glu His Ser Ile Ile Val Ala
 35 40 45
 Ala Leu Arg Tyr Val Val Ser Gly Cys Thr Thr Pro Pro Pro Glu Ile
 50 55 60
 Val Thr Val Ala Cys Gly Glu Ala Cys Ala Leu Cys Gly Ile Asp Gly
 65 70 75 80
 Cys Leu Gly Cys Asp Phe Phe Gly Ala Glu Ala Ala Gly Asn Glu Glu
 85 90 95
 Ala Val Met Ala Thr Asp Tyr Ala Ala Ala Ala Ala Ala Ala Val
 100 105 110
 Ala Gly Gly Ser Gly Gly Lys Arg Val Arg Arg Arg Arg Lys Lys Asn
 115 120 125
 Val Tyr Arg Gly Val Arg His Arg Pro Trp Gly Lys Trp Ala Ala Glu
 130 135 140
 Ile Arg Asp Pro Arg Arg Ala Val Arg Lys Trp Leu Gly Thr Phe Asp
 145 150 155 160
 Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Arg Ala Ala Leu Glu Phe
 165 170 175
 Arg Gly Ala Arg Ala Lys Leu Asn Phe Pro Cys Ser Glu Pro Leu Pro
 180 185 190
 Met Pro Ser Gln Arg Asn Gly Asn Gly Gly Asp Ala Val Thr Ala Ala
 195 200 205
 Thr Thr Thr Ala Glu Gln Met Thr Pro Thr Leu Ser Pro Cys Ser Ala
 210 215 220
 Asp Ala Glu Glu Thr Thr Thr Pro Val Asp Trp Gln Met Gly Ala Asp
 225 230 235 240
 Glu Ala Gly Ser Asn Gln Leu Trp Asp Gly Leu Gln Asp Leu Met Lys
 245 250 255
 Leu Asp Glu Ala Asp Thr Trp Phe Pro Pro Phe Ser Gly Ala Ala Ser
 260 265 270
 Ser Phe

<210> 98

<211> 541

<212> DNA

<213> Glycine max

<220>

<221> misc_feature
<222> (1)..(541)
<223> Ceres CLONE ID no. 679923

<220>
<221> misc_feature
<222> (1)..(541)
<223> Also Known As Ceres ME LINE ME03195

<220>
<221> misc_feature
<222> (1)..(541)
<223> Also Known As Ceres LEAD Number 36

<220>
<221> CDS
<222> (24)..(456)
<223> Referenced by SEQ ID NO: 99

<400> 98
gctcaagttt ccaagaccaa gccaatggaa aacctttcac cattgattta caaaaacccc 60
attagaagaa cttctaggcg atctacaatg tatcttggtg tgagaaaaag gccatgggga 120
agatatgctg ctgagattag gaaccatac accaaagaga gacactggct aggcacattt 180
gacactgctg aagaggctgc tatagcttat gatctttcat ctatcaagat ttgtggcatt 240
aatgctogaa ctaattttca ctaccctttt gtgtctcttc caccacttcc tatgtcgtca 300
ttgcctcctc caccgccacc gccgacocca gagttggatc caagtgttga agtttgtcta 360
gagatgatga atgctgcttc ttacgatggg gatgatgaat ctcttgttat tgcttccatt 420
ttgcaaagtt tttctaattc tggttaactgt tctttttagt ttttggttcc aatgaggcta 480
tggcctgcct cttatcaaat caataattct attttttttc ttigcaaaaa aaaaaaaaaa 540
a 541

<210> 99
<211> 144
<212> PRT
<213> Glycine max

<220>
<221> misc_feature
<222> (1)..(144)
<223> Ceres CLONE ID no. 679923

<220>
<221> misc_feature
<222> (1)..(144)
<223> Also Known As Ceres ME LINE ME03195

<220>
<221> misc_feature
<222> (1)..(144)
<223> Also Known As Ceres LEAD Number 36

<220>
<221> misc_feature
<222> (21)..(84)
<223> Pfam Name: AP2; Pfam Description: AP2 domain

<220>
<221> misc_feature
<222>
<223> Phenotype: Late Flowering
Useful for delaying flowering time

<220>
<221> misc_feature
<222>
<223> Phenotype: Large
Useful for making ornamental plants
with modified flowers

<220>
<221> misc_feature
<222>
<223> Phenotype: ROSETTE LEAVES
Useful for making ornamental plants
with modified leaves

<220>
<221> misc_feature
<222>
<223> Phenotype: Curled 1
Useful for making plants
with altered leaf shape e.g. curled leaves

<220>
<221> misc_feature
<222>
<223> Phenotype: Plant Architecture
Useful for making plants
with enhanced plant architecture

<220>
<221> misc_feature
<222>
<223> Phenotype: Short
Useful for making shorter plants

<220>
<221> misc_feature
<222>
<223> Phenotype: Short Petioles
Useful for making smaller plants

<220>
<221> misc_feature
<222>
<223> Phenotype: Strong
Useful for making stronger plants

<400> 99

Met Glu Asn Leu Ser Pro Leu Ile Tyr Lys Asn Pro Ile Arg Arg Thr
1 5 10 15

Ser Arg Arg Ser Thr Met Tyr Leu Gly Val Arg Lys Arg Pro Trp Gly
 20 25 30
 Arg Tyr Ala Ala Glu Ile Arg Asn Pro Tyr Thr Lys Glu Arg His Trp
 35 40 45
 Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Ile Ala Tyr Asp Leu
 50 55 60
 Ser Ser Ile Lys Ile Cys Gly Ile Asn Ala Arg Thr Asn Phe His Tyr
 65 70 75 80
 Pro Phe Val Ser Leu Pro Pro Leu Pro Met Ser Ser Leu Pro Pro Pro
 85 90 95
 Pro Pro Pro Pro Thr Pro Glu Leu Asp Pro Ser Val Glu Val Cys Leu
 100 105 110
 Glu Met Met Asn Ala Ala Ser Tyr Asp Gly Asp Asp Glu Ser Leu Val
 115 120 125
 Ile Ala Ser Ile Leu Gln Ser Phe Ser Asn Ser Gly Asn Cys Ser Phe
 130 135 140

<210> 100

<211> 129

<212> PRT

<213> *Populus balsamifera* subsp. *trichocarpa*

<220>

<221> misc_feature

<222> (1)..(129)

<223> 1479788

<220>

<221> misc_feature

<222> (1)..(129)

<223> Functional Homolog of Ceres CLONE ID no. 679923
 at SEQ ID NO. 99 with e-value of 3.80E-36 and percent
 identity of 69.0

<400> 100

Met Glu Asn Phe Pro Pro Leu Leu Tyr Arg Asn Pro Lys Arg Ser Ser
 1 5 10 15
 Arg Gln Ser Ser Arg Tyr Leu Gly Val Arg Arg Arg Pro Trp Gly Arg
 20 25 30
 Tyr Ala Ala Glu Ile Arg Asn Pro Tyr Thr Lys Glu Arg His Trp Leu
 35 40 45
 Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Val Ala Tyr Asp Leu Ser
 50 55 60
 Ser Ile Ser Phe Ser Gly Ile Glu Arg Ala Arg Thr Asn Phe Tyr Tyr
 65 70 75 80
 Pro Phe Phe Ala His Pro Ser Pro Ser Gln Glu Ala Pro Pro Pro Pro

				85						90						95
Leu	Pro	Pro	Pro	Glu	Met	Glu	Lys	Gly	Asp	Gln	Leu	Gly	Met	Glu	Asp	
				100				105				110				
Val	Asp	Gly	Asn	Asn	Ala	Leu	Glu	Ile	Leu	Leu	Lys	Ala	Gly	Asn	Gly	
		115					120					125				

Lys

<210> 101
 <211> 143
 <212> PRT
 <213> *Populus balsamifera* subsp. *trichocarpa*

<220>
 <221> misc_feature
 <222> (1)..(143)
 <223> 1533259

<220>
 <221> misc_feature
 <222> (1)..(143)
 <223> Functional Homolog of Ceres CLONE ID no. 679923
 at SEQ ID NO. 99 with e-value of 3.49E-42 and percent
 identity of 66.6

<400> 101
 Met Glu Asn Phe Pro Pro Leu Leu Tyr Arg Asn Pro Lys Arg Ser Ser
 1 5 10 15
 Arg Gln Ser Ser Arg Tyr Leu Gly Val Arg Arg Arg Pro Trp Gly Arg
 20 25 30
 Tyr Ala Ala Glu Ile Arg Asn Pro Tyr Thr Lys Glu Arg His Trp Leu
 35 40 45
 Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Val Ala Tyr Asp Leu Ser
 50 55 60
 Ser Ile Ser Phe Ser Gly Ile Glu Arg Ala Arg Thr Asn Phe Tyr Tyr
 65 70 75 80
 Pro Phe Phe Ala His Pro Ser Pro Ser Gln Glu Ala Pro Pro Pro Pro
 85 90 95
 Leu Pro Pro Pro Glu Met Glu Lys Gly Asp Gln Leu Gly Met Glu Asp
 100 105 110
 Val Gly Thr Thr Gln Asp Asp Glu Ser Ile Val Ile Ala Ser Ile Leu
 115 120 125
 Gln Ser Phe Cys Gln Ser Thr Ser Tyr Ser Phe His Pro Gln Ile
 130 135 140

<210> 102
 <211> 175
 <212> PRT
 <213> *Oryza sativa* subsp. *japonica*

<220>
 <221> misc_feature
 <222> (1)..(175)
 <223> Public GI no. 50941583

<220>
 <221> misc_feature
 <222> (1)..(175)
 <223> Functional Homolog of Ceres CLONE ID no. 679923
 at SEQ ID NO. 99 with e-value of 1.20E-32 and percent
 identity of 65.8

<400> 102
 Met Ala Asp Ala Ala Glu Gln His His Arg Gln Glu Glu Thr Ala Ala
 1 5 10 15
 Ala Thr Thr Thr Pro Gln Gln Met Met Met Arg Arg Arg Arg Ala Arg
 20 25 30
 Ala Ser Ser Glu Tyr Leu Gly Val Arg Arg Arg Pro Trp Gly Arg Tyr
 35 40 45
 Ala Ala Glu Ile Arg Asn Pro Tyr Thr Lys Glu Arg His Trp Leu Gly
 50 55 60
 Thr Phe Asp Thr Ala Glu Glu Ala Ala Val Ala Tyr Asp Leu Ser Ala
 65 70 75 80
 Ile Ser Ile Ser Gly Ala Ala Ala Ala Arg Thr Asn Phe Leu Tyr Pro
 85 90 95
 Asp Met His His His His Pro Ser Pro Pro Gln His Ala Leu Ser Pro
 100 105 110
 Ala Val Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Pro Leu Tyr Asp
 115 120 125
 Asp Asp Tyr Leu Ser Pro Ala Ala Ala Glu Glu Glu Val Glu Ala Gly
 130 135 140
 Asp Asp Glu Ser Leu Thr Ile Ala Thr Ile Leu Gln Ser Phe Gln Tyr
 145 150 155 160
 Gln Gln Ser Val Pro Pro Ala Ser Ser Gly Ser Met Phe Tyr Tyr
 165 170 175

