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HERSCHKOVITZ, Yoav [IL/IL]; 4/4 Arad Street, 53400
Givataim (IL).

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PCT/IL2008/001657

(74) Agents: **G.E. EHRLICH (1995) LTD.** et al.; 11 Men-
achem Begin Street, 52521 Ramat Gan (IL).

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(71) Applicant (*for all designated States except US*): **EVO-
GENE LTD.** [IL/IL]; 13 Gad Finstein Street, 76121 Re-
chovot (IL).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **RONEN, Gil**
[IL/IL]; 20 Moshav Ometz, 38870 Emek Hefer (IL).
VINOCUR, Basia Judith [IL/IL]; 8/10 Eizenberg
Street, 76291 Rechovot (IL). **DIBER, Alex** [IL/IL];
11/12 Grinspan Street, 75502 Rishon-lezion (IL). **AYAL,
Sharon** [IL/IL]; 9 HaShita Street, P.O Box 209, 76951
Kiryat-ekron (IL). **KARCHI, Hagai** [IL/IL]; 249 Sapir
Street, Moshav Sitriya, 76834 Doar-na Emek Soreq (IL).

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(54) Title: ISOLATED POLYPEPTIDES, POLYNUCLEOTIDES USEFUL FOR MODIFYING WATER USER EFFICIENCY, FERTILIZER USE EFFICIENCY, BIOTIC/ABIOTIC STRESS TOLERANCE, YIELD AND BIOMASS IN PLANTS

(57) Abstract: Polynucleotides, polypeptides, plant cells expressing same and methods of using same for increasing abiotic stress tolerance water use efficiency (WUE), fertilizer use efficiency (FUE), biomass, vigor and/or yield of a plant. The method is effected by expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259, thereby increasing the water use efficiency (WUE), the fertil-
izer use efficiency (FUE), the biomass, the vigor and/or the yield of the plant.



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ISOLATED POLYPEPTIDES, POLYNUCLEOTIDES USEFUL FOR MODIFYING
WATER USER EFFICIENCY, FERTILIZER USE EFFICIENCY, BIOTIC/ABIOTIC
STRESS TOLERANCE, YIELD AND BIOMASS IN PLANTS

5 FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to novel aquaporin polynucleotides and polypeptides, and more particularly, but not exclusively, to methods of using same for increasing abiotic stress tolerance, water use efficiency (WUE), fertilizer use efficiency (FUE), biomass, vigor and/or yield of a plant.

10 Abiotic stress conditions such as salinity, drought, flood, suboptimal temperature and toxic chemical pollution, cause substantial damage to agricultural plants. Most plants have evolved strategies to protect themselves against these conditions. However, if the severity and duration of the stress conditions are too great, the effects on plant development, growth and yield of most crop plants are profound. Furthermore, most of
15 the crop plants are highly susceptible to abiotic stress (ABS) and thus necessitate optimal growth conditions for commercial crop yields. Continuous exposure to stress causes major alterations in the plant metabolism which ultimately leads to cell death and consequently yield losses.

The global shortage of water supply is one of the most severe agricultural
20 problems affecting plant growth and crop yield and efforts are made to mitigate the harmful effects of desertification and salinization of the world's arable land. Thus, Agbiotech companies attempt to create new crop varieties which are tolerant to different abiotic stresses focusing mainly in developing new varieties that can tolerate water shortage for longer periods.

25 Studies have shown that plant adaptations to adverse environmental conditions are complex genetic traits with polygenic nature. When water supply is limited, the plant WUE is critical for the survival and yield of crop. Since water scarcity is increasing and water quality is reducing worldwide it is important to increase water productivity and plant WUE. Many of the environmental abiotic stresses, such as
30 drought, low temperature or high salt, decrease root hydraulic conductance, affect plant growth and decrease crop productivity.

Genetic improvement of FUE in plants can be generated either via traditional breeding or via genetic engineering. Attempts to improve FUE in transgenic plants are

described in U.S. Patent Applications 20020046419 to Choo, et al.; U.S. Pat. Appl. 20030233670 to Edgerton et al.; U.S. Pat. Appl. 20060179511 to Chomet et al.; Yanagisawa et al. [Proc. Natl. Acad. Sci. U.S.A. 2004, 101(20):7833-8]; Good AG et al. [Trends Plant Sci. 2004, 9(12):597-605]; and U.S. Pat. No. 6,084,153 to Good et al.

