



(86) Date de dépôt PCT/PCT Filing Date: 2012/04/27
(87) Date publication PCT/PCT Publication Date: 2012/11/08
(85) Entrée phase nationale/National Entry: 2013/11/01
(86) N° demande PCT/PCT Application No.: CN 2012/074811
(87) N° publication PCT/PCT Publication No.: 2012/149883
(30) Priorité/Priority: 2011/05/04 (US61/482,467)

(51) Cl.Int./Int.Cl. *C12N 15/82* (2006.01),
A01H 5/00 (2006.01), *C12N 1/21* (2006.01)
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(54) Titre : PROCEDE POUR L'ACCELERATION DE LA CROISSANCE VEGETALE ET L'AMELIORATION DU
RENDEMENT PAR LA MODIFICATION DES NIVEAUX D'EXPRESSION DE KINASES ET DE PHOSPHATASES
(54) Title: METHOD FOR SPEEDING UP PLANT GROWTH AND IMPROVING YIELD BY ALTERING EXPRESSION
LEVELS OF KINASES AND PHOSPHATASES

(57) **Abrégé/Abstract:**

The invention discloses transgenic plants having increased growth rate and increased yield and methods for making the same. In one embodiment, the method comprises: transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase gene selected from NG6, NG21, NG24, NG28, and NG32, and over-expressing said kinase and/or phosphatase gene in the plant or plant cell.



- (51) **International Patent Classification:**
C12N 15/82 (2006.01) *A01H 5/00* (2006.01)
C12N 1/21 (2006.01)

(21) **International Application Number:**
PCT/CN2012/074811

(22) **International Filing Date:**
27 April 2012 (27.04.2012)

(25) **Filing Language:** English

(26) **Publication Language:** English

(30) **Priority Data:**
61/482,467 4 May 2011 (04.05.2011) US

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

(84) **Designated States** (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

 - *with international search report (Art. 21(3))*
 - *with sequence listing part of description (Rule 5.2(a))*

- (54) **Title:** METHOD FOR SPEEDING UP PLANT GROWTH AND IMPROVING YIELD BY ALTERING EXPRESSION LEVELS OF KINASES AND PHOSPHATASES
- (57) **Abstract:** The invention discloses transgenic plants having increased growth rate and increased yield and methods for making the same. In one embodiment, the method comprises: transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase gene selected from NG6, NG21, NG24, NG28, and NG32, and over-expressing said kinase and/or phosphatase gene in the plant or plant cell.

METHOD FOR SPEEDING UP PLANT GROWTH AND IMPROVING YIELD BY
ALTERING EXPRESSION LEVELS OF KINASES AND PHOSPHATASES

5 **CROSS-REFERENCE TO RELATED APPLICATIONS**

This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Patent Application No. 61/482,467, filed May 4, 2011, which is hereby incorporated by reference in its entirety.

1. INTRODUCTION

10 Described herein are methods for speeding up plant growth and/or elevating plant yields by altering the expression levels of plant kinases and phosphatases. Also described therein are the use of plant kinases and phosphatases, and their respective protein products, as well as fragments, derivatives, homologues, and variants thereof.

15 **2. BACKGROUND OF THE INVENTION**

Purple acid phosphatases (PAPs) catalyze the hydrolysis of a wide range of activated phosphoric acid mono- and di-esters and anhydrides (Klabunde et al., 1996). The PAP proteins are characterized by seven conserved amino acid residues (shown in bold face) in the five conserved motifs **XDXX**, **XDXXY**, **GNH(D/E)**, **XXXH**, **XHXXH**, which are involved in the
20 coordination of the dimetal nuclear center (Fe^{3+} - Me^{2+}) in the active site (Li et al., 2002), where Me is a transition metal; Me^{2+} is mostly found to be Fe^{2+} in mammals, and Zn^{2+} , or Mn^{2+} in plants (Klabunde and Krebs, 1997; Schenk *et al.*, 1999).

Multiple PAP-like sequences are present in plant genomes. In the Arabidopsis genome, twenty-nine potential PAP genes have been identified based on sequence comparison. Most of
25 the functions of characterized plant PAPs are related to phosphorus metabolism. None of the plant PAPs that had been functionally or biochemically characterized carry any transmembrane motif. In addition, no AtPAPs or any other plant PAPs had been discovered to affect sugar signalling and carbon metabolism in plants. Overexpression of AtPAP2 in Arabidopsis, a PAP with a C-terminal motif, can significantly speed up plant growth, increase sugar content in plants
30 and improve seed yield (U.S. Patent Application Publication No. 2010/0159065).

3. SUMMARY

In one aspect, provided herein are methods that speed up or increase the rate of plant growth and elevate plant yields by altering the expression levels of plant kinases and phosphatases. Kinases and phosphatases, and their respectively encoded protein products, as well as fragments, derivatives, homologues, and variants thereof, are disclosed. Methods for introducing these genes into plants to speed up or increase the growth rate of plants, and to increase yield of plants, are provided. The kinases and phosphatases of the present invention are selected from the results of a microarray study. Surprisingly, it is discovered that phosphatases (such as NG6) and kinases (such as NG21, NG24, NG28, and NG32) have growth-promoting effects.

Provided herein, a microarray study was carried out to compare the gene expression profiles of the AtPAP2 overexpression lines, AtPAP2 T-DNA (mutant) line, and the wild-type plants. The results showed that expression levels of a number of genes are significantly altered (upregulated or downregulated) in AtPAP2 overexpression lines, when compared to the wild-type. Among these genes, a number of phosphatases and kinases were selected and analyzed using transgenic studies in Arabidopsis.

At least in part, the present inventors discover that altering the expression levels of plant phosphatases (such as NG6) and kinases (such as NG21, NG24, NG28 and NG32) in plants resulted in rapid plant growth and higher yield. In one aspect, provided herein are methods of producing plants with enhanced growth and/or yield. In one embodiment, the method comprises: transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase gene selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101, and over-expressing said kinase and/or phosphatase gene in the plant or plant cell. In one embodiment, provided herein are methods of regenerating, from said transformed plant or plant cell, a plant having enhanced growth and/or yield.

In one embodiment, the method comprises: transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98%, or 99% identity with SEQ ID NO: 1, 3, 5, 7,

9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101, and over-expressing said kinase and/or phosphatase gene in the plant or plant cell.

In certain embodiments, the method comprises transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase having a nucleic acid
5 fragment from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101. In certain embodiments, the nucleic acid fragment encode a peptide that has the same activity as a peptide encoded by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101.

In certain embodiments, the activity is a kinase and/or phosphatase activity. In certain,
10 embodiments, the method comprises transforming a plant or plant cell with a nucleic and molecule comprising a plant kinase and/or phosphatase having a variant from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101.

In certain embodiments, the variant has 1-5, 6-10, 11-20, 21-30, 31-40, 41-50, 50-70, 71-
15 80, 81-100 nucleic acid deletion, substitution or insertion in the sequence as compared to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101. In certain embodiments, the variants encode a peptide that has the same activity as a peptide encoded by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101. In certain embodiments, the activity
20 is a kinase and/or phosphatase activity.

Provided herein are transgenic plants with enhanced growth and/or yield. In certain
embodiments, the transgenic plant comprises a nucleic acid molecule selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97,
25 99, or 101, wherein said nucleic acid molecule is overexpressed in the transgenic plant when compared to a wild-type plant of the same species cultivated under the same conditions.

In certain embodiments, the transgenic plant comprises a nucleic acid molecule having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101, wherein said nucleic acid molecule is overexpressed in the transgenic

plant when compared to a wild-type plant of the same species cultivated under the same conditions.

In certain embodiments, the transgenic plant comprises a nucleic acid fragment from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101. In certain embodiments, the nucleic acid fragment encodes a peptide that has the same activity as a peptide encoded by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101. In certain embodiments, the activity is a kinase and/or phosphatase activity.

In certain embodiments, the transgenic plant comprises a plant kinase and/or phosphatase homologue, derivative, or variant having a nucleic acid sequence of the SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101. In certain embodiments, the homologue, derivative or variant has 1-5, 6-10, 11-20, 21-30, 31-40, 41-50, 50-70, 71-80, 81-100 nucleic acid deletion, substitution or insertion in the sequence as compared to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, or 101. In certain embodiments, the variants encode a peptide that has the same activity as a peptide encoded by SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101. In certain embodiments, the activity is a kinase and/or phosphatase activity.

In certain embodiments provided herein are the methods of altering the expression levels of plant kinase and/or phosphatase. In certain embodiments, the method comprises transforming a plant or plant cell with a nucleic acid molecule that expresses a plant kinase and/or phosphatase peptide, fragment, derivative or variant from a peptide having an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100, or 102. In certain embodiments, the peptide, fragment, derivative or variant is overexpressed. In certain embodiments, provided herein are methods of regenerating, from said transformed plant or plant cell, a plant having enhanced growth and/or yield.

In certain embodiments, the transgenic plants express a plant kinase and/or phosphatase peptide, fragment, derivative or variant from a protein having an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100, or 102. In certain embodiments, the peptide fragment, derivative or variant is

overexpressed. In certain embodiments, provided herein are regenerated transformed plant having enhanced growth and/or yield.

4. BRIEF DESCRIPTION OF THE FIGURES

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The patent application file contains at least one drawing executed in color. Copies of this patent application with color drawings will be provided by the Office upon request and payment of the necessary fee.

10 **FIG. 1** shows a heat map of the microarray analysis of gene expression profile of Arabidopsis shoots, using three biological replicates for wild-type (WT), 2 biological replicates for AtPAP2 T-DNA line (P2), and 3 biological replicates for two independent AtPAP2 overexpression lines (OE7 and OE21).

15 **FIG. 2** shows scatter plots of the microarray analysis of gene expression profile of Arabidopsis shoots. The results showed that the expression profiles of the two independent AtPAP2 overexpression lines (OE7 and OE21) were significantly different from that of the wild-type (WT), whereas the expression profile of the AtPAP2 T-DNA (mutant) lines resembled closely that of the WT.

20 **FIG. 3** shows a schematic diagram of the expression vector pCXSN. (a). The cDNAs of the NG genes were cloned into the pCXSN vector at the XcmI sites to create the overexpression vectors. (b) shows an exemplified overexpression vector pCXSN-NG6.

25 **FIG. 4** shows the mRNA expression levels of NG genes in the respective overexpression lines. The mRNA expression levels in 10-day-old T3 homologous seedlings were determined by quantitative RT-PCR using gene-specific primers. The fold-changes represent the relative expression levels of mRNAs compared to that of the wild-type (WT = 1.0). The results of two trials were obtained from two batches of plant growth studies.

FIG. 5 shows the growth performance of the wild-type and NG6 over-expression lines in soil. The five columns of plants from left to right were AtPAP2 overexpression lines, WT, T3 homologous NG6 overexpression lines NG6-1, NG6-2, and NG6-3. (a) 22-day-old and (b) 25-day-old plants.

FIG. 6 shows the growth performance of the wild-type and T3 homologous NG21, NG24, NG28 and NG32 overexpression lines in soil. The five columns of plants from left to right were WT, NG21, NG24, NG28 and NG32 overexpression lines. (a) 30-day-old plants and (b) 34-day-old plants grown in black tray. (c) 22-day-old plants, (d) 25-day-old plants, (e) 28-day-old plants, and (f) 36-day-old plants grown in white cups.

4.1. BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NO:1 is a nucleic acid sequence of Arabidopsis phosphatase NG6 gene.

SEQ ID NO:2 is an amino acid sequence of Arabidopsis phosphatase NG6.

SEQ ID NO:3 is a nucleic acid sequence of maize phosphatase NG6 gene.

SEQ ID NO:4 is an amino acid sequence of maize phosphatase NG6.

SEQ ID NO:5 is a nucleic acid sequence of soybean phosphatase NG6 gene.

SEQ ID NO:6 is an amino acid sequence of soybean phosphatase NG6.

SEQ ID NO:7 is a nucleic acid sequence of rice phosphatase NG6 gene.

SEQ ID NO:8 is an amino acid sequence of rice phosphatase NG6.

SEQ ID NO:9 is a nucleic acid sequence of cotton phosphatase NG6 gene.

SEQ ID NO:10 is an amino acid sequence of cotton phosphatase NG6.

SEQ ID NO:11 is a nucleic acid sequence of Arabidopsis kinase NG21 gene.

SEQ ID NO:12 is an amino acid sequence of Arabidopsis kinase NG21.

SEQ ID NO:13 is a nucleic acid sequence of maize kinase NG21 gene.

SEQ ID NO:14 is an amino acid sequence of maize kinase NG21.

SEQ ID NO:15 is a nucleic acid sequence of soybean kinase NG21 gene.

SEQ ID NO:16 is an amino acid sequence of soybean kinase NG21.

SEQ ID NO:17 is a nucleic acid sequence of rice kinase NG21 gene.

SEQ ID NO:18 is an amino acid sequence of rice kinase NG21.

SEQ ID NO:19 is a nucleic acid sequence of cotton kinase NG21 gene.

SEQ ID NO:20 is an amino acid sequence of cotton kinase NG21.

SEQ ID NO:21 is a nucleic acid sequence of Arabidopsis kinase NG24 gene.

SEQ ID NO:22 is an amino acid sequence of Arabidopsis kinase NG24.

SEQ ID NO:23 is a nucleic acid sequence of maize kinase NG24 gene.

SEQ ID NO:24 is an amino acid sequence of maize kinase NG24.
SEQ ID NO:25 is a nucleic acid sequence of soybean kinase NG24 gene.
SEQ ID NO:26 is an amino acid sequence of soybean kinase NG24.
SEQ ID NO:27 is a nucleic acid sequence of rice kinase NG24 gene.
5 SEQ ID NO:28 is an amino acid sequence of rice kinase NG24.
SEQ ID NO:29 is a nucleic acid sequence of cotton kinase NG24 gene.
SEQ ID NO:30 is an amino acid sequence of cotton kinase NG24.
SEQ ID NO:31 is a nucleic acid sequence of Arabidopsis kinase NG28 gene.
SEQ ID NO:32 is an amino acid sequence of Arabidopsis kinase NG28.
10 SEQ ID NO:33 is a nucleic acid sequence of maize kinase NG28 gene.
SEQ ID NO:34 is an amino acid sequence of maize kinase NG28.
SEQ ID NO:35 is a nucleic acid sequence of soybean kinase NG28 gene.
SEQ ID NO:36 is an amino acid sequence of soybean kinase NG28.
SEQ ID NO:37 is a nucleic acid sequence of rice kinase NG28 gene.
15 SEQ ID NO:38 is an amino acid sequence of rice kinase NG28.
SEQ ID NO:39 is a nucleic acid sequence of cotton kinase NG28 gene.
SEQ ID NO:40 is an amino acid sequence of cotton kinase NG28.
SEQ ID NO:41 is a nucleic acid sequence of Arabidopsis kinase NG32 gene.
SEQ ID NO:42 is an amino acid sequence of Arabidopsis kinase NG32.
20 SEQ ID NO:43 is a nucleic acid sequence of maize kinase NG32 gene.
SEQ ID NO:44 is an amino acid sequence of maize kinase NG32.
SEQ ID NO:45 is a nucleic acid sequence of soybean kinase NG32 gene.
SEQ ID NO:46 is an amino acid sequence of soybean kinase NG32.
SEQ ID NO:47 is a nucleic acid sequence of rice kinase NG32 gene.
25 SEQ ID NO:48 is an amino acid sequence of rice kinase NG32.
SEQ ID NO:49 is a nucleic acid sequence of cotton kinase NG32 gene.
SEQ ID NO:50 is an amino acid sequence of cotton kinase NG32.
SEQ ID NO:51 is a primer sequence useful according to the present invention.
SEQ ID NO:52 is a primer sequence useful according to the present invention.
30 SEQ ID NO:53 is a primer sequence useful according to the present invention.

SEQ ID NO:54 is a primer sequence useful according to the present invention.
SEQ ID NO:55 is a primer sequence useful according to the present invention.
SEQ ID NO:56 is a primer sequence useful according to the present invention.
SEQ ID NO:57 is a primer sequence useful according to the present invention.
5 SEQ ID NO:58 is a primer sequence useful according to the present invention.
SEQ ID NO:59 is a primer sequence useful according to the present invention.
SEQ ID NO:60 is a primer sequence useful according to the present invention.
SEQ ID NO:61 is a primer sequence useful according to the present invention.
SEQ ID NO:62 is a primer sequence useful according to the present invention.
10 SEQ ID NO:63 is a primer sequence useful according to the present invention.
SEQ ID NO:64 is a primer sequence useful according to the present invention.
SEQ ID NO:65 is a primer sequence useful according to the present invention.
SEQ ID NO:66 is a primer sequence useful according to the present invention.
SEQ ID NO:67 is a primer sequence useful according to the present invention.
15 SEQ ID NO:68 is a primer sequence useful according to the present invention.
SEQ ID NO:69 is a primer sequence useful according to the present invention.
SEQ ID NO:70 is a primer sequence useful according to the present invention.
SEQ ID NO:71 is a primer sequence useful according to the present invention.
SEQ ID NO:72 is a primer sequence useful according to the present invention.
20 SEQ ID NO:73 is a nucleic acid sequence of Arabidopsis AtPAP2 phosphatase gene.
SEQ ID NO:74 is an amino acid sequence of Arabidopsis AtPAP2 phosphatase.
SEQ ID NO:75 is an amino acid sequence of a conserved motif of an NG6 protein.
SEQ ID NO:76 is an amino acid sequence of a conserved motif of an NG6 protein.
SEQ ID NO:77 is an amino acid sequence of a conserved motif of an NG6 protein.
25 SEQ ID NO:78 is an amino acid sequence of a conserved motif of an NG6 protein.
SEQ ID NO:79 is an amino acid sequence of a conserved motif of an NG21 protein.
SEQ ID NO:80 is an amino acid sequence of a conserved motif of an NG21 protein.
SEQ ID NO:81 is an amino acid sequence of a conserved motif of an NG21 protein.
SEQ ID NO:82 is an amino acid sequence of a conserved motif of an NG21 protein.
30 SEQ ID NO:83 is an amino acid sequence of a conserved motif of an NG24 protein.

SEQ ID NO:84 is an amino acid sequence of a conserved motif of an NG24 protein.

SEQ ID NO:85 is an amino acid sequence of a conserved motif of an NG24 protein.

SEQ ID NO:86 is an amino acid sequence of a conserved motif of an NG28 protein.

SEQ ID NO:87 is an amino acid sequence of a conserved motif of an NG28 protein.

5 SEQ ID NO:88 is an amino acid sequence of a conserved motif of an NG28 protein.

SEQ ID NO:89 is an amino acid sequence of a conserved motif of an NG32 protein.

SEQ ID NO:90 is an amino acid sequence of a conserved motif of an NG32 protein.

SEQ ID NO:91 is an amino acid sequence of a conserved motif of an NG32 protein.

SEQ ID NO:92 is an amino acid sequence of a conserved motif of an NG32 protein.

10 SEQ ID NO:93 is a nucleic acid sequence of rapeseed kinase NG6 gene.

SEQ ID NO:94 is an amino acid sequence of rapeseed kinase NG6.

SEQ ID NO:95 is a nucleic acid sequence of rapeseed kinase NG21 gene.

SEQ ID NO:96 is an amino acid sequence of rapeseed kinase NG21.

SEQ ID NO:97 is a nucleic acid sequence of rapeseed kinase NG24 gene.

15 SEQ ID NO:98 is an amino acid sequence of rapeseed kinase NG24.

SEQ ID NO:99 is a nucleic acid sequence of rapeseed kinase NG28 gene.

SEQ ID NO:100 is an amino acid sequence of rapeseed kinase NG28.

SEQ ID NO:101 is a nucleic acid sequence of rapeseed kinase NG32 gene.

SEQ ID NO:102 is an amino acid sequence of rapeseed kinase NG32.

20

5. DETAILED DESCRIPTION

Provided herein are methods of producing plants with enhanced growth and/or yield. In one embodiment, the method comprises: transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase gene selected from NG6, NG21, NG24, NG28, and NG32, and over-expressing said kinase and/or phosphatase gene in the plant or plant cell. In one embodiment, the method further comprises: regenerating, from said transformed plant or plant cell, a plant having enhanced growth and/or yield. Also provided are transgenic plants with enhanced growth and/or yield, comprising a plant kinase and/or phosphatase gene selected from NG6, NG21, NG24, NG28, and NG32, wherein the kinase and/or phosphatase is overexpressed in the plant or plant cell.

30

The inventors discover that altering the expression levels of one or more phosphatases (such as NG6) and kinases (such as NG21, NG24, NG28, and NG32) results in rapid plant growth and higher yield. The gene expression profiles of the AtPAP2 overexpression lines, AtPAP2 T-DNA (mutant) line, and the wild-type plants are analyzed using microarray. The microarray data show that the expression levels of a range of genes are significantly altered (upregulated or downregulated) in the AtPAP2 overexpression lines, when compared to the wild-type.

The introduction of a representative gene of phosphatases (AT1G05000 (NG6)) and kinases (AT1G13350 (NG21), AT1G28390 (NG24), AT3G24660 (NG28) and AT5G03320 (NG32)), into the genome of Arabidopsis by transgenic technology produced transgenic Arabidopsis that grew faster than the wild-type plants (Table 4, Fig. 5, Fig. 6), and the yield of seeds were elevated by 23 - 70% (Table 5).

While any plant species can be modified using the methods described herein, preferably included without limitation are species from the following genera with representative species in parentheses:

Monocots: genera Asparagus (asparagus), Bromus (cheatgrass), Hemerocallis (daylily), Hordeum (barley), Lolium (ryegrass), Oryza (rice), Panicum (Switchgrass), Pennisetum (fountaingrass), Saccharum (Sugar cane), Sorghum, Trigonella (fenu grass), Triticum (wheat), and Zea (corn); and

Dicots: genera Antirrhinum (flower sp.), Arabidopsis (thaliana), Arachis (peanut), Atropa (deadly nightshade), Brassica (rapeseed), Browallia, Capsicum (pepper), Carthamus (safflower), Cichorium (chicory), Citrus (orange, lemon), Chrysanthemum, Cucumis (cucumber), Datura (thorn apple), Daucus (carrot), Digitalis (foxglove), Fragaria (strawberry), Geranium (flower sp.), Glycine (soybean), Helianthus (sunflower), Hyscyamus, Ipomoea (morning glory), Lactuca (lettuce), Linum (linseed), Lotus (flower sp.), Lycopersicon (tomato), Majorana, Malva (cotton), Manihot, Medicago (alfalfa), Nemesia, Nicotiana (tobacco), Onobrychis, Pelargonium (citrosa), Petunia (flower sp.), Ranunculus (flower sp.), Raphanus (radishes), Salpiglossis, Senecio (flower sp.), Sinapis (albae semen), Solanum (potato), Trifolium (clovers), Vigna (mungbean, fava bean), and Vitis (grape).

In certain embodiments, plant species transgenically modified according to the present invention are selected from soybean, maize, potato, rice, sugar canes, switchgrass, cotton, sorghum, alfalfas, rapeseed, canola, rye, sorghum, sunflower, wheat, tobacco, millet, peanuts sweet potato cassava, coffee, coconut, cocoa, tea, banana, citrus, apple, pineapple, avocado, fig, guava, mango, olive, barley ornamentals, and conifers. In preferred embodiments, plant species transgenically modified according to the present invention are selected from soybean, maize, potato, rice, sugar canes, switchgrass, cotton, sorghum, alfalfas, rapeseed, and canola.

In certain embodiment, plant parts, plant tissue, and plant cells including, but not limited to, shoots, stems, seeds, and roots, can be transgenically modified in accordance with the present invention.

4.2 Definitions

The term “protein or peptide homologue,” as used herein, refers to one or more of the following proteins or peptides: (i) a protein or polypeptide with at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 98% sequence identity with a protein or polypeptide of the invention; (ii) a protein or polypeptide encoded by a nucleotide sequence that is at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 98% identical to a nucleic acid sequence of the invention; (iii) a protein or polypeptide encoded by a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of the invention; (iv) a protein or polypeptide that is derived from conservative substitution of amino acids of a protein or polypeptide of the invention, or that is derived from conservative substitution of amino acids of a protein or polypeptide of (i) – (iii); (v) a fragment of a protein or polypeptide of the invention or a fragment of a protein or polypeptide of (i) through (iv); and (vii) a protein or polypeptide recognized by an antibody that immunospecifically binds to a sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102.

The term “an antibody or an antibody fragment that immunospecifically binds to a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102” or “an antibody or an antibody fragment that immunospecifically binds to a polypeptide, peptide, or protein of the invention,” as

used herein, refers to an antibody or a fragment thereof that immunospecifically binds to a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102, or a fragment of these polypeptide, wherein the antibody or the antibody fragment does not non-specifically bind to other peptides, polypeptides, or proteins.

An antibody or a fragment thereof that immunospecifically binds to a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102, or a fragment of these polypeptide, may cross-react with other antigens. In a preferred embodiment, an antibody or a fragment thereof that immunospecifically binds to a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102, or a fragment of these polypeptides, does not cross-react with other antigens. An antibody or a fragment thereof that immunospecifically binds to a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102, or a fragment of these polypeptide, can be identified by, for example, immunoassays or other techniques known to those skilled in the art. An antibody or an antibody fragment that immunospecifically binds a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102 may be interchangeably referred to as "anti-PAP antibody".

The term "peptide or protein derivative," as used herein, refers to a given peptide or protein that is modified, *e.g.*, by covalent attachment of another molecule, to the peptide or protein, including the incorporation of non-naturally occurring amino acids. The peptide or protein derivative retains one or more biological activities of the peptide or protein.

The term "nucleic acid fragment," as used herein, refers to a fragment of a nucleic acid molecule of the invention, wherein the fragment comprises at least about 400, at least about 450, at least about 500, at least about 550, at least about 600, at least about 650, at least about 700, at least about 750, at least about 800, at least about 850, at least about 900, at least about 950, at least about 1000, at least about 1050, at least about 1100, at least about 1150, at least about 1200, at least about 1250, at least about 1300, or at least about 1350 contiguous nucleic acid bases of the nucleic acid molecule.

The term "protein or peptide fragment," as used herein, refers to a fragment of a protein or peptide of the invention, wherein the fragment comprises at least about 160, at least about 180, at least about 200, at least about 220, at least about 240, at least about 260, at least about 280, at least about 300, at least about 320, at least about 340, or at least about 360 contiguous amino acid residues of the protein or peptide.

The term "protein or peptide variant," as used herein, includes 1) a naturally occurring allelic variation of a given protein or peptide, and 2) a recombinantly prepared variation of a given protein or peptide, in which one or more amino acid residues have been modified by amino acid substitution, addition, and/or deletion.

An "isolated" nucleic acid molecule has been removed from any environment in which it may exist in nature. For instance, an "isolated" nucleic acid molecule, such as a cDNA molecule, is substantially free of other cellular materials, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. In a preferred embodiment, nucleic acid molecules encoding the polypeptides/proteins of the present invention are isolated or purified.

The term "under stringent conditions" refers to hybridization and washing conditions under which nucleotide sequences having homology to each other remain hybridized to each other. Such hybridization conditions are described in, for example, but not limited to, *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6.; *Basic Methods in Molecular Biology*, Elsevier Science Publishing Co., Inc., N.Y. (1986), pp. 75-78, and 84-87; and *Molecular Cloning*, Cold Spring Harbor Laboratory, N.Y. (1982), pp. 387-389, and are well known to those skilled in the art. A preferred example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC), 0.5% SDS at about 68°C followed by one or more washes in 2X SSC, 0.5% SDS at room temperature. Another preferred, example of stringent hybridization conditions is hybridization in 6X SSC at about 45°C followed by one or more washes in 0.2X SSC, 0.1% SDS at about 50-65°C.