<210> 103
 <211> 1681
 <212> DNA
 <213> Glycine max

<220>
 <221> misc_feature

<222> (1)..(1681)
<223> Ceres CLONE ID no. 691319

<220>
<221> misc_feature
<222> (1)..(1681)
<223> Also Known As Ceres ME LINE ME05057

<220>
<221> misc_feature
<222> (1)..(1681)
<223> Also Known As Ceres ME LINE ME09233

<220>
<221> CDS
<222> (111)..(1470)
<223> Referenced by SEQ ID NO: 104

<400> 103
aaaagggtgt ccaaagaagg aatcacacaa gagaaatddd ggggtggatct tggtaattta 60
aattdgtgtcc aaaaatagta agaaaaaaaa accatagttc atttaatttd catgtccttg 120
ctaacggtgg cgcaccaaag ggggtcaggt gagtttatcc ggttcacgga aagtcatggc 180
ggdggdggcg atgacgtcag tggdgcaggt gaacatggtd gtggacatga tgatggaagt 240
ggdgtctggag gttcactagg gtdgaatttd aaccaagtga tgcaacaagg tgaggdgaca 300
atgcaaggtd gttcattggt ttcagggtdt aacaggggtd atccagagtd gagagaaata 360
gttdcagctt tgacacacgt ggtgtcttda gggdctggcc agaggagcac cgaattgacc 420
cagcaaagtd gtttdctat gatgtctgt tcttdcttdt cacgttdgtc tgcttdctct 480
tcttdcttdc ctdctccttd ttdtgagcc tctdgggtd gccacaaaag aggcagagaa 540
gaagaagaga atagtacttd acataacttd atgcaacaac aacaacaaag tgctccaaga 600
cttdtcagaa acattggtga ctdcatggtg ctdtdtcaag gagactcatc atcagtgaca 660
gaagaagccc ccactccac aactacaact gtaaccgccg tcttgaaaa cccaccagga 720
ggdggggaaa ggaggagaaa gtacagagga gtgaggcaga ggccatgggg aaatgggca 780
gcagaaatcc gtgatccaca caaagcagca agagtdtdgc taggcacatt tgacacagaa 840
gaagcagcag caagagccta tgatgaagct gcattgaggt tcagaggcaa cagagcaaag 900
cttaacttdc ctgaaaatgt aagagcagtd ccaccattc aaccttdtda agccaccact 960
aggctaaccg ttdtdgattd caccacctct caattccggc cactctccgc ggtggcgcca 1020
cccttdattc agcagccaca gattcagggc tcttdtgact tgatcagaga ctacttdcaa 1080
tactctcagc ttdtacagag tgatttdtaa cagcaacaaa tacaacaaca acagcagcag 1140
cagcggcagc agcagcagcg gcagcggcag cagcggcagc agcagcagca acaacaacaa 1200
caaccatcta gtdtdgttda gcagtdgtac tataatgcac aatttdgttd acttdaatca 1260

ccttcaatgc tatcatcatc tccttcattt tcttctctctg tgtctccagc accattccca 1320
 ttattcaciaa cctctgcttc tttcccttg ttttcaagtc aacaaatggg ctatttccag 1380
 ccaccggaaa gccgcaatcc cgctggcggc gtgccggagt ttccaacgtc cacatggctg 1440
 gataccagta gccagccacc accttctggg tgatacagtg ttttagtttc cttcatattt 1500
 tcctttttct tttttctttc ttctattctt agcataaaaa aaaaagactt gttatactta 1560
 tttctttttt caagggtgaa actatgatat agtttttttt aagtattttt ggtactattc 1620
 tcgtatcaga attagagttt cagtaattta tgttgatatt caatacaaat ctttattatg 1680
 t 1681

<210> 104
 <211> 453
 <212> PRT
 <213> Glycine max

<220>
 <221> misc_feature
 <222> (1)..(453)
 <223> Ceres CLONE ID no. 691319

<220>
 <221> misc_feature
 <222> (1)..(453)
 <223> Also Known As Ceres ME LINE ME05057

<220>
 <221> misc_feature
 <222> (1)..(453)
 <223> Also Known As Ceres ME LINE ME09233

<220>
 <221> misc_feature
 <222> (209)..(272)
 <223> Pfam Name: AP2; Pfam Description: AP2 domain

<220>
 <221> misc_feature
 <222>
 <223> Phenotype: ROSETTE LEAVES
 Useful for making ornamental plants
 with modified leaves

<220>
 <221> misc_feature
 <222>
 <223> Phenotype: Disorganized Rosette
 Useful for making plants
 with increased biomass

<220>
 <221> misc_feature
 <222>
 <223> Phenotype: Lanceolate Shaped
 Useful for making plants with increased biomass

and foliage

<220>

<221> misc_feature

<222>

<223> Phenotype: Short

Useful for making shorter plants

<400> 104

Met Ser Leu Leu Thr Val Ala His Gln Arg Gly Ser Gly Glu Phe Ile
1 5 10 15

Arg Phe Thr Glu Ser His Gly Gly Gly Gly Asp Asp Val Ser Gly Asp
20 25 30

Gly Glu His Gly Cys Gly His Asp Asp Gly Ser Gly Ala Gly Gly Ser
35 40 45

Leu Gly Leu Asn Phe Asn Gln Val Met Gln Gln Gly Glu Val Thr Met
50 55 60

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

Arg Glu Ile Val Ser Ala Leu Thr His Val Val Ser Ser Gly Ser Gly
85 90 95

Gln Arg Ser Thr Glu Leu Thr Gln Gln Ser Gly Phe Pro Met Met Ser
100 105 110

Ala Ser Ser Leu Ser Arg Leu Ser Ala Phe Ser Ser Ser Ser Pro Ser
115 120 125

Pro Ser Ser Gly Ala Ser Trp Val Gly His Lys Arg Gly Arg Glu Glu
130 135 140

Glu Glu Asn Ser Thr Ser His Asn Leu Met Gln Gln Gln Gln Gln Ser
145 150 155 160

Ala Pro Arg Leu Phe Arg Asn Ile Gly Asp Phe Met Val Pro Ser Gln
165 170 175

Gly Asp Ser Ser Ser Val Thr Glu Glu Ala Pro Thr Ser Thr Thr Thr
180 185 190

Thr Val Thr Ala Val Thr Glu Asn Pro Pro Gly Gly Gly Glu Arg Arg
195 200 205

Arg Lys Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala
210 215 220

Glu Ile Arg Asp Pro His Lys Ala Ala Arg Val Trp Leu Gly Thr Phe
225 230 235 240

Asp Thr Glu Glu Ala Ala Ala Arg Ala Tyr Asp Glu Ala Ala Leu Arg
245 250 255

Phe Arg Gly Asn Arg Ala Lys Leu Asn Phe Pro Glu Asn Val Arg Ala
260 265 270

Val Pro Pro Ile Gln Pro Phe Gln Ala Thr Thr Arg Leu Thr Val Ser

```

                275                280                285
Asp Ser Thr Thr Ser Gln Phe Arg Pro Leu Ser Ala Val Ala Pro Pro
290                295                300

Phe Ile Gln Gln Pro Gln Ile Gln Gly Ser Ser Asp Leu Ile Arg Asp
305                310                315                320

Tyr Leu Gln Tyr Ser Gln Leu Leu Gln Ser Asp Phe Gln Gln Gln Gln
                325                330                335

Ile Gln Gln Gln Gln Gln Gln Gln Arg Gln Gln Gln Gln Arg Gln Arg
                340                345                350

Gln Gln Arg Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Ser Ser Leu
                355                360                365

Leu Gln Gln Leu Tyr Tyr Asn Ala Gln Phe Ala Ser Leu Gln Ser Pro
                370                375                380

Ser Met Leu Ser Ser Ser Pro Ser Phe Ser Ser Ser Val Ser Pro Ala
385                390                395                400

Pro Phe Pro Leu Phe Thr Thr Ser Ala Ser Phe Pro Leu Phe Ser Ser
                405                410                415

Gln Gln Met Gly Tyr Phe Gln Pro Pro Glu Ser Arg Asn Pro Ala Gly
                420                425                430

Gly Val Pro Glu Phe Pro Thr Ser Thr Trp Ser Asp Thr Ser Ser Gln
                435                440                445

```

Pro Pro Pro Ser Gly

<210> 105

<211> 398

<212> PRT

<213> *Populus balsamifera* subsp. *trichocarpa*

<220>

<221> misc_feature

<222> (1)..(398)

<223> 1443093

<220>

<221> misc_feature

<222> (1)..(398)

<223> Functional Homolog of Ceres CLONE ID no. 691319
at SEQ ID NO. 104 with e-value of 3.19E-73 and percent
identity of 56.0

<400> 105

```

Met Gly Tyr Ser Ser Ser Thr Glu Met Ser Met Val Ser Glu Leu Thr
1                5                10                15

```

```

His Val Val Ser Gly Gln Arg Gly Ser Thr Ser Asp Trp Gly Ser Tyr
                20                25                30

```

```

Gly Ala Val Gly Leu Gly Gly Ala Thr Ile Thr Ser Asn Phe Gly Gln
                35                40                45

```

Ala Ala Pro Gly Ser Asn Thr Ser Thr Pro Ala Ser Pro Pro Leu Ser
 50 55 60
 Ala Tyr Ser Ser Thr Ser Gly Ser Gly Leu Trp Ile Gly Gln Lys Arg
 65 70 75 80
 Gly Arg Glu Glu Glu Ala Gly Ala Ala Ala Gln Leu Met Glu Ser Leu
 85 90 95
 Pro Arg Val Tyr Arg Gly Phe Asn Asp Phe Arg Ser Ser Gln Gly Asp
 100 105 110
 Ser Ser Ser Ser Gly Ala Thr Ala Thr Glu Glu Val Ser Ala Ser Thr
 115 120 125
 Ile Val Ile Pro Thr Thr Thr Thr Pro Ser Thr Thr Ala Thr Pro Ser
 130 135 140
 Ser Glu Ile Ala Ser Leu Glu Glu Thr Gly Glu Gln Arg Arg Arg Tyr
 145 150 155 160
 Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
 165 170 175
 Asp Pro His Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Asp Thr Ala
 180 185 190
 Glu Ala Ala Ala Arg Ala Tyr Asp Asp Ala Ala Leu Arg Phe Arg Gly
 195 200 205
 Asn Arg Ala Lys Leu Asn Phe Pro Glu Asn Val Arg Leu Leu Pro Ala
 210 215 220
 Gln Thr Gln Asn Val Thr Ala Ser Gln Val Pro Ile Ser His Ser Gln
 225 230 235 240
 Leu Ser Ser His Leu Gln Leu Gln Pro Ile Ser Ser Pro Arg Gln Gln
 245 250 255
 Ala Gln Arg Pro Gln Ala Pro Ala Pro Ala Leu Phe Gln Ser Gln Ala
 260 265 270
 Asp Ile Ile Arg Asp Tyr Trp Glu Tyr Ser Gln Leu Leu Gln Ser Ser
 275 280 285
 Gly Glu Phe His His His Gln Gln Gln Gln Gln Gln Gln Gln Pro
 290 295 300
 Ser Ser Leu Leu Gln Pro Met Phe Tyr Asn Pro Gln Val Ala Ser Leu
 305 310 315 320
 Gln Ser Ser Ala Leu Thr Ser Leu Ser Ser Ser Thr Ser Val Ser Ser
 325 330 335
 Leu Ala Ala Ile Ser Ser Gly Ser Ser Pro Ser Thr Phe Ser Pro Ser
 340 345 350
 Ala Ser Ser Phe Pro Leu Leu Phe Ala Gly Gln Gln Leu Gly Tyr Phe
 355 360 365