5 Aquaporins (AQPs), the water channel proteins, are involved in transport of water through the membranes, maintenance of cell water balance and homeostasis under changing environmental and developmental conditions [Maurel C. Plant aquaporins: Novel functions and regulation properties. FEBS Lett. 2007, 581(12):2227-36]. These proteins are considered to be the main passage enabling transport of water and small
10 neutral solutes such as urea and CO₂ through the membrane [Maurel C. Plant aquaporins: Novel functions and regulation properties. FEBS Lett. 2007 Jun 12; 581(12):2227-36]. In plants, AQPs are present as four subfamilies of intrinsic proteins: plasma membrane (PIP), tonoplast (TIP), small and basic (SIP) and NOD26-like (NIP). The total number of AQP members in plants, as compared to animals, appears to be
15 surprisingly high [Maurel C., 2007 (Supra)]. For instance, 35 AQP genes have been identified in the Arabidopsis genome [Quigley F, et al., "From genome to function: the Arabidopsis aquaporins". Genome Biol. 2002, 3(1):RESEARCH0001.1-1.17], 36 in maize [Chaumont F, et al., 2001, "Aquaporins constitute a large and highly divergent protein family in maize. Plant Physiol", 125(3):1206-15], and 33 in rice [Sakurai, J., et
20 a., 2005, Identification of 33 rice aquaporin genes and analysis of their expression and function. Plant Cell Physiol. 46, 1568-1577]. The high number of AQPs in plants suggests a diverse role and differential regulation under variable environmental conditions [Maurel C., 2007 (Supra)].

WO2004/104162 to the present inventors teaches polynucleotide sequences and
25 methods of utilizing same for increasing the tolerance of a plant to abiotic stresses and/or increasing the biomass of a plant.

WO2007/020638 to the present inventors teaches polynucleotide sequences and methods of utilizing same for increasing the tolerance of a plant to abiotic stresses and/or increasing the biomass, vigor and/or yield of a plant.

30 Lian HL, et al., 2006 (Cell Res. 16: 651-60) over-expressed members of the PIP1 subgroup of AQPs in rice. Aharon R., et al. 2003 (Plant Cell, 15: 439-47) over-

expressed the Arabidopsis plasma membrane aquaporin, PIP1b, in transgenic tobacco plants.

SUMMARY OF THE INVENTION

5 According to an aspect of some embodiments of the present invention there is provided a method of increasing abiotic stress tolerance of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs: 33, 34, 30, 27-29, 31, 32,
10 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259, thereby increasing the abiotic stress tolerance of the plant.

According to an aspect of some embodiments of the present invention there is
15 provided a method of increasing water use efficiency (WUE), fertilizer use efficiency (FUE), biomass, vigor and/or yield of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of
20 SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259, thereby increasing the water use efficiency (WUE), the fertilizer use efficiency (FUE), the biomass, the vigor and/or the yield of the plant.

According to an aspect of some embodiments of the present invention there is
25 provided an isolated polynucleotide comprising a nucleic acid sequence at least 80 % identical to the nucleic acid sequence selected from the group consisting of SEQ ID NOs:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857 and 2859-3051.

30 According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct, comprising the isolated polynucleotide of the invention and a promoter for directing transcription of the nucleic acid sequence.

According to an aspect of some embodiments of the present invention there is provided an isolated polypeptide, comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

According to an aspect of some embodiments of the present invention there is provided a plant cell comprising an exogenous polypeptide having an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

According to an aspect of some embodiments of the present invention there is provided a plant cell comprising an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % homologous to the nucleic acid sequence selected from the group consisting of SEQ ID NOs:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857 and 2859-3051.

According to an aspect of some embodiments of the present invention there is provided a method of increasing abiotic stress tolerance of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising the amino acid sequence set forth by SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259, thereby increasing the abiotic stress tolerance of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing water use efficiency (WUE), fertilizer use efficiency (FUE), biomass, vigor and/or yield of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising the amino acid sequence set forth by SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-

1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259, thereby increasing the water use efficiency (WUE), the fertilizer use efficiency (FUE), the biomass, the vigor and/or the yield of the plant.

5 According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857, 2859-3050 or 3051.

10 According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct, comprising the isolated polynucleotide of the invention and a promoter for directing transcription of the nucleic acid sequence.

 According to an aspect of some embodiments of the present invention there is provided an isolated polypeptide, comprising the amino acid sequence set forth by SEQ
15 ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

 According to an aspect of some embodiments of the present invention there is provided a plant cell comprising an exogenous polypeptide having the amino acid
20 sequence set forth by SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

 According to an aspect of some embodiments of the present invention there is
25 provided a plant cell comprising an exogenous polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857, 2859-3050 or 3051.

 According to some embodiments of the invention, the polynucleotide is selected
30 from the group consisting of SEQ ID NOs:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857 and 2859-3051.

According to some embodiments of the invention, the amino acid sequence is selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-
5 2769, 3052-3065 and 3067-3259.

According to some embodiments of the invention, the polypeptide is selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-
10 3065 and 3067-3259.

According to some embodiments of the invention, the abiotic stress is selected from the group consisting of salinity, water deprivation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

15 According to some embodiments of the invention, the method further comprising growing the plant expressing the exogenous polynucleotide under the abiotic stress.