To determine the percent identity of two amino acid sequences or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino acid or nucleic acid sequence). The amino acid residues or nucleotides at

corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = number of identical overlapping positions/total number of positions x 100%). In one embodiment, the two sequences are the same length.

The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2264 2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. U.S.A. 90:5873 5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.*, 1990, J. Mol. Biol. 215:403. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, *e.g.*, for score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the present invention. BLAST protein searches can be performed with the XBLAST program parameters set, *e.g.*, to score 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecule of the present invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, 1997, Nucleic Acids Res. 25:3389 3402. Alternatively, PSI BLAST can be used to perform an iterated search which detects distant relationships between molecules (*Id.*). When utilizing BLAST, Gapped BLAST, and PSI Blast programs, the default parameters of the respective programs (*e.g.*, of XBLAST and NBLAST) can be used (see, *e.g.*, the NCBI website). Another preferred, non limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, CABIOS 4:11 17. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

As used herein, the term “derivative” (*e.g.*, proteins, polypeptides, peptides, and antibodies) refers to an agent that comprises an amino acid sequence which has been altered by the introduction of amino acid residue substitutions, deletions, and/or additions. The term “derivative” as used herein also refers to an agent which has been modified, *i.e.*, by the covalent attachment of any type of molecule to the agent. For example, but not by way of limitation, an antibody may be modified, *e.g.*, by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. A derivative of an agent may be produced by chemical modifications using techniques known to those of skill in the art, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Further, a derivative of an agent may contain one or more non-classical amino acids. A derivative of an agent possesses a similar or identical function as the agent from which it was derived.

The term “enhance or promote plant growth and/or yield” refers to for example, increased plant weight, increased leaf number and/or weight, increased number of inflorescence, increased seed production (such as weight/seed and total weight of seeds), increased carbon metabolism, increased carbohydrate (*e.g.*, starch, sugars, cellulose), amino acid, and/or lipid production, early bolting, and also can include combinations of the foregoing, when compared to a wild-type plant of the same species cultivated under the same conditions.

5.1 Growth-promoting Phosphatases and Kinases

Provided herein are phosphatases and kinases that promote plant growth and/or yield. In one embodiment, the growth-promoting phosphatase is NG6, and the growth-promoting kinases are selected from NG6, NG21, NG24, NG28, and NG32. In certain specific embodiments, the growth-promoting phosphatases and kinases are derived from plant species including, but not limited to, Arabidopsis, rice, soybean, maize, and cotton.

In certain embodiments, the phosphatase gene that promotes plant growth and/or yield is an NG6 gene comprising a nucleic acid sequence selected from SEQ ID NO: 1, 3, 5, 7, 9 or 93. In certain embodiments, the phosphatase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99%

identity with SEQ ID NO: 1, 3, 5, 7, 9 or 93. In certain embodiments, the phosphatase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule derives from a nucleic acid molecule having nucleic acid sequence comprising SEQ ID NO: 1, 3, 5, 7, 9 or 93.

5 In certain embodiments, the phosphatase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 1, 3, 5, 7, 9 or 93. In certain embodiments, the phosphatase gene that promotes plant growth and/or yield comprises the nucleic acid sequence that encodes a protein that comprises one or more of the following conserved motifs: GIFRSGFP (SEQ ID
10 NO:75), YLCPEPYP (SEQ ID NO:76), KEPFVXIP (SEQ ID NO:77), and HCXRGKHRTG (SEQ ID NO:78).

In certain embodiments, the phosphatase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid molecule having nucleic acid sequences comprising SEQ ID NO: 1, 3, 5, 7, 9 or 93. In certain
15 embodiments, the phosphatase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: GIFRSGFP (SEQ ID NO:75), YLCPEPYP (SEQ ID NO:76), KEPFVXIP (SEQ ID NO:77), and HCXRGKHRTG (SEQ ID NO:78).

In certain embodiments, the kinase gene that promotes plant growth and/or yield is an NG21 gene comprising a nucleic acid sequence selected from SEQ ID NO: 11, 13, 15, 17, 19 or
20 95. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 11, 13, 15, 17, 19 or 95. In certain embodiments, the kinase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid molecule having nucleic acid sequence
25 comprising SEQ ID NO: 11, 13, 15, 17, 19 or 95.

In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 11, 13, 15, 17, or 19 or 95. In certain embodiments, the
30 kinase gene that promotes plant growth and/or yield comprises the nucleic acid sequence that encodes a protein that comprises one or more of the following conserved motifs:

DNWDDA(D/E)GYG (SEQ ID NO:79), YRNHLCLVFESL (SEQ ID NO:80),
VLHCDIKPDNMLVNE (SEQ ID NO:81), and TPYLVSRLFYRXPEI (SEQ ID NO:82).

In certain embodiments, the kinase gene that promotes plant growth and/or yield is a
homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid
molecule having nucleic acid sequences comprising SEQ ID NO: 11, 13, 15, 17, 19 or 95. In
certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or
more of the following conserved motifs: DNWDDA(D/E)GYG (SEQ ID NO:79),
YRNHLCLVFESL (SEQ ID NO:80), VLHCDIKPDNMLVNE (SEQ ID NO:81), and
TPYLVSRLFYRXPEI (SEQ ID NO:82). In certain embodiments, the kinase gene that promotes
plant growth and/or yield is an NG24 gene comprising a nucleic acid sequence selected from
SEQ ID NO: 21, 23, 25, 27, 29 or 97. In certain embodiments, the kinase gene that promotes
plant growth and/or yield comprises a nucleic acid sequence having at least 65%, 70%, 75%,
80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 21, 23, 25, 27,
29 or 97. In certain embodiments, the kinase gene that promotes plant growth and/or yield is a
homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid
molecule having nucleic acid sequence comprising SEQ ID NO: 21, 23, 25, 27, 29 or 97.

In certain embodiments, the kinase gene that promotes plant growth and/or yield
comprises a nucleic acid sequence having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98%
or 99% identity with SEQ ID NO: 21, 23, 25, 27, 29 or 97. In certain embodiments, the kinase
gene that promotes plant growth and/or yield comprises one or more of the following conserved
motifs: VRHRDXKS (SEQ ID NO:83), GTLXGYLDP (SEQ ID NO:84), and
DV(F/Y)S(F/Y)G(I/V)LLLEI (SEQ ID NO:85).

In certain embodiments, the kinase gene that promotes plant growth and/or yield is a
homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid
molecule having nucleic acid sequence comprising SEQ ID NO: 21, 23, 25, 27, 29 or 97. In
certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or
more of the following conserved motifs: VRHRDXKS (SEQ ID NO:83), GTLXGYLDP (SEQ
ID NO:84), and DV(F/Y)S(F/Y)G(I/V)LLLEI (SEQ ID NO:85). In certain embodiments, the
kinase gene that promotes plant growth and/or yield is an NG28 gene comprising a nucleic acid
sequence selected from SEQ ID NO: 31, 33, 35, 37, 39 or 99. In certain embodiments, the NG24

kinase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 31, 33, 35, 37, 39 or 99. In certain embodiments, the NG24 kinase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid molecule having nucleic acid sequence comprising SEQ ID NO: 31, 33, 35, 37, 39 or 99.

In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 31, 33, 35, 37, 39 or 99. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: RRHKIALG (SEQ ID NO:86), Y(K/R)APEL (SEQ ID NO:87), and DVYAFGILLLE (SEQ ID NO:88).

In certain embodiments, the kinase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid molecule having nucleic acid sequence comprising SEQ ID NO: 31, 33, 35, 37, 39 or 99. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: RRHKIALG (SEQ ID NO:86), Y(K/R)APEL (SEQ ID NO:87), and DVYAFGILLLE (SEQ ID NO:88).

In certain embodiments, the kinase gene that promotes plant growth and/or yield is an NG32 gene comprising a nucleic acid sequence selected from SEQ ID NO: 41, 43, 45, 47, 49 or 101. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 41, 43, 45, 47, 49 or 101. In certain embodiments, the kinase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid molecule having nucleic acid sequence comprising SEQ ID NO: 41, 43, 45, 47, 49 or 101.

In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises a nucleic acid sequence having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 41, 43, 45, 47, 49 or 101. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved

motifs: CAXDDERG (SEQ ID NO:89), AKLSDFGLAR (SEQ ID NO:90), YELITGR(R/K) (SEQ ID NO:91), and RPKMSEV (SEQ ID NO:92).

In certain embodiments, the kinase gene that promotes plant growth and/or yield is a homologue, derivative, or variant of a nucleic acid molecule that derives from nucleic acid molecule having nucleic acid sequence comprising SEQ ID NO: 41, 43, 45, 47, 49 or 101. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: CAXDDERG (SEQ ID NO:89), AKLSDFGLAR (SEQ ID NO:90), YELITGR(R/K) (SEQ ID NO:91), and RPKMSEV (SEQ ID NO:92). In certain embodiments, the phosphatase or kinase gene that promotes plant growth and/or yield encodes a protein selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the phosphatase or kinase gene that promotes plant growth and/or yield encodes a protein having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, , 50, 94, 96, 98, 100 or 102. In certain embodiments, the phosphatase or kinase gene that promotes plant growth and/or yield encodes a protein that is a homologue, derivative, or variant of a protein derived from the amino acid molecule having the amino acid sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102.

In certain embodiments, the phosphatase gene that promotes plant growth and/or yield encodes an NG6 protein having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 2, 4, 6, 8, 10 or 94. In certain embodiments, the phosphatase gene that promotes plant growth and/or yield one or more of the following conserved motifs: GIFRSGFP (SEQ ID NO:75), YLCPEPYP (SEQ ID NO:76), KEPFVXIP (SEQ ID NO:77), and HCXRGKHRTG (SEQ ID NO:78).

In certain embodiments, the phosphatase gene that promotes plant growth and/or yield encodes an NG6 protein that is a homologue, derivative, or variant of a protein derived from the amino acid molecule having the amino acid sequence comprising SEQ ID NO: 2, 4, 6, 8, 10 or 94. In certain embodiments, the phosphatase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: GIFRSGFP (SEQ ID NO:75),

YLCPEPYP (SEQ ID NO:76), KEPFVXIP (SEQ ID NO:77), and HCXRGKHRTG (SEQ ID NO:78).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG 21 protein having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 12, 14, 16, 18, 20 or 96. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: DNWDDA(D/E)GYG (SEQ ID NO:79), YRNHLCLVFESL (SEQ ID NO:80), VLHCDIKPDNMLVNE (SEQ ID NO:81), and TPYLVSRFYRXPEI (SEQ ID NO:82).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG21 protein that is a homologue, derivative, or variant of a protein derived from the amino acid molecule having the amino acid sequence selected from SEQ ID NO: 12, 14, 16, 18, 20 or 96. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: DNWDDA(D/E)GYG (SEQ ID NO:79), YRNHLCLVFESL (SEQ ID NO:80), VLHCDIKPDNMLVNE (SEQ ID NO:81), and TPYLVSRFYRXPEI (SEQ ID NO:82).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG24 protein having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 22, 24, 26, 28, 30 or 98. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: VRHRDXKS (SEQ ID NO:83), GTLXGYLDP (SEQ ID NO:84), and DV(F/Y)S(F/Y)G(I/V)LLLEI (SEQ ID NO:85).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG24 protein that is a homologue, derivative, or variant of a protein derived from the amino acid molecule having the amino acid sequence selected from SEQ ID NO: 22, 24, 26, 28, 30 or 98. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: VRHRDXKS (SEQ ID NO:83), GTLXGYLDP (SEQ ID NO:84), and DV(F/Y)S(F/Y)G(I/V)LLLEI (SEQ ID NO:85).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG28 protein having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 32, 34, 36, 38, 40 or 100. In certain embodiments, the kinase gene that

promotes plant growth and/or yield comprises one or more of the following conserved motifs: RRHKIALG (SEQ ID NO:86), Y(K/R)APEL (SEQ ID NO:87), and DVYAFGILLLE (SEQ ID NO:88).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG28 protein that is a homologue, derivative, or variant of a protein derived from the amino acid molecule having the amino acid sequence selected from SEQ ID NO: 32, 34, 36, 38, 40 or 100, wherein the protein comprises one or more of the following conserved motifs: RRHKIALG (SEQ ID NO:86), Y(K/R)APEL (SEQ ID NO:87), and DVYAFGILLLE (SEQ ID NO:88).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG32 protein having at least 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 42, 44, 46, 48, 50 or 102. In certain embodiments, the kinase gene that promotes plant growth and/or yield comprises one or more of the following conserved motifs: CAXDDERG (SEQ ID NO:89), AKLSDFGLAR (SEQ ID NO:90), YELITGR(R/K) (SEQ ID NO:91), and RPKMSEV (SEQ ID NO:92).

In certain embodiments, the kinase gene that promotes plant growth and/or yield encodes an NG32 protein that is a homologue, derivative, or variant of a protein derived from the amino acid molecule having the amino acid sequence selected from SEQ ID NO: 42, 44, 46, 48, 50 or 102, wherein the protein comprises one or more of the following conserved motifs: CAXDDERG (SEQ ID NO:89), AKLSDFGLAR (SEQ ID NO:90), YELITGR(R/K) (SEQ ID NO:91), and RPKMSEV (SEQ ID NO:92).

5.2 Production of Transgenic Plants with Enhanced Growth and/or Yield

Another aspect of the present invention provides methods of producing plants with enhanced growth and/or yield. In one embodiment, the method comprises: transforming a plant or plant cell with a nucleic acid molecule comprising a plant kinase and/or phosphatase gene of the present invention. In one embodiment, the method comprises overexpressing said kinase and/or phosphatase gene in the plant or plant cell. In one embodiment, the present invention further comprises: regenerating, from said transformed plant or plant cell, a plant having enhanced growth and/or yield.

The term “overexpressing,” “overexpression,” or any of the grammatical variations thereof (*e.g.*, over-expressing, over-expression) refers to an increase in the level of expression of a gene, or the level of a protein product encoded by a gene, wherein such increase is at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 150%, or 200%,
5 when compared to cells of the same type in a wild-type plant of the same species cultivated under the same conditions.

In one embodiment, the method further comprises: transforming a plant or a plant cell with a nucleic acid molecule comprising an AtPAP2 gene. In certain embodiments, the method comprises overexpressing the AtPAP2 gene in the plant or plant cell. In one embodiment, the
10 AtPAP2 gene comprises SEQ ID NO: 73. In certain embodiments, the AtPAP2 gene comprises a nucleic acid molecule having a nucleic acid molecule having sequence having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98%, or 99% identity with SEQ ID NO: 73.

In one embodiment, the method further comprises: transforming a plant or a plant cell with a nucleic acid molecule encoding AtPAP2 phosphatase. In certain embodiment, the method
15 comprises overexpressing the nucleic acid molecule encoding AtPAP2 phosphatase in the plant or plant cell. In one embodiment, AtPAP2 phosphatase comprises SEQ ID NO: 74. In certain embodiments, AtPAP2 phosphatase comprises an amino acid molecule having an amino acid nucleic acid sequence having at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98%, or 99% identity with SEQ ID NO: 74.

20 Provided herein are transgenic plants with enhanced growth and/or yield. In certain embodiments, the transgenic plant comprises a nucleic acid molecule having a nucleic acid sequence selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant when compared to a wild-type plant of the
25 same species cultivated under the same conditions. In certain embodiments, the transgenic plant comprises a nucleic acid molecule having a nucleic acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant when
30 compared to a wild-type plant of the same species cultivated under the same conditions. In

certain embodiments, the transgenic plant comprises a nucleic acid molecule that is a homologue, derivative, or variant of a nucleic acid molecule derived from the nucleic acid molecule having a nucleic acid sequence selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant when compared to a wild-type plant of the same species cultivated under the same conditions.

In certain embodiments, the transgenic plant comprises a nucleic acid that encodes a protein having an amino acid sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant when compared to a wild-type plant of the same species cultivated under the same conditions. In certain embodiments, the transgenic plant comprises a nucleic acid that encodes a protein having an amino acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant when compared to a wild-type plant of the same species cultivated under the same conditions. In certain embodiments, the transgenic plant comprises a nucleic acid that encodes a protein that is a homologue, derivative, or variant of a protein derived from the peptide having an amino acid sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant when compared to a wild-type plant of the same species cultivated under the same conditions.

In certain embodiments, the transgenic plant comprises a protein having an amino acid sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the level of the protein in the transgenic plant is higher than that of a wild-type plant of the same species cultivated under the same conditions. In certain embodiments, the transgenic plant comprises a protein having an amino acid sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 93%, 95%, 96%, 97%, 98% or 99% identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24,

26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the level of the protein in the transgenic plant is higher than that of a wild-type plant of the same species cultivated under the same conditions. In certain embodiments, the transgenic plant comprises a protein that is a homologue, derivative, or variant of a protein derived from the peptide having an amino acid and sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102. In certain embodiments, the level of the protein in the transgenic plant is higher than that of a wild-type plant of the same species cultivated under the same conditions.

In addition, the present invention provides transgenic plant cells transformed with a nucleic acid molecule of the present invention. In one embodiment, the invention provides transgenic plant cells comprising a kinase or phosphatase nucleic acid molecule of the invention. In certain embodiments, the nucleic acid molecule is overexpressed in the transgenic plant cells when compared to plant cells of the same type in a wild-type plant of the same species cultivated under the same conditions. In another embodiment, the invention provides transgenic plant cells comprising a kinase or phosphatase protein of the invention, wherein the level of said protein in the transgenic plant cells is higher (*e.g.*, at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 150%, or 200% higher) than that of plant cells of the same type in a wild-type plant of the same species cultivated under the same conditions.

In certain embodiments, the transgenic plant comprises a nucleic acid molecule encoding a phosphatase having an amino acid sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, or 94 and/or a kinase selected from SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 96, 98, 100 or 102. In another embodiment, the transgenic plant comprises a nucleic acid molecule encoding a phosphatase having an amino acid sequence selected from SEQ ID NO: 2, 4, 6, 8, 10, or 94 and/or a kinase selected from SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 96, 98, 100 or 102. In certain embodiment, all or a portion, particularly an N-terminal portion, of amino acid residues 1 to 80, preferably all or a portion of amino acid residues 1 to 30, are replaced by a heterologous plant signal peptide by genetic engineering. In such a transgenic plant, the phosphatases or kinases are directed to various organelles/compartments of the cells.

In certain embodiments, the present invention provides chimeric gene constructs for genetic modification of plants to increase growth rate and to improve yield. In a specific embodiment, the chimeric gene constructs comprise a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101. In another specific embodiment, the chimeric gene constructs comprise a sequence that hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101, or a complement thereof, wherein the nucleic acid sequence encodes a protein or a polypeptide that exhibits at least one structural and/or functional feature of the polypeptides and enhances plant growth and/or yield.

The phosphatase or kinase- coding sequence is operatively linked to upstream and downstream regulatory components, preferably heterologous to the phosphatase or kinase sequence, such as for example, CMV 35S promoter, which acts to cause expression of the gene (production of the enzyme) in plant cells (*see* Fig. 3). Preferably, when a construct comprising a gene encoding a phosphatase or kinase of the present invention is introduced into plant cells by a conventional transformation method, such as microparticle bombardment, *Agrobacterium* infection, or microinjection, the gene is expressed in the cells under the control of the regulatory sequences. The expressed phosphatase interacts with the biosynthetic machinery that is naturally present in the plant cells to alter the carbon metabolism. By altering the carbon metabolism, the method of the present invention promotes the growth rate of the plant, resulting in faster growth rate and higher yield. As a result, the time required for the maturation of the plant and the time required for flowering is shortened. Also provided are methods for increasing growth rate and yield of plants, comprising the step of inserting into such plant cells, or cells of such whole plants, a chimeric gene construct.

In one specific embodiment, *Arabidopsis* is genetically modified by introducing an overexpression construct comprising nucleic acid molecules encoding a growth-promoting phosphatase or kinase of the present invention.

In an embodiment, the growth-promoting phosphatase and kinase genes are derived from *Arabidopsis*. As shown in the examples, transgenic *Arabidopsis* plants with over-expression of

NG6, NG21, NG24, NG28, and/or NG32 have enhanced growth and/or yield, when compared to wild-type *Arabidopsis* plants (*see* Table 5, and Figs. 5 and 6).

In one embodiment, a transgenic plant overexpressing a nucleic acid comprises the sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101 or homologues thereof, wherein the nucleic acid molecule encodes polypeptides or proteins of the invention.

5.3 Homologues, Derivatives, and Variants of Kinases and Phosphatases

The present invention also provides homologues, derivatives, and variants of kinases and phosphatases of the present invention; nucleic acid molecules encoding the polypeptides and homologues, derivatives, and variants; vectors, plant cells and transgenic plants comprising these nucleic acid molecules; and uses thereof for promoting plant growth and/or yield. The homologues, derivatives and variants of kinases and phosphatases are derived from the wild-type kinases and phosphatases, respectively. The methods of deriving the homologues, derivatives and variants are well known in the art which include routine conventional techniques of chemical modifications of amino acid residues or using molecular biology and recombinant DNA manipulation and production. Such techniques are available to the skilled artisan in laboratory manuals such as Sambrook and Russell, *Molecular cloning: A Laboratory Manual*, 3rd edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (2001).

In one embodiment, a homologue of the nucleic acid or polypeptide molecule of the present invention includes: (i) a polypeptide with at least about 65%, at least about 70%, at least about 80%, at least about 90%, or at least about 98% sequence identity of the polypeptide of the invention; (ii) a polypeptide encoded by a nucleotide sequence that is at least about 65%, at least about 70%, at least about 80%, at least about 90%, or at least about 98% identical to one or more of the nucleotide sequences encoding a polypeptide of the invention, or a fragment thereof; (iii) a polypeptide encoded by a nucleotide sequence that hybridizes, under stringent conditions, to a nucleotide sequence of the present invention; (iv) a polypeptide having an amino acid sequence that is at least about 65%, at least about 70%, at least about 80%, at least about 90%, or at least about 98% identical to a polypeptide of the present invention, and wherein the polypeptide of the invention is conservatively substituted; (v) a nucleic acid sequence encoding an amino acid

sequence that is at least about 70%, at least about 80%, at least about 90%, or at least about 98% identical to a polypeptide of the present invention and wherein the polypeptide of the invention is conservatively substituted; and (vi) a fragment of a polypeptide described in (i) through (iv), wherein the polypeptide fragment has at least 175, 200, 225, 250, 275, 300, 325, 350, 375, 400,
5 450, 500, 550, 600, 650, 700, or 750 contiguous amino acid residues of a polypeptide of the invention.

In one embodiment, a homologue polypeptide has an amino acid sequence that is at least about 65%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, or at least about 98% identical to a kinase or phosphatase of the present invention. In one
10 embodiment, the homologue polypeptide is obtained by conservative substitution.

In one aspect, the homologues derivatives and variants are derived from the wild type kinase and phosphatase by substitution, deletion, insertion of one or more nucleic acid in a nucleic acid molecule or one or more amino acid residues in an amino acid molecule. The term “derived” as used herein includes the modifications of a wild type nucleic acid molecule or
15 amino acid molecule as described below. For example, non-natural amino acids can be substituted for the amino acids of the kinases and phosphatases so long as the kinases and phosphatases having the substituted amino acids retain substantially the same functional activity as the kinases and phosphatases in which amino acids have not been substituted. Those having skill in the art will recognize that mutations can be made to polynucleotides encoding protein and
20 peptides, or complementary thereto, and that such mutations do not cause structural changes that affect functionality.

Conservative substitutions whereby a modified protein or polypeptide of the present invention having an amino acid of one class is replaced with another amino acid of the same class fall within the scope of the subject invention so long as the modified protein or polypeptide
25 having the substitution still retains substantially the same functional activity as the protein or polypeptide that does not have the substitution. For instance, amino acid residue of any of the following 11 groups may be conservatively substituted with another amino acid of the same group: (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
30 amino acids, such as glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (4)

neutral nonpolar (hydrophobic) amino acids, such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (5) amino acids having aliphatic side chains, such as glycine, alanine, valine, leucine, and isoleucine; (6) amino acids having aliphatic-hydroxyl side chains, such as serine and threonine; (7) amino acids having amide-containing side chains, such as asparagine and glutamine; (8) amino acids having aromatic side chains, such as phenylalanine, tyrosine, and tryptophan; (9) amino acids having basic side chains, such as lysine, arginine, and histidine; (10) amino acids having sulfur-containing side chains, such as cysteine and methionine; and (11) amino acids having similar geometry and hydrogen bonding patterns, such as aspartic acid, asparagine, glutamic acid and glutamine.

Examples of non-natural amino acids include, but are not limited to, ornithine, citrulline, hydroxyproline, homoserine, phenylglycine, taurine, iodotyrosine, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, 2-amino butyric acid, γ -amino butyric acid, ϵ -amino hexanoic acid, 6-amino hexanoic acid, 2-amino isobutyric acid, 3-amino propionic acid, norleucine, norvaline, sarcosine, homocitrulline, cysteic acid, τ -butylglycine, τ -butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, and amino acid analogues in general. Non-natural amino acids also include amino acids having derivatized side groups. Furthermore, any of the amino acids in the protein can be of the D (dextrorotary) form or L (levorotary) form.

The structure of a polypeptide can be determined by methods known to those skilled in the art, including but not limited to, X-ray crystallography, nuclear magnetic resonance, and crystallographic electron microscopy. A sequence having sequence homology can be made using standard molecular biology techniques, including site-directed mutagenesis and by insertion or deletion of sequences.

In one aspect, the homologues, derivatives and variants are derived from the wild type kinase and phosphatase. In certain embodiments, provided herein are derivatives of the disclosed polypeptides. For example, but not by way of limitation, derivatives may include peptides or proteins that have been modified, *e.g.*, by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical

modifications may be carried out by known techniques including, but not limited to, specific chemical cleavage, acetylation, formylation, etc. Additionally, the derivative may contain one or more non-classical amino acids. The subject invention also concerns variants of the polynucleotides of the present invention. Variant sequences include those sequences wherein
5 one or more nucleotides of the sequence have been substituted, deleted, and/or inserted.

The nucleotides that can be substituted for natural nucleotides of DNA have a base moiety that can include, but is not limited to, inosine, 5-fluorouracil, 5-bromouracil, hypoxanthine, 1-methylguanine, 5-methylcytosine, and tritylated bases. The sugar moiety of the nucleotide in a sequence can also be modified and includes, but is not limited to, arabinose,
10 xylulose, and hexose. In addition, the adenine, cytosine, guanine, thymine, and uracil bases of the nucleotides can be modified with acetyl, methyl, and/or thio groups. Sequences containing nucleotide substitutions, deletions, and/or insertions can be prepared and tested using standard techniques known in the art.

Unless otherwise specified, as used herein percent sequence identity and/or similarity of
15 two sequences can be determined using the algorithm of Karlin and Altschul (1990), modified as in Karlin and Altschul (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990). BLAST searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain sequences with the desired percent sequence identity. To obtain gapped alignments for comparison purposes, Gapped BLAST can
20 be used as described in Altschul *et al.* (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (NBLAST and XBLAST) can be used. See NCBI/NIH website.

The subject invention also contemplates those polynucleotide molecules having sequences which are sufficiently homologous with the polynucleotide sequences exemplified
25 herein so as to permit hybridization with that sequence under standard stringent conditions and standard methods (Maniatis *et al.*, 1982).

In one embodiment, the present invention further provides isolated nucleic acid molecules that comprise, or consist of, at least about 550, at least about 600, at least about 650, at least about 700, at least about 750, at least about 800, at least about 850, at least about 900, at
30 least about 950, at least about 1000, at least about 1050, at least about 1100, at least about 1150,

at least about 1200, at least about 1250, at least about 1300, or at least about 1350 contiguous nucleotides of a nucleic acid molecule of the present invention.