Arg Pro Pro Gln Asn Gln Asn Pro Ala Ser Gly Ser Asp Phe Pro Val
 370 375 380

Pro Pro Trp Thr Asp Ser Ser His Asn Pro Ser Ser Ser Gly
 385 390 395

<210> 106

<211> 393

<212> PRT

<213> Populus balsamifera subsp. trichocarpa

<220>

<221> misc_feature

<222> (1)..(393)

<223> 1452324

<220>

<221> misc_feature

<222> (1)..(393)

<223> Functional Homolog of Ceres CLONE ID no. 691319
 at SEQ ID NO. 104 with e-value of 1.69E-67 and percent
 identity of 54.8

<400> 106

Met Gly Tyr Ser Ser Ser Ala Glu Met Ser Ala Met Val Ser Ala Leu
 1 5 10 15

Thr His Val Val Ser Gly His Arg Gly Ser Thr Ser Asp Trp Gly Ser
 20 25 30

Tyr Gly Ala Ser Gly Leu Gly Gly Ala Thr Ile Thr Ser Thr Ile Val
 35 40 45

Gln Ala Ala Pro Gly Ser Asn Thr Ser Pro Ala Ser Pro Ser Leu Ser
 50 55 60

Ala Tyr Ser Ser Thr Ser Gly Ser Gly Ser Trp Ile Gly Gln Lys Arg
 65 70 75 80

Gly Arg Glu Lys Glu Ala Gly Ala Ala Ala Gln Leu Lys Glu Ser Leu
 85 90 95

Pro Arg Val His Arg Gly Phe Asp Asp Phe Arg Ser Ser Leu Gly Asp
 100 105 110

Ser Pro Ser Ser Gly Ala Thr Ala Thr Glu Glu Val Ser Ala Ser Thr
 115 120 125

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

Ser Glu Thr Ala Ser Leu Gly Glu Thr Gly Glu Arg Lys Arg Arg Tyr
 145 150 155 160

Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
 165 170 175

Asp Pro His Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu Thr Ala

180								185				190			
Glu	Ala	Ala	Ala	Arg	Ala	Tyr	Asp	Glu	Ala	Ala	Leu	Arg	Phe	Arg	Gly
		195				200						205			
Ser	Arg	Ala	Lys	Leu	Asn	Phe	Pro	Glu	Asn	Ala	Arg	Leu	Leu	Pro	Ala
		210				215						220			
Gln	Met	Gln	Asn	Val	Thr	Ala	Ser	Gln	Val	Pro	Ile	Ser	Arg	Ser	Gln
225				230						235				240	
Leu	Pro	Ser	His	His	Gln	Leu	Gln	Ser	Ile	Ser	Ser	Pro	Arg	Gln	Gln
				245				250						255	
Ala	Gln	Arg	Pro	Gln	Val	Pro	Ala	Pro	Ala	Leu	Phe	Gln	Ser	Gln	Pro
		260						265				270			
Asp	Ile	Ile	Arg	Asp	Tyr	Trp	Glu	Tyr	Ser	Gln	Leu	Leu	Gln	Ser	Ser
		275				280						285			
Gly	Asp	Phe	His	Gly	Gln	Gln	Gln	Pro	Pro	Pro	Ser	Asn	Leu	Leu	Glu
290						295						300			
Gln	Met	Phe	Tyr	Asn	Pro	Gln	Leu	Ala	Ser	Leu	Gln	Ser	Ser	Thr	Leu
305				310						315				320	
Ser	Ser	Leu	Pro	Ser	Ser	Thr	Ser	Gly	Ser	Ser	Phe	Ala	Ala	Ile	Pro
				325				330						335	
Ser	Gly	Ser	Ile	Ser	Ser	Thr	Leu	Ser	Pro	Ser	Ala	Ser	Ser	Phe	Pro
		340						345				350			
Leu	Leu	Phe	Ala	Gly	Gln	Gln	Leu	Gly	Tyr	Phe	Arg	Pro	Pro	Glu	Asn
		355				360						365			
Gln	Asn	Pro	Ala	Ala	Gly	Ser	Asp	Phe	Pro	Val	Pro	Pro	Trp	Thr	Asp
370						375						380			
Cys	Ser	Arg	Arg	Pro	Ser	Ser	Thr	Gly							
385				390											

```
<210> 107
<211> 877
<212> DNA
<213> Arabidopsis thaliana
```

```
<220>
<221> misc_feature
<222> (1)..(877)
<223> Ceres CLONE ID no. 98850
```

```
<220>
<221> CDS
<222> (47)..(626)
<223> Referenced by SEQ ID NO: 108
```

<400> 107
agattaggat taaattaggg cataaccctt atcggagatt tgaagccatg ggaagaagaa 60

```

aaatcgagat caagogaatc gagaacaaaa gcagtcgaca agtcactttc tccaaacgac 120
gcaatggtct catcgacaaa gctcgacaac ttctgattct ctgtgaatcc tccgtcgctg 180
ttgtcgctgt atctgcctcc ggaaaactct atgactcttc ctccggtgac gagatagaag 240
cgctgttcaa gccggagaaa cctcaatggt ttgaactcga tcttgaagaa aaaattcaga 300
attatcttcc acacaaggag ttactagaaa cagtccaaag caagcttgaa gaaccaaagt 360
tcgataatgt aagtgtagat tctctaattt ctctggagga acaacttgag actgctctgt 420
ccgtaagtag agctaggaag gcagaactga tgatggagta tatcgagtcc cttaaagaaa 480
aggagaaatt gctgagagaa gagaaccagg ttctggctag ccagatggga aagaatacgt 540
tgctggcaac agatgatgag agaggaatgt ttccgggaag tagctccggc aacaaaatac 600
cggagactct cccgctgctc aattagccac catcatcaac ggctgagttt tcaccttaaa 660
ctcaaagcct gattcataat taagagaata aatttgtata ttataaaaag ctgtgtaatc 720
tcaaaccttt tatcttctc tagtgtggaa ttaaggtca aaaagaaaac gagaaagtat 780
ggatcagtggt tgtacctctc tcggagacaa gatcagagtt tgtgtgtttg tgtctgaatg 840
taoggattgg atttttaaag ttgtgctttc tttctcc 877

```

<210> 108

<211> 192

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(192)

<223> Ceres CLONE ID no. 98850

<220>

<221> misc_feature

<222> (69)..(162)

<223> Pfam Name: K-box; Pfam Description: K-box re.g.ion

<220>

<221> misc_feature

<222> (9)..(59)

<223> Pfam Name: SRF-TF; Pfam Description: SRF-type transcription factor
(DNA-binding and dimerisation domain)

<400> 108

```

Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1           5           10           15

```

```

Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala
          20           25           30

```

```

Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Val
          35           40           45

```

Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu
50 55 60

Ala Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu
65 70 75 80

Glu Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val
85 90 95

Gln Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser
100 105 110

Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg
115 120 125

Ala Arg Lys Ala Glu Leu Met Met Glu Tyr Ile Glu Ser Leu Lys Glu
130 135 140

Lys Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu Ala Ser Gln Met
145 150 155 160

Gly Lys Asn Thr Leu Leu Ala Thr Asp Asp Glu Arg Gly Met Phe Pro
165 170 175

Gly Ser Ser Ser Gly Asn Lys Ile Pro Glu Thr Leu Pro Leu Leu Asn
180 185 190

<210> 109

<211> 1614

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(1614)

<223> Ceres CDNA ID no. 36533702

<220>

<221> misc_feature

<222> (1)..(1614)

<223> Also Known As Ceres ME LINE ME04012

<220>

<221> CDS

<222> (14)..(1523)

<223> Referenced by SEQ ID NO: 110

<400> 109

aaacactttc atacatgagc aatattcaag aaatggagat gatattgatg gtctctttgt 60

gottaacgac cctcattacc cttttctttgc ttaaacaatt cctcaaacga accgccaaca 120

aagtgaactt accaccatct ccatggaggc ttccgttgat tggtaacctc caccagctta 180

gcctccaccc tcaccgttcc ctccattccc taagccttcg gtacggacca ctcatgctcc 240

ttcatttttg ccgtgtcccc atactcgtag taccctccgg ggaagcagct caagaggtat 300

tgaaaacaca cgatcttaag ttgccaacc gcccgagatc aaaagccgtt catgggctta 360

tgaatggggg gcgatgatgtg gtgtttgggtc cctatggaga atattggaga cagatgaaga 420
gtgtatgcat tctcaatctg ctcacgaaca aaatgggttc gtcctttgag aagataagag 480
aagaagagct aaatgaaatg atcaagaagc tggagaaagc aagttcttct tcttcgtcag 540
aaaatctgag cgaactcttt gttactctcc caagcgatgt tacgagtaga attgccttgg 600
gaagaaaaca tagtgaggac gaaaccgcaa gggatctcaa gaagcgagtg aggcagatca 660
tggagctttt aggcgagttc ccaatcgggg actatgtccc ggctttggca tggatagaca 720
ggatcaacgg tttcaatgct agaataaagg aagtaagtca agggtttagc gatcttatgg 780
acaagtggg gcaagaacat ttagaggcag gtaatcataa agaggacttt gtcgatatac 840
tgttatcaat cgaaagcgag aagagtattg gattccaagc tcaaagagac gacatcaaatt 900
tcatgatatt ggatatgttt ataggaggga cgtcaacaag ttcaactcta ctagaatgga 960
taatgacgga gctgatcaga aatccaaatg ttatgaagaa actccaagac gagattcggg 1020
caaccattag gccacatggg tcatacataa aagaaaaaga tgttgaaaat atgaaatact 1080
tgaaagccgt gattaaagag gtgtttcggg tgcactctcc tcttccacta atacttccca 1140
gattattaag tgaagatgtc aaagtaaagg gatataacat agccgcagga accgaggtga 1200
taatcaatgc ttggggccatc caaagagacc ccgcgatatg gggaccggat gcagaagaat 1260
tcaaaccaga aagacattta gattcaactt tggattatca tggaaaagat ttaaacttca 1320
tcccattcgg atcagggaga aggatttgtc cagggataaa tcttgctttg ggtttggtag 1380
aggtgacagt ggccaacctt gtaggccgat ttgactggag ggccgaggct ggaccaaattg 1440
gggatcaacc tgatctaact gaagcttttg gtctcgatgt ttgccgaaag ttccctctca 1500
ttgcatttcc atcttccgtt atttaaaatg tttctctttt tatcttttac cttgttatgc 1560
acttaattaa taagaagcat tgtaagatat aataaaatcc ttcatttttag aaaa 1614