According to some embodiments of the invention, the promoter is a constitutive promoter.

20 According to some embodiments of the invention, the plant cell forms a part of a plant.

Unless otherwise defined, all technical and/or scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of the invention, 25 exemplary methods and/or materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be necessarily limiting.

BRIEF DESCRIPTION OF THE DRAWINGS

30 Some embodiments of the invention are herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for

purposes of illustrative discussion of embodiments of the invention. In this regard, the description taken with the drawings makes apparent to those skilled in the art how embodiments of the invention may be practiced.

In the drawings:

5 FIG. 1 is a schematic illustration of the pGI binary plasmid used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; H- *HindIII* restriction enzyme; X - *XbaI* restriction enzyme; B - *BamHI* restriction enzyme; S - *SalI* restriction enzyme; Sm - *SmaI* restriction enzyme; R-I - *EcoRI* restriction enzyme; Sc - *SacI/SstI/Ecl136II*; (numbers) - Length in base-
10 pairs; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); GUSintron - the GUS reporter gene (coding sequence and intron). The isolated polynucleotide sequences of some embodiments of the invention were cloned into the vector while replacing the GUSintron reporter gene.

15 FIGs. 2A-B are images depicting root development of plants grown in transparent agar plates. The different transgenes were grown in transparent agar plates for 10-15 days and the plates were photographed every 2-5 days starting at day 1. FIG. 2A - An exemplary image of plants taken following 12 days on agar plates. FIG. 2B - An exemplary image of root analysis in which the length of the root measured is
20 represented by a red arrow.

FIGs. 3A-F are histograms depicting the total economic fruit yield, plant biomass and harvest index for TOM-ABST36 (black bar) vs. control (white bar) plants growing in the commercial greenhouse under a 200 mM sodium chloride (NaCl) irrigation regime (FIG. 3A-C, respectively), or under two different water-stress regimes (WLI-1 and WLI-
25 2; FIG. 3D-F, respectively). Yield performance was compared to plants growing under standard irrigation conditions (0 mM NaCl and WLI-0). Results are the average of the four independent events. *Significantly different at $P \leq 0.05$.

FIGs. 3G-J are photographs of transgenic tomato plants or control plants grown under various conditions. FIG. 3G - TOM-ABST36 plants growing under regular
30 irrigation conditions; FIG. 3H - control plants growing under regular irrigation conditions; FIG. 3I - TOM-ABST36 plants after growing under a 200-mM NaCl-

irrigation regime during the entire growing season; FIG. 3J - control plants after growing under a 200-mM NaCl-irrigation regime during the entire growing season.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

5 The present invention, in some embodiments thereof, relates to novel aquaporin polynucleotides and polypeptides, and more particularly, but not exclusively, to methods of using same for increasing abiotic stress tolerance, water use efficiency, fertilizer use efficiency, biomass, vigor and/or yield of a plant.

10 Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not necessarily limited in its application to the details set forth in the following description or exemplified by the Examples. The invention is capable of other embodiments or of being practiced or carried out in various ways.

 While reducing the invention to practice, the present inventors have identified novel aquaporin (AQP) polynucleotides and polypeptides encoded thereby.

15 Thus, as shown in the Examples section which follows, the present inventors have employed a bioinformatics approach which combines digital expression analysis and cross-species comparative genomics and screened 7.2 million expressed sequence tags (ESTs) from 1,195 relevant EST's libraries of both monocot and dicot plant species. Using this approach 1,114 different AQP genes have been identified and were
20 further classified to 11 subgroups (Table 1). Further analysis revealed that ESTs of the TIP2 subgroup are significantly over-represented in both plants' roots and in plants exposed to abiotic stress (ABS), and that polypeptides (e.g., SEQ ID NOs: 27-28, 45-48, Table 2) encoded by polynucleotides of the TIP2 subgroup (e.g., SEQ ID NOs: 1, 2, 19-22, Table 2) share a common consensus sequence TLXFXFAGVGS (SEQ ID
25 NO:2826). Based on over-representation in roots, ABS conditions and tissues with low water levels (such as seed and pollen) additional polynucleotides of the aquaporin gene family were identified (SEQ ID NOs: 3-18, 23-26, Table 2), as well as homologues or orthologues thereof (SEQ ID NOs: 53-1400, 2844-3051 for polynucleotides and SEQ ID NOs: 1401-2746, 3052-3259 for polypeptides; Table 3). Moreover, quantitative RT-
30 PCR analysis demonstrated increased expression of representative AQP genes (e.g., SEQ ID NOs: 5, 6 and 7) under salt stress, which was higher in plants exhibiting salt tolerance as compared to plants which are sensitive to salt stress (Table 5, Example 2 of

the Examples section which follows). As is further described in Examples 3-4 of the Examples section which follows, representative AQP polynucleotides were cloned (Tables 7, 8 and 9) and transgenic plants over-expressing same were generated (Example 4). These plants were shown to exhibit increased tolerance to various abiotic stresses such as osmotic stress (Tables 10-14; Example 5) and salinity stress (Tables 30-45; Example 6), increased fertilizer use efficiency (under nitrogen limiting conditions, Tables 59-68, Example 7) and increased growth, biomass and yield under normal [Tables 15-29 (Example 5), 46-58 (Example 6)] or abiotic stress conditions conditions (Examples 5-8). Altogether, these results suggest the use of the AQP polynucleotides and polypeptides of the invention for increasing abiotic stress tolerance, water use efficiency, fertilizer use efficiency, biomass, vigor and/or yield of a plant.