In another embodiment, an isolated nucleic acid molecule encodes a variant of a polypeptide whose amino acid sequence has been modified by genetic engineering so that biological activities of the polypeptides are either enhanced or reduced, or the local structures thereof are changed without significantly altering the biological activities. Amino acid modifications can be made by methods known in the art.

In one embodiment, the present invention embodies isolated nucleic acid molecules that hybridize, under stringent conditions, to nucleic acid molecules having the nucleic acid sequence comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101, or homologues thereof. In certain embodiments, the nucleic acid molecules encode proteins or polypeptides that exhibit at least one structural and/or functional feature of the polypeptides of the invention (e.g. enhance plant growth and/or yield).

A further embodiment includes methods for preparing a polypeptide as provided herein by recombinant DNA technology. In one embodiment, the preparation method comprises culturing host cells containing a recombinant expression vector encoding a polypeptide as provided herein, or a nucleotide sequence encoding a polypeptide as provided herein operably linked to a heterologous promoter, and producing the polypeptide as provided herein.

5.4 Vectors and Expression Constructs

Another embodiment includes nucleic acid molecules suitable for use as primers or hybridization probes for the detection of nucleic acids encoding a phosphatase or kinase polypeptide as provided herein or other sequences.

Yet another embodiment includes vectors, *e.g.*, recombinant expression vectors, comprising a nucleic acid molecule as provided herein. Furthermore, host cells containing such a vector or engineered to contain and/or express a nucleic acid molecule as provided herein and host cells containing a nucleotide sequence as provided herein operably linked to a heterologous promoter are disclosed.

As used herein, the term “expression construct” refers to a combination of nucleic acid sequences that provides for transcription of an operably linked nucleic acid sequence. In general, operably linked components are in contiguous relation.

Expression constructs of the invention will also generally include regulatory elements that are functional in the intended host cell in which the expression construct is to be expressed. Regulatory elements include promoters, transcription termination sequences, translation termination sequences, enhancers, and polyadenylation elements.

An expression construct as provided herein can comprise a promoter sequence operably linked to a polynucleotide sequence encoding a peptide. Promoters can be incorporated into a polynucleotide using standard techniques known in the art. Multiple copies of promoters or multiple promoters can be used in an expression construct. In a preferred embodiment, a promoter can be positioned about the same distance from the transcription start site as it is from the transcription start site in its natural genetic environment. Some variation in this distance is permitted without substantial decrease in promoter activity. A transcription start site is typically included in the expression construct.

Unique restriction enzyme sites can be included at the 5' and 3' ends of the expression construct to allow for insertion into a polynucleotide vector. As used herein, the term “vector” refers to any genetic element, including for example, plasmids, cosmids, chromosomes, phage, virus, and the like, which is capable of replication when associated with proper control elements and which can transfer polynucleotide sequences between cells. Vectors contain a nucleotide sequence that permits the vector to replicate in a selected host cell.

The term “operably linked,” as used herein, refers to when transcription under the control of the “operably linked” promoter produces a functional messenger RNA, translation of which results in the production of the polypeptide encoded by the DNA operably linked to the promoter.

5.5 Fusion Proteins

Also provided herein are fusion proteins. In one embodiment, the polypeptides as provided herein, or fragments thereof, are recombinantly fused or chemically conjugated (*e.g.*, covalent and non-covalent conjugations) to heterologous polypeptides (*i.e.*, an unrelated polypeptide or portion thereof, preferably at least 10, at least 20, at least 30, at least 40, at least

50, at least 60, at least 70, at least 80, at least 90 or at least 100 amino acids of the polypeptide) to generate fusion proteins. The fusion can be direct, or may occur through linker sequences.

In one embodiment, the fusion protein comprises a polypeptide fused to a heterologous signal sequence at its N-terminus. For example, the signal sequence naturally found in the polypeptide can be replaced by a signal sequence that is derived from a heterologous origin. Various signal sequences are commercially available.

In another embodiment, a polypeptide can be fused to tag sequences, *e.g.*, a hexa-histidine peptide, among others, many of which are commercially available. As described in Gentz *et al.*, 1989, *Proc. Natl. Acad. Sci. USA*, 86:821-824, for instance, hexa-histidine provides for convenient purification of the fusion protein. Other examples of peptide tag include the hemagglutinin "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson *et al.*, 1984, *Cell*, 37:767), and the "flag" tag (Knappik *et al.*, 1994, *Biotechniques*, 17(4):754-761). These tags are useful for purification of recombinantly produced polypeptides.

Fusion proteins can be produced by standard recombinant DNA techniques or by protein synthetic techniques, *e.g.*, by use of a DNA synthesizer. For example, a nucleic acid molecule encoding a fusion protein can be synthesized by conventional techniques including, for example, automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers, which give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, *e.g.*, *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds., John Wiley & Sons, 1992).

The nucleotide sequence encoding a fusion protein can be inserted into an appropriate expression vector, *i.e.*, a vector that contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. In a specific embodiment, the expression of a fusion protein is regulated by an inducible promoter.

In another embodiment, the present invention provides methods for detecting the presence, activity or expression of a polypeptide of the invention or similar polypeptide in a biological material, such as cells, or culture media. The increased or decreased activity or expression of the polypeptide in a sample relative to a control sample can be determined by

contacting the biological material with an agent that can detect directly or indirectly the presence, activity or expression of the polypeptide. In a particular embodiment, such an agent is an antibody or a fragment thereof which immunospecifically binds to one of the disclosed polypeptides.

5 In a still another embodiment, a fusion protein comprising a bioactive molecule and one or more domains of a disclosed polypeptide or fragment thereof is provided. In particular, fusion proteins comprising a bioactive molecule recombinantly fused or chemically conjugated (including both covalent and non-covalent conjugations) to one or more domains of a disclosed polypeptide or fragments thereof.

10 5.6 Preparation of Transgenic Plants

Genetic engineering of plants can be achieved in several ways. The most common method is *Agrobacterium*-mediated transformation. In this method, *A. tumefaciens*, which naturally infects plants by inserting tumor-causing genes into a plant's genome, is genetically altered. Selected genes can be engineered into the T-DNA of the bacterial Ti (tumor-inducing) plasmid of *A. tumefaciens* in laboratory conditions so that they become integrated into the plant chromosomes when the T-DNA is transferred to the plant by the bacteria's own internal transfer mechanisms.

20 The only essential parts of the T-DNA are its two small (25 base pair) border repeats, at least one of which is needed for plant transformation. The bacterial genes encoding for plant hormones that promote tumor growth are excised from the T-DNA and replaced with a sequence of DNA that typically contains: a selectable marker (e.g. an antibiotic-resistance gene; usually kanamycin resistance), a restriction site - a site with a specific sequence of nucleotides where a restriction enzyme will cut the DNA, and the desired genes to be incorporated into the plant (B. Tinland, 1996. The integration of T-DNA into plant genomes. Trends in Plant Science 1,178-184; 25 D. Grierson (ed.) 1991. Plant Genetic Engineering. Blackie, Glasgow).

Agrobacterium can be added to plant protoplasts (plant cells with cell walls removed) in culture; the plant protoplasts then regenerate cell walls at which point non-transformed plants are killed with antibiotics for which the transformed plants have been given resistance genes.

Plantlets are then regenerated from the surviving transformed cells using standard plant tissue culture techniques.

In an alternative technique, sterile disks or fragments of vegetative portions of plants are placed in liquid culture medium with *Agrobacterium*, and then hormones are used to induce rooting, thereby regenerating plantlets grown on selection media. Another technique for delivering genes is possible for some plants such as *Arabidopsis*, where the *Agrobacterium* or even "naked" DNA can be infused through the seed coat to cause transformation (Clough SJ and Bent AF, 1998. Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. *Plant J* 16:735-43).

The biolistic method for genetic engineering of plants was developed more recently and is becoming more widely employed. In this method, very small particles (microprojectiles) of tungsten or gold coated with biologically active DNA are propelled at high-velocities into plant cells using an electrostatic pulse, air pressure, or gunpowder percussion. As the particles pass through the cell, the DNA dissolves and can then integrate into the genome of that cell and its progeny. This method can produce stable transformants (Christou, P., *et al.*, 1988. Stable transformation of soybean callus by DNA-coated gold particles, *Plant Physiology* 87:671-674). The method can be practiced on whole plants and is particularly effective on meristematic tissue. It is also capable of delivering DNA either to the nucleus or into mitochondria (Johnston, S.A., *et al.*, 1988. Mitochondrial transformation in yeast by bombardment with microprojectiles (*Science* 240,1538-41) and chloroplasts (Svab, Z., *et al.*, 1990, Stable transformation of plastids in higher plants, *Proc Natl Acad Sci. USA* 87, 8526-8530).

The electroporation method of plant genetic engineering has met with less success. In this technique, protoplasts in culture take up pure DNA when treated with certain membrane-active agents or with electroporation - a rapid pulse of high-voltage direct current. Once the DNA enters the protoplast, it can be integrated into the cells genome. Standard tissue culture techniques are then used to regenerate transgenic plants.

The microinjection method of plant genetic engineering is perhaps the most difficult. In this method, DNA is microinjected into target plant cells using very thin glass needles in a method similar to that used with animals. The technique is laborious, ineffective, and impractical for generating large numbers of transgenic plants.

It is within the ability of a skilled artisan to select known methods for producing genetically engineering plants, taking into account various factors such as the targeted plant species and which methods have been proven effective therein.

5.7 Preparation of Antibodies

In one aspect, provided herein are antibodies against the kinase and phosphatase. Antibodies which specifically recognize one of the described phosphatase polypeptides or fragments thereof can be used for detecting, screening, and isolating the polypeptide that is provided herein or fragments thereof, or similar sequences that encode similar enzymes from other organisms. For example, an antibody which immunospecifically binds a protein or protein fragments thereof can be used for various *in vitro* detection assays, including enzyme-linked immunosorbent assays (ELISA), radioimmunoassays, Western blot, etc., for the detection of the polypeptide that is provided herein or fragments, derivatives, homologues, or variants thereof, or similar molecules having the similar enzymatic activities as the phosphatase and/or kinase polypeptides.

Embodiments further provide antibodies that immunospecifically bind a polypeptide that is provided herein. Such antibodies include, but are not limited to, antibodies from various animals, humanized, chimeric, polyclonal, monoclonal, bi-specific, multi-specific, single chain antibodies, Fab fragments, F(ab')₂ fragments, disulfide-linked Fvs, fragments containing a VL or VH domain or a complementary determining region (CDR), wherein the antibody or antibody fragment immunospecifically binds to a polypeptide that is provided herein.

Antibodies specific for the described phosphatase polypeptides can be generated by any suitable method known in the art. Once an antibody molecule has been produced, it may then be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (*e.g.*, ion exchange, affinity, particularly by affinity for the specific antigen after Protein A or Protein G purification, and sizing column chromatography), centrifugation, differential solubility, or by any other standard techniques for the purification of proteins. Further, the antibodies or fragments thereof may be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

Antibodies fused or conjugated to heterologous polypeptides may be used in *in vitro* immunoassays and in purification methods (*e.g.*, affinity chromatography) well known in the art. See *e.g.*, PCT publication Number WO 93/21232; EP 439,095; Naramura *et al.*, 1994, *Immunol. Lett.* 39:91-99; U.S. Patent 5,474,981; Gillies *et al.*, 1992, PNAS 89:1428-1432; and Fell *et al.*,
5 1991, *J. Immunol.* 146:2446-2452, which are incorporated herein by reference in their entireties.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the described polypeptides or fragments, derivatives, homologues, or variants thereof, or similar molecules having the similar enzymatic activities as the polypeptide of the invention. Such solid supports include, but are not limited to, glass,
10 cellulose, polyacrylamide, nylon, and polystyrene.

5.8 Detection Assays

An exemplary method for detecting the presence or absence of an over-expressed phosphatase/ kinase polypeptide or an inserted phosphatase/kinase-encoding nucleic acid in a
15 biological sample involves obtaining a biological sample from various sources and contacting the sample with a compound or an agent capable of detecting a polypeptide or nucleic acid (*e.g.*, mRNA, genomic DNA) such that the presence of a heterologous polypeptide or nucleic acid is detected in the sample.

An exemplary agent for detecting mRNA or genomic DNA encoding an inserted
20 phosphatase polypeptide is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA encoding any of the described phosphatase and kinase polypeptides. The nucleic acid probe can be, for example, a full-length cDNA, such as the nucleic acid of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99, 101 or a portion thereof, such as an oligonucleotide of at least one of at least about 15, at least
25 about 20, at least about 25, at least about 30, at least about 50, at least about 100, at least about 250, at least about 500, or more nucleotides in length and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a polypeptide of the invention.

An exemplary agent for detecting an over-expressed phosphatase / kinase polypeptide is an antibody capable of binding to a phosphatase / kinase polypeptide product of an inserted gene,

preferably an antibody with a detectable label. Antibodies can be polyclonal and monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used.

The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

The detection method can be used to detect mRNA, protein, or genomic DNA in a sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a heterologous polypeptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a heterologous polypeptide include introducing into a subject organism a labeled antibody directed against the polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in the subject organism can be detected by standard imaging techniques, including autoradiography.

In a specific embodiment, the methods further involve: 1) obtaining a control sample from a control subject, 2) contacting the control sample with a compound or agent capable of detecting an over-expressed polypeptide product, or the mRNA transcription product, or genomic DNA encoding an inserted phosphatase gene, such that the presence of the polypeptide or mRNA or genomic DNA encoding the phosphatase polypeptide is detected in the sample, and 3) comparing the level of the phosphatase / kinase polypeptide or mRNA or genomic DNA encoding the polypeptide in a control sample with the level of the polypeptide or mRNA or genomic DNA encoding endogenous phosphatase polypeptides in the test sample.

5.9 Applications of Transgenic Plants

The transgenic plants generated can have many useful applications, including in food, feed, biomass, biofuels (starch, cellulose, seed lipids) and wood pulp industry. The enhanced

growth rate of the transgenic plants can provide additional carbon dioxide fixation per hectare of land per year, and, thus is useful for generating carbon credits.

6.0 EXAMPLES

Following are examples that illustrate embodiments for practicing the invention. These examples should not be construed as limiting. Unless otherwise noted, all percentages are by weight, all solvent mixture proportions are by volume, all temperatures are in Centigrade, and all pressure is at or near atmospheric pressure.

6.1 SCREENING OF GROW-PROMOTING NG GENES

Two independent AtPAP2 overexpression lines (OE7 and OE21, homozygous T3 plants), an AtPAP2 T-DNA mutant line that cannot express the full length AtPAP2, and the wild-type Arabidopsis (Col-0) were employed for microarray analysis. The AtPAP2 overexpression lines (OE7 and OE21, homozygous T3 plants), the AtPAP2 T-DNA mutant line, and the wild-type Arabidopsis (Col-0) line have been disclosed by the present inventor in U.S. Patent Application Serial No. 12/640,674 (U.S. Patent Application Publication No. 2010/0159065), which is hereby incorporated by reference in its entirety.

Briefly, seeds were germinated on MS medium supplemented with 2% (w/v) sucrose, grew in a growth room under 12 hour-light/12 hour-dark cycle at 22°C for 10 days, and were then transferred to soil and grew in a growth chamber under a 16-hour light (22°C) and 8-hour dark (18°C) cycle. Shoots of 20-day-old Arabidopsis (WT, T-DNA, OE7 and OE21) prior to bolting were collected in the middle of day (4 plants/line/tube, 3 biological triplicates/line, 3 tubes/line) and ground in liquid nitrogen. RNA extraction was performed with on-column DNase digestion according to the manufacturer's instruction (RNeasy Plant Mini Kit, Cat.No.74904, Qiagen). Total RNA was dissolved in DEPC water and quantified by the Bioanalyzer 2100 (Agilent Technologies, Boblingen, Germany). Double strand DNA synthesis and Cy 3 labeling from three biological replicates were performed by NimbleGen Systems, Inc. (Madison, WI). Statistical analyses of normalized microarray data (RMA algorithm, quantile normalization) and drawing of scatter plots, heatmaps were performed using ArrayStar 3.0 (DNASTAR, Madison, WI). Identification of GO and classification were carried out using software available from TAIR

database and KEGG pathway database. In all three replications, genes were considered to be significantly regulated if their fold change values were positively or negatively beyond 1.3 ($p < 0.05$).

20-day-old plants did not show any differences in appearance so that any differences in gene expression between the lines were not due to difference in developmental stage or additional tissues (e.g. inflorescence). The transcripts levels of 30360 genes in shoots were determined using the Arabidopsis Genome NimbleGen chips. The average hybridization signals detected in each line were normalized from the log2 average signal and compared with the signal strengths in the wild-type Arabidopsis.

An overview of the expression data of OE7, OE21 and T-DNA plants versus wild-type control is presented as a heat map (Fig. 1) and scatter plots (Fig. 2) that show a linear bias in the graphs. Gene expression patterns in transgenic shoots are different comparative to their wild-type controls.

The data show that AtPAP2 overexpression altered expression levels of other genes, nearly half of which have not been characterized yet. AtPAP2 overexpression lines exhibit more dramatic changes in gene expression than the AtPAP2 T-DNA line.

Differentially expressed genes are identified using P -value < 0.05 and fold change > 1.3 as the cutoff, and the results show that the expression of about 6312, 7831, and 672 genes in the shoots of OE7, OE21 and T-DNA lines are significantly altered. An overall view of the altered genes in the heat map (Fig. 1) revealed that most genes were down-regulated in the fold change ≥ 2.0 . In addition, the fold change in expression levels is smaller in up-regulated genes than in down-regulated genes.

Based on the microarray data, 33 putative phosphatase and kinase genes were selected, and were introduced into Arabidopsis to produce overexpression lines. The results show that the overexpression of NG6, NG21, NG24, NG28 and NG32 in Arabidopsis promotes the growth of Arabidopsis and increases seed yield (see Example 2). The expression level of the five growth-promoting NG genes in the AtPAP2 OE lines and T-DNA lines are shown in Table 1.

Table 1. Microarray data of the 5 growth-promoting genes in AtPAP2 overexpression lines (OE7, OE21), T-DNA line and wild type (WT) Arabidopsis.

NG		WT-	T-DNA	OE7	OE21	OE7/WT	OE21/WT	T-DNA/	
No.	AGI code	Mean	Mean	Mean	Mean	Fold	Fold	WT Fold	Gene Description
NG 6	AT1G05000	637	533	976	1131	1.52*	1.78**	0.83	Protein phosphatase
NG21	AT1G13350	2406	2151	3543	3441	1.47*	1.43*	0.89	Protein kinase
NG24	AT1G28390	778	710	1853	1915	2.37**	2.42**	0.91	Protein kinase
NG28	AT3G24660	2514	1839	3313	4422	1.32**	1.74**	0.73	Protein kinase
NG32	AT5G03320	1325	1063	1884	2053	1.43*	1.56**	0.80	Protein kinase

6.2 PRODUCTION OF NG OVEREXPRESSION LINES IN ARABIDOPSIS

5 To create transgenic NG gene overexpressing lines, the full length coding region of each NG gene's cDNA was amplified by PCR using the following primers (Table 2). The PCR products were inserted into the pCXS vector with classical TA cloning method (Fig. 3).

Table 2. Primers used for to amplify the full CDS of the aimed NG genes

Gene name		Sequence(5'---3')
NG6	Forward Primer	5'-TCGAGCTAGCATGAAGCTTGTGGAGAAGAC-3' (SEQ ID NO: 51)
	Reverse Primer	5'-CGACGAGCTCTTACCTGATGGAACAAGAG-3 (SEQ ID NO: 52)
NG21	Forward Primer	5'-ATGGTGAGTGACAAGCATGTAG-3' (SEQ ID NO: 53)
	Reverse Primer	5'-TCACTTGCCCGTGATGAATG-3' (SEQ ID NO: 54)
NG24	Forward Primer	5'-ATGGGTTATCTCTCTTGCAAC-3' (SEQ ID NO: 55)
	Reverse Primer	5'-TCAGTATCTCTCCGCGACG-3' (SEQ ID NO: 56)
NG28	Forward Primer	5'-ATGGGCATGGAAGCTTTGAG-3' (SEQ ID NO: 57)
	Reverse Primer	5'-TCAAATGGAGTTTCGGCGT-3' (SEQ ID NO: 58)
NG32	Forward Primer	5'-ATGAAATGCTTCTTATCCC-3' (SEQ ID NO: 59)
	Reverse Primer	5'-TCAACAAGCTCTCACATTCT-3' (SEQ ID NO: 60)

The vector was introduced into *Agrobacterium tumefaciens* strain GV3101 and then transformed by the floral dip method (Clough and Bent, 1998) into wild-type Col-0 to generate NG-overexpressing lines. Through two generations of selection on MS agar plate with 30 mg/l hygromycin, homologous NG transgenic lines were obtained. The resistant plants were transferred to soil to grow to maturity, and their transgenic status was confirmed by qRT-PCR analysis.

6.3 CONFIRMATION OF OVEREXPRESSION OF NG GENES IN TRANSGENIC PLANTS

The transcription levels of the NG genes in the hygromycin resistant, homologous T3 overexpression lines were confirmed by quantitative Real Time-PCR. Total RNA was extracted from 10-day-old seedlings grown on Murashige and Skoog (MS) with 3% (w/v) sucrose using the TRIzol RNA isolation method with DNase I treatment. cDNAs were generated using Superscript III reverse transcriptase (Invitrogen, Carlsbad, CA, USA) using an oligo15 dT primer. Two gene-specific primers were used to amplify the 80-150bp coding region of each NG gene. The ACTIN primers were used for control experiment. As shown in Figure 4, the transcript levels of each overexpression line were consistently higher than their respective expression levels in the wild-type.

Table 3. Primers used in the quantitative RT-PCR

NG6	Forward Primer	5'-TGTGCCCCGAGCCCTACC-3' (SEQ ID NO: 61)
	Reverse Primer	5'-CTTTCAGTGCCATGCGGATTTT-3 (SEQ ID NO: 62)
NG21	Forward Primer	5'-GGCACAAGTCCCGTCATCACC-3' (SEQ ID NO: 63)
	Reverse Primer	5'-TCCCCAATCCCTTCTTTTCCTA-3' (SEQ ID NO: 64)
NG24	Forward Primer	5'-GCCGCCGTCAAGAGAACAAC-3' (SEQ ID NO: 65)
	Reverse Primer	5'-CTCCGGTGGTCAACGCAGTAA-3' (SEQ ID NO: 66)
NG28	Forward Primer	5'-TGTTGTTGTGGCCTCGTTGTTA-3' (SEQ ID NO: 67)
	Reverse Primer	5'-CTTTCCTTCACCGCCTTCTTTC-3' (SEQ ID NO: 68)
NG32	Forward Primer	5'-AAGCTTTCGGATTTCGGTTTG-3' (SEQ ID NO: 69)

	Reverse Primer	5'-TGGCCTTCTTCCTGTAATGAGC-3' (SEQ ID NO: 70)
ACTIN	Forward Primer	5'- CCCGCTATGTATGTCGC -3' (SEQ ID NO: 71)
	Reverse Primer	5'- AAGGTCAAGACGGAGGAT -3' (SEQ ID NO: 72)

6.4 GROWTH PHENOTYPES OF NG GENE OVER-EXPRESSION LINES

Arabidopsis seeds were soaked in water at 4°C for 3 days. The seeds were surface sterilized and sown on MS medium supplemented with 3% (w/v) sucrose for 10 days. Seedlings with 2 rosette leaves of the same size were transferred to soil under Long Day condition (16h light at 22°C/ 8h dark at 18°C) in a plant growth chamber. Bolting time was measured when the primary inflorescence reached 1 cm above the rosette leaves. (Liu *et al.*, 2008; Wu *et al.*, 2008).

The inflorescences of NG gene OE lines emerged earlier (4-5 days) than the WT at Long Day conditions (Table 4, Fig. 5 and Fig. 6). This phenotype observation was repeated at least 3 times and the results of two of the experiments are shown here.

Table 4A. Earlier bolting time of NG OE lines (Trial 1)

	WT	NG6	NG21	NG24	NG28	NG32
Average bolting time (Day)	24.4	21.2	20.1	21.4	20.8	19.8
SD	1.4	1.0	1.4	0.9	1.0	1.3
N	12	12	12	9	9	9

Table 4B. Earlier bolting time of NG OE lines (Trial 2)

	WT	NG6	NG21	NG24	NG28	NG32
Average bolting time (Day)	24.3	19.2	19	19	18.3	19
SD	0.8	0.8	1.1	1	1.0	0.9
N	12	6	6	9	6	6

At maturity (Long Day), the number of inflorescence and the total weight of seeds harvested from each line were recorded. The results of two separate experimental trials are shown in Tables 5A and B. The results show that the overexpression of each of the five NG

genes (NG6, NG21, NG24, NG28, and NG32) resulted in increased number of inflorescences and seed yield. Compared to that of the wild-type, the seed yield of each NG over-expression line increased 30-50% (Table 5).

Table 5A.OE lines produced more seeds (Trial 1).

Lines	Weight of seeds (mg)/plant	SD
WT(Col-0)	80.4	4.9
NG6	113.6	12.2
NG21	127.8	26.9
NG24	99.6	17.3
NG28	130.6	26.7
NG32	135.9	23.5

5 The plants were grown in small black trays (N = 6 – 9).

Table 5B. OE lines produced more seeds (Trial 2).

Lines	Weight of seeds (mg)/plant	SD
WT(Col-0)	142.0	14.6
NG6	190.3	15.7
NG21	180.4	26.3
NG24	203.8	20.0
NG28	186.0	39.5
NG32	241.8	23.8

The plants were grown in large white cups (N = 6 – 9).

10 The results show that, when compared to the wild-type, Arabidopsis plants transformed with NG6, NG21, NG24, NG28 and/or NG32 have the following advantageous phenotypes: (1) faster growth rate; (2) higher seed yield.

6.5 SEQUENCE ALIGNMENT AND PHYLOGENETIC ANALYSIS

All the CDS of 5 NG genes in the Arabidopsis Col-0 ecotype were obtained from the TAIR website. Sequence alignment of each NG gene was retrieved by tblastn program from
5 Plant GDB database and NCBI database using the amino acid sequence of each Arabidopsis NG gene as the bait sequences. Partial sequences recovered were aligned and compared to produce a full length coding sequence if feasible. Sequence alignment and phylogenetic tree were conducted using MEGA4 (Kumar *et al.*, 2004) and *ClustalW* program. Amino acid sequence comparisons were performed using CLC Sequence Viewer 5.1.1.

10 Those skilled in the art will recognize, or be able to ascertain many equivalents to the specific embodiments of the invention described herein using no more than routine experimentation. Such equivalents are intended to be encompassed by the following claims.

All publication, patents and patent applications mentioned in this specification are incorporated herein by reference in their entireties into the specification to the same extent as if
15 each individual publication, patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety.

Citation or discussion of a reference herein shall not be construed as an admission that such is prior art to the present invention.

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Clough, S.J. and Bent, A.F. (1998) Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. *Plant J*, 16, 735-743.

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Klabunde, T. and Krebs, B. (1997) The dimetal center in purple acid phosphatases. *Metal Sites in Proteins and Models*, 89, 177-198.

10

Li, D., Zhu, H., Liu, K., Liu, X., Leggewie, G., Udvardi, M. and Wang, D. (2002) Purple acid phosphatases of *Arabidopsis thaliana*. Comparative analysis and differential regulation by phosphate deprivation. *J.Biol.Chem.*, 277, 27772-27781.

- 15 Schenk, G., Ge, Y., Carrington, L.E., Wynne, C.J., Searle, I.R., Carroll, B.J., Hamilton, S. and de-Jersey, J. (1999) Binuclear metal centers in plant purple acid phosphatases: Fe-Mn in sweet potato and Fe-Zn in soybean. *Arch.Biochem Biophys*, 370, 183-189.