<210> 110

<211> 503

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(503)

<223> Ceres CDNA ID no. 36533702

<220>

<221> misc_feature

<222> (1)..(503)

<223> Also Known As Ceres ME LINE ME04012

<220>

<221> misc_feature

<222> (40)..(498)

<223> Pfam Name: p450; Pfam Description: Cytochrome P450

<220>

<221> misc_feature

<222>

<223> Phenotype: Dark Green

Useful for increasing chlorophyll
and photosynthetic capacity

<400> 110

Met Ser Asn Ile Gln Glu Met Glu Met Ile Leu Met Val Ser Leu Cys
1 5 10 15

Leu Thr Thr Leu Ile Thr Leu Phe Leu Leu Lys Gln Phe Leu Lys Arg
20 25 30

Thr Ala Asn Lys Val Asn Leu Pro Pro Ser Pro Trp Arg Leu Pro Leu
35 40 45

Ile Gly Asn Leu His Gln Leu Ser Leu His Pro His Arg Ser Leu His
50 55 60

Ser Leu Ser Leu Arg Tyr Gly Pro Leu Met Leu Leu His Phe Gly Arg
65 70 75 80

Val Pro Ile Leu Val Val Ser Ser Gly Glu Ala Ala Gln Glu Val Leu
85 90 95

Lys Thr His Asp Leu Lys Phe Ala Asn Arg Pro Arg Ser Lys Ala Val
100 105 110

His Gly Leu Met Asn Gly Gly Arg Asp Val Val Phe Gly Pro Tyr Gly
115 120 125

Glu Tyr Trp Arg Gln Met Lys Ser Val Cys Ile Leu Asn Leu Leu Thr
130 135 140

Asn Lys Met Val Ala Ser Phe Glu Lys Ile Arg Glu Glu Glu Leu Asn
145 150 155 160

Glu Met Ile Lys Lys Leu Glu Lys Ala Ser Ser Ser Ser Ser Ser Glu
165 170 175

Asn Leu Ser Glu Leu Phe Val Thr Leu Pro Ser Asp Val Thr Ser Arg
180 185 190

Ile Ala Leu Gly Arg Lys His Ser Glu Asp Glu Thr Ala Arg Asp Leu
195 200 205

Lys Lys Arg Val Arg Gln Ile Met Glu Leu Leu Gly Glu Phe Pro Ile
210 215 220

Gly Asp Tyr Val Pro Ala Leu Ala Trp Ile Asp Arg Ile Asn Gly Phe
225 230 235 240

Asn Ala Arg Ile Lys Glu Val Ser Gln Gly Phe Ser Asp Leu Met Asp
245 250 255

Lys Val Val Gln Glu His Leu Glu Ala Gly Asn His Lys Glu Asp Phe
260 265 270

Val Asp Ile Leu Leu Ser Ile Glu Ser Glu Lys Ser Ile Gly Phe Gln
 275 280 285
 Ala Gln Arg Asp Asp Ile Lys Phe Met Ile Leu Asp Met Phe Ile Gly
 290 295 300
 Gly Thr Ser Thr Ser Ser Thr Leu Leu Glu Trp Ile Met Thr Glu Leu
 305 310 315 320
 Ile Arg Asn Pro Asn Val Met Lys Lys Leu Gln Asp Glu Ile Arg Ser
 325 330 335
 Thr Ile Arg Pro His Gly Ser Tyr Ile Lys Glu Lys Asp Val Glu Asn
 340 345 350
 Met Lys Tyr Leu Lys Ala Val Ile Lys Glu Val Phe Arg Val His Pro
 355 360 365
 Pro Leu Pro Leu Ile Leu Pro Arg Leu Leu Ser Glu Asp Val Lys Val
 370 375 380
 Lys Gly Tyr Asn Ile Ala Ala Gly Thr Glu Val Ile Ile Asn Ala Trp
 385 390 395 400
 Ala Ile Gln Arg Asp Pro Ala Ile Trp Gly Pro Asp Ala Glu Glu Phe
 405 410 415
 Lys Pro Glu Arg His Leu Asp Ser Thr Leu Asp Tyr His Gly Lys Asp
 420 425 430
 Leu Asn Phe Ile Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Ile
 435 440 445
 Asn Leu Ala Leu Gly Leu Val Glu Val Thr Val Ala Asn Leu Val Gly
 450 455 460
 Arg Phe Asp Trp Arg Ala Glu Ala Gly Pro Asn Gly Asp Gln Pro Asp
 465 470 475 480
 Leu Thr Glu Ala Phe Gly Leu Asp Val Cys Arg Lys Phe Pro Leu Ile
 485 490 495

Ala Phe Pro Ser Ser Val Ile

<210> 111

<211> 503

<212> PRT

<213> Arabidopsis thaliana

<220>

<221> misc_feature

<222> (1)..(503)

<223> Public GI no. 42569483

<220>

<221> misc_feature

<222> (1)..(503)

<223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 1.49E-242 and percent
 identity of 89.4

<400> 111

```

Met Ser Asn Ile Gln Glu Met Glu Met Ile Leu Ser Ile Ser Leu Cys
1           5           10           15

Leu Thr Thr Leu Ile Thr Leu Leu Leu Leu Arg Arg Phe Leu Lys Arg
20           25           30

Thr Ala Thr Lys Val Asn Leu Pro Pro Ser Pro Trp Arg Leu Pro Val
35           40           45

Ile Gly Asn Leu His Gln Leu Ser Leu His Pro His Arg Ser Leu Arg
50           55           60

Ser Leu Ser Leu Arg Tyr Gly Pro Leu Met Leu Leu His Phe Gly Arg
65           70           75           80

Val Pro Ile Leu Val Val Ser Ser Gly Glu Ala Ala Gln Glu Val Leu
85           90           95

Lys Thr His Asp His Lys Phe Ala Asn Arg Pro Arg Ser Lys Ala Val
100          105          110

His Gly Leu Met Asn Gly Gly Arg Asp Val Val Phe Ala Pro Tyr Gly
115          120          125

Glu Tyr Trp Arg Gln Met Lys Ser Val Cys Ile Leu Asn Leu Leu Thr
130          135          140

Asn Lys Met Val Glu Ser Phe Glu Lys Val Arg Glu Asp Glu Val Asn
145          150          155          160

Ala Met Ile Glu Lys Leu Glu Lys Ala Ser Ser Ser Ser Ser Ser Glu
165          170          175

Asn Leu Ser Glu Leu Phe Ile Thr Leu Pro Ser Asp Val Thr Ser Arg
180          185          190

Val Ala Leu Gly Arg Lys His Ser Glu Asp Glu Thr Ala Arg Asp Leu
195          200          205

Lys Lys Arg Val Arg Gln Ile Met Glu Leu Leu Gly Glu Phe Pro Ile
210          215          220

Gly Glu Tyr Val Pro Ile Leu Ala Trp Ile Asp Gly Ile Arg Gly Phe
225          230          235          240

Asn Asn Lys Ile Lys Glu Val Ser Arg Gly Phe Ser Asp Leu Met Asp
245          250          255

Lys Val Val Gln Glu His Leu Glu Ala Ser Asn Asp Lys Ala Asp Phe
260          265          270

Val Asp Ile Leu Leu Ser Ile Glu Lys Asp Lys Asn Ser Gly Phe Gln
275          280          285

Val Gln Arg Asn Asp Ile Lys Phe Met Ile Leu Asp Met Phe Ile Gly
290          295          300

Gly Thr Ser Thr Thr Ser Thr Leu Leu Glu Trp Thr Met Thr Glu Leu

```

```

305              310              315              320
Ile Arg Ser Pro Lys Ser Met Lys Lys Leu Gln Asp Glu Ile Arg Ser
              325              330              335
Thr Ile Arg Pro His Gly Ser Tyr Ile Lys Glu Lys Glu Val Glu Asn
              340              345              350
Met Lys Tyr Leu Lys Ala Val Ile Lys Glu Val Leu Arg Leu His Pro
              355              360              365
Ser Leu Pro Met Ile Leu Pro Arg Leu Leu Ser Glu Asp Val Lys Val
              370              375              380
Lys Gly Tyr Asn Ile Ala Ala Gly Thr Glu Val Ile Ile Asn Ala Trp
385              390              395              400
Ala Ile Gln Arg Asp Thr Ala Ile Trp Gly Pro Asp Ala Glu Glu Phe
              405              410              415
Lys Pro Glu Arg His Leu Asp Ser Gly Leu Asp Tyr His Gly Lys Asn
              420              425              430
Leu Asn Tyr Ile Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Ile
              435              440              445
Asn Leu Ala Leu Gly Leu Ala Glu Val Thr Val Ala Asn Leu Val Gly
              450              455              460
Arg Phe Asp Trp Arg Val Glu Ala Gly Pro Asn Gly Asp Gln Pro Asp
465              470              475              480
Leu Thr Glu Ala Ile Gly Ile Asp Val Cys Arg Lys Phe Pro Leu Ile
              485              490              495
Ala Phe Pro Ser Ser Val Val
              500

```

```

<210> 112
<211> 497
<212> PRT
<213> Arabidopsis thaliana

```

```

<220>
<221> misc_feature
<222> (1)..(497)
<223> Public GI no. 2880054

```

```

<220>
<221> misc_feature
<222> (1)..(497)
<223> Functional Homolog of Ceres CDNA ID no. 36533702
      at SEQ ID NO. 110 with e-value of 1.69E-239 and percent
      identity of 89.3

```

```

<400> 112
Met Glu Met Ile Leu Ser Ile Ser Leu Cys Leu Thr Thr Leu Ile Thr
1              5              10              15

```

Leu Leu Leu Leu Arg Arg Phe Leu Lys Arg Thr Ala Thr Lys Val Asn
 20 25 30
 Leu Pro Pro Ser Pro Trp Arg Leu Pro Val Ile Gly Asn Leu His Gln
 35 40 45
 Leu Ser Leu His Pro His Arg Ser Leu Arg Ser Leu Ser Leu Arg Tyr
 50 55 60
 Gly Pro Leu Met Leu Leu His Phe Gly Arg Val Pro Ile Leu Val Val
 65 70 75 80
 Ser Ser Gly Glu Ala Ala Gln Glu Val Leu Lys Thr His Asp His Lys
 85 90 95
 Phe Ala Asn Arg Pro Arg Ser Lys Ala Val His Gly Leu Met Asn Gly
 100 105 110
 Gly Arg Asp Val Val Phe Ala Pro Tyr Gly Glu Tyr Trp Arg Gln Met
 115 120 125
 Lys Ser Val Cys Ile Leu Asn Leu Leu Thr Asn Lys Met Val Glu Ser
 130 135 140
 Phe Glu Lys Val Arg Glu Asp Glu Val Asn Ala Met Ile Glu Lys Leu
 145 150 155 160
 Glu Lys Ala Ser Ser Ser Ser Ser Ser Glu Asn Leu Ser Glu Leu Phe
 165 170 175
 Ile Thr Leu Pro Ser Asp Val Thr Ser Arg Val Ala Leu Gly Arg Lys
 180 185 190
 His Ser Glu Asp Glu Thr Ala Arg Asp Leu Lys Lys Arg Val Arg Gln
 195 200 205
 Ile Met Glu Leu Leu Gly Glu Phe Pro Ile Gly Glu Tyr Val Pro Ile
 210 215 220
 Leu Ala Trp Ile Asp Gly Ile Arg Gly Phe Asn Asn Lys Ile Lys Glu
 225 230 235 240
 Val Ser Arg Gly Phe Ser Asp Leu Met Asp Lys Val Val Gln Glu His
 245 250 255
 Leu Glu Ala Ser Asn Asp Lys Ala Asp Phe Val Asp Ile Leu Leu Ser
 260 265 270
 Ile Glu Lys Asp Lys Asn Ser Gly Phe Gln Val Gln Arg Asn Asp Ile
 275 280 285
 Lys Phe Met Ile Leu Asp Met Phe Ile Gly Gly Thr Ser Thr Thr Ser
 290 295 300
 Thr Leu Leu Glu Trp Thr Met Thr Glu Leu Ile Arg Ser Pro Lys Ser
 305 310 315 320
 Met Lys Lys Leu Gln Asp Glu Ile Arg Ser Thr Ile Arg Pro His Gly
 325 330 335