It should be noted that polypeptides or polynucleotides which affect (e.g., increase) plant metabolism, growth, reproduction and/or viability under stress, can also affect the plant growth, biomass, yield and/or vigor under optimal conditions.

Thus, according to one aspect of the invention, there is provided a method of increasing abiotic stress tolerance, water use efficiency, fertilizer use efficiency, growth, biomass, yield and/or vigor of a plant. The method is effected by expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising the amino acid consensus sequence TLXFXFAGVGS as set forth by SEQ ID NO:2826, wherein expression of the polypeptide promotes plants' biomass/ vigor and/or yield under normal or stress conditions.

It is suggested that the polypeptide's activity is structurally associated with the integrity of the above consensus sequence (SEQ ID NO:2826). In some embodiments of this aspect of the present invention, the activity is a water channel activity which typically resides in the vacuolar membrane (tonoplast) and/or the plasma membrane of the plant cell and enables the transport of water and/or small neutral solutes such as urea, nitrates and carbon dioxide (CO₂) through the membrane.

The phrase "abiotic stress" as used herein refers to any adverse effect on metabolism, growth, reproduction and/or viability of a plant. Accordingly, abiotic stress can be induced by suboptimal environmental growth conditions such as, for example, salinity, water deprivation, flooding, freezing, low or high temperature, heavy

metal toxicity, anaerobiosis, nutrient deficiency, atmospheric pollution or UV irradiation. The implications of abiotic stress are discussed in the Background section.

The phrase "abiotic stress tolerance" as used herein refers to the ability of a plant to endure an abiotic stress without suffering a substantial alteration in metabolism, growth, productivity and/or viability.

As used herein the phrase "water use efficiency (WUE)" refers to the level of organic matter produced per unit of water consumed by the plant, *i.e.*, the dry weight of a plant in relation to the plant's water use, *e.g.*, the biomass produced per unit transpiration.

As used herein the phrase "fertilizer use efficiency" refers to the uptake, spread, absorbent, accumulation, relocation (within the plant) and use of one or more of the minerals and organic moieties absorbed from the soil, such as nitrogen, phosphates and/or potassium.

As used herein the phrase "plant biomass" refers to the amount (measured in grams of air-dry tissue) of a tissue produced from the plant in a growing season, which could also determine or affect the plant yield or the yield per growing area.

As used herein the phrase "plant yield" refers to the amount (as determined by weight/size) or quantity (numbers) of tissue produced per plant or per growing season. Hence increased yield could affect the economic benefit one can obtain from the plant in a certain growing area and/or growing time.

As used herein the phrase "plant vigor" refers to the amount (measured by weight) of tissue produced by the plant in a given time. Hence increase vigor could determine or affect the plant yield or the yield per growing time or growing area.

As used herein the term "increasing" refers to at least about 2 %, at least about 3 %, at least about 4 %, at least about 5 %, at least about 10 %, at least about 15 %, at least about 20 %, at least about 30 %, at least about 40 %, at least about 50 %, at least about 60 %, at least about 70 %, at least about 80 %, increase in plant abiotic stress tolerance, water use efficiency, fertilizer use efficiency, growth, biomass, yield and/or vigor as compared to a native plant [*i.e.*, a plant not modified with the biomolecules (polynucleotide or polypeptides) of the invention, *e.g.*, a non-transformed plant of the same species which is grown under the same growth conditions).

As used herein, the phrase "exogenous polynucleotide" refers to a heterologous nucleic acid sequence which may not be naturally expressed within the plant or which overexpression in the plant is desired. The exogenous polynucleotide may be introduced into the plant in a stable or transient manner, so as to produce a ribonucleic acid (RNA) molecule and/or a polypeptide molecule. It should be noted that the exogenous polynucleotide may comprise a nucleic acid sequence which is identical or partially homologous to an endogenous nucleic acid sequence of the plant.

According to some embodiments of the invention, the exogenous polynucleotide of the invention encodes a polypeptide having an amino acid sequence at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs: 27-28, 45-48, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561, 2449-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2484 and 2765.