United States Patent Application Publication No. 2010/0159065

SEQUENCE LISTING IN ELECTRONIC FORM

In accordance with Section 111(1) of the Patent Rules, this description contains a sequence listing in electronic form in ASCII text format (file: 73140-38 Seq 15-OCT-13 v1.txt).

A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

The sequences in the sequence listing in electronic form are reproduced in the following table.

SEQUENCE TABLE

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LIM, Boon Leong

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ALTERING EXPRESSION LEVELS OF KINASES AND PHOSPHATASES

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<140> CA national phase of PCT/CN2012/074811

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 Pro Phe Val Asn Ile Pro Glu Asp Thr Ile Arg Glu Ala Leu Arg Leu
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 Val Leu Asp Val Arg Asn His Pro Val Leu Ile His Cys Asn Arg Gly
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 Lys His Arg Thr Gly Arg Leu Val Gly Cys Leu Arg Lys Leu Gln Arg
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Lys Lys Lys Leu Glu Ser Val Asp Glu Phe Gly Asp Ile Lys Ser Gly
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Gln Phe Arg Glu Asn Asn Leu Gly Arg Asn Gln Arg Arg Glu Arg Glu
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Cys Glu Lys Arg Lys Glu Ile Glu Pro Asp Arg Glu Arg Arg Lys Glu
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Tyr Ser Ser Arg Glu Arg Gly Arg Glu Asn Glu Arg Glu Arg Arg Ser
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Glu Lys Asp Arg Asp Lys Gly Arg Glu Phe Gln Ser Asp Arg Glu Lys
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Gly His Ser Arg His Asp Ala Glu Asp Asp Leu Glu Leu Arg Ser Pro
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Arg	Ile	Phe	Ile	Leu	Asp	Pro	Gln	Lys	Arg	Ile	Thr	Val	Ser	Gln	Ala	740	745	750
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Ala	Ser	Lys	Asp	Asp	Pro	Glu	Glu	Val	Ala	Ile	Lys	Ile	Ile	Arg	Asn	
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Ile	Ser	Ser	Phe	Met	Tyr	Arg	Asn	His	Leu	Cys	Leu	Val	Phe	Glu	Ser	
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Ala	Leu	Lys	His	Leu	Lys	Asn	Cys	Lys	Val	Leu	His	Cys	Asp	Ile	Lys	
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Pro	Asp	Asn	Met	Leu	Val	Asn	Glu	Ala	Lys	Asn	Val	Leu	Lys	Val	Cys	
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Asp	Phe	Gly	Asn	Ala	Met	Leu	Ala	Gly	Met	Asn	Glu	Val	Thr	Pro	Tyr	
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Leu	Val	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Ile	Val	Leu	Gly	Leu	Ala	
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Tyr	Asp	His	Pro	Leu	Asp	Met	Trp	Ser	Val	Gly	Cys	Cys	Leu	Tyr	Glu	
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Leu	Tyr	Thr	Gly	Lys	Val	Leu	Phe	Pro	Gly	Pro	Ser	Asn	Asn	Ala	Met	
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Leu Arg Leu His Met Glu Leu Lys Gly Pro Phe Pro Lys Lys Met Leu
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 His Ala Thr Glu Glu Asp Pro Val Thr Lys Thr Ala Val Arg Arg Leu
 885 890 895
 Ile Leu Asn Ile Lys Pro Lys Asp Val Gly Ser Leu Phe Pro Asn Phe
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 Pro Gly Glu Asp Pro Lys Met Leu Ser Ser Phe Lys Asp Leu Leu Asp
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 Leu Ser His Pro Phe Ile Thr Gly Lys
 945 950

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 <212> DNA
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<212> PRT
<213> glycine max

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Asn Ser His Arg His Arg His Gly Ser Lys Lys Arg Asp Glu Glu Val
35          40          45
Glu Phe Asp Asp Arg Thr Ile Ala Ala Val Pro Ser Pro Thr Ser His
50          55          60
Arg Tyr Leu His Asp Asp Asp Val Glu Glu Gly Glu Ile Leu Glu Asp
65          70          75          80
Glu Ala Leu Asp Gly Glu Val Gly Lys Lys Glu Thr Glu Ser Asp Val
85          90          95
Glu Pro Gly Glu Ile Lys Val Thr Gly Asp Arg Asp Val Arg Ser Asp
100         105         110
Asn Gln Asn Ser Glu Pro Leu Thr Lys Ile Ser Glu Thr Arg Asn Glu
115         120         125
Asp Ile Arg Asp Asp Lys Phe Ile Ser Pro Ala Ile Asp Ala Gln Asp
130         135         140
Asp Val Ser Pro Asn Arg Ser Ser Ser Glu Thr Arg Asp Gly Lys His
145         150         155         160
Ala Gln Ala Arg Thr Asp Gly Val Gly Asn Gly Tyr Leu Asp Pro Lys
165         170         175
Ser Ser Lys Gly Asp Lys Trp Gln Asn Gly Glu Leu Gly His Phe Lys
180         185         190
Gly Glu Lys Tyr Arg Met Ser Gly Ser Ser Pro Ser His Gly Arg Tyr
195         200         205
Arg Ser Arg Ser Arg Ser Ile Gly His Thr Arg Asp Arg Ser Arg Ser
210         215         220
Arg Ser Ile Ile Asp Glu Tyr Pro His Ser Lys Arg Arg Arg Phe Asp
225         230         235         240
Tyr Asp His Asp Glu Glu Arg Val Arg Ala Arg Gly Arg Glu His Glu
245         250         255
Ala Arg Asp Arg Asp Val Asp Arg Asp Leu His Gly Glu Lys Lys Gln
260         265         270
Glu Glu Thr Ser Arg Gly Lys Glu Ile Glu Ser Arg Asp Arg Tyr Arg
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Tyr	Arg	His	Lys	Asp	Arg	Asp	Thr	Ala	Asn	Asp	Arg	Tyr	Arg	Lys	His	
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Asp	Asn	Pro	Val	Lys	Val	Tyr	Ser	Ser	Met	Gly	Ser	Thr	Ala	Glu	Val	
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Glu	Asp	Thr	Leu	Gln	Leu	Pro	Glu	Gln	Glu	Glu	Glu	Asp	Leu	Asn	Arg	
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Ile	Lys	Glu	Glu	Ser	Arg	Arg	Arg	Arg	Glu	Ala	Ile	Met	Glu	Lys	Tyr	
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Lys	Lys	Gln	His	Gln	Gln	Val	Glu	Glu	Ala	Val	Gly	Asn	Glu	Gly	Asn	
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Gly	Ile	Ile	Phe	Pro	Ile	Ser	Leu	Thr	Ile	Cys	Asn	Tyr	Ser	Tyr	Lys	
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Asp	Asp	Ala	Asp	Tyr	Leu	Glu	Pro	Ser	Phe	Ala	Val	Gly	Lys	Ser	Pro	
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Ala	Glu	Gly	Tyr	Tyr	Ser	Tyr	Arg	Ile	Gly	Glu	Ile	Leu	Asp	Gly	Arg	
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Tyr	Glu	Val	Thr	Ala	Ala	His	Gly	Arg	Gly	Val	Phe	Ser	Thr	Val	Val	
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Arg	Gly	Lys	Asn	Leu	Lys	Met	Gly	Asn	Gly	Glu	Pro	Glu	Glu	Val	Ala	
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Ile	Lys	Ile	Ile	Arg	Ser	Asn	Asp	Thr	Met	Tyr	Lys	Ala	Gly	Met	Asp	
				645					650					655		
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Lys	Phe	Gly	Arg	Asn	Ile	Gly	Leu	Arg	Leu	Thr	Ala	Val	Arg	Ala	Tyr	
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Ala	Lys	Gln	Leu	Phe	Ile	Ala	Leu	Lys	His	Leu	Arg	Asn	Cys	Gly	Val	
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Leu His Cys Asp Ile Lys Pro Asp Asn Met Leu Val Asn Glu Ser Lys
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 755 760 765
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 770 775 780
 Ile Ile Leu Gly Leu Pro Tyr Asp His Pro Leu Asp Ile Trp Ser Val
 785 790 795 800
 Gly Cys Cys Leu Tyr Glu Leu Tyr Ile Gly Lys Val Leu Phe Pro Gly
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 835 840 845
 Asp Gln Asp Leu Asn Phe Leu Ala Thr Glu Glu Asp Pro Val Thr Lys
 850 855 860
 Lys Thr Ile Lys Arg Leu Ile Leu Asn Ile Lys Pro Lys Asp Ile Gly
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 <212> PRT
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<400> 18

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Ser	Gln	Arg	Val	Pro	Lys	Ser	Pro	Leu	Leu	Thr	Arg	Glu	Lys	Glu	Arg
	50				55					60					
Lys	His	Lys	Asp	Glu	His	Arg	Lys	Ser	Tyr	Pro	Lys	Asp	Ser	His	Ser
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Thr	Glu	Arg	Ser	Ser	Ser	Tyr	Ala	Val	Arg	Asp	Glu	Ala	Tyr	Asp	Glu
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Arg	Glu	Arg	Tyr	Lys	His	Glu	Arg	Arg	His	Arg	Ser	Asn	Pro	Val	Asp
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Ser	Ser	Ser	Arg	Ser	Arg	Ser	Asp	Arg	Arg	Glu	Ser	Ala	His	His	Ile
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Gln	Leu	Gln	Lys	Gln	Gln	Leu	Glu	Ser	Leu	Pro	Arg	Ser	Asn	Asp	Glu	
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Lys	Leu	Gly	Lys	Asp	Asp	Gly	Leu	Arg	Ile	Glu	Lys	Asn	Ala	Leu	His	
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Leu	Leu	Asp	Gly	Arg	Tyr	Glu	Ile	Thr	Ala	Ala	His	Gly	Lys	Gly	Val	
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Phe	Ser	Thr	Val	Val	Arg	Ala	Lys	Asp	Leu	Lys	Ala	Gly	Lys	Asp	Asp	
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Pro	Glu	Glu	Val	Ala	Ile	Lys	Ile	Ile	Arg	Asn	Asn	Glu	Thr	Met	Tyr	
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Lys	Ala	Gly	Lys	Gln	Glu	Val	Ser	Ile	Leu	Glu	Lys	Leu	Ala	Ser	Ala	
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Asp	Arg	Glu	Asp	Arg	Arg	His	Cys	Val	Arg	Phe	Ile	Ser	Ser	Phe	Met	
			580					585					590			
Tyr	Arg	Asn	His	Leu	Cys	Leu	Val	Phe	Glu	Ser	Leu	Asn	Met	Asn	Leu	
		595					600					605				
Arg	Glu	Val	Leu	Lys	Lys	Phe	Gly	Arg	Asn	Ile	Gly	Leu	Lys	Leu	Thr	
	610					615					620					
Ala	Val	Arg	Ala	Tyr	Ser	Lys	Gln	Leu	Phe	Ile	Ala	Leu	Lys	His	Leu	
625					630					635					640	
Lys	Asn	Cys	Lys	Val	Leu	His	Cys	Asp	Ile	Lys	Pro	Asp	Asn	Met	Leu	
				645					650					655		
Val	Asn	Glu	Ala	Lys	Asn	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Asn	Ala	
			660					665					670			
Met	Leu	Ala	Gly	Met	Asn	Glu	Val	Thr	Pro	Tyr	Leu	Val	Ser	Arg	Phe	
		675					680						685			

Tyr Arg Ala Pro Glu Ile Ile Leu Gly Leu Pro Tyr Asp His Pro Leu
 690 695 700
 Asp Met Trp Ser Val Gly Cys Cys Leu Tyr Glu Leu Tyr Thr Gly Lys
 705 710 715 720
 Val Leu Phe Pro Gly Pro Ser Asn Asn Asp Met Leu Arg Leu His Met
 725 730 735
 Glu Leu Lys Gly Pro Phe Pro Lys Lys Met Leu Arg Lys Gly Ala Phe
 740 745 750
 Thr Met Gln His Phe Asp Gln Asp Leu Asn Phe His Ala Thr Glu Glu
 755 760 765
 Asp Pro Val Thr Lys Lys Ala Val Thr Arg Met Ile Leu Asn Ile Lys
 770 775 780
 Pro Lys Asp Ile Gly Ser Leu Ile Ser Asn Phe Pro Gly Glu Asp Pro
 785 790 795 800
 Lys Met Leu Ser Asn Phe Lys Asp Leu Leu Glu Lys Ile Phe Val Leu
 805 810 815
 Asp Pro Glu Lys Arg Ile Thr Ile Ser Gln Ala Leu Ser His Pro Phe
 820 825 830
 Ile Thr Gly Lys
 835

<210> 19
 <211> 1134
 <212> DNA
 <213> gossypium hirsutum

<400> 19
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 aaaggagttt tttcaacggt tgtacgtgcg aaggatctta aggctggtgc tactgggggg 180
 gaagaagtag ctataaagat cattcgtaat aatgaaacga tgcacaaggc tggtcagctg 240
 gaggttcaaa tattgaaaaa attagcaggt gcagatccag atgataagcg acattgtgtt 300
 cgttttttgt caagtttcaa gtacaggaat catctttgtt tagtttttga gtctcttcat 360
 atgaatctgc gtgaagttct caagaagttt ggtagcaata ttggtcttaa actaactgct 420
 gtcagggctt atgctaagca actttttatt gcgcttaagc atctaaaaaa ctgtggtgtt 480
 cttcattgtg atataaagcc tgataacatg ctggtaaagt aggcaaaaaa tgtgctgaag 540
 ctttgtgatt ttggtaatgc catgtttgct ggtaaaaatg aaattacacc ataccttgtt 600
 agccgctttt atcgtgcacc agaaattatt cttggtttgc cttacgatca tccaatggat 660
 atctggtctg ttggttgctg tttgtatgag ctatatactg gaaaagttct tttccctggt 720
 ccaacaaaca atgacatgct acgtcttcat atggaactca aaggtccttt tccaaagaag 780
 atgttgcgta agggagcatt tacagaacaa cactttgatc aagatctgaa ttttcatgct 840
 acagaagagg atcctgttac taaaaagagt ataaagagga tgattcttaa cataaagcca 900
 aaagatatca gttcaattat tgttggtctc ccaggtagg atccaaagat ggtagccaac 960
 ttcaaagacc ttctagaaaa aatttttgtg cttgatccag agaagagaat gacagttact 1020
 caggcattgg ctcatccatt catcacgggc aagtggaaac atgttgctga ttttatgtct 1080
 ccagaaatgt gttgcgctag atatttgtac attatgaccc taactcatat ttag 1134

<210> 20
 <211> 377
 <212> PRT
 <213> gossypium hirsutum

<400> 20
 Gly Thr Arg Pro Val Ile Arg Ser Gly Leu His Asp Asn Trp Asp Asp
 1 5 10 15

Ala Glu Gly Tyr Tyr Ser Tyr Arg Phe Gly Glu Ile Leu Asp Gly Arg
 20 25 30
 Tyr Glu Val Thr Ala Ala His Gly Lys Gly Val Phe Ser Thr Val Val
 35 40 45
 Arg Ala Lys Asp Leu Lys Ala Gly Ala Thr Gly Gly Glu Glu Val Ala
 50 55 60
 Ile Lys Ile Ile Arg Asn Asn Glu Thr Met His Lys Ala Gly Gln Leu
 65 70 75 80
 Glu Val Gln Ile Leu Lys Lys Leu Ala Gly Ala Asp Pro Asp Asp Lys
 85 90 95
 Arg His Cys Val Arg Phe Leu Ser Ser Phe Lys Tyr Arg Asn His Leu
 100 105 110
 Cys Leu Val Phe Glu Ser Leu His Met Asn Leu Arg Glu Val Leu Lys
 115 120 125
 Lys Phe Gly Arg Asn Ile Gly Leu Lys Leu Thr Ala Val Arg Ala Tyr
 130 135 140
 Ala Lys Gln Leu Phe Ile Ala Leu Lys His Leu Lys Asn Cys Gly Val
 145 150 155 160
 Leu His Cys Asp Ile Lys Pro Asp Asn Met Leu Val Asn Glu Ala Lys
 165 170 175
 Asn Val Leu Lys Leu Cys Asp Phe Gly Asn Ala Met Phe Ala Gly Lys
 180 185 190
 Asn Glu Ile Thr Pro Tyr Leu Val Ser Arg Phe Tyr Arg Ala Pro Glu
 195 200 205
 Ile Ile Leu Gly Leu Pro Tyr Asp His Pro Met Asp Ile Trp Ser Val
 210 215 220
 Gly Cys Cys Leu Tyr Glu Leu Tyr Thr Gly Lys Val Leu Phe Pro Gly
 225 230 235 240
 Pro Thr Asn Asn Asp Met Leu Arg Leu His Met Glu Leu Lys Gly Pro
 245 250 255
 Phe Pro Lys Lys Met Leu Arg Lys Gly Ala Phe Thr Glu Gln His Phe
 260 265 270
 Asp Gln Asp Leu Asn Phe His Ala Thr Glu Glu Asp Pro Val Thr Lys
 275 280 285
 Lys Ser Ile Lys Arg Met Ile Leu Asn Ile Lys Pro Lys Asp Ile Ser
 290 295 300
 Ser Ile Ile Val Gly Ser Pro Gly Glu Asp Pro Lys Met Val Ala Asn
 305 310 315 320
 Phe Lys Asp Leu Leu Glu Lys Ile Phe Val Leu Asp Pro Glu Lys Arg
 325 330 335
 Met Thr Val Thr Gln Ala Leu Ala His Pro Phe Ile Thr Gly Lys Trp
 340 345 350
 Lys His Val Ala Asp Phe Met Ser Pro Glu Met Cys Cys Ala Arg Tyr
 355 360 365
 Leu Tyr Ile Met Thr Leu Thr His Ile
 370 375

<210> 21
 <211> 1413
 <212> DNA
 <213> Arabidopsis thaliana

<400> 21
 atggggttatc tctcttgcaa cggcgaatcc gccgtcgcaa tctgcgatac ttataactgg 60
 aatcctcgtc gacgatctaa agtaccggag aaacgtcatc ctctaaagct tcgggttttc 120
 aactacgacg aactcgccgt cgctactaac ggcttctccg ccaataactt cctcggaaaa 180

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ggaagtcacg gcagagttta caaagcagtt ctcgacgacg gaaagcttct cgccgccgtc 240
aagagaacaa caatcaccac taccgttggt aataacaata acaacgtgag tcaggtagac 300
aatgagatcg agattctttc acgggttcgt caccgttgga tgggtcaactt aatcggttac 360
tgcgttgacc accggaggaa aacaaagctg ttagtcgtcg agtacatgcc taacggtacg 420
cttcacgacg agttacattc tcgtagttcg ttagattcac ggttaagtag ttggaatcgg 480
agaattaaac acgcgcttca gatcgcgatt gctgtccacg ctcttcacac cgcagagact 540
caagtgatcc accgtgacat taaatcgtgt aacgttttaa tagacggtga cggtaacgct 600
aggttagctg atttcggatt agcattgatc ggaaacgttg acgatgagcg tttgaaatat 660
actccgccgg cgggtacggt gggatattta gatccgctcg acttagcacc ggccgacttg 720
acggctaaga gcgatgtttt cagctttggg atattgttgt tggagattat tagtggtaga 780
gaagccattg atttgaatta tagtccgctg tgtatcggtt attgggcggg gccgcttacc 840
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gtgattcggg agttggccgt tatggcggct aggtgtgtta gatcgacggc gaagaaacgt 960
ccagatatgt tagaggttgt tgagtgtttg aaaacgggtg ggcagttacc tccggcgtgg 1020
aataaactgc ggcggaggag tgaagagaga tcggaaaatg ttttggcggg tgaggaagag 1080
aaggaagaga ttcattgtgag gattgtgaga ggaggaagca ggaagaatcg gaaggtatcg 1140
aacgtgacga cgagtgtgga tgatgtttac gagagattag ttccggagga aacgctgccg 1200
tttcgctcgc ggaattttgt gctgagatcg agatcagtag gagcgaaagt tggaccggat 1260
ccatacgacg ggtttggtga tgagacgggt gttacaatga gattacttat tgagaaagaa 1320
agaccggtga cgacggcagc gatgaggctg agtaagtcca ggtcgggtggg gattgtacgt 1380
agtcataaaa cggcgtcgcg gaagagatac tga 1413

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<210> 22
<211> 470
<212> PRT
<213> Arabidopsis thaliana

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<400> 22
Met Gly Tyr Leu Ser Cys Asn Gly Glu Ser Ala Val Ala Ile Cys Asp
1          5          10          15
Thr Tyr Asn Trp Asn Pro Arg Arg Arg Ser Lys Val Pro Glu Lys Arg
          20          25          30
His Pro Pro Lys Leu Arg Val Phe Asn Tyr Asp Glu Leu Ala Val Ala
          35          40          45
Thr Asn Gly Phe Ser Ala Asn Asn Phe Leu Gly Lys Gly Ser His Gly
          50          55          60
Arg Val Tyr Lys Ala Val Leu Asp Asp Gly Lys Leu Leu Ala Ala Val
          65          70          75          80
Lys Arg Thr Thr Ile Thr Thr Thr Val Gly Asn Asn Asn Asn Asn Val
          85          90          95
Ser Gln Val Asp Asn Glu Ile Glu Ile Leu Ser Arg Val Arg His Arg
          100          105          110
Trp Met Val Asn Leu Ile Gly Tyr Cys Val Asp His Arg Arg Lys Thr
          115          120          125
Lys Leu Leu Val Val Glu Tyr Met Pro Asn Gly Thr Leu His Asp Gln
          130          135          140
Leu His Ser Arg Ser Ser Leu Asp Ser Arg Leu Ser Ser Trp Asn Arg
          145          150          155          160
Arg Ile Lys His Ala Leu Gln Ile Ala Ile Ala Val His Ala Leu His
          165          170          175
Thr Ala Glu Thr Gln Val Ile His Arg Asp Ile Lys Ser Cys Asn Val
          180          185          190
Leu Ile Asp Gly Asp Gly Asn Ala Arg Leu Ala Asp Phe Gly Leu Ala
          195          200          205
Leu Ile Gly Asn Val Asp Asp Glu Arg Leu Lys Tyr Thr Pro Pro Ala
          210          215          220

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Gly Thr Leu Gly Tyr Leu Asp Pro Ser Tyr Leu Ala Pro Ala Asp Leu
 225 230 235 240
 Thr Ala Lys Ser Asp Val Phe Ser Phe Gly Ile Leu Leu Leu Glu Ile
 245 250 255
 Ile Ser Gly Arg Glu Ala Ile Asp Leu Asn Tyr Ser Pro Ser Cys Ile
 260 265 270
 Val Asp Trp Ala Val Pro Leu Ile Lys Arg Gly Asp Tyr Asp Ala Ile
 275 280 285
 Cys Asp Leu Lys Ile Lys Asn Arg Pro Tyr Tyr Ala Val Ile Arg Lys
 290 295 300
 Leu Ala Val Met Ala Ala Arg Cys Val Arg Ser Thr Ala Lys Lys Arg
 305 310 315 320
 Pro Asp Met Leu Glu Val Val Glu Cys Leu Lys Thr Val Arg Gln Leu
 325 330 335
 Ser Pro Ala Trp Asn Lys Leu Arg Arg Arg Ser Glu Glu Arg Ser Glu
 340 345 350
 Asn Val Leu Ala Val Glu Glu Glu Lys Glu Glu Ile His Val Arg Ile
 355 360 365
 Val Arg Gly Gly Ser Arg Lys Asn Arg Lys Val Ser Asn Val Thr Thr
 370 375 380
 Ser Val Asp Asp Val Tyr Glu Arg Leu Val Pro Glu Glu Thr Leu Pro
 385 390 395 400
 Phe Arg Arg Arg Asn Phe Val Leu Arg Ser Arg Ser Val Gly Ala Lys
 405 410 415
 Val Gly Pro Asp Pro Tyr Asp Gly Phe Gly Asp Glu Thr Val Val Thr
 420 425 430
 Met Arg Leu Leu Ile Glu Lys Glu Arg Pro Val Thr Thr Ala Ala Met
 435 440 445
 Arg Leu Ser Lys Ser Arg Ser Val Gly Ile Val Arg Ser His Lys Thr
 450 455 460
 Ala Ser Arg Lys Arg Tyr
 465 470

<210> 23
 <211> 1830
 <212> DNA
 <213> zea mays

<400> 23
 atgggctacc tctcctgccg cgcggactcg tccgtggcga cgtgccgctc catcacggcc 60
 atctcgccgc tcccactctc gcgcgcgctcg gggtcggggg cggggggcgg ctcgctccagg 120
 cccccgctgc cgccggcgca ggccggccatc gagcgcttcg actacgcgga gctggaggcg 180
 gccacgtccc acttcgcgga cgcggcgctg ctgggcccgg gcagccacgg ggccgtctac 240
 aaggccgtgc tcccctcggg ccgcgcgcgtc gccgtcaagc gcccctcccc gcgcgcgccc 300
 gaggtggaca acgagatccg catcctctcc tccgtccggg gccgcgggct cgtcaacctc 360
 ctcggtttct ctgaccccgg ccccgcgccg cgcctgctcg tcgtcgagta catgcccac 420
 ggcaacgtct acgacctgct ccactccaac ccgcgcccgc cgggctggcc gcgcgcgctg 480
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 acgcccagaga gcctcagcac caagacagac gtcttcagct tcgggacct gctgctcgag 780
 atcatgagcg gccgcaaggc catcgacgtc cagcactcgc cgccgtccgt cgtcgagtgg 840
 gccgtccgcg tcttacggaa aggcaaggtc gcctcgctgt tcgacccgcg tgtggcgccg 900
 ccacgagacc cggtcacccg caaggacctt gccgcgctgg ccgccagctg tgtgcgctcc 960
 tgcagggagc ggcgcgccgtc catggccgac atcgtccagc gtctcgtgct tctcagcaaa 1020

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gccgtgtcgg ccaaggtgtg gaacgggctc gccgacgggc ttgccgtggt agggaaacct 1080
tgtgcggttg ttgatgttca gaagaccatc tccaagcgag gtgctgccag ccgcagggct 1140
gaatcagaga gggagtcgac ttcagcattg gtgtttgacg acgatgaaaa ggaggatgta 1200
gatgcagagg ccttgaggga agatcagggt ccatccaaca agtcaccacc ccgaccactg 1260
aagaacggga tagtgttttc cgaggcaggg gtcgaggaga ggagaaatct cttggacctg 1320
atggctcgga tcgatgggtg tgccggccaa agattcggca ttaccagagc aagaacagtg 1380
cgtgctaata gtgagctcat cgaaaaggat gcagtgttgc tctaaggag gaaccagacg 1440
gtaagagttg ttggatcaga ggcactgccg aagtctggaa ggatttctcg ctatgatgtg 1500
aagatcaaac acaaagcagg ggaagagcaa gaggagacag ggaaagccca agacaaagta 1560
gagaaaatcc aagttaatgc aagcgggatt caagaaagtt ccaaggaaat attaggcaag 1620
acagataaat tgttggatgc actggagcca aaccttgaca aagaagagaa ggttcaagaa 1680
aaggaagagc aacacctcga tgaagtggat aatgttcaag agaatgaagg caaagtccaa 1740
tgcccggcag agaaaatcca ggaaggtgga gaagtccaat gccccgggca gagaaaatcc 1800
aggaaagtgc aggattctga gacaaagtag                                     1830

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<210> 24
<211> 609
<212> PRT
<213> zea mays