Ser Tyr Ile Lys Glu Lys Glu Val Glu Asn Met Lys Tyr Leu Lys Ala
 340 345 350

Val Ile Lys Glu Val Leu Arg Leu His Pro Ser Leu Pro Met Ile Leu
 355 360 365

Pro Arg Leu Leu Ser Glu Asp Val Lys Val Lys Gly Tyr Asn Ile Ala
 370 375 380

Ala Gly Thr Glu Val Ile Ile Asn Ala Trp Ala Ile Gln Arg Asp Thr
 385 390 395 400

Ala Ile Trp Gly Pro Asp Ala Glu Glu Phe Lys Pro Glu Arg His Leu
 405 410 415

Asp Ser Gly Leu Asp Tyr His Gly Lys Asn Leu Asn Tyr Ile Pro Phe
 420 425 430

Gly Ser Gly Arg Arg Ile Cys Pro Gly Ile Asn Leu Ala Leu Gly Leu
 435 440 445

Ala Glu Val Thr Val Ala Asn Leu Val Gly Arg Phe Asp Trp Arg Val
 450 455 460

Glu Ala Gly Pro Asn Gly Asp Gln Pro Asp Leu Thr Glu Ala Ile Gly
 465 470 475 480

Ile Asp Val Cys Arg Lys Phe Pro Leu Ile Ala Phe Pro Ser Ser Val
 485 490 495

Val

<210> 113
 <211> 497
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(497)
 <223> Public GI no. 22329490

<220>
 <221> misc_feature
 <222> (1)..(497)
 <223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 1.49E-233 and percent
 identity of 86.6

<400> 113
 Met Glu Met Thr Leu Met Val Ser Leu Cys Leu Thr Thr Leu Leu Thr
 1 5 10 15

Leu Leu Leu Leu Lys Lys Phe Leu Lys Arg Thr Ala Lys Lys Val Asn
 20 25 30

Leu Pro Pro Ser Pro Trp Arg Ile Pro Val Ile Gly Asn Leu His Gln

35					40					45					
Leu	Ser	Leu	His	Pro	His	Arg	Ser	Leu	His	Ser	Leu	Ser	Leu	Arg	Tyr
50						55					60				
Gly	Pro	Leu	Met	Leu	Leu	His	Phe	Gly	Arg	Val	Pro	Ile	Leu	Val	Val
65					70					75					80
Ser	Ser	Ser	Glu	Ala	Ala	His	Glu	Ile	Leu	Lys	Thr	His	Asp	Leu	Lys
			85						90					95	
Phe	Ala	Asn	Arg	Pro	Lys	Ser	Lys	Ala	Val	His	Gly	Leu	Met	Asn	Gly
			100					105						110	
Gly	Arg	Asp	Val	Val	Phe	Gly	Pro	Tyr	Gly	Glu	Tyr	Trp	Arg	Gln	Met
		115					120					125			
Lys	Ser	Val	Cys	Ile	Leu	Asn	Leu	Leu	Thr	Asn	Lys	Met	Val	Ala	Ser
	130					135					140				
Phe	Glu	Lys	Val	Arg	Glu	Glu	Glu	Val	Asn	Ala	Met	Met	Glu	Lys	Leu
145					150					155					160
Glu	Lys	Ala	Ser	Cys	Ser	Ser	Ser	Ala	Glu	Asn	Leu	Ser	Glu	Leu	Phe
			165						170					175	
Val	Thr	Leu	Thr	Ser	Asp	Val	Thr	Ser	Arg	Val	Ser	Leu	Gly	Lys	Lys
			180					185					190		
Tyr	Trp	Glu	Asp	Glu	Thr	Ala	Gly	Gly	Leu	Lys	Lys	Arg	Val	Arg	Gln
		195					200					205			
Ile	Met	Glu	Leu	Leu	Arg	Glu	Phe	Pro	Ile	Gly	Asp	Tyr	Val	Pro	Ala
	210					215					220				
Leu	Ala	Trp	Ile	Asp	Arg	Ile	Asn	Gly	Phe	Asn	Ser	Lys	Ile	Val	Glu
225					230					235					240
Val	Ser	Arg	Ala	Tyr	Ser	Asp	Leu	Met	Glu	Lys	Val	Val	Gln	Glu	His
				245					250					255	
Leu	Glu	Ala	Gly	Glu	His	Lys	Ala	Asp	Phe	Val	Asn	Ile	Leu	Leu	Ser
			260					265					270		
Ile	Glu	Lys	Glu	Lys	Asn	Asn	Gly	Phe	Lys	Val	Gln	Arg	Asn	Asp	Ile
	275						280					285			
Lys	Phe	Met	Ile	Leu	Asp	Met	Phe	Ile	Gly	Gly	Ile	Ser	Thr	Ser	Ser
	290					295					300				
Thr	Leu	Leu	Glu	Trp	Ile	Met	Thr	Glu	Leu	Ile	Arg	Asn	Pro	Glu	Cys
305					310					315					320
Met	Lys	Lys	Leu	Gln	Asn	Glu	Ile	Arg	Ser	Thr	Ile	Arg	Pro	His	Gly
				325					330					335	
Ser	Tyr	Ile	Lys	Glu	Lys	Glu	Val	Glu	Asn	Met	Arg	Tyr	Leu	Lys	Ala
			340					345					350		
Val	Ile	Lys	Glu	Val	Phe	Arg	Val	His	Pro	Pro	Leu	Pro	Leu	Ile	Leu
		355					360					365			

Pro Arg Leu Leu Thr Glu Asp Val Lys Val Lys Gly Tyr Asp Ile Ala
 370 375 380
 Ala Gly Thr Glu Val Leu Ile Asn Ala Trp Ser Ile His Arg Asp Pro
 385 390 395 400
 Ala Ile Trp Gly Pro Asp Ala Glu Glu Phe Lys Pro Glu Arg His Leu
 405 410 415
 Asp Ser Thr Leu Asp Tyr His Gly Gln Asp Leu Lys Tyr Ile Pro Phe
 420 425 430
 Gly Ser Gly Arg Arg Ile Cys Pro Gly Ile Asn Leu Ala Met Gly Leu
 435 440 445
 Val Glu Val Thr Leu Ala Asn Leu Val Gly Arg Phe Asp Trp Ser Val
 450 455 460
 Asp Pro Gly Pro Asn Gly Asp Gln Pro Asp Leu Ala Glu Asp Phe Gly
 465 470 475 480
 Leu Asp Val Cys Arg Lys Asn Pro Leu Ile Ala Phe Pro Ser Ser Val
 485 490 495
 Ala

<210> 114
 <211> 477
 <212> PRT
 <213> Arabidopsis thaliana

<220>
 <221> misc_feature
 <222> (1)..(477)
 <223> Public GI no. 4835796

<220>
 <221> misc_feature
 <222> (1)..(477)
 <223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 9.10E-218 and percent
 identity of 86.1

<400> 114
 Met Glu Met Thr Leu Met Val Ser Leu Cys Leu Thr Thr Leu Leu Thr
 1 5 10 15
 Leu Leu Leu Leu Lys Lys Phe Leu Lys Arg Thr Ala Lys Lys Val Asn
 20 25 30
 Leu Pro Pro Ser Pro Trp Arg Ile Pro Val Ile Gly Asn Leu His Gln
 35 40 45
 Leu Ser Leu His Pro His Arg Ser Leu His Ser Leu Ser Leu Ser Glu
 50 55 60

Ala Ala His Glu Ile Leu Lys Thr His Asp Leu Lys Phe Ala Asn Arg
 65 70 75 80
 Pro Lys Ser Lys Ala Val His Gly Leu Met Asn Gly Gly Arg Asp Val
 85 90 95
 Val Phe Gly Pro Tyr Gly Glu Tyr Trp Arg Gln Met Lys Ser Val Cys
 100 105 110
 Ile Leu Asn Leu Leu Thr Asn Lys Met Val Ala Ser Phe Glu Lys Val
 115 120 125
 Arg Glu Glu Glu Val Asn Ala Met Met Glu Lys Leu Glu Lys Ala Ser
 130 135 140
 Cys Ser Ser Ser Ala Glu Asn Leu Ser Glu Leu Phe Val Thr Leu Thr
 145 150 155 160
 Ser Asp Val Thr Ser Arg Val Ser Leu Gly Lys Lys Tyr Trp Glu Asp
 165 170 175
 Glu Thr Ala Gly Gly Leu Lys Lys Arg Val Arg Gln Ile Met Glu Leu
 180 185 190
 Leu Arg Glu Phe Pro Ile Gly Asp Tyr Val Pro Ala Leu Ala Trp Ile
 195 200 205
 Asp Arg Ile Asn Gly Phe Asn Ser Lys Ile Val Glu Val Ser Arg Ala
 210 215 220
 Tyr Ser Asp Leu Met Glu Lys Val Val Gln Glu His Leu Glu Ala Gly
 225 230 235 240
 Glu His Lys Ala Asp Phe Val Asn Ile Leu Leu Ser Ile Glu Lys Glu
 245 250 255
 Lys Asn Asn Gly Phe Lys Val Gln Arg Asn Asp Ile Lys Phe Met Ile
 260 265 270
 Leu Asp Met Phe Ile Gly Gly Ile Ser Thr Ser Ser Thr Leu Leu Glu
 275 280 285
 Trp Ile Met Thr Glu Leu Ile Arg Asn Pro Glu Cys Met Lys Lys Leu
 290 295 300
 Gln Asn Glu Ile Arg Ser Thr Ile Arg Pro His Gly Ser Tyr Ile Lys
 305 310 315 320
 Glu Lys Glu Val Glu Asn Met Arg Tyr Leu Lys Ala Val Ile Lys Glu
 325 330 335
 Val Phe Arg Val His Pro Pro Leu Pro Leu Ile Leu Pro Arg Leu Leu
 340 345 350
 Thr Glu Asp Val Lys Val Lys Gly Tyr Asp Ile Ala Ala Gly Thr Glu
 355 360 365
 Val Leu Ile Asn Ala Trp Ser Ile His Arg Asp Pro Ala Ile Trp Gly
 370 375 380
 Pro Asp Ala Glu Glu Phe Lys Pro Glu Arg His Leu Asp Ser Thr Leu