Homology (e.g., percent homology) can be determined using any homology comparison software, including for example, the BlastP or TBLASTN software of the National Center of Biotechnology Information (NCBI) such as by using default parameters, when starting from a polypeptide sequence; or the tBLASTX algorithm (available via the NCBI) such as by using default parameters, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database.

Homologous sequences include both orthologous and paralogous sequences. The term "paralogous" relates to gene-duplications within the genome of a species leading to paralogous genes. The term "orthologous" relates to homologous genes in different organisms due to ancestral relationship.

One option to identify orthologues in monocot plant species is by performing a reciprocal blast search. This may be done by a first blast involving blasting the sequence-of-interest against any sequence database, such as the publicly available NCBI

database which may be found at: Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov. If orthologues in rice were sought, the sequence-of-interest would be blasted against, for example, the 28,469 full-length cDNA clones from *Oryza sativa* Nipponbare available at NCBI. The blast results may be filtered. The full-length sequences of either the filtered results or the non-filtered results are then blasted back (second blast) against the sequences of the organism from which the sequence-of-interest is derived. The results of the first and second blasts are then compared. An orthologue is identified when the sequence resulting in the highest score (best hit) in the first blast identifies in the second blast the query sequence (the original sequence-of-interest) as the best hit. Using the same rationale a paralogue (homolog to a gene in the same organism) is found. In case of large sequence families, the ClustalW program may be used [Hypertext Transfer Protocol://World Wide Web (dot) ebi (dot) ac (dot) uk/Tools/clustalw2/index (dot) html], followed by a neighbor-joining tree (Hypertext Transfer Protocol://en (dot) wikipedia (dot) org/wiki/Neighbor-joining) which helps visualizing the clustering.

According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide consisting of the amino acid sequence set forth by SEQ ID NO:27-28, 45-48, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561, 2449-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2484 or 2765.

According to some embodiments of the invention the exogenous polynucleotide comprises a nucleic acid sequence which is at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1, 2, 19, 20-22, 53-55, 57-87, 89-141, 143-147, 149-195, 197-206, 208-212, 214, 1102-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 2751-2752 and 2748-2750.

Identity (e.g., percent homology) can be determined using any homology comparison software, including for example, the BlastN software of the National Center of Biotechnology Information (NCBI) such as by using default parameters.

According to some embodiments of the invention the exogenous polynucleotide
5 is set forth by SEQ ID NO:1, 2, 19, 20-22, 53-55, 57-87, 89-141, 143-147, 149-195, 197-206, 208-212, 214, 1102-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 2751-2752, 2748-2749, or 2750.

Notwithstanding the above, additional AQP polynucleotides and polypeptides encoded thereby are contemplated by the present teachings.

10 According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide having an amino acid sequence at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about
15 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % homologous to SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

20 According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide consisting of the amino acid sequence set forth by SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

25 In an exemplary embodiment the exogenous polynucleotide does not encode a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NOs: 1828, 1867, 1404, 1436, 1495, 1543, 1554, 1560, 2451, 2452, 2459, 2464, 2482, 2484 and 3066.

According to some embodiments of the invention, the exogenous polynucleotide
30 is at least at least about 60 %, least at least about 65 %, least at least about 70 %, least at least about 75 %, least at least about 80 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least

about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to SEQ ID NO:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857, 2859-3050 or 3051.

According to some embodiments of the invention, the polynucleotide is set forth by SEQ ID NO:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857, 2859-3050 or 3051.

10 In an exemplary embodiment the exogenous polynucleotide is not the polynucleotide set forth by SEQ ID NO: 481, 520, 56, 88, 148, 196, 207, 213, 1104, 1105, 1112, 1117, 1135, 1137 or 2858.

As used herein the term "polynucleotide" refers to a single or double stranded nucleic acid sequence which is isolated and provided in the form of an RNA sequence, a complementary polynucleotide sequence (cDNA), a genomic polynucleotide sequence and/or a composite polynucleotide sequences (e.g., a combination of the above).

As used herein the phrase "complementary polynucleotide sequence" refers to a sequence, which results from reverse transcription of messenger RNA using a reverse transcriptase or any other RNA dependent DNA polymerase. Such a sequence can be subsequently amplified *in vivo* or *in vitro* using a DNA dependent DNA polymerase.

As used herein the phrase "genomic polynucleotide sequence" refers to a sequence derived (isolated) from a chromosome and thus it represents a contiguous portion of a chromosome.

As used herein the phrase "composite polynucleotide sequence" refers to a sequence, which is at least partially complementary and at least partially genomic. A composite sequence can include some exonal sequences required to encode the polypeptide of the present invention, as well as some intronic sequences interposing therebetween. The intronic sequences can be of any source, including of other genes, and typically will include conserved splicing signal sequences. Such intronic sequences may further include cis acting expression regulatory elements.