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<400> 24
Met Gly Tyr Leu Ser Cys Arg Ala Asp Ser Ser Val Ala Thr Cys Arg
1          5          10          15
Ser Ile Thr Ala Ile Ser Pro Leu Pro Leu Ser Arg Arg Ser Gly Ser
          20          25          30
Gly Ser Gly Gly Gly Ser Ser Arg Pro Pro Leu Pro Pro Ala Gln Ala
          35          40          45
Ala Ile Glu Arg Phe Asp Tyr Ala Glu Leu Glu Ala Ala Thr Ser His
          50          55          60
Phe Ala Asp Ala Ala Leu Leu Gly Arg Gly Ser His Gly Ala Val Tyr
65          70          75          80
Lys Ala Val Leu Pro Ser Gly Arg Ala Val Ala Val Lys Arg Pro Ser
          85          90          95
Pro Arg Arg Pro Glu Val Asp Asn Glu Ile Arg Ile Leu Ser Ser Val
          100         105         110
Arg Gly Pro Arg Leu Val Asn Leu Leu Gly Phe Ser Asp Pro Gly Pro
          115         120         125
Ala Pro Arg Leu Leu Val Val Glu Tyr Met Pro Asn Gly Thr Leu Tyr
          130         135         140
Asp Leu Leu His Ser Asn Pro Arg Pro Pro Gly Trp Pro Arg Arg Leu
145         150         155         160
Arg Leu Ala Leu Gln Thr Ala Arg Ala Leu Arg Ala Leu His Asp Ala
          165         170         175
Asp Pro Pro Val Ile His Arg Asp Val Lys Ser Ala Asn Val Leu Leu
          180         185         190
Asp Ala Asn Leu Gly Ala Arg Leu Gly Asp Phe Gly Leu Ala Leu Arg
          195         200         205
Val Pro Lys Ala Thr Ala Gly Ala Asn Ala Ala Ala Ala Ala Ala Pro
          210         215         220
Thr Pro Pro Pro Ala Gly Thr Leu Gly Tyr Leu Asp Pro Ala Tyr Val
225         230         235         240
Thr Pro Glu Ser Leu Ser Thr Lys Thr Asp Val Phe Ser Phe Gly Ile
          245         250         255
Leu Leu Leu Glu Ile Met Ser Gly Arg Lys Ala Ile Asp Val Gln His
          260         265         270

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Ser Pro Pro Ser Val Val Glu Trp Ala Val Pro Leu Leu Arg Lys Gly
 275 280 285
 Lys Val Ala Ser Leu Phe Asp Pro Arg Val Ala Pro Pro Arg Asp Pro
 290 295 300
 Val Thr Arg Lys Asp Leu Ala Ala Leu Ala Ala Ser Cys Val Arg Ser
 305 310 315 320
 Cys Arg Glu Arg Arg Pro Ser Met Ala Asp Ile Val Gln Arg Leu Val
 325 330 335
 Leu Leu Ser Lys Ala Val Ser Ala Lys Val Trp Asn Gly Leu Ala Asp
 340 345 350
 Gly Leu Ala Val Val Gly Asn Pro Cys Ala Val Val Asp Val Gln Lys
 355 360 365
 Thr Ile Ser Lys Arg Gly Ala Ala Ser Arg Arg Ala Glu Ser Glu Arg
 370 375 380
 Glu Ser Thr Ser Ala Leu Val Phe Asp Asp Asp Glu Lys Glu Asp Val
 385 390 395 400
 Asp Ala Glu Ala Leu Glu Glu Asp Gln Val Pro Ser Asn Lys Ser Pro
 405 410 415
 Pro Arg Pro Leu Lys Asn Gly Ile Val Phe Ser Glu Ala Gly Ala Arg
 420 425 430
 Glu Arg Arg Asn Leu Leu Asp Leu Met Ala Arg Ile Asp Gly Val Ala
 435 440 445
 Gly Gln Arg Phe Gly Ile Thr Arg Ala Arg Thr Val Arg Ala Asn Gly
 450 455 460
 Glu Leu Ile Glu Lys Asp Ala Val Leu Leu Leu Arg Arg Asn Gln Thr
 465 470 475 480
 Val Arg Val Val Gly Ser Glu Ala Leu Pro Lys Ser Gly Arg Ile Ser
 485 490 495
 Arg Tyr Asp Val Lys Ile Lys His Lys Ala Gly Glu Glu Gln Glu Glu
 500 505 510
 Thr Gly Lys Ala Gln Asp Lys Val Glu Lys Ile Gln Val Asn Ala Ser
 515 520 525
 Gly Ile Gln Glu Ser Ser Lys Glu Ile Leu Gly Lys Thr Asp Lys Leu
 530 535 540
 Leu Asp Ala Leu Glu Pro Asn Leu Asp Lys Glu Glu Lys Val Gln Glu
 545 550 555 560
 Lys Glu Glu Gln His Leu Asp Glu Val Asp Asn Val Gln Glu Asn Glu
 565 570 575
 Gly Lys Val Gln Cys Pro Ala Glu Lys Ile Gln Glu Gly Gly Glu Val
 580 585 590
 Gln Cys Pro Arg Gln Arg Lys Ser Arg Lys Val Glu Asp Ser Glu Thr
 595 600 605
 Lys

<210> 25
 <211> 1287
 <212> DNA
 <213> glycine max

<220>
 <221> misc_feature
 <222> (747)..(747)
 <223> n is a, c, g, or t

<400> 25
 atgccctacc tcacttgcaa cgccgagtcc gcaatagcca catgcgaccc tcactccctc

60

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aagaagaaga aaaagcccaa aagcccagcc caggcccagc ccggtgcgaca cttegcctac 120
tccgacatcc tgcacgccac caacaacttc tctgccgaca ccttcctagg taaaggcagc 180
cacggcacag tctacaaggc cgccttccac ggcggcgctc tcgtcgccgc cgtcaaaata 240
accaaaccce aaacctcaaa cgaaatcgaa attctctccc acctcaaaaa aaaccctcgt 300
cttggttaacc taattggctt ctgcaacgac caaacccaaa ctaacaacat taacaacaac 360
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<210> 26
<211> 428
<212> PRT
<213> glycine max

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<400> 26
Met Pro Tyr Leu Thr Cys Asn Ala Glu Ser Ala Ile Ala Thr Cys Asp
1          5          10          15
Pro His Ser Leu Lys Lys Lys Lys Lys Pro Lys Ser Pro Ala Gln Ala
20          25          30
Gln Pro Val Arg His Phe Ala Tyr Ser Asp Ile Leu Asp Ala Thr Asn
35          40          45
Asn Phe Ser Ala Asp Thr Phe Leu Gly Lys Gly Ser His Gly Thr Val
50          55          60
Tyr Lys Ala Ala Phe His Gly Gly Ala Leu Val Ala Ala Val Lys Ile
65          70          75          80
Thr Lys Pro Lys Thr Ser Asn Glu Ile Glu Ile Leu Ser His Leu Lys
85          90          95
Lys Asn Pro Arg Leu Val Asn Leu Ile Gly Phe Cys Asn Asp Gln Thr
100          105          110
Gln Thr Asn Asn Ile Asn Asn Asn Lys Leu Ile Val Val Glu Tyr Met
115          120          125
Pro Asn Gly Ser Leu His Glu Leu Leu His Ser Thr Lys Lys Pro Val
130          135          140
Arg Pro Pro Ser Trp Thr Ala Arg Val Arg Phe Ala Val Gln Val Ala
145          150          155          160
Lys Ala Val Arg Leu Leu His Ser Ser Glu Pro Pro Val Ile His Arg
165          170          175
Asp Ile Lys Ser Ser Asn Val Leu Ile Asp Glu Lys Trp Asn Ala Arg
180          185          190
Leu Gly Asp Phe Gly Leu Ala Val Arg Gly His Val Ala Asp Ser Arg
195          200          205
Val Pro Pro Ala Gly Thr Leu Gly Tyr Leu Asp Pro Cys Tyr Leu Ala
210          215          220

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Pro Gly Asp Leu Ser Ser Lys Ser Asp Val Phe Ser Phe Gly Val Leu
 225 230 235 240
 Leu Leu Glu Ile Ala Ser Gly Arg His Ala Leu Asp Val Arg His Ser
 245 250 255
 Pro Pro Ser Val Leu Asp Trp Ala Val Pro Leu Val Arg Arg Gly Glu
 260 265 270
 Phe Lys Glu Ile Cys Asp Pro Arg Ile Gly Ala Pro Pro Asp Met Ala
 275 280 285
 Ala Phe Arg Arg Met Ala Val Leu Ala Ala Arg Cys Val Arg Ser Thr
 290 295 300
 Pro Glu Arg Arg Pro Ser Met Val Glu Val Leu Glu Cys Leu Thr Ala
 305 310 315 320
 Val Arg Lys Cys Phe Arg Ala Pro Val Met Trp Lys Arg Ile Lys Arg
 325 330 335
 Arg Val Glu Ile Ala Arg Gly Asp Leu Phe His Asp Trp Asp Arg Ser
 340 345 350
 Glu Glu Val Val Arg Val Val Lys Leu Gly Ser Ser Ser Ser Arg Arg
 355 360 365
 Asn Gly Lys Val Ser Ser Val Ser Gly Val Glu Tyr Glu Gly Gly His
 370 375 380
 Ala Asn Pro Ala Val Arg Ser Arg Ser Val Gly Ser Gly Ser Gly Leu
 385 390 395 400
 Val Gly Phe Gly Phe Lys Asn Arg Lys Gly Lys Val Arg Leu Lys Arg
 405 410 415
 Ser Arg Ser Met Gly Ser Pro Val Pro Leu Arg Trp
 420 425

<210> 27
 <211> 2040
 <212> DNA
 <213> oryza sativa

<400> 27
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 atatcgccgc tgccgctgtc gcggcggtcg ggggtcggcg gcaggcggcg cgcgctgccg 120
 gcggcggcga gggaggggga tgggtggggag gcgtcgctcg ccgccgccac catcgagcgg 180
 ttcgcgtacg acgaactgga ggcggcgacc tcccacttcg cggacgcggc gctgctcggg 240
 aggggcagcc acggggcggt gtacaaggcg gtgctcgctt ccggcgcgcg cgtcgccgtc 300
 aagcgcccct ccccgcgccg ccccgagggtg gacaacgaga tccgcatcct ctctccgtc 360
 cgcgggccgc gcctcgtaaa cctcctcggc ttctccgact ccggcgccgg cgccggcgcc 420
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 ctcgcgctcc agacggcgcg cgcgtccgc gcgctccacg acgccgatcc ccccgctcatc 600
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 gacttcggcc tagccctccg cgtgcccaag cggctacccg gcgacgcgcg cgccaatgcc 720
 gccgccacgc cggcgccggc gggcacgctc gggtaacctg acccggccta cgtcacgccg 780
 gagagcctca gcaccaagac cgacgtcttc agcttcggga tctgtctgct cgagatcatg 840
 agcggccgca aggccatcga cgtccagcac tcgccgccgt cgggtggtgga gtgggcgggtg 900
 cccctgctgc ggaaggggaa ggtggcctcg ctgttcgacc cacgggtggc gccgccgcgt 960
 gacccggtca cccggagaga cctagccgct ctggcggcga gctgcgtgcg gtcgtgcagg 1020
 gagcggcggc cgtcgatggc cgacatagtt gatcggttg tggttctcag caaggccgtg 1080
 tcggggcaaaa tgtggaacgg actcgccgtg gttgggaacc cctgcgctgt cgtggatgtc 1140
 cagaagacca tcgcgaagcg agctgctgct gctgctgcag gcgatagagc cgcgtcgcag 1200
 cgggagctga cttcggcatt ggcatttgat gatgatgaga agaaagagga ggaggatgcg 1260
 ccgaatgcag gtgcgttaga ggaggatgag gtgccattgg tgggtgcgaa gaaagcacc 1320
 cggccattga agaattggaa gatgttctct gagccagggg caaggagag gagaaatctc 1380

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agaaatcaaa ctgtgaaagt acttggtatcg gaggcctttt ctaaagctga tatcttttca 1560
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atccaagaaa aacttgggga aatctttgat aaagcaatga aatctgaaga aaagacaggg 1920
caaaatcctg gcatagaaaa gaaaatccaa gacacggcag agaagaaaca agagcatgat 1980
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<210> 28
<211> 679
<212> PRT
<213> oryza sativa

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<400> 28
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20     25     30
Gly Gly Arg Arg Arg Ala Leu Pro Ala Ala Ala Arg Glu Gly Asp Gly
35     40     45
Gly Glu Ala Ser Ser Ala Ala Ala Thr Ile Glu Arg Phe Ala Tyr Asp
50     55     60
Glu Leu Glu Ala Ala Thr Ser His Phe Ala Asp Ala Ala Leu Leu Gly
65     70     75     80
Arg Gly Ser His Gly Ala Val Tyr Lys Ala Val Leu Ala Ser Gly Arg
85     90     95
Ala Val Ala Val Lys Arg Pro Ser Pro Arg Arg Pro Glu Val Asp Asn
100    105    110
Glu Ile Arg Ile Leu Ser Ser Val Arg Gly Pro Arg Leu Val Asn Leu
115    120    125
Leu Gly Phe Ser Asp Ser Gly Ala Gly Ala Gly Ala Asp Gln Gln Gln
130    135    140
Gln Gln His Arg Pro Arg Leu Leu Val Val Glu Tyr Met Pro Asn Gly
145    150    155    160
Thr Leu Tyr Glu Leu Leu His Ser Asn Pro Arg Pro Pro Gly Trp Pro
165    170    175
Arg Arg Val Arg Leu Ala Leu Gln Thr Ala Arg Ala Leu Arg Ala Leu
180    185    190
His Asp Ala Asp Pro Pro Val Ile His Arg Asp Val Lys Ser Ala Asn
195    200    205
Val Leu Leu Asp Ala Asn Leu Asp Ala Arg Leu Gly Asp Phe Gly Leu
210    215    220
Ala Leu Arg Val Pro Lys Arg Leu Pro Gly Asp Ala Ala Ala Asn Ala
225    230    235    240
Ala Ala Thr Pro Ala Pro Ala Gly Thr Leu Gly Tyr Leu Asp Pro Ala
245    250    255
Tyr Val Thr Pro Glu Ser Leu Ser Thr Lys Thr Asp Val Phe Ser Phe
260    265    270
Gly Ile Leu Leu Leu Glu Ile Met Ser Gly Arg Lys Ala Ile Asp Val
275    280    285
Gln His Ser Pro Pro Ser Val Val Glu Trp Ala Val Pro Leu Leu Arg
290    295    300

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Lys Gly Lys Val Ala Ser Leu Phe Asp Pro Arg Val Ala Pro Pro Arg
 305 310 315 320
 Asp Pro Val Thr Arg Arg Asp Leu Ala Ala Leu Ala Ala Ser Cys Val
 325 330 335
 Arg Ser Cys Arg Glu Arg Arg Pro Ser Met Ala Asp Ile Val Asp Arg
 340 345 350
 Leu Val Val Leu Ser Lys Ala Val Ser Gly Lys Met Trp Asn Gly Leu
 355 360 365
 Ala Val Val Gly Asn Pro Cys Ala Val Val Asp Val Gln Lys Thr Ile
 370 375 380
 Ala Lys Arg Ala Ala Ala Ala Ala Gly Asp Arg Ala Ala Ser Gln
 385 390 395 400
 Arg Glu Leu Thr Ser Ala Leu Ala Phe Asp Asp Asp Glu Lys Lys Glu
 405 410 415
 Glu Glu Asp Ala Pro Asn Ala Gly Ala Leu Glu Glu Asp Glu Val Pro
 420 425 430
 Leu Val Gly Ala Lys Lys Ala Pro Arg Pro Leu Lys Asn Gly Lys Met
 435 440 445
 Phe Ser Glu Pro Gly Ala Arg Glu Arg Arg Asn Leu Leu Glu Leu Met
 450 455 460
 Ala Arg Ile Asp Gly Val Ala Gly Gln Arg Phe Gly Ile Thr Arg Ala
 465 470 475 480
 Arg Thr Val Arg Ala Ala Ser Glu Ser Ile Glu Lys Asp Ala Ala Val
 485 490 495
 Leu Leu Leu Arg Arg Asn Gln Thr Val Lys Val Leu Gly Ser Glu Ala
 500 505 510
 Leu Ser Lys Ala Asp Ile Phe Ser Ser Leu Asp Ala Lys Ile Lys His
 515 520 525
 Glu Leu Gly Lys Glu Gln Gln Glu Glu Ala Gly Lys Ile Lys His Glu
 530 535 540
 Leu Val Lys Glu Gln Gln Glu Lys Ala Gly Asn Ile Lys Gln Glu Leu
 545 550 555 560
 Val Lys Glu Gln Gln Glu Lys Ala Gly Asn Ile Lys Gln Glu Ser Gly
 565 570 575
 Glu Glu Gln Glu Lys Ala Gly Lys Thr Lys His Asp Ala Gly Lys Gly
 580 585 590
 His Val Glu Lys Ala Val Gly Ile Asn Leu Glu Ala Gly Lys Glu Gln
 595 600 605
 Glu Lys Val Glu Lys Asn Gln Glu Lys Glu Met Lys Ile Gln Glu Lys
 610 615 620
 Leu Gly Glu Ile Phe Asp Lys Ala Met Lys Ser Glu Glu Lys Thr Gly
 625 630 635 640
 Gln Asn Pro Gly Ile Glu Lys Lys Ile Gln Asp Thr Ala Glu Lys Lys
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 Gln Glu His Asp Ala Arg Val Val Gln Asp Lys Val Glu Lys Ile Gln
 660 665 670
 Asp Glu Ala Lys Lys Ile Gln
 675

<210> 29
 <211> 1235
 <212> DNA
 <213> gossypium hirsutum

<400> 29
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60

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gatcttctta ccgccaccaa tggcttctct tccgatagct tctcggtaa aggtagtcac 180
ggttccgtct acaaagccgt acttgacgat ggcaagttaa tcaccgccgt taagaaaacg 240
tcaaagaact gtaacagtcc tgccgacaac gagatcgaga ttctttcccg agttgatcat 300
cctcgactcg ttaatctcat cggttactgc tccgattcgc tttgtaagaa taaattaatc 360
gtcgtggaat atatgcccac cggttcattg tacgatcttt tacattcttc ttcttgtaaa 420
ccgccggggt ggtccagccg ggttcgattc gctttacagg tagcaaaagc ggttcaagct 480
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gatcaaaggt ggaacgctcg attgggtgat ttcgggcttg cattgatagg acacgtggag 600
gatgtacgga ttaagtgcac cccaccggcg gggacgttag gatattctga cccgagttat 660
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gagattatta gcgggaggca tgctattgat ttgaagtata gtccgccgtc agttgttgac 780
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<210> 30
<211> 411
<212> PRT
<213> gossypium hirsutum

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

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Asp	Val	Ser	Thr	Lys	Ser	Asp	Val	Phe	Ser	Tyr	Gly	Ile	Leu	Leu	Leu	225	230	235	240
Glu	Ile	Ile	Ser	Gly	Arg	His	Ala	Ile	Asp	Leu	Lys	Tyr	Ser	Pro	Pro	245	250	255	
Ser	Val	Val	Asp	Trp	Ala	Val	Pro	Leu	Ile	Lys	Lys	Gly	Asn	Ile	Val	260	265	270	
Ala	Val	Tyr	Asp	Pro	Arg	Ile	Leu	Pro	Pro	Lys	Asp	Pro	Ile	Val	Arg	275	280	285	
Lys	Gln	Leu	Ala	Val	Ile	Ala	Ala	Lys	Cys	Val	Arg	Ser	Cys	Arg	Glu	290	295	300	
Arg	Arg	Pro	Ala	Met	Lys	Glu	Val	Val	Gly	Trp	Leu	Thr	Gly	Leu	Ser	305	310	315	320
Lys	Leu	Val	Pro	Leu	His	Ser	Trp	Asn	Gly	Phe	Ser	Asn	Pro	Cys	Met	325	330	335	
Met	Val	Glu	Thr	Val	Gly	Arg	Pro	Val	Asp	Phe	Arg	Asn	Ala	Gln	Glu	340	345	350	
Asn	Leu	Asp	Ala	Val	His	Gly	Thr	Leu	Ala	Ala	Lys	Asp	Ser	Arg	Arg	355	360	365	
Ala	Tyr	Ser	Asp	Leu	Gly	Phe	Arg	Ser	Asn	Leu	Met	Glu	Leu	Met	Gly	370	375	380	
Ile	Thr	Ser	Ile	Asp	Gly	Glu	Ala	Lys	Ala	Ser	Ser	Ser	His	Arg	Phe	385	390	395	400
Gly	Asn	Lys	Ser	Tyr	Gly	Asn	Leu	Cys	Leu	Val						405	410		

<210> 31
 <211> 2025
 <212> DNA
 <213> Arabidopsis thaliana

<400> 31
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 aagtcttcac tacaaggaaa cagtggagagc ttactgttgt cttcttggaa ctccctctgtt 180
 cctgtttgtc aatggagagg tgtaaaatgg gtattttcaa atgggtctcc tcttcaatgt 240
 agtgacctct cttcaccaca atggactaat acctctctgt tcaacgactc ttctcttcac 300
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 aggttttaaag gtgtgaagtc acttgatctt tcaagtaatg tctttgaagg tcttgttcct 720
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 caaggtggtg agaactctgac gttggatgat gttttgaatg ctactgggca agttatggag 1140
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 gaaagtaaac ctcgaaagcc agctttgaat tgggctagga gacacaagat tgcacttgga 1440
 atagcgaggg gacttgctta tcttcatact ggacaagaag ttcctatcat ccatggaaat 1500

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attagatcaa agaacgtgct tgtggacgac tttttctttg caaggctaac tgagtttggg 1560
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gggtacaaag cacctgaact ccacaagatg aagaaatgca atccaaggag tgatgtttac 1680
gcctttggga tccttctctt ggagatattg atgggtaaga aaccaggaaa gagtggaagg 1740
aacggtaatg agtttgtgga cttgccttct ttggtttaaag ctgcggtgtt ggaagagacg 1800
acaatggagg ttttcgactt ggaggcaatg aaagggatta ggagcccaat ggaagaagg 1860
ttggttcatg cattgaagct agcgatggga tgttgtgctc ctgttacaac agttagaccc 1920
agcatggaag aggttgtgaa gcagttggaa gagaacagac cgaggaatag atccgcattg 1980
tacagcccaa ccgaaaccag gagcgacgcc gaaactccat ttgga 2025

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<210> 32
<211> 674
<212> PRT
<213> Arabidopsis thaliana

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<400> 32
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Leu Ile Leu His Cys His Cys Gly Thr Ser Leu Ser Gly Ser Ser Asp
20          25          30
Val Lys Leu Leu Leu Gly Lys Ile Lys Ser Ser Leu Gln Gly Asn Ser
35          40          45
Glu Ser Leu Leu Leu Ser Ser Trp Asn Ser Ser Val Pro Val Cys Gln
50          55          60
Trp Arg Gly Val Lys Trp Val Phe Ser Asn Gly Ser Pro Leu Gln Cys
65          70          75          80
Ser Asp Leu Ser Ser Pro Gln Trp Thr Asn Thr Ser Leu Phe Asn Asp
85          90          95
Ser Ser Leu His Leu Leu Ser Leu Gln Leu Pro Ser Ala Asn Leu Thr
100         105         110
Gly Ser Leu Pro Arg Glu Ile Gly Glu Phe Ser Met Leu Gln Ser Val
115         120         125
Phe Leu Asn Ile Asn Ser Leu Ser Gly Ser Ile Pro Leu Glu Leu Gly
130         135         140
Tyr Thr Ser Ser Leu Ser Asp Val Asp Leu Ser Gly Asn Ala Leu Ala
145         150         155         160
Gly Val Leu Pro Pro Ser Ile Trp Asn Leu Cys Asp Lys Leu Val Ser
165         170         175
Phe Lys Ile His Gly Asn Asn Leu Ser Gly Val Leu Pro Glu Pro Ala
180         185         190
Leu Pro Asn Ser Thr Cys Gly Asn Leu Gln Val Leu Asp Leu Gly Gly
195         200         205
Asn Lys Phe Ser Gly Glu Phe Pro Glu Phe Ile Thr Arg Phe Lys Gly
210         215         220
Val Lys Ser Leu Asp Leu Ser Ser Asn Val Phe Glu Gly Leu Val Pro
225         230         235         240
Glu Gly Leu Gly Val Leu Glu Leu Glu Ser Leu Asn Leu Ser His Asn
245         250         255
Asn Phe Ser Gly Met Leu Pro Asp Phe Gly Glu Ser Lys Phe Gly Ala
260         265         270
Glu Ser Phe Glu Gly Asn Ser Pro Ser Leu Cys Gly Leu Pro Leu Lys
275         280         285
Pro Cys Leu Gly Ser Ser Arg Leu Ser Pro Gly Ala Val Ala Gly Leu
290         295         300
Val Ile Gly Leu Met Ser Gly Ala Val Val Val Ala Ser Leu Leu Ile
305         310         315         320

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Gly Tyr Leu Gln Asn Lys Lys Arg Lys Ser Ser Ile Glu Ser Glu Asp
 325 330 335
 Asp Leu Glu Glu Gly Asp Glu Glu Asp Glu Ile Gly Glu Lys Glu Gly
 340 345 350
 Gly Glu Gly Lys Leu Val Val Phe Gln Gly Gly Glu Asn Leu Thr Leu
 355 360 365
 Asp Asp Val Leu Asn Ala Thr Gly Gln Val Met Glu Lys Thr Ser Tyr
 370 375 380
 Gly Thr Val Tyr Lys Ala Lys Leu Ser Asp Gly Gly Asn Ile Ala Leu
 385 390 395 400
 Arg Leu Leu Arg Glu Gly Thr Cys Lys Asp Arg Ser Ser Cys Leu Pro
 405 410 415
 Val Ile Arg Gln Leu Gly Arg Ile Arg His Glu Asn Leu Val Pro Leu
 420 425 430
 Arg Ala Phe Tyr Gln Gly Lys Arg Gly Glu Lys Leu Leu Ile Tyr Asp
 435 440 445
 Tyr Leu Pro Asn Ile Ser Leu His Asp Leu Leu His Glu Ser Lys Pro
 450 455 460
 Arg Lys Pro Ala Leu Asn Trp Ala Arg Arg His Lys Ile Ala Leu Gly
 465 470 475 480
 Ile Ala Arg Gly Leu Ala Tyr Leu His Thr Gly Gln Glu Val Pro Ile
 485 490 495
 Ile His Gly Asn Ile Arg Ser Lys Asn Val Leu Val Asp Asp Phe Phe
 500 505 510
 Phe Ala Arg Leu Thr Glu Phe Gly Leu Asp Lys Ile Met Val Gln Ala
 515 520 525
 Val Ala Asp Glu Ile Val Ser Gln Ala Lys Ser Asp Gly Tyr Lys Ala
 530 535 540
 Pro Glu Leu His Lys Met Lys Lys Cys Asn Pro Arg Ser Asp Val Tyr
 545 550 555 560
 Ala Phe Gly Ile Leu Leu Leu Glu Ile Leu Met Gly Lys Lys Pro Gly
 565 570 575
 Lys Ser Gly Arg Asn Gly Asn Glu Phe Val Asp Leu Pro Ser Leu Val
 580 585 590
 Lys Ala Ala Val Leu Glu Glu Thr Thr Met Glu Val Phe Asp Leu Glu
 595 600 605
 Ala Met Lys Gly Ile Arg Ser Pro Met Glu Glu Gly Leu Val His Ala
 610 615 620
 Leu Lys Leu Ala Met Gly Cys Cys Ala Pro Val Thr Thr Val Arg Pro
 625 630 635 640
 Ser Met Glu Glu Val Val Lys Gln Leu Glu Glu Asn Arg Pro Arg Asn
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 Arg Ser Ala Leu Tyr Ser Pro Thr Glu Thr Arg Ser Asp Ala Glu Thr
 660 665 670
 Pro Phe