385 390 395 400
 Asp Tyr His Gly Gln Asp Leu Lys Tyr Ile Pro Phe Gly Ser Gly Arg
 405 410 415
 Arg Ile Cys Pro Gly Ile Asn Leu Ala Met Gly Leu Val Glu Val Thr
 420 425 430
 Leu Ala Asn Leu Val Gly Arg Phe Asp Trp Ser Val Asp Pro Gly Pro
 435 440 445
 Asn Gly Asp Gln Pro Asp Leu Ala Glu Asp Phe Gly Leu Asp Val Cys
 450 455 460
 Arg Lys Asn Pro Leu Ile Ala Phe Pro Ser Ser Val Ala
 465 470 475

<210> 115
 <211> 509
 <212> PRT
 <213> *Nepeta racemosa*

<220>
 <221> misc_feature
 <222> (1)..(509)
 <223> Public GI no. 3582021

<220>
 <221> misc_feature
 <222> (1)..(509)
 <223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 3.60E-113 and percent
 identity of 46.3

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

Arg Ser Ile Cys Val Leu Gln Leu Leu Ser Asn Lys Arg Val Gln Ser
 130 135 140
 Phe Arg Arg Val Arg Glu Glu Thr Ser Ile Met Val Glu Lys Ile
 145 150 155 160
 Met Gln Leu Gly Ser Ser Ser Ser Thr Pro Val Asn Leu Ser Glu Leu
 165 170 175
 Leu Leu Ser Leu Thr Asn Asp Val Val Cys Arg Val Thr Leu Gly Lys
 180 185 190
 Lys Tyr Gly Gly Gly Asn Gly Ser Glu Glu Val Asp Lys Leu Lys Glu
 195 200 205
 Met Leu Thr Glu Ile Gln Asn Leu Met Gly Ile Ser Pro Val Trp Glu
 210 215 220
 Phe Ile Pro Trp Leu Asn Trp Thr Arg Arg Phe Asp Gly Val Asp Gln
 225 230 235 240
 Arg Val Asp Arg Ile Val Lys Ala Phe Asp Gly Phe Leu Glu Ser Val
 245 250 255
 Ile Gln Glu His Lys Glu Arg Asp Gly Asp Lys Asp Gly Asp Gly Asp
 260 265 270
 Gly Ala Leu Asp Phe Val Asp Ile Leu Leu Gln Phe Gln Arg Glu Asn
 275 280 285
 Lys Asn Arg Ser Pro Val Glu Asp Asp Thr Val Lys Ala Leu Ile Leu
 290 295 300
 Asp Met Phe Val Ala Gly Thr Asp Thr Thr Ala Thr Ala Leu Glu Trp
 305 310 315 320
 Ala Val Ala Glu Leu Ile Lys Asn Pro Arg Ala Met Lys Arg Leu Gln
 325 330 335
 Asn Glu Val Arg Glu Val Ala Gly Ser Lys Ala Glu Ile Glu Glu Glu
 340 345 350
 Asp Leu Glu Lys Met Pro Tyr Leu Lys Ala Ser Ile Lys Glu Ser Leu
 355 360 365
 Arg Leu His Val Pro Val Val Leu Leu Val Pro Arg Glu Ser Thr Arg
 370 375 380
 Asp Thr Asn Val Leu Gly Tyr Asp Ile Ala Ser Gly Thr Arg Val Leu
 385 390 395 400
 Ile Asn Ala Trp Ala Ile Ala Arg Asp Pro Ser Val Trp Glu Asn Pro
 405 410 415
 Glu Glu Phe Leu Pro Glu Arg Phe Leu Asp Ser Ser Ile Asp Tyr Lys
 420 425 430
 Gly Leu His Phe Glu Leu Leu Pro Phe Gly Ala Gly Arg Arg Gly Cys
 435 440 445

Pro Gly Ala Thr Phe Ala Val Ala Ile Asp Glu Leu Ala Leu Ala Lys
 450 455 460

Leu Val His Lys Phe Asp Phe Gly Leu Pro Asn Gly Ala Arg Met Glu
 465 470 475 480

Glu Leu Asp Met Ser Glu Thr Ser Gly Met Thr Val His Lys Lys Ser
 485 490 495

Pro Leu Leu Leu Leu Pro Ile Pro His His Ala Ala Pro
 500 505

<210> 116

<211> 494

<212> PRT

<213> Ammi majus

<220>

<221> misc_feature

<222> (1)..(494)

<223> Public GI no. 46947673

<220>

<221> misc_feature

<222> (1)..(494)

<223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 1.10E-102 and percent
 identity of 46.0

<400> 116

Met Lys Met Leu Glu Gln Asn Pro Gln Tyr Leu Tyr Phe Phe Ser Leu
 1 5 10 15

Phe Leu Val Thr Ile Phe Leu Tyr Lys Trp Leu Thr Leu Lys Lys Thr
 20 25 30

Pro Leu Lys Asn Leu Pro Pro Ser Pro Pro Gln Tyr Pro Ile Ile Gly
 35 40 45

Asn Leu His Gln Ile Gly Pro Asp Pro Gln Ala Ser Leu Arg Asp Leu
 50 55 60

Ala Gln Lys Tyr Gly Pro Leu Met Phe Leu Lys Phe Gly Thr Val Pro
 65 70 75 80

Val Leu Val Val Ser Ser Ala Asp Ala Ala Arg Glu Ala Leu Lys Thr
 85 90 95

His Asp Leu Val Phe Ala Asp Arg Pro Tyr Ser Ser Val Ala Asn Lys
 100 105 110

Ile Phe Tyr Asn Gly Lys Asp Met Val Phe Ala Arg Tyr Thr Glu Tyr
 115 120 125

Trp Arg Gln Val Lys Ser Ile Cys Val Thr Gln Leu Leu Ser Asn Lys
 130 135 140

Arg Val Asn Ser Phe His Tyr Val Arg Glu Glu Glu Val Asp Leu Leu

145		150		155		160
Val Gln Asn Leu Glu Asn Ser His Ser Lys Val Ala Asn Leu Thr Glu						
	165			170		175
Leu Leu Ile Glu Val Thr Gly Asn Val Val Cys Arg Val Ser Val Gly						
	180		185			190
Ser Gly Asp Lys Val Asp Ser Tyr Lys Ile Leu Ile Leu Glu Ile Met						
	195		200			205
Asp Met Leu Gly Tyr Ser Arg Ser Ile Glu Asp Phe Phe Pro Leu Leu						
	210		215			220
Gly Trp Val Asp Trp Leu Thr Gly Leu Arg Gly Lys Val Ala Glu Ala						
225		230		235		240
Ala Lys Gly Val Asp Thr Phe Leu Glu Gly Val Leu Lys Glu His Leu						
	245		250			255
Ser Thr Thr Gly Ser Lys Tyr Asn Asp Phe Val Ser Ile Leu Leu Glu						
	260		265			270
Ile Gln Glu Ala Asp Ala Gly Ser Ser Met Asp Asn Glu Cys Ile Lys						
	275		280			285
Ser Leu Ile Trp Asp Met Leu Gly Ala Gly Thr Glu Thr Ile Ser Thr						
	290		295			300
Ala Leu Glu Trp Thr Leu Ala Ala Leu Ile Lys Asn Pro Asp Ala Met						
305		310		315		320
Phe Lys Leu Gln Asn Glu Val Arg Glu Ile Gly Lys Gly Lys Ser Lys						
	325		330			335
Ile Ser Glu Ala Asp Leu Val Lys Met Asn Tyr Leu Gln Ala Val Met						
	340		345			350
Lys Glu Ser Met Arg Leu Tyr Phe Thr Ala Pro Leu Leu Val Pro Arg						
	355		360			365
Glu Ala Arg Gln Asp Ile Lys Phe Met Gly Tyr Asp Ile Ser Ser Gly						
	370		375			380
Thr Gln Val Leu Ile Asn Ala Trp Ala Ile Ala Arg Asp Pro Leu Leu						
385		390		395		400
Trp Asp Lys Pro Glu Glu Phe Arg Pro Glu Arg Phe Leu Asn Ser Pro						
	405		410			415
Ile Asp Tyr Lys Gly Phe His Tyr Glu Phe Leu Pro Phe Gly Ala Gly						
	420		425			430
Arg Arg Gly Cys Pro Gly Ile Gln Phe Ala Met Cys Ile Asn Glu Leu						
	435		440			445
Val Val Ala Asn Leu Val His Lys Phe Asn Phe Glu Leu Pro Asp Gly						
	450		455			460
Lys Arg Leu Glu Asp Leu Asp Met Thr Ala Ala Ser Gly Ile Thr Leu						
465		470		475		480

Arg Lys Lys Ser Pro Leu Leu Val Val Ala Arg Pro His Val
 485 490

<210> 117
 <211> 471
 <212> PRT
 <213> Persea americana

<220>
 <221> misc_feature
 <222> (1)..(471)
 <223> Public GI no. 117188

<220>
 <221> misc_feature
 <222> (1)..(471)
 <223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 3.09E-107 and percent
 identity of 45.9

<400> 117
 Met Ala Ile Leu Val Ser Leu Leu Phe Leu Ala Ile Ala Leu Thr Phe
 1 5 10 15
 Phe Leu Leu Lys Leu Asn Glu Lys Arg Glu Lys Lys Pro Asn Leu Pro
 20 25 30
 Pro Ser Pro Pro Asn Leu Pro Ile Ile Gly Asn Leu His Gln Leu Gly
 35 40 45
 Asn Leu Pro His Arg Ser Leu Arg Ser Leu Ala Asn Glu Leu Gly Pro
 50 55 60
 Leu Ile Leu Leu His Leu Gly His Ile Pro Thr Leu Ile Val Ser Thr
 65 70 75 80
 Ala Glu Ile Ala Glu Glu Ile Leu Lys Thr His Asp Leu Ile Phe Ala
 85 90 95
 Ser Arg Pro Ser Thr Thr Ala Ala Arg Arg Ile Phe Tyr Asp Cys Thr
 100 105 110
 Asp Val Ala Phe Ser Pro Tyr Gly Glu Tyr Trp Arg Gln Val Arg Lys
 115 120 125
 Ile Cys Val Leu Glu Leu Leu Ser Ile Lys Arg Val Asn Ser Tyr Arg
 130 135 140
 Ser Ile Arg Glu Glu Glu Val Gly Leu Met Met Glu Arg Ile Ser Gln
 145 150 155 160
 Ser Cys Ser Thr Gly Glu Ala Val Asn Leu Ser Glu Leu Leu Leu Leu
 165 170 175
 Leu Ser Ser Gly Thr Ile Thr Arg Val Ala Phe Gly Lys Lys Tyr Glu
 180 185 190