According to some embodiments of the invention, the polynucleotide of the invention comprises no more than 5000 nucleic acids in length. According to some

embodiments of the invention, the polynucleotide of the invention comprises no more than 4000 nucleic acids in length, e.g., no more than 3000 nucleic acids, e.g., no more than 2500 nucleic acids.

5 Nucleic acid sequences encoding the polypeptides of the present invention may be optimized for expression. A non-limiting example of an optimized nucleic acid sequence is provided in SEQ ID NO:2751, which encodes an optimized polypeptide comprising the amino acid sequence set forth by SEQ ID NO:27. Examples of such sequence modifications include, but are not limited to, an altered G/C content to more closely approach that typically found in the plant species of interest, and the removal of
10 codons atypically found in the plant species commonly referred to as codon optimization.

The phrase "codon optimization" refers to the selection of appropriate DNA nucleotides for use within a structural gene or fragment thereof that approaches codon usage within the plant of interest. Therefore, an optimized gene or nucleic acid
15 sequence refers to a gene in which the nucleotide sequence of a native or naturally occurring gene has been modified in order to utilize statistically-preferred or statistically-favored codons within the plant. The nucleotide sequence typically is examined at the DNA level and the coding region optimized for expression in the plant species determined using any suitable procedure, for example as described in Sardana et
20 al. (1996, Plant Cell Reports 15:677-681). In this method, the standard deviation of codon usage, a measure of codon usage bias, may be calculated by first finding the squared proportional deviation of usage of each codon of the native gene relative to that of highly expressed plant genes, followed by a calculation of the average squared deviation. The formula used is: $1 \text{ SDCU} = n = 1/N \left[\left(X_n - Y_n \right) / Y_n \right]^2 / N$, where X_n
25 refers to the frequency of usage of codon n in highly expressed plant genes, where Y_n to the frequency of usage of codon n in the gene of interest and N refers to the total number of codons in the gene of interest. A Table of codon usage from highly expressed genes of dicotyledonous plants is compiled using the data of Murray et al. (1989, Nuc Acids Res. 17:477-498).

30 One method of optimizing the nucleic acid sequence in accordance with the preferred codon usage for a particular plant cell type is based on the direct use, without performing any extra statistical calculations, of codon optimization Tables such as those

provided on-line at the Codon Usage Database through the NIAS (National Institute of Agrobiological Sciences) DNA bank in Japan (Hypertext Transfer Protocol://World Wide Web (dot) kazusa (dot) or (dot) jp/codon/). The Codon Usage Database contains codon usage tables for a number of different species, with each codon usage Table
5 having been statistically determined based on the data present in Genbank.

By using the above Tables to determine the most preferred or most favored codons for each amino acid in a particular species (for example, rice), a naturally-occurring nucleotide sequence encoding a protein of interest can be codon optimized for that particular plant species. This is effected by replacing codons that may have a low
10 statistical incidence in the particular species genome with corresponding codons, in regard to an amino acid, that are statistically more favored. However, one or more less-favored codons may be selected to delete existing restriction sites, to create new ones at potentially useful junctions (5' and 3' ends to add signal peptide or termination cassettes, internal sites that might be used to cut and splice segments together to produce a correct
15 full-length sequence), or to eliminate nucleotide sequences that may negatively effect mRNA stability or expression.

The naturally-occurring encoding nucleotide sequence may already, in advance of any modification, contain a number of codons that correspond to a statistically-favored codon in a particular plant species. Therefore, codon optimization of the native
20 nucleotide sequence may comprise determining which codons, within the native nucleotide sequence, are not statistically-favored with regards to a particular plant, and modifying these codons in accordance with a codon usage table of the particular plant to produce a codon optimized derivative. A modified nucleotide sequence may be fully or partially optimized for plant codon usage provided that the protein encoded by the
25 modified nucleotide sequence is produced at a level higher than the protein encoded by the corresponding naturally occurring or native gene. Construction of synthetic genes by altering the codon usage is described in for example PCT Patent Application 93/07278.

Thus, the invention encompasses nucleic acid sequences described hereinabove;
30 fragments thereof, sequences hybridizable therewith, sequences homologous thereto, sequences encoding similar polypeptides with different codon usage, altered sequences characterized by mutations, such as deletion, insertion or substitution of one or more

nucleotides, either naturally occurring or man induced, either randomly or in a targeted fashion.

As mentioned, the present inventors have uncovered previously uncharacterized polypeptides which share the amino acid consensus sequence set forth by SEQ ID NO:2826.

Thus, the invention provides an isolated polypeptide having an amino acid sequence at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to an amino acid sequence selected from the group consisting of SEQ ID NO: 27-28, 45-48, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561, 2449-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2484 and 2765.

According to some embodiments of the invention, the invention provides an isolated polypeptide having an amino acid sequence at least about 60 %, at least about 65 %, at least about 70 %, at least about 75 %, at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to an amino acid sequence selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

According to some embodiments of the invention, the polypeptide is set forth by SEQ ID NO: 33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

In an exemplary embodiment the polypeptide is not the polypeptide set forth by SEQ ID NO: 1828, 1867, 1404, 1436, 1495, 1543, 1554, 1560, 2451, 2452, 2459, 2464, 2482, 2484 or 3066.