<210> 33
 <211> 2037
 <212> DNA
 <213> zea mays

<400> 33
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gtgcaggcgc	tgaagctggc	gatgggctgc	tgcgcgccgg	tgccagcggc	gaggccgagc	1920
atggcggagg	tggtgcggca	gctggaggag	agccggccca	agaacgtcca	cccgcggtct	1980
gcgctgtaca	gccctacgga	gagcaggagc	gacgcgggca	cgcgcgaccac	cgcctag	2037

<210> 34
 <211> 678
 <212> PRT
 <213> zea mays

<400> 34
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 1 5 10 15
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 20 25 30
 Val Lys Pro Ala Leu Gln Gly Glu Arg Ala Asn Ala Gln Leu Ala Thr
 35 40 45
 Trp Asn Ala Ser Thr Pro Leu Cys Leu Trp Arg Gly Leu Arg Trp Ala
 50 55 60
 Thr Pro Asp Gly Arg Pro Leu Arg Cys Asp Ala Ala Ala Thr Arg Ala
 65 70 75 80
 Asn Leu Ser Leu Ala Ser Asp Pro Ala Leu Leu Leu Leu Ser Val Arg
 85 90 95
 Leu Pro Ala Ser Ala Leu Ala Gly Arg Leu Pro Pro Asp Leu Gly Ala
 100 105 110
 Phe Ser Ala Leu Asp Ser Val Tyr Leu Ala Ala Asn Ser Leu Ser Gly
 115 120 125
 Pro Val Pro Leu Glu Leu Gly Asn Ala Pro Ala Leu Ser Ala Leu Asp
 130 135 140

Leu	Ala	Gly	Asn	Arg	Leu	Ser	Gly	Asp	Leu	Pro	Ala	Ser	Ile	Trp	Asn	145	150	155	160
Leu	Cys	Asp	Arg	Ala	Thr	Glu	Leu	Arg	Leu	His	Gly	Asn	Ala	Leu	Thr	165	170		175
Gly	Ala	Val	Pro	Glu	Pro	Ala	Gly	Pro	Asn	Thr	Thr	Cys	Asp	Arg	Leu	180	185		190
Arg	Val	Leu	Asp	Leu	Gly	Ala	Asn	Arg	Phe	Ser	Gly	Ala	Phe	Pro	Ala	195	200		205
Phe	Val	Thr	Ala	Phe	Arg	Gly	Leu	Gln	Arg	Leu	Asp	Leu	Gly	Ala	Asn	210	215		220
Arg	Leu	Glu	Gly	Pro	Ile	Pro	Glu	Ala	Leu	Ala	Gly	Met	Ala	Ala	Thr	225	230		235
Gln	Gln	Leu	Gln	Ala	Leu	Asn	Val	Ser	Tyr	Asn	Asn	Phe	Ser	Gly	Gln	245	250		255
Leu	Pro	Pro	Ser	Phe	Ala	Ala	Ser	Arg	Phe	Thr	Ala	Asp	Ser	Phe	Val	260	265		270
Gly	Asn	Glu	Pro	Ala	Leu	Cys	Gly	Pro	Pro	Leu	Arg	Gln	Cys	Val	Thr	275	280		285
Ala	Ser	Gly	Leu	Ser	Ser	Arg	Gly	Val	Ala	Gly	Met	Val	Ile	Gly	Ile	290	295		300
Met	Ala	Gly	Ala	Val	Val	Leu	Ala	Ser	Val	Ser	Ile	Gly	Trp	Ala	Gln	305	310		315
Gly	Arg	Trp	Arg	Arg	Ser	Gly	Arg	Ile	Pro	Glu	Gln	Asp	Glu	Met	Leu	325	330		335
Glu	Ser	Ala	Asp	Asp	Ala	Gln	Asp	Ala	Ser	Ser	Glu	Gly	Arg	Leu	Val	340	345		350
Val	Phe	Glu	Gly	Gly	Glu	His	Leu	Thr	Leu	Glu	Glu	Val	Leu	Asn	Ala	355	360		365
Thr	Gly	Gln	Val	Val	Asp	Lys	Ala	Ser	Tyr	Cys	Thr	Val	Tyr	Lys	Ala	370	375		380
Lys	Leu	Ala	Ser	Gly	Gly	Ser	Ser	Ile	Glu	Leu	Arg	Leu	Leu	Arg	Glu	385	390		395
Gly	Ser	Cys	Lys	Asp	Ala	Ala	Ser	Cys	Ala	Pro	Val	Val	Arg	Arg	Ile	405	410		415
Gly	Arg	Ala	Arg	His	Glu	Asn	Leu	Val	Pro	Leu	Arg	Ala	Phe	Tyr	Gln	420	425		430
Gly	Arg	Arg	Gly	Glu	Lys	Leu	Leu	Val	Tyr	Asp	Tyr	Phe	Pro	Arg	Ser	435	440		445
Arg	Thr	Leu	Gln	Glu	Leu	Leu	His	Gly	Gly	Ser	Glu	Pro	Ala	Ala	Gly	450	455		460
Arg	Pro	Ala	Leu	Thr	Trp	Gly	Arg	Arg	His	Lys	Ile	Ala	Leu	Gly	Ala	465	470		475
Ala	Arg	Ala	Leu	Ala	Tyr	Leu	His	Ala	Gly	Gln	Gly	Glu	Ala	His	Gly	485	490		495
Asn	Val	Arg	Ser	Ser	Ile	Val	Val	Val	Asp	Asp	Leu	Phe	Val	Pro	Arg	500	505		510
Leu	Ala	Glu	Tyr	Ala	Val	Asp	Arg	Leu	Leu	Val	Pro	Ala	Ala	Ala	Glu	515	520		525
Ala	Val	Leu	Ala	Ala	Ala	Lys	Ala	Asp	Gly	Tyr	Lys	Ala	Pro	Glu	Leu	530	535		540
His	Ser	Met	Lys	Lys	Cys	Ser	Ala	Arg	Thr	Asp	Val	Tyr	Ala	Phe	Gly	545	550		555
Ile	Leu	Leu	Leu	Glu	Leu	Leu	Met	Gly	Arg	Lys	Pro	Ser	Ala	Ser	Ala	565	570		575
Gly	Gly	Ala	Ala	Arg	Ala	Met	Asp	Leu	Pro	Ser	Val	Val	Lys	Val	Ala	580	585		590

Val Leu Glu Glu Thr Ala Leu Glu Glu Val Leu Asp Ala Glu Val Val
595 600 605
Lys Gly Leu Arg Val Ser Pro Ala Glu Glu Gly Leu Val Gln Ala Leu
610 615 620
Lys Leu Ala Met Gly Cys Cys Ala Pro Val Pro Ala Ala Arg Pro Ser
625 630 635 640
Met Ala Glu Val Val Arg Gln Leu Glu Glu Ser Arg Pro Lys Asn Val
645 650 655
His Pro Arg Ser Ala Leu Tyr Ser Pro Thr Glu Ser Arg Ser Asp Ala
660 665 670
Gly Thr Pro Thr Thr Ala
675

<210> 35
<211> 2100
<212> DNA
<213> glycine max

<400> 35
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cccccttctt caccctccac tacttctctc tctgacgttg agcttctctt gggaaagatc 180
aaagcttcac tgcaaggtag taactctgac aaccttggtt tgtcttcatg gaactcctcc 240
accccaacttt gtcagtggaa aggcctcata tgggtcttct ccaatggcac tcctctctca 300
tgcactgact tgcctctctc tcaatggacc aatctcacac tcctcaaaga ccttctctt 360
cacttggtttt ccctccggct cccttctgca aacctctctg gttccctccc tagagagctt 420
ggagggttcc ctatgctcca aagtctctac cttaacatta actcattgga gggtagcatc 480
cctcttgagc ttgggttatag ctctctctct tctgagattg atttggtgga caatatgcta 540
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cacggttaatt ctttatctgg gttagtttct gagectgcat tgcctaactc ttcttgcaag 660
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acaaagtttg gtggcctaaa gcagcttgac ttgggggaata acatgtttat ggggtgcaatt 780
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aatgatgaag aggaagatga tgaagagaat ggtggtaatg ctattggtgg agctggtgag 1140
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cttcatgatc ttttacatgg agctaaagct ggaaaaccag tgttgaactg ggctaggcga 1500
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cctatggaag atgggttggt gcaggcctg aagctggcaa tggggtgctg tgcaccagtg 1980
gcatctgtta ggccaagcat ggatgaagtt gtgaggcagt tggaggagaa tagaccaagg 2040
aacaggtctg cattatacag ccctacagaa acaagaagtg gaagtgttac cccattttga 2100

<210> 36
 <211> 699
 <212> PRT
 <213> glycine max

<400> 36

Met	Ala	Phe	Leu	Asn	Pro	Phe	Ser	Leu	His	Ile	Pro	Met	Ser	Leu	Leu
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Phe	Phe	Phe	Leu	Phe	Phe	Phe	Cys	Phe	Cys	Lys	Ala	Ser	Ser	Thr	Thr
			20					25					30		
Thr	Ser	Thr	Thr	Lys	Ser	Leu	Ser	Pro	Pro	Ser	Ser	Pro	Ser	Thr	Thr
		35					40					45			
Ser	Ser	Ser	Asp	Val	Glu	Leu	Leu	Leu	Gly	Lys	Ile	Lys	Ala	Ser	Leu
	50					55					60				
Gln	Gly	Ser	Asn	Ser	Asp	Asn	Leu	Val	Leu	Ser	Ser	Trp	Asn	Ser	Ser
65					70					75					80
Thr	Pro	Leu	Cys	Gln	Trp	Lys	Gly	Leu	Ile	Trp	Val	Phe	Ser	Asn	Gly
				85					90					95	
Thr	Pro	Leu	Ser	Cys	Thr	Asp	Leu	Ser	Ser	Pro	Gln	Trp	Thr	Asn	Leu
			100					105						110	
Thr	Leu	Leu	Lys	Asp	Pro	Ser	Leu	His	Leu	Phe	Ser	Leu	Arg	Leu	Pro
			115				120						125		
Ser	Ala	Asn	Leu	Ser	Gly	Ser	Leu	Pro	Arg	Glu	Leu	Gly	Gly	Phe	Pro
	130					135					140				
Met	Leu	Gln	Ser	Leu	Tyr	Leu	Asn	Ile	Asn	Ser	Leu	Glu	Gly	Thr	Ile
145					150					155					160
Pro	Leu	Glu	Leu	Gly	Tyr	Ser	Ser	Ser	Leu	Ser	Glu	Ile	Asp	Leu	Gly
				165					170					175	
Asp	Asn	Met	Leu	Gly	Gly	Val	Leu	Pro	Pro	Ser	Ile	Trp	Asn	Leu	Cys
			180					185					190		
Glu	Arg	Leu	Val	Ser	Leu	Arg	Leu	His	Gly	Asn	Ser	Leu	Ser	Gly	Leu
		195					200					205			
Val	Ser	Glu	Pro	Ala	Leu	Pro	Asn	Ser	Ser	Cys	Lys	Asn	Leu	Gln	Val
	210						215					220			
Leu	Asp	Leu	Gly	Gly	Asn	Lys	Phe	Ser	Gly	Ser	Phe	Pro	Glu	Phe	Ile
225					230					235					240
Thr	Lys	Phe	Gly	Gly	Leu	Lys	Gln	Leu	Asp	Leu	Gly	Asn	Asn	Met	Phe
				245					250					255	
Met	Gly	Ala	Ile	Pro	Gln	Gly	Leu	Ala	Gly	Leu	Ser	Leu	Glu	Lys	Leu
			260					265					270		
Asn	Leu	Ser	His	Asn	Asn	Phe	Ser	Gly	Val	Leu	Pro	Leu	Phe	Gly	Gly
		275					280					285			
Glu	Ser	Lys	Phe	Gly	Val	Asp	Ala	Phe	Glu	Gly	Asn	Ser	Pro	Ser	Leu
	290					295					300				
Cys	Gly	Pro	Pro	Leu	Gly	Ser	Cys	Ala	Arg	Thr	Ser	Thr	Leu	Ser	Ser
305					310					315					320
Gly	Ala	Val	Ala	Gly	Ile	Val	Ile	Ser	Leu	Met	Thr	Gly	Ala	Val	Val
				325					330					335	
Leu	Ala	Ser	Leu	Leu	Ile	Gly	Tyr	Met	Gln	Asn	Lys	Lys	Lys	Lys	Gly
			340					345					350		
Ser	Gly	Glu	Ser	Glu	Asp	Glu	Leu	Asn	Asp	Glu	Glu	Glu	Asp	Asp	Glu
		355					360					365			
Glu	Asn	Gly	Gly	Asn	Ala	Ile	Gly	Gly	Ala	Gly	Glu	Gly	Lys	Leu	Met
	370					375					380				
Leu	Phe	Ala	Gly	Gly	Glu	Asn	Leu	Thr	Leu	Asp	Asp	Val	Leu	Asn	Ala
385					390					395					400

Thr Gly Gln Val Leu Glu Lys Thr Cys Tyr Gly Thr Ala Tyr Lys Ala
 405 410 415
 Lys Leu Ala Asp Gly Gly Thr Ile Ala Leu Arg Leu Leu Arg Glu Gly
 420 425 430
 Ser Cys Lys Asp Lys Ala Ser Cys Leu Ser Val Ile Lys Gln Leu Gly
 435 440 445
 Lys Ile Arg His Glu Asn Leu Ile Pro Leu Arg Ala Phe Tyr Gln Gly
 450 455 460
 Lys Arg Gly Glu Lys Leu Leu Ile Tyr Asp Tyr Leu Pro Leu Arg Thr
 465 470 475 480
 Leu His Asp Leu Leu His Gly Ala Lys Ala Gly Lys Pro Val Leu Asn
 485 490 495
 Trp Ala Arg Arg His Lys Ile Ala Leu Gly Ile Ala Arg Gly Leu Ala
 500 505 510
 Tyr Leu His Thr Gly Leu Glu Val Pro Val Thr His Ala Asn Val Arg
 515 520 525
 Ser Lys Asn Val Leu Val Asp Asp Phe Phe Thr Ala Arg Leu Thr Asp
 530 535 540
 Phe Gly Leu Asp Lys Leu Met Ile Pro Ser Ile Ala Asp Glu Met Val
 545 550 555 560
 Ala Leu Ala Lys Thr Asp Gly Tyr Lys Ala Pro Glu Leu Gln Arg Met
 565 570 575
 Lys Lys Cys Asn Ser Arg Thr Asp Val Tyr Ala Phe Gly Ile Leu Leu
 580 585 590
 Leu Glu Ile Leu Ile Gly Lys Lys Pro Gly Lys Asn Gly Arg Asn Gly
 595 600 605
 Glu Tyr Val Asp Leu Pro Ser Met Val Lys Val Ala Val Leu Glu Glu
 610 615 620
 Thr Thr Met Glu Val Phe Asp Val Glu Leu Leu Lys Gly Ile Arg Ser
 625 630 635 640
 Pro Met Glu Asp Gly Leu Val Gln Ala Leu Lys Leu Ala Met Gly Cys
 645 650 655
 Cys Ala Pro Val Ala Ser Val Arg Pro Ser Met Asp Glu Val Val Arg
 660 665 670
 Gln Leu Glu Glu Asn Arg Pro Arg Asn Arg Ser Ala Leu Tyr Ser Pro
 675 680 685
 Thr Glu Thr Arg Ser Gly Ser Val Thr Pro Phe
 690 695

<210> 37
 <211> 1989
 <212> DNA
 <213> oryza sativa

<400> 37
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 ggcgaagtag gagggaacgc gcagctggcc acctggaccg cctccacccc gctctgccag 180
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 aacgccctcc acggcccaat ccccgacccc gccgcctcg ccccaaacac cacctgcgac 600
 gccctcagcc tctcgacct ctccgccaac cgctctccg gcccttccc ctctcccta 660

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ggccaacttc cccccgacct cgctctcttg ccgcccgcgc ccttctctgc caacagcccc 840
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cccaccatgg cggaggtggt gcggcagctg gaggaggtcc ggccccgaa cagcagccgg 1920
ccgtcggcga tctacagccc cgccagccc aggagcgacg ccggcacgcc caccgccgcc 1980
gccgtctaa 1989

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<210> 38
<211> 662
<212> PRT
<213> oryza sativa

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<400> 38
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20 25 30
Val Lys Pro Ala Leu Gln Gly Glu Gly Glu Val Gly Gly Asn Ala Gln
35 40 45
Leu Ala Thr Trp Thr Ala Ser Thr Pro Leu Cys Gln Trp Arg Gly Leu
50 55 60
Arg Trp Ser Thr Ala Ala Thr Leu Pro Arg Glu Leu Pro Cys Gly Asn
65 70 75 80
Leu Ser Ala Gly Leu Ala His His Pro Val Pro Asp Asp Leu Leu Leu
85 90 95
Leu Leu Ser Ile Arg Leu Pro Ala Ser Ala Leu Ala Gly His Leu Pro
100 105 110
Pro Glu Leu Ala Ala Phe Ser Ala Leu Ala Ser Ile Phe Leu Ala His
115 120 125
Asn Ser Leu Ser Gly Pro Ile Pro Leu Ala Leu Gly Asn Ala Pro Ala
130 135 140
Leu Ser Leu Leu Asp Leu Ala Ser Asn Arg Leu Ser Gly Ser Leu Pro
145 150 155 160
Leu Ser Ile Trp Asn Leu Cys Ser Gly Asn Ala Arg Leu Ser Leu Leu
165 170 175
Arg Leu His Gly Asn Ala Leu His Gly Pro Ile Pro Asp Pro Ala Ala
180 185 190
Leu Ala Pro Asn Thr Thr Cys Asp Ala Leu Ser Leu Leu Asp Leu Ser
195 200 205

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Ala	Asn	Arg	Leu	Ser	Gly	Pro	Phe	Pro	Ser	Ser	Leu	Val	Thr	Thr	Ala
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Phe	Pro	Ala	Leu	Arg	Ser	Leu	Asp	Leu	Ser	Asp	Asn	Arg	Leu	His	Gly
225					230					235					240
Pro	Ile	Pro	His	Gly	Leu	Ala	Pro	Ile	His	Ser	Leu	Asn	Leu	Ser	Tyr
				245					250					255	
Asn	Asn	Phe	Ser	Gly	Gln	Leu	Pro	Pro	Asp	Leu	Ala	Ser	Leu	Pro	Pro
			260					265					270		
Asp	Ala	Phe	Leu	Ala	Asn	Ser	Pro	Ala	Leu	Cys	Gly	Pro	Pro	Leu	Pro
		275					280					285			
His	His	Cys	Leu	Pro	Ser	Asn	Pro	Leu	Thr	Ser	Ser	Ala	Val	Ala	Ala
	290					295					300				
Ile	Val	Ile	Ala	Leu	Met	Ala	Ala	Ala	Val	Val	Leu	Ala	Ser	Leu	Ser
305					310					315					320
Ile	Gly	Trp	Ala	Gln	Gly	Arg	Trp	Arg	Arg	Ala	Pro	Leu	Pro	Pro	Glu
				325					330					335	
Glu	Gly	Thr	Leu	Thr	Glu	Asp	Gly	Glu	Gly	Lys	Leu	Val	Val	Phe	Gln
			340					345					350		
Gly	Gly	Glu	His	Leu	Thr	Leu	Glu	Glu	Val	Leu	Asn	Ala	Thr	Gly	Gln
		355					360					365			
Val	Val	Asn	Lys	Ala	Ser	Tyr	Cys	Thr	Val	Tyr	Lys	Ala	Lys	Leu	Ala
	370					375					380				
Glu	Gly	Gly	Gly	Ser	Ile	Glu	Leu	Arg	Leu	Leu	Arg	Glu	Gly	Cys	Cys
385					390					395					400
Lys	Asp	Ala	Glu	Ser	Cys	Ala	Pro	Ala	Val	Arg	Arg	Ile	Gly	Arg	Ala
				405					410					415	
Arg	His	Asp	Asn	Leu	Val	Pro	Leu	Arg	Ala	Phe	Tyr	Gln	Gly	Arg	Arg
			420					425					430		
Gly	Glu	Lys	Leu	Leu	Val	Tyr	Asp	Tyr	Phe	Pro	Gly	Asn	Arg	Thr	Leu
		435					440					445			
His	Glu	Leu	Leu	His	Gly	His	Gly	Glu	Gln	Ser	Gln	Gly	Met	Arg	Pro
	450				455						460				
Ala	Leu	Thr	Trp	Ala	Arg	Arg	His	Lys	Ile	Ala	Leu	Gly	Val	Ala	Arg
465					470					475					480
Ala	Leu	Ala	Tyr	Val	His	Ala	Gly	His	Gly	Glu	Ala	His	Gly	Ser	Val
				485					490					495	
Arg	Ser	Ser	Asn	Val	Leu	Val	Asp	Glu	Trp	Phe	Val	Ala	Arg	Val	Ala
			500					505					510		
Glu	Tyr	Ala	Val	His	Arg	Leu	Leu	Val	Ala	Ala	Ala	Val	Gly	Lys	Ala
	515						520					525			
Asp	Gly	Tyr	Arg	Ala	Pro	Glu	Leu	Gln	Ser	Arg	Gly	Arg	Cys	Ser	Pro
	530					535					540				
Arg	Thr	Asp	Val	Tyr	Ala	Phe	Gly	Ile	Leu	Leu	Leu	Glu	Leu	Leu	Met
545					550					555					560
Gly	Arg	Lys	Ala	Ser	Gly	Glu	Leu	Pro	Ala	Val	Val	Lys	Ala	Ala	Val
				565					570					575	
Leu	Glu	Glu	Val	Thr	Met	Met	Glu	Val	Phe	Asp	Ala	Glu	Val	Ala	Arg
			580					585					590		
Gly	Val	Arg	Ser	Pro	Ala	Glu	Glu	Gly	Leu	Leu	Gln	Ala	Leu	Lys	Leu
		595					600					605			
Ala	Met	Gly	Cys	Cys	Ala	Pro	Val	Ala	Ser	Ala	Arg	Pro	Thr	Met	Ala
	610					615					620				
Glu	Val	Val	Arg	Gln	Leu	Glu	Glu	Val	Arg	Pro	Arg	Asn	Ser	Ser	Arg
625					630					635					640

Pro Ser Ala Ile Tyr Ser Pro Ala Glu Pro Arg Ser Asp Ala Gly Thr
 645 650 655
 Pro Thr Ala Ala Ala Val
 660

<210> 39
 <211> 1254
 <212> DNA
 <213> *Gossypium hirsutum*

<400> 39
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 caagctctta gagagcttga tctttcgagt aacatgcttt caggtcaaat tccacagagt 120
 ttggccactt taaacgtgga aaaattaaac ctttcccaca ataacttcac tggaatgttg 180
 cctgtttttg gtgaaagaaa gtttggcccg gaggctttcg aagggaacaa tccagggcta 240
 tgtgggttgc ctttgaatag ttgtagtggc aggtcacagc tgagtccagg tgcaattgct 300
 ggcattgtga ttggtctaata gactggagtg gtagtttttg catcattgtt cgttggctat 360
 atgcaaaaca ggaagaggag cagcaatgga gatagtgagg aggaactgga agaaggagag 420
 ggggatgaaa acgggggtcgg gggagtgtgc agcgagagca agcttatttt gtttcaaggc 480
 ggggagcatt tgacattaga ggatgtactg aatgcaactg gtcaagtcat ggagaagaca 540
 aattatggga ctgtttataa ggcaaagctt gctgatgggtg gaaatatagc attgaggttg 600
 ttgaggggaag gcagttgtaa ggacgggagt tcatgtctgc ctgtcataaa gcagctgggg 660
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 caagcaggaa agccagttct aaattgggct cgacggcaca aaatcgcatg ggggatagcc 840
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 aagctaataa tcccggctgt ggctgatgaa atggttggcc tcgcaaagac cgaatgttac 1020
 aaggcaccgg aacttcaaag catgaagaaa tgcaacacca gaactgacgt ttatgcattt 1080
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 gatgttgggg atttgccttc gattgtgaaa gcagcagttt tggaagagac aacaatggag 1200
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<210> 40
 <211> 417
 <212> PRT
 <213> *Gossypium hirsutum*

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

Asn Gly Asp Ser Glu Glu Glu Leu Glu Glu Gly Glu Gly Asp Glu Asn
 130 135 140
 Gly Val Gly Gly Val Val Ser Glu Ser Lys Leu Ile Leu Phe Gln Gly
 145 150 155 160
 Gly Glu His Leu Thr Leu Glu Asp Val Leu Asn Ala Thr Gly Gln Val
 165 170 175
 Met Glu Lys Thr Asn Tyr Gly Thr Val Tyr Lys Ala Lys Leu Ala Asp
 180 185 190
 Gly Gly Asn Ile Ala Leu Arg Leu Leu Arg Glu Gly Ser Cys Lys Asp
 195 200 205
 Gly Ser Ser Cys Leu Pro Val Ile Lys Gln Leu Gly Lys Val Arg His
 210 215 220
 Glu Asn Leu Val Pro Leu Arg Ala Phe Tyr Gln Gly Lys Arg Gly Glu
 225 230 235 240
 Lys Leu Leu Ile Tyr Asp Tyr Leu Pro Asn Arg Ser Leu His Asp Phe
 245 250 255
 Leu His Gly Met Gln Ala Gly Lys Pro Val Leu Asn Trp Ala Arg Arg
 260 265 270
 His Lys Ile Ala Leu Gly Ile Ala Lys Gly Leu Ala His Leu His Thr
 275 280 285
 Gly Leu Glu Met Pro Ile Thr His Gly Asn Val Arg Ser Lys Asn Val
 290 295 300
 Leu Val Asp Asp Phe Phe Val Ala Arg Leu Thr Glu Tyr Gly Leu Asp
 305 310 315 320
 Lys Leu Met Ile Pro Ala Val Ala Asp Glu Met Val Ala Leu Ala Lys
 325 330 335
 Thr Glu Cys Tyr Lys Ala Pro Glu Leu Gln Ser Met Lys Lys Cys Asn
 340 345 350
 Thr Arg Thr Asp Val Tyr Ala Phe Gly Ile Leu Leu Leu Glu Ile Leu
 355 360 365
 Ile Gly Lys Lys Pro Glu Lys Asn Ala Arg Arg Asn Asp Val Gly Asp
 370 375 380
 Leu Pro Ser Ile Val Lys Ala Ala Val Leu Glu Glu Thr Thr Met Glu
 385 390 395 400
 Val Phe Asp Val Glu Val Leu Lys Val Phe Glu Val Arg Trp Lys Thr
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<210> 41
 <211> 1263
 <212> DNA
 <213> arabidopsis thaliana

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 gatgtttctg gaacgagcac agtatcatcc actggttaga actcgaacac tagcatgtca 180
 gctagagaaa acaaccttag agagttcact attggtgatc ttaaattctgc cacaaggaac 240
 ttcagcaggt caggtatgat cggggaaggc ggttttggtt gtgtcttctg gggaacaatc 300
 aagaacttag aagacccatc gaagaaaatc gaagtcgcgg ttaaacagct cggcaaaaga 360
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 tcaaacttgg tgaagttgct gggacattgt gcagaagacg atgaacgtgg aatccaaagg 480
 cttttgggtt atgaatatat gccaaaccaa agtgctcagat tccatttatc tccgcggtca 540
 ccgacagtac ttacttgga cctcagattg agaatagcac aagacgcagc tcgaggttta 600
 acataccttc atgaagaaat ggactttcag ataattatcc gtgatttcaa gtcattccaa 660
 attctactag acgagaattg gacagcgaag ctttcggatt tcggtttggc tcgcttaggt 720

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cagaagcttt tagaatgggt gagaccttac ttatccgaca caaggagggt ccggctaata 960
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<210> 42
<211> 420
<212> PRT
<213> arabidopsis thaliana