Gly Glu Glu Glu Arg Lys Asn Lys Phe Ala Asp Leu Ala Thr Glu Leu
 195 200 205
 Thr Thr Leu Met Gly Ala Phe Phe Val Gly Asp Tyr Phe Pro Ser Phe
 210 215 220
 Ala Trp Val Asp Val Leu Thr Gly Met Asp Ala Arg Leu Lys Arg Asn
 225 230 235 240
 His Gly Glu Leu Asp Ala Phe Val Asp His Val Ile Asp Asp His Leu
 245 250 255
 Leu Ser Arg Lys Ala Asn Gly Ser Asp Gly Val Glu Gln Lys Asp Leu
 260 265 270
 Val Asp Val Leu Leu His Leu Gln Lys Asp Ser Ser Leu Gly Val His
 275 280 285
 Leu Asn Arg Asn Asn Leu Lys Ala Val Ile Leu Asp Met Phe Ser Gly
 290 295 300
 Gly Thr Asp Thr Thr Ala Val Thr Leu Glu Trp Ala Met Ala Glu Leu
 305 310 315 320
 Ile Lys His Pro Asp Val Met Glu Lys Ala Gln Gln Glu Val Arg Arg
 325 330 335
 Val Val Gly Lys Lys Ala Lys Val Glu Glu Glu Asp Leu His Gln Leu
 340 345 350
 His Tyr Leu Lys Leu Ile Ile Lys Glu Thr Leu Arg Leu His Pro Val
 355 360 365
 Ala Pro Leu Leu Val Pro Arg Glu Ser Thr Arg Asp Val Val Ile Arg
 370 375 380
 Gly Tyr His Ile Pro Ala Lys Thr Arg Val Phe Ile Asn Ala Trp Ala
 385 390 395 400
 Ile Gly Arg Asp Pro Lys Ser Trp Glu Asn Ala Glu Glu Phe Leu Pro
 405 410 415
 Glu Arg Phe Val Asn Asn Ser Val Asp Phe Lys Gly Gln Asp Phe Gln
 420 425 430
 Leu Ile Pro Phe Gly Ala Gly Arg Arg Gly Cys Pro Gly Ile Ala Phe
 435 440 445
 Gly Ile Ser Ser Val Glu Ile Ser Leu Ala Asn Leu Leu Tyr Trp Phe
 450 455 460
 Asn Trp Glu Leu Pro Gly Ile
 465 470

<210> 118

<211> 529

<212> PRT

<213> *Oryza sativa* subsp. *japonica*

<220>
<221> misc_feature
<222> (1)..(529)
<223> Public GI no. 34904242

<220>
<221> misc_feature
<222> (1)..(529)
<223> Functional Homolog of Ceres CDNA ID no. 36533702
at SEQ ID NO. 110 with e-value of 2.70E-99 and percent
identity of 45.5

<400> 118

Met	Ala	Val	Ser	Leu	Val	Val	Val	Val	Val	Val	Val	Ile	Ala	Ile	Val
1				5					10					15	
Val	Pro	Leu	Leu	Tyr	Leu	Val	Leu	Leu	Pro	Ala	Trp	Lys	Pro	Ala	Arg
			20					25					30		
Arg	Asp	Asp	Gly	Asp	Gly	Gly	Met	Arg	Arg	Arg	Leu	Pro	Pro	Ser	Pro
		35					40					45			
Pro	Trp	Gly	Leu	Pro	Leu	Leu	Gly	His	Leu	His	Leu	Leu	Gly	Ala	Leu
	50					55					60				
Pro	His	Arg	Ala	Leu	Arg	Ser	Leu	Ala	Ala	Ala	His	Gly	Pro	Val	Leu
65				70						75				80	
Leu	Leu	Arg	Leu	Gly	Arg	Val	Pro	Val	Val	Val	Val	Ser	Ser	Ala	Ala
				85					90					95	
Ala	Ala	Glu	Glu	Val	Met	Arg	Thr	Arg	Asp	Leu	Glu	Phe	Ala	Ser	Arg
			100					105					110		
Pro	Arg	Val	Ala	Met	Ala	Glu	Arg	Leu	Leu	Tyr	Gly	Gly	Arg	Asp	Val
		115						120					125		
Ala	Phe	Ala	Pro	Tyr	Gly	Glu	Tyr	Trp	Arg	Gln	Thr	Arg	Arg	Ile	Cys
	130					135						140			
Val	Val	His	Leu	Leu	Ser	Ala	Arg	Arg	Val	Leu	Ser	Phe	Arg	Arg	Val
145					150					155				160	
Arg	Glu	Glu	Glu	Ala	Ala	Ala	Leu	Val	Ala	Arg	Val	Arg	Ala	Ala	Gly
				165					170					175	
Gly	Ala	Val	Asp	Leu	Val	Glu	His	Leu	Thr	Ala	Tyr	Ser	Asn	Thr	Val
			180					185					190		
Val	Ser	Arg	Ala	Val	Phe	Gly	Asp	Glu	Ser	Ala	Arg	Gly	Leu	Tyr	Gly
		195					200						205		
Asp	Val	Asp	Arg	Gly	Arg	Val	Leu	Arg	Lys	Leu	Phe	Asp	Asp	Phe	Val
	210					215					220				
Glu	Leu	Leu	Gly	Gln	Glu	Pro	Met	Gly	Glu	Leu	Leu	Pro	Trp	Leu	Gly
225					230					235				240	
Trp	Val	Asp	Ala	Leu	Asn	Gly	Met	Glu	Val	Lys	Val	Gln	Arg	Thr	Phe
			245						250					255	

Glu Ala Leu Asp Gly Ile Leu Glu Lys Val Ile Asp Asp His Arg Arg
 260 265 270
 Arg Arg Arg Glu Val Gly Arg Gln Met Asp Asp Gly Gly Gly Gly Asp
 275 280 285
 His Arg Asp Phe Val Asp Val Leu Leu Asp Val Asn Glu Thr Asp Met
 290 295 300
 Asp Ala Gly Val Gln Leu Gly Thr Ile Glu Ile Lys Ala Ile Ile Leu
 305 310 315 320
 Asp Met Phe Ala Ala Gly Thr Asp Thr Thr Thr Thr Val Ile Glu Trp
 325 330 335
 Ala Met Ala Glu Leu Ile Thr His Pro Asp Ala Met Arg Asn Ala Gln
 340 345 350
 Asp Glu Ile Lys Ala Val Val Gly Ile Thr Ser His Ile Thr Glu Asp
 355 360 365
 His Leu Asp Arg Leu Pro Tyr Leu Lys Ala Val Leu Lys Glu Thr Leu
 370 375 380
 Arg Leu His Pro Pro Leu Pro Leu Leu Val Pro His Glu Pro Ser Ser
 385 390 395 400
 Asp Thr Lys Ile Leu Gly Tyr Ser Ile Pro Ala Cys Thr Arg Ile Val
 405 410 415
 Ile Asn Ala Trp Thr Ile Gly Arg Asp Gln Ala Thr Trp Gly Glu His
 420 425 430
 Ala Glu Glu Phe Ile Pro Glu Arg Phe Leu Glu Ser Gly Leu Asp Tyr
 435 440 445
 Ile Gly Gln Asp Phe Val Leu Val Pro Phe Gly Ala Gly Arg Arg Gly
 450 455 460
 Cys Pro Gly Val Gly Phe Ala Val Gln Ala Met Glu Met Ala Leu Ala
 465 470 475 480
 Ser Leu Leu Tyr Asn Phe Asp Trp Glu Thr Arg Val Val Asp Arg Arg
 485 490 495
 Ser Glu Phe Gly Thr Ser Ser Leu Asp Met Ser Glu Met Asn Gly Leu
 500 505 510
 Ser Val Arg Leu Lys Tyr Gly Leu Pro Leu Ile Ala Ile Ser Arg Phe
 515 520 525

Pro

<210> 119

<211> 482

<212> PRT

<213> Triticum aestivum

<220>

<221> misc_feature

<222> (1)..(482)

<223> Ceres CLONE ID no. 921721

<220>

<221> misc_feature

<222> (1)..(482)

<223> Functional Homolog of Ceres CDNA ID no. 36533702
 at SEQ ID NO. 110 with e-value of 6.10E-102 and percent
 identity of 45.2

<400> 119

Met Glu Gly Arg Arg His Leu Pro Pro Ser Pro Arg Gly Leu Pro Leu
 1 5 10 15

Leu Gly His Leu His Leu Leu Gly Ser Leu Pro His Arg Ala Leu Arg
 20 25 30

Ser Leu Ala Ala Ala His Gly Pro Val Leu Leu Leu Arg Leu Gly Arg
 35 40 45

Val Pro Ala Val Val Val Ser Ser Pro Ala Ala Ala Glu Glu Val Met
 50 55 60

Arg Ala Arg Asp Leu Ala Phe Ala Ser Arg Pro Arg Ser Ala Met Ala
 65 70 75 80

Asp Arg Leu Leu Tyr Gly Arg Asp Val Ala Phe Ala Pro Tyr Gly Glu
 85 90 95

Tyr Trp Arg Gln Ala Arg Arg Val Cys Val Val His Leu Leu Ser Pro
 100 105 110

Leu Arg Ile Leu Ser Phe Arg Gly Val Arg Glu Glu Glu Ala Ala Ala
 115 120 125

Leu Val Glu Arg Val Arg Gly Ala Ala Ala Gly Gly Ala Ala Val Asp
 130 135 140

Leu Cys Glu Leu Leu Val Ala Tyr Ala Asn Thr Val Val Ser Arg Ala
 145 150 155 160

Ala Phe Gly Asp Asp Ser Ala Arg Gly Leu Tyr Glu Glu Gly Asn Lys
 165 170 175

Glu Arg Glu Leu Arg Lys Val Phe Asn Asp Phe Gln Glu Leu Leu Gly
 180 185 190

Thr Ala Pro Leu Gly Glu Leu Leu Pro Trp Leu Gly Trp Leu Asp Ala
 195 200 205

Val Arg Gly Met Glu Gly Lys Ile Arg Arg Thr Phe Lys Ala Leu Asp
 210 215 220

Gly Val Leu Glu Lys Val Ile Gly Asp His Arg Arg Arg Arg Gln Ala
 225 230 235 240

Gly Gln Gln Thr Gly Asp Asp Gly Gly Asp His Arg Asp Phe Val Asp

245 250 255
Val Leu Leu Asp Val Ser Asp Thr Asp Asp Glu Ala Gly Met Arg Leu
260 265 270
Ser Thr Thr Glu Ile Lys Ala Ile Ile Leu Asp Met Phe Ala Ala Gly
275 280 285
Thr Asp Thr Thr Ser Thr Ala Met Glu Trp Ala Met Ala Glu Val Ile
290 295 300
Thr His Pro Asp Ser Met Arg Lys Leu Gln Asp Glu Leu Arg Ala Ala
305 310 315 320
Val Gly Gly Ser Gly His Val Ile Thr Glu Asp His Ile Asp Lys Leu
325 330 335
His Tyr Leu Lys Ala Val Val Lys Glu Thr Leu Arg Leu His Pro Pro
340 345 350
Ile Pro Leu Leu Val Pro Arg Glu Pro Gln Asp Asp Ala Glu Ile Leu
355 360 365
Gly His His Val Pro Ala Gly Thr Arg Val Val Ile Asn Ala Trp Ala
370 375 380
Val Gly Arg Asp Pro Ala Ala Trp Glu Arg Ala Glu Glu Phe Val Pro
385 390 395 400
Glu Arg Phe Leu Asp Gly Ala Val Asp Tyr Lys Gly Gln Asp Phe Gln
405 410 415
Leu Ile Pro Phe Gly Ala Gly Arg Arg Gly Cys Pro Gly Val Gly Phe
420 425 430
Ala Ala Ala Thr Val Glu Met Ala Leu Ala Ser Leu Met Tyr His Phe
435 440 445
Asp Trp Glu Pro Ala Gly Ala Ser Leu Asp Met Arg Glu Val Asn Gly
450 455 460
Leu Ala Val His Leu Lys Ser Gly Leu Pro Leu Val Ala Lys Leu Arg
465 470 475 480
Phe Arg