5 The invention also encompasses fragments of the above described polypeptides and polypeptides having mutations, such as deletions, insertions or substitutions of one or more amino acids, either naturally occurring or man induced, either randomly or in a targeted fashion.

The term "plant" as used herein encompasses whole plants, ancestors and progeny of the plants and plant parts, including seeds, shoots, stems, roots (including tubers), and plant cells, tissues and organs. The plant may be in any form including suspension cultures, embryos, meristematic regions, callus tissue, leaves, gametophytes, sporophytes, pollen, and microspores. Plants that are particularly useful in the methods of the invention include all plants which belong to the superfamily Viridiplantae, in particular monocotyledonous and dicotyledonous plants including a fodder or forage legume, ornamental plant, food crop, tree, or shrub selected from the list comprising

10 Acacia spp., Acer spp., Actinidia spp., Aesculus spp., Agathis australis, Albizia amara, Alsophila tricolor, Andropogon spp., Arachis spp, Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula spp., Brassica spp., Bruguiera gymnorrhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra spp, Camellia sinensis,

20 Canna indica, Capsicum spp., Cassia spp., Centroema pubescens, Chacoomeles spp., Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coronillia varia, Cotoneaster serotina, Crataegus spp., Cucumis spp., Cupressus spp., Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon spp., Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium spp., Dicksonia squarosa, Dibeteropogon amplexans, Dioclea spp, Dolichos spp., Dorycnium rectum, Echinochloa pyramidalis, Ehraffia spp., Eleusine coracana, Eragrostis spp., Erythrina spp., Eucalyptus spp., Euclea schimperi, Eulalia villosa, Pagopyrum spp., Feijoa sellowiana, Fragaria spp., Flemingia spp, Freycinetia banksii, Geranium thunbergii, Ginago biloba, Glycine javanica, Gliricidia spp, Gossypium hirsutum, Grevillea spp.,

25 Guibourtia coleosperma, Hedysarum spp., Hemaphysalis altissima, Heteropogon contortus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hypephyllia dissolute, Indigo incamata, Iris spp., Leptarrhena pyrrolifolia, Lespedeza spp., Lettuce spp., Leucaena

leucocephala, Loudetia simplex, Lotonus bainesli, Lotus spp., Macrotyloma axillare, Malus spp., Manihot esculenta, Medicago saliva, Metasequoia glyptostroboides, Musa sapientum, Nicotianum spp., Onobrychis spp., Ornithopus spp., Oryza spp., Peltophorum africanum, Pennisetum spp., Persea gratissima, Petunia spp., Phaseolus
 5 spp., Phoenix canariensis, Phormium cookianum, Photinia spp., Picea glauca, Pinus spp., Pisum sativum, Podocarpus totara, Pogonarthria fleckii, Pogonaffhria squarrosa, Populus spp., Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus spp., Rhamphiolepis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes spp., Robinia pseudoacacia, Rosa spp., Rubus spp.,
 10 Salix spp., Schyzachyrium sanguineum, Sciadopitys vefficillata, Sequoia sempervirens, Sequoiadendron giganteum, Sorghum bicolor, Spinacia spp., Sporobolus fimbriatus, Stiburus alopecuroides, Stylosanthos humilis, Tadehagi spp, Taxodium distichum, Themeda triandra, Trifolium spp., Triticum spp., Tsuga heterophylla, Vaccinium spp., Vicia spp., Vitis vinifera, Watsonia pyramidata, Zantedeschia aethiopica, Zea mays,
 15 amaranth, artichoke, asparagus, broccoli, Brussels sprouts, cabbage, canola, carrot, cauliflower, celery, collard greens, flax, kale, lentil, oilseed rape, okra, onion, potato, rice, soybean, straw, sugar beet, sugar cane, sunflower, tomato, squash tea, maize, wheat, barely, rye, oat, peanut, pea, lentil and alfalfa, cotton, rapeseed, canola, pepper, sunflower, tobacco, eggplant, eucalyptus, a tree, an ornamental plant, a perennial grass
 20 and a forage crop. Alternatively algae and other non-Viridiplantae can be used for the methods of the present invention.

According to some embodiments of the invention, the plant used by the method of the invention is a crop plant such as rice, maize, wheat, barley, peanut, potato, sesame, olive tree, palm oil, banana, soybean, sunflower, canola, sugarcane, alfalfa,
 25 millet, leguminosae (bean, pea), flax, lupinus, rapeseed, tobacco, poplar and cotton.