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

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Glu Trp Val Arg Pro Tyr Leu Ser Asp Thr Arg Arg Phe Arg Leu Ile
 305 310 315 320
 Val Asp Pro Arg Leu Glu Gly Lys Tyr Met Ile Lys Ser Val Gln Lys
 325 330 335
 Leu Ala Val Val Ala Asn Leu Cys Leu Thr Arg Asn Ala Lys Ala Arg
 340 345 350
 Pro Lys Met Ser Glu Val Leu Glu Met Val Thr Lys Ile Val Glu Ala
 355 360 365
 Ser Ser Pro Gly Asn Gly Gly Lys Lys Pro Gln Leu Val Pro Leu Lys
 370 375 380
 Ser Gln Glu Thr Ser Arg Val Glu Glu Gly Lys Asn Lys Lys Val Leu
 385 390 395 400
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 405 410 415
 Val Arg Ala Cys
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<210> 43
 <211> 1296
 <212> DNA
 <213> zea mays

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<210> 44
 <211> 431
 <212> PRT
 <213> zea mays

<400> 44
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Arg	Asp	Val	Arg	Ser	Gly	Ser	Asp	Phe	Thr	Ser	Leu	Asn	Val	Ser	Asp
		35					40					45			
Met	Ser	Ala	Glu	Ser	Ile	Arg	Arg	Thr	Gln	Tyr	Pro	Ser	Phe	Thr	Asp
	50					55					60				
Arg	Pro	Ser	Asn	Leu	Arg	Val	Phe	Ser	Phe	Ala	Glu	Leu	Lys	Ser	Ala
65					70					75					80
Thr	Arg	Asn	Phe	Ser	Arg	Ser	Leu	Met	Val	Gly	Glu	Gly	Gly	Phe	Gly
			85					90						95	
Cys	Val	Tyr	Arg	Gly	Val	Ile	Lys	Thr	Ser	Asp	Glu	Pro	Asn	Glu	Arg
			100					105					110		
Ile	Glu	Ile	Ala	Val	Lys	Gln	Leu	Asn	Arg	Lys	Gly	Leu	Gln	Gly	Gln
	115					120						125			
Lys	Glu	Trp	Leu	Thr	Glu	Met	Asn	Val	Leu	Gly	Ile	Val	Asp	His	Pro
	130					135					140				
Asn	Leu	Val	Lys	Leu	Ile	Gly	Tyr	Cys	Ala	Glu	Asp	Asp	Glu	Arg	Gly
145					150					155					160
Val	Gln	Arg	Leu	Leu	Val	Tyr	Glu	Tyr	Met	Pro	Asn	Gly	Ser	Val	Asp
			165					170						175	
Asp	His	Leu	Ser	Ser	Arg	Ser	Thr	Ser	Thr	Leu	Ser	Trp	Pro	Met	Arg
		180						185					190		
Leu	Lys	Val	Ala	Leu	Asp	Ser	Ala	Arg	Gly	Leu	Lys	Tyr	Leu	His	Glu
	195						200					205			
Glu	Met	Glu	Phe	Gln	Val	Ile	Phe	Arg	Asp	Leu	Lys	Thr	Ser	Asn	Ile
	210					215					220				
Leu	Leu	Asp	Glu	Asn	Trp	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Ala
225					230					235					240
Arg	His	Gly	Pro	Ala	Glu	Gly	Leu	Thr	His	Val	Ser	Thr	Ala	Val	Val
			245					250						255	
Gly	Thr	Leu	Gly	Tyr	Ala	Ala	Pro	Glu	Tyr	Met	Gln	Thr	Gly	Arg	Leu
		260						265					270		
Thr	Ala	Lys	Ser	Asp	Ile	Trp	Ser	Tyr	Gly	Val	Leu	Leu	Tyr	Glu	Leu
	275						280					285			
Ile	Thr	Gly	Arg	Arg	Pro	Ile	Asp	Arg	Asn	Arg	Pro	Lys	Ser	Glu	Gln
	290					295					300				
Lys	Leu	Leu	Asp	Trp	Val	Lys	Pro	Tyr	Ile	Ser	Asp	Val	Lys	Arg	Phe
305					310					315					320
Pro	Ile	Ile	Val	Asp	Pro	Arg	Leu	Glu	Gly	His	Tyr	Asn	Leu	Lys	Ser
			325						330					335	
Met	Thr	Lys	Leu	Ser	Ser	Val	Ala	Asn	Arg	Cys	Leu	Val	Arg	Met	Pro
		340						345					350		
Lys	Ser	Arg	Pro	Lys	Met	Ser	Glu	Val	Tyr	Asp	Met	Val	Gln	Lys	Ile
	355						360					365			
Val	Asp	Cys	Val	Gly	Thr	Gly	Pro	Pro	Gln	Pro	Pro	Leu	Leu	His	Tyr
	370					375					380				
His	Gly	Ser	Ala	Ser	Glu	Pro	Gly	Pro	Gly	Asp	Lys	Arg	Ala	Arg	Lys
385					390					395					400
Gly	Ser	Val	Lys	Arg	Arg	Arg	Leu	Trp	Glu	Leu	Arg	Phe	Gly	Cys	Arg
			405					410					415		
His	Ile	Val	Trp	Arg	Gly	Trp	Lys	Pro	Ala	Ile	Val	Lys	Asp	Ile	
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<210> 45

<211> 1287

<212> DNA

<213> glycine max

<400> 45

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ggttctgagt	taaattctca	ggatgtttcg	gacaatggca	gctcagaatc	ccagaggagg	180
aatgcaattc	ccagtttgtc	ccagagaccc	agcaacctca	gagtgtttac	tgtatctgaa	240
ctgaaatcag	ccaccaagaa	tttcagtcgc	tctgttatga	tccgagaggg	tgggtttggg	300
tgtgtctacc	tgggattgat	aagaagcgca	gaggactcct	ccagaagaat	tgaagttgca	360
gttaaacaac	ttagtaaaag	aggaatgcag	ggccataggg	aatgggtgac	agaagtgaat	420
gttctgggca	ttgttgagca	tcccaatctt	gtgaaactag	tgggttactg	tgctgatgat	480
gatgaaagag	gaatccagag	gcttctaatt	tatgaataca	tgccaaacag	aagtgtggaa	540
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cgagatgcag	ctcgtggggt	aacataacctg	catgaggaaa	tggatttcca	gataattttc	660
agagattttca	aatcttcaaa	tatcctattg	gatgaacagt	ggaatgcaaa	gctatcagac	720
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ggaacaatgg	gatatgccgc	tcttgaatat	gttcaaaccg	gacgtctaac	ttcaaagaat	840
gatgtatgga	gctacgggtg	cttcctttat	gaactcatca	ctggtaggcg	ccctttagat	900
cgaaatcgcc	ccaggcgtga	gcagaagttg	ttggaatgga	taaggccata	cctatcagat	960
gggaagaaat	ttcaactaat	attagatcca	agacttgata	agaaacaagt	cttcaagtca	1020
gcccagagac	tcgctatgat	tgctaaccaa	tgcttggcaa	aaaatcccaa	gaatcgccca	1080
aagatgagtg	aggtattgga	aatggtaa	aatggttag	aatcatcatc	cagttctagt	1140
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aacaagaaac	gaaccatgga	tcagaagctc	ggagaaagta	attggtttgt	taggatgtgg	1260
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<210> 46

<211> 428

<212> PRT

<213> glycine max

<400> 46

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

Arg Ser Val Glu His His Leu Ser His Arg Ser Glu Thr Pro Leu Pro
 180 185 190
 Trp Thr Arg Arg Leu Lys Ile Ala Arg Asp Ala Ala Arg Gly Leu Thr
 195 200 205
 Tyr Leu His Glu Glu Met Asp Phe Gln Ile Ile Phe Arg Asp Phe Lys
 210 215 220
 Ser Ser Asn Ile Leu Leu Asp Glu Gln Trp Asn Ala Lys Leu Ser Asp
 225 230 235 240
 Phe Gly Leu Ala Arg Leu Gly Pro Ser Asp Gly Leu Thr His Val Ser
 245 250 255
 Thr Ala Val Val Gly Thr Met Gly Tyr Ala Ala Pro Glu Tyr Val Gln
 260 265 270
 Thr Gly Arg Leu Thr Ser Lys Asn Asp Val Trp Ser Tyr Gly Val Phe
 275 280 285
 Leu Tyr Glu Leu Ile Thr Gly Arg Arg Pro Leu Asp Arg Asn Arg Pro
 290 295 300
 Arg Arg Glu Gln Lys Leu Leu Glu Trp Ile Arg Pro Tyr Leu Ser Asp
 305 310 315 320
 Gly Lys Lys Phe Gln Leu Ile Leu Asp Pro Arg Leu Asp Lys Lys Gln
 325 330 335
 Val Phe Lys Ser Ala Gln Arg Leu Ala Met Ile Ala Asn Gln Cys Leu
 340 345 350
 Ala Lys Asn Pro Lys Asn Arg Pro Lys Met Ser Glu Val Leu Glu Met
 355 360 365
 Val Asn Gly Met Val Glu Ser Ser Ser Ser Ser Pro Gln Leu Pro
 370 375 380
 Leu Arg Ser Val Val Thr Leu Glu Ala Ser Gln Asp Thr Glu Thr Asn
 385 390 395 400
 Asn Lys Lys Arg Thr Met Asp Gln Lys Leu Gly Glu Ser Asn Trp Phe
 405 410 415
 Val Arg Met Trp Arg Pro Lys Leu Val Arg Thr Cys
 420 425

<210> 47
 <211> 1284
 <212> DNA
 <213> oryza sativa

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 aatcgcaaag gacttcaggg gcagaaagaa tggttaacag aactgaatgt gcttgggatt 420
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<210> 48
<211> 428
<212> PRT
<213> oryza sativa
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91

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 Ile Val Ala Ser Ile Glu Thr Gly Thr Pro Gln Pro Pro Leu His Tyr
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 His Gly Ser Val Ser Glu Pro Gly Ser Lys Arg Pro Lys Lys Gly Ser
 385 390 395 400
 Leu Lys Arg Arg Phe Gln Glu Phe Lys Phe Gly Cys Arg Gln Ile Val
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 Trp Arg Ser Trp Lys Pro Glu Ile Ile Lys Thr Cys
 420 425

<210> 49
 <211> 1041
 <212> DNA
 <213> Gossypium hirsutum

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 gcaggacca gaactcctga accaccattg aatgatgtct ctctggaaac tgctagggaa 960
 cgtaaaagaa ggattataga ttttagaagc ggtgaagagt ttgtttgggtc atggactcca 1020
 aagctcataa gaccatgcta a 1041

<210> 50
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 <213> Gossypium hirsutum

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

Tyr Met Pro Asn Arg Ser Val Glu Asn His Leu Ser Val Arg Ser Glu
 100 105 110
 Thr Thr Leu Ser Trp Ala Met Arg Leu Lys Ile Ala Gln Asp Ala Ala
 115 120 125
 Arg Gly Leu Ala Tyr Leu His Glu Gly Met Glu Phe Gln Ile Ile Phe
 130 135 140
 Arg Asp Phe Lys Ser Ser Asn Ile Leu Leu Asp Glu Gln Trp Asn Ala
 145 150 155 160
 Lys Leu Ser Asp Phe Gly Leu Ala Arg Leu Gly Pro Ser Glu Gly Leu
 165 170 175
 Thr His Ile Ser Thr Ala Val Val Gly Thr Met Gly Tyr Ala Ala Pro
 180 185 190
 Glu Tyr Ile Gln Thr Gly Arg Leu Thr Ser Lys Ile Asp Val Trp Ser
 195 200 205
 Tyr Gly Val Phe Leu Tyr Glu Leu Ile Thr Gly Arg Arg Pro Phe Asp
 210 215 220
 Lys Asn Arg Pro Lys Asn Glu Gln Arg Leu Leu Glu Trp Val Lys Pro
 225 230 235 240
 Tyr Leu Ser Asp Arg Lys Phe Gln Leu Ile Leu Asp Pro Arg Leu Lys
 245 250 255
 Gly Lys Tyr Gln Leu Lys Ser Ala Gln Arg Leu Ala Val Val Ala Asn
 260 265 270
 Arg Cys Leu Val Arg Asn Pro Lys Ser Arg Pro Lys Met Ser Glu Val
 275 280 285
 Leu Glu Met Val Asn Arg Ile Val Glu Ala Ser Ser Ala Gly Pro Arg
 290 295 300
 Thr Pro Glu Pro Pro Leu Asn Asp Val Ser Leu Glu Thr Ala Arg Glu
 305 310 315 320
 Arg Lys Arg Arg Ile Ile Asp Phe Arg Ser Gly Glu Glu Phe Val Trp
 325 330 335
 Ser Trp Thr Pro Lys Leu Ile Arg Pro Cys
 340 345

<210> 51
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NG6 Forward Primer

<400> 51
 tcgagctagc atgaagcttg tggagaagac

30

<210> 52
 <211> 29
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 <213> Artificial Sequence

<220>
 <223> NG6 Reverse Primer

<400> 52
 cgacgagctc ttacctgatg gaacaagag

29

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> NG21 Forward Primer

<400> 53
atggtgagtg acaagcatgt ag 22

<210> 54
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<220>
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<400> 54
tcacttgccc gtgatgaatg 20

<210> 55
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<212> DNA
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<220>
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<400> 55
atgggttatc tctcttgcaa c 21

<210> 56
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<220>
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<400> 56
tcagtatctc ttccgcgacg 20

<210> 57
<211> 20
<212> DNA
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<220>
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<400> 57
atgggcatgg aagctttgag 20

<210> 58
<211> 20
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<220>
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<400> 58
tcaaaatgga gtttcggcgt 20

<210> 59
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<220>
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<400> 59
atgaaatgct tcttattccc 20

<210> 60
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<220>
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<400> 60
tcaacaagct ctcacattct 20

<210> 61
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> NG6 Forward Primer

<400> 61
tgtgcccgga gccctacc 18

<210> 62
<211> 22
<212> DNA
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<220>
 <223> NG6 Reverse Primer

 <400> 62
 ctttcagtgcatgcggatttt 22

<210> 63
 <211> 21
 <212> DNA
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 <220>
 <223> NG21 Forward Primer

 <400> 63
 ggcacaagtc cgcctcatcac c 21

<210> 64
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG21 Reverse Primer

 <400> 64
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<210> 65
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG24 Forward Primer

 <400> 65
 gccgccgtca agagaacaac 20

<210> 66
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG24 Reverse Primer

 <400> 66
 ctccggtggt caacgcagta a 21

<210> 67
 <211> 22

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG28 Forward Primer

 <400> 67
 tgttgttggtg gcctcgttgt ta 22

<210> 68
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG28 Reverse Primer

 <400> 68
 ctttccttca ccgccttctt tc 22

<210> 69
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG32 Forward Primer

 <400> 69
 aagctttcgg atttcggttt g 21

<210> 70
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> NG32 Reverse Primer

 <400> 70
 tggccttctt cctgtaatga gc 22

<210> 71
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> ACTIN Forward Primer

 <400> 71
 cccgctatgt atgtcgc 17

<210> 72
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ACTIN Reverse Primer

<400> 72
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18

<210> 73
 <211> 1971
 <212> DNA
 <213> Arabidopsis thaliana

<400> 73
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 gtgatacaat ggtccggtgt cgattctccg tcagatctcg attgggttagg actctactcg 180
 ccgccggagt ctctaatga tcactttatt gggtacaaat tcctcaatga atcgteccact 240
 tggaaagatg gtttcgggttc gatttctctt cctttaacca atctccgatc aaattacaca 300
 ttccggatct tccggttgag cgaatccgag attgatccga aacataagga tcatgatcag 360
 aatcctttac caggaactaa acatcttcta gctgaatcgg agcagctgac ttccggatcc 420
 ggtggttggtg tgccggagca gatccatttg tcgttcacaa atatgggttaa cacgatgcgt 480
 gttatgtttg tagctggaga tgggtgaagaa cgttttggtg gatacgggtga atcgaaggat 540
 ttgttaggta attccgcggc ggcgcgtggg atgagggtacg agagagagca catgtgtgat 600
 tcgccggcga attccactat tgggttgaga gatcctggtt ggatttttga taccgtcatg 660
 aagaatttga atgatggcgt tagatactat tatcagggtg ggagtgattc taagggatgg 720
 agtgagatcc atagctacat tgctcgagat gtgactgcag aagaaaccgt agctttcatg 780
 tttggagata tgggttggtg tacaccatac acgacattta tccgcacaca agatgagagc 840
 atatctacag tgaagtggat cctccgtgac attgaagctc ttgggtgataa gccagctatg 900
 atttcacaca ttggagatat aagttatgct cgtgggttact cgtgggtatg ggatgagttc 960
 tttgctcagg ttgagcctat tgctcgaca gttccttacc atgtttgcat tggtaacct 1020
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 gatggtggtg gcgaatgtgg tgtgccgtat agcttgaagt ttaacatgcc tgggaattct 1140
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 ggaacggtcc atttcgttta tatctccaca gagacgaatt ttcttaaagg aggtagtcaa 1260
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 gtgcaaggac atagaccaat gtacactacg agcaacgagg ttagagacac tatgattcga 1380
 caaaagatgg ttgagcatct agaacccttg tttgtgaaaa acaatgtcac acttgctcta 1440
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 cagtggcaag gaaatccggt tcatcttggt atcgggtatgg ctgggtcaaga ttggcaaccg 1560
 atttggcagc ctagacaaaa ccatccagat ctctctatat tccctcagcc tgaacaatca 1620
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 gtttcttttg tgggtaatca cgatggcgaa gttcatgata ctggttgagat gttagcatct 1740
 ggggtagtaa tcagtgggag caaagagagt actaaaatcc caaatctgaa aaccgttcct 1800
 gcttctgcta cacttatggg aaaatcagaa tctaattgct tgtgggtatgc caaaggagca 1860
 ggcttgatgg ttgtgggtgt gcttttaggg ttcattatcg ggttttttac ccggggaaag 1920
 aaatcttcgt ctggaaaccg ttggatccca gtcaagaacg aggagacata a 1971

<210> 74
 <211> 656
 <212> PRT
 <213> Arabidopsis thaliana

<400> 74

Met	Ile	Val	Asn	Phe	Ser	Phe	Phe	Leu	Leu	Leu	Phe	Val	Ser	Val	Phe
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Val	Ser	Ser	Ala	Asp	Ser	Lys	Ala	Thr	Ile	Ser	Ile	Ser	Pro	Asn	Ala
			20					25					30		
Leu	Asn	Arg	Ser	Gly	Asp	Ser	Val	Val	Ile	Gln	Trp	Ser	Gly	Val	Asp
		35					40					45			
Ser	Pro	Ser	Asp	Leu	Asp	Trp	Leu	Gly	Leu	Tyr	Ser	Pro	Pro	Glu	Ser
	50					55					60				
Pro	Asn	Asp	His	Phe	Ile	Gly	Tyr	Lys	Phe	Leu	Asn	Glu	Ser	Ser	Thr
65					70					75					80
Trp	Lys	Asp	Gly	Phe	Gly	Ser	Ile	Ser	Leu	Pro	Leu	Thr	Asn	Leu	Arg
				85				90						95	
Ser	Asn	Tyr	Thr	Phe	Arg	Ile	Phe	Arg	Trp	Ser	Glu	Ser	Glu	Ile	Asp
			100					105					110		
Pro	Lys	His	Lys	Asp	His	Asp	Gln	Asn	Pro	Leu	Pro	Gly	Thr	Lys	His
		115					120					125			
Leu	Leu	Ala	Glu	Ser	Glu	Gln	Leu	Thr	Phe	Gly	Ser	Gly	Val	Gly	Met
	130					135						140			
Pro	Glu	Gln	Ile	His	Leu	Ser	Phe	Thr	Asn	Met	Val	Asn	Thr	Met	Arg
145					150					155					160
Val	Met	Phe	Val	Ala	Gly	Asp	Gly	Glu	Glu	Arg	Phe	Val	Arg	Tyr	Gly
				165					170					175	
Glu	Ser	Lys	Asp	Leu	Leu	Gly	Asn	Ser	Ala	Ala	Ala	Arg	Gly	Met	Arg
			180					185					190		
Tyr	Glu	Arg	Glu	His	Met	Cys	Asp	Ser	Pro	Ala	Asn	Ser	Thr	Ile	Gly
		195					200					205			
Trp	Arg	Asp	Pro	Gly	Trp	Ile	Phe	Asp	Thr	Val	Met	Lys	Asn	Leu	Asn
	210					215					220				
Asp	Gly	Val	Arg	Tyr	Tyr	Tyr	Gln	Val	Gly	Ser	Asp	Ser	Lys	Gly	Trp
225					230					235					240
Ser	Glu	Ile	His	Ser	Tyr	Ile	Ala	Arg	Asp	Val	Thr	Ala	Glu	Glu	Thr
				245					250					255	
Val	Ala	Phe	Met	Phe	Gly	Asp	Met	Gly	Cys	Ala	Thr	Pro	Tyr	Thr	Thr
			260					265					270		
Phe	Ile	Arg	Thr	Gln	Asp	Glu	Ser	Ile	Ser	Thr	Val	Lys	Trp	Ile	Leu
		275					280					285			
Arg	Asp	Ile	Glu	Ala	Leu	Gly	Asp	Lys	Pro	Ala	Met	Ile	Ser	His	Ile
	290					295					300				
Gly	Asp	Ile	Ser	Tyr	Ala	Arg	Gly	Tyr	Ser	Trp	Val	Trp	Asp	Glu	Phe
305					310					315					320
Phe	Ala	Gln	Val	Glu	Pro	Ile	Ala	Ser	Thr	Val	Pro	Tyr	His	Val	Cys
				325					330					335	
Ile	Gly	Asn	His	Glu	Tyr	Asp	Phe	Ser	Thr	Gln	Pro	Trp	Lys	Pro	Asp
			340					345					350		
Trp	Ala	Ala	Ser	Ile	Tyr	Gly	Asn	Asp	Gly	Gly	Gly	Glu	Cys	Gly	Val
		355					360					365			
Pro	Tyr	Ser	Leu	Lys	Phe	Asn	Met	Pro	Gly	Asn	Ser	Ser	Glu	Ser	Thr
	370					375					380				
Gly	Met	Lys	Ala	Pro	Pro	Thr	Arg	Asn	Leu	Tyr	Tyr	Ser	Tyr	Asp	Met
385					390					395					400
Gly	Thr	Val	His	Phe	Val	Tyr	Ile	Ser	Thr	Glu	Thr	Asn	Phe	Leu	Lys
				405					410					415	
Gly	Gly	Ser	Gln	Tyr	Glu	Phe	Ile	Lys	Arg	Asp	Leu	Glu	Ser	Val	Asp
			420					425					430		
Arg	Lys	Lys	Thr	Pro	Phe	Val	Val	Val	Gln	Gly	His	Arg	Pro	Met	Tyr
		435					440					445			

Thr	Thr	Ser	Asn	Glu	Val	Arg	Asp	Thr	Met	Ile	Arg	Gln	Lys	Met	Val
450						455					460				
Glu	His	Leu	Glu	Pro	Leu	Phe	Val	Lys	Asn	Asn	Val	Thr	Leu	Ala	Leu
465					470					475					480
Trp	Gly	His	Val	His	Arg	Tyr	Glu	Arg	Phe	Cys	Pro	Ile	Ser	Asn	Asn
				485					490					495	
Thr	Cys	Gly	Thr	Gln	Trp	Gln	Gly	Asn	Pro	Val	His	Leu	Val	Ile	Gly
			500					505					510		
Met	Ala	Gly	Gln	Asp	Trp	Gln	Pro	Ile	Trp	Gln	Pro	Arg	Pro	Asn	His
		515					520					525			
Pro	Asp	Leu	Pro	Ile	Phe	Pro	Gln	Pro	Glu	Gln	Ser	Met	Tyr	Arg	Thr
		530				535						540			
Gly	Glu	Phe	Gly	Tyr	Thr	Arg	Leu	Val	Ala	Asn	Lys	Glu	Lys	Leu	Thr
545					550					555					560
Val	Ser	Phe	Val	Gly	Asn	His	Asp	Gly	Glu	Val	His	Asp	Thr	Val	Glu
				565					570					575	
Met	Leu	Ala	Ser	Gly	Val	Val	Ile	Ser	Gly	Ser	Lys	Glu	Ser	Thr	Lys
			580					585					590		
Ile	Pro	Asn	Leu	Lys	Thr	Val	Pro	Ala	Ser	Ala	Thr	Leu	Met	Gly	Lys
		595					600					605			
Ser	Glu	Ser	Asn	Ala	Leu	Trp	Tyr	Ala	Lys	Gly	Ala	Gly	Leu	Met	Val
		610				615					620				
Val	Gly	Val	Leu	Leu	Gly	Phe	Ile	Ile	Gly	Phe	Phe	Thr	Arg	Gly	Lys
625					630					635					640
Lys	Ser	Ser	Ser	Gly	Asn	Arg	Trp	Ile	Pro	Val	Lys	Asn	Glu	Glu	Thr
				645					650					655	

<210> 75
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motifs

<400> 75
 Gly Ile Phe Arg Ser Gly Phe Pro
 1 5

<210> 76
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motifs

<400> 76
 Tyr Leu Cys Pro Glu Pro Tyr Pro
 1 5

<210> 77
 <211> 8

<212> PRT
 <213> Artificial sequence

<220>
 <223> motifs

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

<400> 77
 Lys Glu Pro Phe Val Xaa Ile Pro
 1 5

<210> 78
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> motifs

<220>
 <221> SITE
 <222> (3)..(3)
 <223> Xaa can be any naturally occurring amino acid

<400> 78
 His Cys Xaa Arg Gly Lys His Arg Thr Gly
 1 5 10

<210> 79
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> NG21 motif

<220>
 <221> SITE
 <222> (7)..(7)
 <223> Xaa = Asp or Glu

<400> 79
 Asp Asn Trp Asp Asp Ala Xaa Gly Tyr Tyr
 1 5 10

<210> 80
 <211> 12
 <212> PRT
 <213> Artificial sequence

<220>

<223> NG21 motif

<400> 80

Tyr	Arg	Asn	His	Leu	Cys	Leu	Val	Phe	Glu	Ser	Leu
1				5					10		

<210> 81

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> NG21 motif

<400> 81

Val	Leu	His	Cys	Asp	Ile	Lys	Pro	Asp	Asn	Met	Leu	Val	Asn	Glu
1				5					10					15

<210> 82

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> NG21 motif

<220>

<221> SITE

<222> (8)..(8)

<223> Xaa = Phe or Val

<220>

<221> SITE

<222> (11)..(11)

<223> Xaa can be any naturally occurring amino acid

<400> 82

Thr	Pro	Tyr	Leu	Val	Ser	Arg	Phe	Tyr	Arg	Xaa	Pro	Glu	Ile
1				5						10			

<210> 83

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> NG24 motif

<220>

<221> SITE

<222> (6)..(6)

<223> Xaa can be any naturally occurring amino acid

<400> 83
 Val Arg His Arg Asp Xaa Lys Ser
 1 5

<210> 84
 <211> 9
 <212> PRT
 <213> Artificial sequence

<220>
 <223> NG24 motif

<220>
 <221> SITE
 <222> (4)..(4)
 <223> Xaa can be any naturally occurring amino acid