<210> 120
<211> 515
<212> PRT
<213> Triticum aestivum

<220>
<221> misc_feature
<222> (1)..(515)
<223> Ceres CLONE ID no. 703961

<220>
<221> misc_feature

<222> (1)..(515)

<223> Functional Homolog of Ceres CDNA ID no. 36533702

at SEQ ID NO. 110 with e-value of 6.10E-102 and percent identity of 45.2

<400> 120

Met	Ala	Val	Ser	Pro	Leu	Ala	Leu	Val	Leu	Leu	Leu	Leu	Ala	Phe	Ala
1				5					10					15	

Val	Ser	Leu	Leu	Tyr	Ile	Leu	Arg	Arg	Pro	Ala	Pro	Leu	Arg	Ser	Gly
		20					25						30		

Ser	Asp	Gly	Gly	Arg	Arg	His	Leu	Pro	Pro	Ser	Pro	Arg	Gly	Leu	Pro
		35					40					45			

Leu	Leu	Gly	His	Leu	His	Leu	Leu	Gly	Ser	Leu	Pro	His	Arg	Ala	Leu
	50					55						60			

Arg	Ser	Leu	Ala	Ala	Ala	His	Gly	Pro	Val	Leu	Leu	Leu	Arg	Leu	Gly
65					70				75					80	

Arg	Val	Pro	Ala	Val	Val	Val	Ser	Ser	Pro	Ala	Ala	Ala	Glu	Glu	Val
				85					90					95	

Met	Arg	Ala	Arg	Asp	Leu	Ala	Phe	Ala	Ser	Arg	Pro	Arg	Ser	Ala	Met
			100					105					110		

Ala	Asp	Arg	Leu	Leu	Tyr	Gly	Arg	Asp	Val	Ala	Phe	Ala	Pro	Tyr	Gly
	115					120						125			

Glu	Tyr	Trp	Arg	Gln	Ala	Arg	Arg	Val	Cys	Val	Val	His	Leu	Leu	Ser
	130					135						140			

Pro	Leu	Arg	Ile	Leu	Ser	Phe	Arg	Gly	Val	Arg	Glu	Glu	Glu	Ala	Ala
145					150					155					160

Ala	Leu	Val	Glu	Arg	Val	Arg	Gly	Ala	Ala	Ala	Gly	Gly	Ala	Ala	Val
				165					170					175	

Asp	Leu	Cys	Glu	Leu	Leu	Val	Ala	Tyr	Ala	Asn	Thr	Val	Val	Ser	Arg
		180						185						190	

Ala	Ala	Phe	Gly	Asp	Asp	Ser	Ala	Arg	Gly	Leu	Tyr	Glu	Glu	Gly	Asn
		195					200					205			

Lys	Glu	Arg	Glu	Leu	Arg	Lys	Val	Phe	Asn	Asp	Phe	Gln	Glu	Leu	Leu
	210					215					220				

Gly	Thr	Ala	Pro	Leu	Gly	Glu	Leu	Leu	Pro	Trp	Leu	Gly	Trp	Leu	Asp
225					230					235					240

Ala	Val	Arg	Gly	Met	Glu	Gly	Lys	Ile	Arg	Arg	Thr	Phe	Lys	Ala	Leu
				245					250					255	

Asp	Gly	Val	Leu	Glu	Lys	Val	Ile	Gly	Asp	His	Arg	Arg	Arg	Arg	Gln
		260						265						270	

Ala	Gly	Gln	Gln	Thr	Gly	Asp	Asp	Gly	Gly	Asp	His	Arg	Asp	Phe	Val
		275					280						285		

Asp Val Leu Leu Asp Val Ser Asp Thr Asp Asp Glu Ala Gly Met Arg
 290 295 300
 Leu Ser Thr Thr Glu Ile Lys Ala Ile Ile Leu Asp Met Phe Ala Ala
 305 310 315 320
 Gly Thr Asp Thr Thr Ser Thr Ala Met Glu Trp Ala Met Ala Glu Val
 325 330 335
 Ile Thr His Pro Asp Ser Met Arg Lys Leu Gln Asp Glu Leu Arg Ala
 340 345 350
 Ala Val Gly Gly Ser Gly His Val Ile Thr Glu Asp His Ile Asp Lys
 355 360 365
 Leu His Tyr Leu Lys Ala Val Val Lys Glu Thr Leu Arg Leu His Pro
 370 375 380
 Pro Ile Pro Leu Leu Val Pro Arg Glu Pro Gln Asp Asp Ala Glu Ile
 385 390 395 400
 Leu Gly His His Val Pro Ala Gly Thr Arg Val Val Ile Asn Ala Trp
 405 410 415
 Ala Val Gly Arg Asp Pro Ala Ala Trp Glu Arg Ala Glu Glu Phe Val
 420 425 430
 Pro Glu Arg Phe Leu Asp Gly Ala Val Asp Tyr Lys Gly Gln Asp Phe
 435 440 445
 Gln Leu Ile Pro Phe Gly Ala Gly Arg Arg Gly Cys Pro Gly Val Gly
 450 455 460
 Phe Ala Ala Ala Thr Val Glu Met Ala Leu Ala Ser Leu Met Tyr His
 465 470 475 480
 Phe Asp Trp Glu Pro Ala Gly Ala Ser Leu Asp Met Arg Glu Val Asn
 485 490 495
 Gly Leu Ala Val His Leu Lys Ser Gly Leu Pro Leu Val Ala Lys Leu
 500 505 510
 Arg Phe Arg
 515

<210> 121

<211> 502

<212> PRT

<213> Persea americana

<220>

<221> misc_feature

<222> (1)..(502)

<223> Public GI no. 25282608

<220>

<221> misc_feature

<222> (1)..(502)

<223> Functional Homolog of Ceres CDNA ID no. 36533702

at SEQ ID NO. 110 with e-value of 3.69E-111 and percent identity of 45.2

<400> 121

```

Met Ala Ile Leu Val Ser Leu Leu Phe Leu Ala Ile Ala Leu Thr Phe
1           5           10           15

Phe Leu Leu Lys Leu Asn Glu Lys Arg Glu Lys Lys Pro Asn Leu Pro
20           25           30

Pro Ser Pro Pro Asn Leu Pro Ile Ile Gly Asn Leu His Gln Leu Gly
35           40           45

Asn Leu Pro His Arg Ser Leu Arg Ser Leu Ala Asn Glu Leu Gly Pro
50           55           60

Leu Ile Leu Leu His Leu Gly His Ile Pro Thr Leu Ile Val Ser Thr
65           70           75           80

Ala Glu Ile Ala Glu Glu Ile Leu Lys Thr His Asp Leu Ile Phe Ala
85           90           95

Ser Arg Pro Ser Thr Thr Ala Ala Arg Arg Ile Phe Tyr Asp Cys Thr
100          105          110

Asp Val Ala Phe Ser Pro Tyr Gly Glu Tyr Trp Arg Gln Val Arg Lys
115          120          125

Ile Cys Val Leu Glu Leu Leu Ser Ile Lys Arg Val Asn Ser Tyr Arg
130          135          140

Ser Ile Arg Glu Glu Glu Val Gly Leu Met Met Glu Arg Ile Ser Gln
145          150          155          160

Ser Cys Ser Thr Gly Glu Ala Val Asn Leu Ser Glu Leu Leu Leu Leu
165          170          175

Leu Ser Ser Gly Thr Ile Thr Arg Val Ala Phe Gly Lys Lys Tyr Glu
180          185          190

Gly Glu Glu Glu Arg Lys Asn Lys Phe Ala Asp Leu Ala Thr Glu Leu
195          200          205

Thr Thr Leu Met Gly Ala Phe Phe Val Gly Asp Tyr Phe Pro Ser Phe
210          215          220

Ala Trp Val Asp Val Leu Thr Gly Met Asp Ala Arg Leu Lys Arg Asn
225          230          235          240

His Gly Glu Leu Asp Ala Phe Val Asp His Val Ile Asp Asp His Leu
245          250          255

Leu Ser Arg Lys Ala Asn Gly Ser Asp Gly Val Glu Gln Lys Asp Leu
260          265          270

Val Asp Val Leu Leu His Leu Gln Lys Asp Ser Ser Leu Gly Val His
275          280          285

Leu Asn Arg Asn Asn Leu Lys Ala Val Ile Leu Asp Met Phe Ser Gly
290          295          300

```

Gly Thr Asp Thr Thr Ala Val Thr Leu Glu Trp Ala Met Ala Glu Leu
 305 310 315 320
 Ile Lys His Pro Asp Val Met Glu Lys Ala Gln Gln Glu Val Arg Arg
 325 330 335
 Val Val Gly Lys Lys Ala Lys Val Glu Glu Glu Asp Leu His Gln Leu
 340 345 350
 His Tyr Leu Lys Leu Ile Ile Lys Glu Thr Leu Arg Leu His Pro Val
 355 360 365
 Ala Pro Leu Leu Val Pro Arg Glu Ser Thr Arg Asp Val Val Ile Arg
 370 375 380
 Gly Tyr His Ile Pro Ala Lys Thr Arg Val Phe Ile Asn Ala Trp Ala
 385 390 395 400
 Ile Gly Arg Asp Pro Lys Ser Trp Glu Asn Ala Glu Glu Phe Leu Pro
 405 410 415
 Glu Arg Phe Val Asn Asn Ser Val Asp Phe Lys Gly Gln Asp Phe Gln
 420 425 430
 Leu Ile Pro Phe Gly Ala Gly Arg Arg Gly Cys Pro Gly Ile Ala Phe
 435 440 445
 Gly Ile Ser Ser Val Glu Ile Ser Leu Ala Asn Leu Leu Tyr Trp Phe
 450 455 460
 Asn Trp Glu Leu Pro Gly Asp Leu Thr Lys Glu Asp Leu Asp Met Ser
 465 470 475 480
 Glu Ala Val Gly Ile Thr Val His Met Lys Phe Pro Leu Gln Leu Val
 485 490 495
 Ala Lys Arg His Leu Ser
 500