<400> 84
 Gly Thr Leu Xaa Gly Tyr Leu Asp Pro
 1 5

<210> 85
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NG24 motif

<220>
 <221> SITE
 <222> (3)..(3)
 <223> Xaa = Phe or Tyr

<220>
 <221> SITE
 <222> (5)..(5)
 <223> Xaa = Phe or Tyr

<220>
 <221> SITE
 <222> (7)..(7)
 <223> Xaa = Ile or Val

<400> 85
 Asp Val Xaa Ser Xaa Gly Xaa Leu Leu Leu Glu Ile
 1 5 10

<210> 86
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>

<223> NG28 motif

<400> 86

Arg	Arg	His	Lys	Ile	Ala	Leu	Gly
1				5			

<210> 87

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> NG28 motif

<220>

<221> SITE

<222> (2)..(2)

<223> Xaa = Lys or Arg

<400> 87

Tyr	Xaa	Ala	Pro	Glu	Leu
1			5		

<210> 88

<211> 11

<212> PRT

<213> Artificial sequence

<220>

<223> NG28 motif

<400> 88

Asp	Val	Tyr	Ala	Phe	Gly	Ile	Leu	Leu	Leu	Glu
1			5					10		

<210> 89

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> NG32 motif

<220>

<221> SITE

<222> (3)..(3)

<223> Xaa can be any naturally occurring amino acid

<400> 89

Cys	Ala	Xaa	Asp	Asp	Glu	Arg	Gly
1			5				

<210> 90
 <211> 10
 <212> PRT
 <213> Artificial sequence

<220>
 <223> NG32 motif

<400> 90
 Ala Lys Leu Ser Asp Phe Gly Leu Ala Arg
 1 5 10

<210> 91
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NG32 motif

<220>
 <221> SITE
 <222> (8)..(8)
 <223> Xaa = Arg or Lys

<400> 91
 Tyr Glu Leu Ile Thr Gly Arg Xaa
 1 5

<210> 92
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
 <223> NG32 motif

<400> 92
 Arg Pro Lys Met Ser Glu Val
 1 5

<210> 93
 <211> 648
 <212> DNA
 <213> Brassica napus

<400> 93
 atgaagctag ttgagaatac gccggcgggcg actgacaagt tcaccaccac ggaggaggag 60
 gacggtgaag acgcctgccg cacgatcgag gtcgtcgaga gaaacgtggt tcaggctcag 120
 ttgatgaag ctgctgatgc gggtgaggag cttaacctta taccgccgct caacttctct 180
 atggtggata acggaatatt ccgttctgga ttccctgatc cggctaactt ctccttcctc 240
 cagactctcg gactccgctc aattatttat ctgtgtccgg agccttacc agagagtaac 300
 atccagttcc tcaaatccaa tgggattact cttttccagt ttggcattga aggcaataag 360
 gaaccatttg tgattattcc agaccagaaa atccgcaagg cactcaatgt ccttttagat 420

gagaaaaacc atccggttct gattcattgt aagcgaggca agcatcgtagc tgggtgtctt	480
gtgggttgct tgagaaaact tcagaaatgg tgtttgactt cgatatttga cgagtaccag	540
cgatttgcag cagctaaagc tagagtttca gatcaaagat tcatggagat attcgacgtc	600
tccagcttca gtcattgtcc gatgtctttc tcttgttcca gcaggtaa	648

<210> 94
 <211> 215
 <212> PRT
 <213> Brassica napus

<400> 94
 Met Lys Leu Val Glu Asn Thr Pro Ala Ala Thr Asp Lys Phe Thr Thr
 1 5 10 15
 Thr Glu Glu Glu Asp Gly Glu Asp Ala Cys Arg Thr Ile Glu Val Val
 20 25 30
 Glu Arg Asn Val Phe Gln Ala Gln Phe Asp Glu Ala Ala Asp Ala Val
 35 40 45
 Glu Glu Leu Asn Leu Ile Pro Pro Leu Asn Phe Ser Met Val Asp Asn
 50 55 60
 Gly Ile Phe Arg Ser Gly Phe Pro Asp Pro Ala Asn Phe Ser Phe Leu
 65 70 75 80
 Gln Thr Leu Gly Leu Arg Ser Ile Ile Tyr Leu Cys Pro Glu Pro Tyr
 85 90 95
 Pro Glu Ser Asn Ile Gln Phe Leu Lys Ser Asn Gly Ile Thr Leu Phe
 100 105 110
 Gln Phe Gly Ile Glu Gly Asn Lys Glu Pro Phe Val Ile Ile Pro Asp
 115 120 125
 Gln Lys Ile Arg Lys Ala Leu Asn Val Leu Leu Asp Glu Lys Asn His
 130 135 140
 Pro Val Leu Ile His Cys Lys Arg Gly Lys His Arg Thr Gly Cys Leu
 145 150 155 160
 Val Gly Cys Leu Arg Lys Leu Gln Lys Trp Cys Leu Thr Ser Ile Phe
 165 170 175
 Asp Glu Tyr Gln Arg Phe Ala Ala Ala Lys Ala Arg Val Ser Asp Gln
 180 185 190
 Arg Phe Met Glu Ile Phe Asp Val Ser Ser Phe Ser His Val Pro Met
 195 200 205
 Ser Phe Ser Cys Ser Ser Arg
 210 215

<210> 95
 <211> 2325
 <212> DNA
 <213> Brassica napus

<400> 95
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 gagaactctg aagagaagta taagagtagt aaccgggtctc ttacggagag ccggcagtat 180
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 35 40 45
 Ser Ser Asn Arg Ser Leu Thr Glu Ser Arg Gln Tyr Asn Glu Val Arg
 50 55 60
 Ala Arg Ser Arg Ser Lys Ser Arg Val Val Ala Glu Asp Glu Phe Ser
 65 70 75 80
 Val Arg Gly Arg His Arg Asp Ser Ser Arg Glu Tyr Arg His Asp Arg
 85 90 95
 Val Asp Ser Arg Arg Ser Glu Gly Arg Gly Arg Tyr Glu Gly Tyr Asp
 100 105 110
 Arg Glu Tyr Thr Arg Glu Asp Val Glu Arg Glu Arg Ser Lys Glu Arg
 115 120 125
 Asp Met Asp Arg Glu Gly Ser Ile Arg Asp Arg Asp Ser Glu Gly Ser
 130 135 140

Lys	Arg	Arg	Glu	Arg	Asp	Ile	Asp	Arg	Arg	Arg	Glu	Arg	Glu	Arg	Glu	145	150	155	160
Glu	Arg	Arg	Glu	Ile	Glu	Ala	Asp	Arg	Glu	Arg	Arg	Lys	Asp	Lys	Glu	165	170	175	
Arg	Glu	Arg	Ser	Ile	Asp	Arg	Asp	Arg	Arg	Arg	Glu	Arg	Glu	Gly	Arg	180	185	190	
Asp	Arg	Asp	Asn	Glu	Arg	Gly	Gly	Ser	Val	Asp	Arg	Glu	Arg	Arg	Arg	195	200	205	
Glu	Arg	Glu	Gly	Asp	Tyr	Leu	Arg	Asp	Arg	Asp	Asn	Arg	Arg	Gly	Arg	210	215	220	
Ser	Arg	Asp	Arg	Thr	Arg	Tyr	Asp	Ser	Arg	Glu	Arg	Met	Arg	Glu	Lys	225	230	235	240
Glu	Arg	Glu	Ser	Asp	Lys	Asp	Arg	Glu	Ile	Gln	Ala	Asp	Lys	Glu	Lys	245	250	255	
His	Lys	Ser	Val	Glu	Val	Asp	Asn	Gly	Glu	Arg	Ser	Lys	Tyr	Glu	Asn	260	265	270	
Asp	Gln	Asp	Asp	Asn	Asp	Lys	Glu	Phe	Ile	Trp	Lys	Ser	Pro	Glu	Glu	275	280	285	
Ile	Glu	Glu	Glu	Glu	Leu	Asn	Lys	Ile	Arg	Glu	Ser	Ile	Glu	Lys	Phe	290	295	300	
Lys	Lys	Lys	Pro	Glu	Gln	Gln	Ser	Glu	Leu	Ile	Ser	Gln	Asp	Lys	Glu	305	310	315	320
Ile	Asp	Phe	Val	Gln	Glu	Ser	Ser	Ala	Pro	Asp	Ser	Ala	Ser	Phe	Ala	325	330	335	
Val	Val	Thr	Asp	Ala	Asn	Ala	Gly	Ala	Ala	Lys	Ala	Lys	Ser	Asp	Phe	340	345	350	
Asp	Pro	Val	Val	Ser	Asp	Val	Ala	Lys	Thr	Ser	Leu	Thr	Ala	Gly	Gly	355	360	365	
Pro	Pro	Asn	Met	Phe	Gly	Ile	Ser	Asn	Ser	Glu	Lys	Thr	Gln	Ala	Pro	370	375	380	
Ala	Gly	Leu	Gly	Glu	Gly	Ser	Pro	Lys	Ser	Glu	Arg	Ser	Ala	Asp	Met	385	390	395	400
Phe	His	Asp	Asp	Ile	Phe	Gly	Glu	Ser	Pro	Ala	Ala	Asn	Gln	Lys	Val	405	410	415	
Asp	His	Met	Arg	Gly	Lys	Gly	Asp	Gly	Val	Pro	Met	Val	Arg	Ser	Gly	420	425	430	
Leu	His	Asp	Asn	Trp	Asp	Asp	Ala	Glu	Gly	Tyr	Tyr	Ser	Tyr	Gln	Phe	435	440	445	
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Gly	Val	Phe	Ser	Thr	Val	Val	Arg	Ala	Lys	Asp	Leu	Arg	Ala	Gly	Pro	465	470	475	480
Ala	Glu	Pro	Asp	Glu	Val	Ala	Ile	Lys	Ile	Ile	Arg	Asn	Asn	Glu	Thr	485	490	495	
Met	His	Lys	Ala	Gly	Gln	Thr	Glu	Val	Gln	Ile	Leu	Lys	Lys	Leu	Ala	500	505	510	
Gly	Ala	Asp	Arg	Asp	Asp	Lys	Arg	His	Cys	Val	Arg	Leu	Leu	Ser	Ser	515	520	525	
Phe	Lys	Tyr	Arg	Asn	His	Leu	Cys	Leu	Val	Phe	Glu	Ser	Leu	His	Leu	530	535	540	
Asn	Leu	Arg	Glu	Leu	Leu	Lys	Lys	Phe	Gly	Arg	Asn	Ile	Gly	Leu	Lys	545	550	555	560
Leu	Ser	Ala	Val	Arg	Ser	Tyr	Ser	Lys	Gln	Leu	Phe	Ile	Ala	Leu	Lys	565	570	575	
His	Leu	Lys	Asn	Cys	Gly	Val	Leu	His	Cys	Asp	Ile	Lys	Pro	Asp	Asn	580	585	590	

Met Leu Val Asn Glu Asn Lys Thr Val Leu Lys Leu Cys Asp Phe Gly
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Asn Ala Met Phe Ala Gly Lys Asn Glu Val Thr Pro Tyr Leu Val Ser
610 615 620
Arg Phe Tyr Arg Ser Pro Glu Ile Ile Leu Gly Leu Ala Tyr Asp His
625 630 635 640
Pro Leu Asp Ile Trp Ser Val Gly Cys Cys Leu Tyr Glu Leu Tyr Cys
645 650 655
Gly Lys Val Leu Phe Pro Gly Ala Thr Asn Asn Asp Met Leu Arg Leu
660 665 670
His Met Glu Leu Lys Gly Leu Phe Pro Lys Lys Met Leu Arg Lys Gly
675 680 685
Ala Phe Ile Asp Gln His Phe Asp His Asp Leu Asn Phe Tyr Ala Thr
690 695 700
Glu Glu Asp Thr Val Ser Gly Lys Met Met Lys Arg Met Ile Leu Asn
705 710 715 720
Val Lys Pro Lys Asp Phe Gly Ser Ile Ile Lys Gly Tyr Pro Gly Glu
725 730 735
Asp Pro Lys Met Leu Ala His Phe Arg Asp Leu Leu Asp Lys Met Phe
740 745 750
Ile Leu Asp Pro Glu Lys Arg Leu Thr Val Ser Gln Ala Leu Ala His
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<212> DNA
<213> Brassica napus

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gatgcaaggt cttctaaaga ctcagcgttt accaaagata acgaccgtcc ggatcttgat 180
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 65 70 75 80
 Glu Gly Phe Lys Glu Glu Ser Ile Val Gly Lys Gly Ser Phe Ser Cys
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 Val Tyr Lys Gly Val Leu Arg Asp Gly Thr Thr Val Ala Val Lys Lys
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 Ala Ile Met Ser Ser Asp Lys Gln Lys Asn Ser Asn Glu Phe Arg Thr
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 Leu Gly Tyr Cys Glu Glu Gly Gly Glu Arg Leu Leu Val Tyr Glu Phe
 145 150 155 160
 Met Ala His Gly Ser Leu Tyr Asn His Leu His Gly Lys Asn Lys Ala
 165 170 175
 Leu Lys Glu Gln Leu Asp Trp Val Lys Arg Val Thr Ile Ala Val Gln
 180 185 190
 Ala Ala Arg Gly Ile Glu Tyr Leu His Gly Tyr Ala Cys Pro Pro Val
 195 200 205
 Ile His Arg Asp Ile Lys Ser Ser Asn Ile Leu Ile Asp Glu Glu His
 210 215 220
 Asn Ala Arg Val Ala Asp Phe Gly Leu Ser Leu Leu Gly Pro Val Asp
 225 230 235 240
 Ser Gly Ser Pro Leu Ala Glu Leu Pro Ala Gly Thr Leu Gly Tyr Leu
 245 250 255
 Asp Pro Glu Tyr Tyr Arg Leu His Tyr Leu Thr Thr Lys Ser Asp Val
 260 265 270
 Tyr Ser Phe Gly Val Leu Leu Leu Glu Ile Leu Ser Gly Arg Lys Ala
 275 280 285
 Ile Asp Met His Tyr Glu Glu Gly Asn Ile Val Glu Trp Ala Val Pro
 290 295 300
 Leu Ile Lys Ala Gly Asp Ile Thr Ser Ile Leu Asp Pro Val Leu Lys
 305 310 315 320
 Gln Pro Thr Glu Ile Glu Ala Leu Arg Arg Ile Val Ser Val Ala Cys
 325 330 335
 Lys Cys Val Arg Met Arg Gly Lys Asp Arg Pro Ser Met Asp Lys Val
 340 345 350
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 355 360 365
 Ser Glu Gln Pro Ile Leu Pro Thr Glu Val Val Leu Gly Ser Ser Arg
 370 375 380
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 385 390 395 400

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 <213> Brassica napus

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<210> 100
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 <212> PRT
 <213> Brassica napus

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 35 40 45
 Gly Leu Asp Lys Ile Met Val Gln Ala Val Ala Asp Glu Ile Val Ser
 50 55 60
 Gln Ala Lys Ser Asp Gly Tyr Lys Ala Pro Glu Leu His Lys Met Lys
 65 70 75 80
 Lys Cys Asn Pro Arg Ser Asp Val Tyr Ala Phe Gly Ile Leu Leu Leu
 85 90 95
 Glu Ile Leu Met Gly Lys Lys Pro Gly Lys Ser Gly Arg Asn Gly Gly
 100 105 110
 Glu Tyr Val Asp Leu Pro Ser Leu Val Lys Ala Ala Val Leu Glu Glu
 115 120 125
 Thr Thr Met Glu Val Phe Asp Leu Glu Ala Met Lys Gly Ile Arg Ser
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 Pro Met Glu Glu Gly Leu Val His Ala Leu Lys Leu Ala Met Gly Cys
 145 150 155 160
 Cys Ala Pro Val Thr Thr Val Arg Pro Ser Met Glu Glu Val Val Lys
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<210> 101
 <211> 1278
 <212> DNA
 <213> Brassica napus

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 <211> 425
 <212> PRT
 <213> Brassica napus

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 35 40 45
 Ser Thr Glu Ser Ser Met Gly Arg Lys Asn Ser Tyr Pro Ser Met Ser
 50 55 60
 Ala Arg Glu Ser Asn Leu Arg Glu Phe Ser Val Thr Asp Leu Lys Ala
 65 70 75 80
 Ala Thr Lys Asn Phe Ser Arg Ser Val Met Ile Gly Glu Gly Gly Phe
 85 90 95
 Gly Cys Val Phe Arg Gly Thr Val Arg Asp Leu Glu Asp Pro Ser Ile
 100 105 110

Lys	Ile	Glu	Val	Ala	Val	Lys	Gln	Leu	Gly	Lys	Arg	Gly	Leu	Gln	Gly		
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His	Lys	Glu	Trp	Val	Thr	Glu	Val	Asn	Phe	Leu	Gly	Val	Val	Glu	His		
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Ser	Asn	Leu	Val	Lys	Leu	Leu	Gly	Tyr	Cys	Ala	Glu	Asp	Asp	Glu	Arg		
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Glu	Ser	His	Leu	Ser	Pro	Arg	Ser	Leu	Thr	Val	Leu	Thr	Trp	Asp	Leu		
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Arg	Leu	Arg	Ile	Ala	Gln	Asp	Ala	Ala	Arg	Gly	Leu	Thr	Tyr	Leu	His		
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225					230					235					240		
Ala	Arg	Leu	Gly	Pro	Ser	Glu	Gly	Leu	Thr	His	Val	Thr	Thr	Asp	Val		
			245					250						255			
Val	Gly	Thr	Met	Ala	Tyr	Ala	Ala	Pro	Glu	Tyr	Ile	Gln	Thr	Gly	Arg		
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Leu	Thr	Ser	Lys	Ser	Asp	Val	Trp	Gly	Tyr	Gly	Val	Phe	Ile	Tyr	Glu		
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Leu	Ile	Thr	Gly	Arg	Lys	Pro	Val	Asp	Arg	Asn	Lys	Pro	Lys	Gly	Glu		
	290				295					300							
Gln	Lys	Leu	Leu	Glu	Trp	Val	Arg	Pro	Tyr	Leu	Ser	Asp	Thr	Arg	Lys		
305					310					315					320		
Phe	Lys	Leu	Ile	Leu	Asp	Pro	Arg	Leu	Glu	Gly	Lys	Tyr	Pro	Leu	Lys		
			325					330						335			
Ser	Val	Gln	Lys	Leu	Ala	Val	Val	Ala	Asn	Arg	Cys	Leu	Val	Arg	Asn		
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Pro	Lys	Ala	Arg	Pro	Lys	Met	Ser	Glu	Val	Leu	Glu	Met	Val	Asn	Lys		
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Ile	Val	Glu	Ala	Pro	Ser	Cys	Ser	Gly	Thr	Ser	Pro	Gln	Leu	Val	Pro		
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Leu	Gln	Gly	Leu	Glu	Thr	Ser	Arg	Asp	Ala	Gly	Gly	Gly	Lys	Lys	Lys		
385					390					395					400		
Arg	Gly	Leu	Glu	Asn	Gly	Gly	Gly	Glu	Gly	Gly	Trp	Phe	Gly	Lys	Leu		
			405					410						415			
Trp	Asn	Pro	Lys	Thr	Ile	Arg	Ala	Cys									
		420						425									

CLAIMS

What is claimed is:

1. A method to make a transgenic plant having increased rate of plant growth and/or elevated plant yields comprising:
 - a) introducing a nucleic acid molecule encoding a putative phosphatase or kinase into a plant or plant cell, wherein the nucleic acid molecule comprises:
 - i) a sequence having at least 65% identity with SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101; and/or
 - ii) a sequence encoding a polypeptide having at least 65% identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100, or 102; and
 - b) over-expressing the nucleic acid molecule in the plant or plant cell.
2. The method of claim 1, wherein the nucleic acid molecule comprises:
 - i) a sequence selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101; and/or
 - ii) a sequence encoding a polypeptide selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102.
3. The method of claim 1, further comprising regenerating, from said transformed plant or plant cell, a plant having enhanced growth and/or yield.
4. The method of claim 1, wherein plant growth rate and/or plant yield is increased.
5. The method of claim 1, wherein the plant is of a species selected from the group consisting of: Asparagus, Bromus, Hemerocalli, Hordeum, Lolium, Panicum, Pennisetum, Saccharum, Sorghum, Trigonell, Triticum, Zea, Antirrhinum, Arabidopsis, Arachis, Atropa, Brassica, Browallia, Capsicum, Carthamus, Cichorium, Citrus, Chrysanthemum, Cucumis, Datura, Daucus, Digitalis, Fragaria, Geranium, Glycine, Helianthus, Hyoscyamus, Ipomoea, Lactuca, Linum, Lotus, Solanum lycopersicon, Majorana, Malva, Gossypium, Manihot, Medicago, Nemesis, Nicotiana, Onobrychis, Pelargonium, Petunia, Ranunculus, Raphanus, Salpiglossis, Senecio, Sinapis, Solanum, Trifolium, Vigna, and Vitis; or
a species selected from the family Brassica; a species selected from soybean, maize, potato, rice, sugar canes, switchgrass, cotton, sorghum, alfalfas, rapeseed, or canola.

6. The method of claim 1, wherein the plant cell is a seed, stem, shoot, or root cell.
7. The method of claim 1, wherein plant weight, total weight of leaf or seed, total number of inflorescence, carbon metabolism, and/or level of carbohydrate, amino acid, and/or lipid production is increased, when compared to a wild-type plant of the same species cultivated under the same conditions.
8. A transgenic plant cell, comprising:
- i) a nucleic acid molecule selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101, wherein said nucleic acid molecule is over-expressed in the transgenic plant cell when compared to plant cells of the same type in a wild-type plant of the same species; and/or
 - ii) a nucleic acid molecule that encodes a protein selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102,
- wherein said nucleic acid molecule is over-expressed in the transgenic plant cell when compared to plant cells of the same type in a wild-type plant of the same species.
9. The transgenic plant cell of claim 8, comprising:
- i) a nucleic acid molecule selected from SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 93, 95, 97, 99 or 101, wherein said nucleic acid molecule is over-expressed in the transgenic plant cell when compared to plant cells of the same type in a wild-type plant of the same species; and/or
 - ii) a nucleic acid that encodes a protein selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 94, 96, 98, 100 or 102,
- wherein said nucleic acid molecule is over-expressed in the transgenic plant cell when compared to plant cells of the same type in a wild-type plant of the same species.
10. The transgenic plant cell of claim 8, wherein the plant cell comprises a nucleotide sequence having at least 65% identity with SEQ ID NO: 1, 3, 5, 7, or 9.
11. The transgenic plant cell of claim 8, wherein the plant cell comprises a nucleotide sequence encoding a sequence having at least 65% identity with SEQ ID NO: 2, 4, 6, 8, or 10.

12. The transgenic plant cell of claim 8, wherein said plant cell is of a monocotyledonous species or a dicotyledonous species.

13. The transgenic plant cell of claim 8, wherein the plant cell is of a species selected from the group consisting of: Asparagus, Bromus, Hemerocalli, Hordeum, Lolium, Panicum, Pennisetum, Saccharum, Sorghum, Trigonell, Triticum, Zea, Antirrhinum, Arabidopsis, Arachis, Atropa, Brassica, Browallia, Capsicum, Carthamus, Cichorium, Citrus, Chrysanthemum, Cucumis, Datura, Daucus, Digitalis, Fragaria, Geranium, Glycine, Helianthus, Hyscyamus, Ipomoea, Lactuca, Linum, Lotus, Solanum lycopersicon, Majorana, Malva, Gossypium, Manihot, Medicago, Nemesis, Nicotiana, Onobrychis, Pelargonium, Petunia, Ranunculus, Raphanus, Salpiglossis, Senecio, Sinapis, Solanum, Trifolium, Vigna, and Vitis.

14. The transgenic plant cell of claim 8, wherein the plant cell is of a species selected from the family Brassica.

15. A transgenic plant, comprising a transgenic plant cell of claim 8.

16. The transgenic plant of claim 15, wherein plant weight, total weight of leaf or seed, total number of inflorescence, carbon metabolism, and/or level of carbohydrate, amino acid, and/or lipid production is increased, when compared to a wild-type plant of the same species cultivated under the same conditions.

Application number / Numéro de demande: 2,834,945

Figures: _____

Pages: 1,2,4,5 _____

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(Request original documents in File Prep. Section on the 10th floor)

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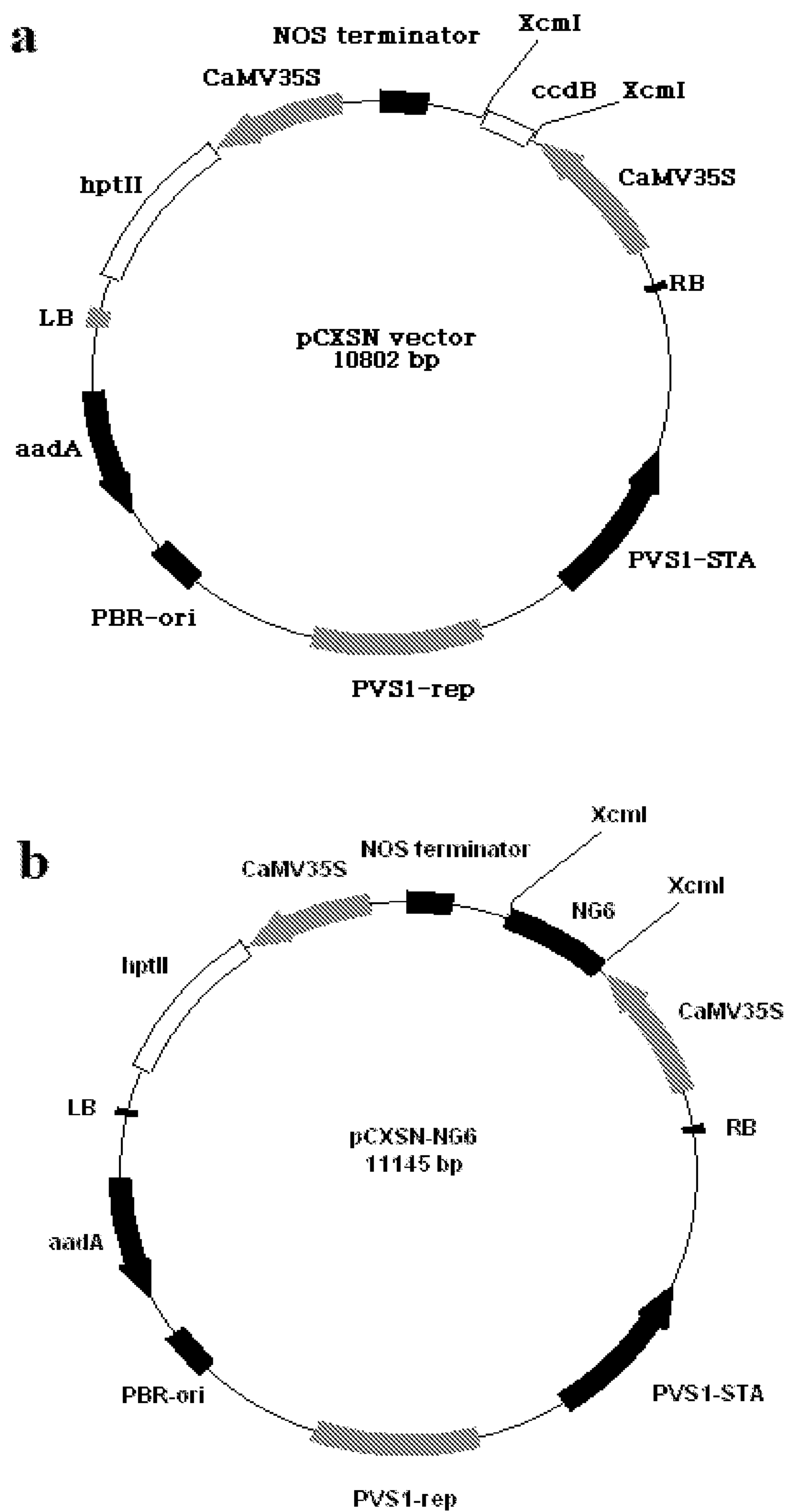


FIG. 3