Expressing the exogenous polynucleotide of the invention within the plant can be effected by transforming one or more cells of the plant with the exogenous polynucleotide, followed by generating a mature plant from the transformed cells and cultivating the mature plant under conditions suitable for expressing the exogenous
 30 polynucleotide within the mature plant.

According to some embodiments of the invention, the transformation is effected by introducing to the plant cell a nucleic acid construct which includes the exogenous

polynucleotide of some embodiments of the invention and at least one promoter capable of directing transcription of the exogenous polynucleotide in the plant cell. Further details of suitable transformation approaches are provided hereinbelow.

As used herein, the term "promoter" refers to a region of DNA which lies
5 upstream of the transcriptional initiation site of a gene to which RNA polymerase binds to initiate transcription of RNA. The promoter controls where (e.g., which portion of a plant) and/or when (e.g., at which stage or condition in the lifetime of an organism) the gene is expressed.

Any suitable promoter sequence can be used by the nucleic acid construct of the
10 present invention. Preferably the promoter is a constitutive promoter, a tissue-specific, or an abiotic stress-inducible promoter.

Suitable constitutive promoters include, for example, CaMV 35S promoter (SEQ ID NO:2825; Odell et al., Nature 313:810-812, 1985); Arabidopsis At6669 promoter (SEQ ID NO:2823; see PCT Publication No. WO04081173A2); maize Ubi 1
15 (Christensen et al., Plant Sol. Biol. 18:675-689, 1992); rice actin (McElroy et al., Plant Cell 2:163-171, 1990); pEMU (Last et al., Theor. Appl. Genet. 81:581-588, 1991); CaMV 19S (Nilsson et al., Physiol. Plant 100:456-462, 1997); GOS2 (de Pater et al, Plant J Nov;2(6):837-44, 1992); ubiquitin (Christensen et al, Plant Mol. Biol. 18: 675-689, 1992); Rice cyclophilin (Bucholz et al, Plant Mol Biol. 25(5):837-43, 1994); Maize
20 H3 histone (Lepetit et al, Mol. Gen. Genet. 231: 276-285, 1992); Actin 2 (An et al, Plant J. 10(1);107-121, 1996) and Synthetic Super MAS (Ni et al., The Plant Journal 7: 661-76, 1995). Other constitutive promoters include those in U.S. Pat. Nos. 5,659,026, 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; and 5,608,142.

25 Suitable tissue-specific promoters include, but not limited to, leaf-specific promoters [such as described, for example, by Yamamoto et al., Plant J. 12:255-265, 1997; Kwon et al., Plant Physiol. 105:357-67, 1994; Yamamoto et al., Plant Cell Physiol. 35:773-778, 1994; Gotor et al., Plant J. 3:509-18, 1993; Orozco et al., Plant Mol. Biol. 23:1129-1138, 1993; and Matsuoka et al., Proc. Natl. Acad. Sci. USA
30 90:9586-9590, 1993], seed-preferred promoters [e.g., from seed specific genes (Simon, et al., Plant Mol. Biol. 5. 191, 1985; Scofield, et al., J. Biol. Chem. 262: 12202, 1987; Baszczynski, et al., Plant Mol. Biol. 14: 633, 1990), Brazil Nut albumin (Pearson' et al.,

Plant Mol. Biol. 18: 235- 245, 1992), legumin (Ellis, et al. Plant Mol. Biol. 10: 203-214, 1988), Glutelin (rice) (Takaiwa, et al., Mol. Gen. Genet. 208: 15-22, 1986; Takaiwa, et al., FEBS Letts. 221: 43-47, 1987), Zein (Matzke et al Plant Mol Biol, 143).323-32 1990), napA (Stalberg, et al, Planta 199: 515-519, 1996), Wheat SPA (Albanietal, Plant
 5 Cell, 9: 171- 184, 1997), sunflower oleosin (Cummins, etal., Plant Mol. Biol. 19: 873-876, 1992)], endosperm specific promoters [e.g., wheat LMW and HMW, glutenin-1 (Mol Gen Genet 216:81-90, 1989; NAR 17:461-2), wheat a, b and g gliadins (EMBO3:1409-15, 1984), Barley ltr1 promoter, barley B1, C, D hordein (Theor Appl Gen 98:1253-62, 1999; Plant J 4:343-55, 1993; Mol Gen Genet 250:750- 60, 1996),
 10 Barley DOF (Mena et al, The Plant Journal, 116(1): 53- 62, 1998), Biz2 (EP99106056.7), Synthetic promoter (Vicente-Carbajosa et al., Plant J. 13: 629-640, 1998), rice prolamin NRP33, rice -globulin Glb-1 (Wu et al, Plant Cell Physiology 39(8) 885- 889, 1998), rice alpha-globulin REB/OHP-1 (Nakase et al. Plant Mol. Biol. 33: 513-S22, 1997), rice ADP-glucose PP (Trans Res 6:157-68, 1997), maize ESR gene
 15 family (Plant J 12:235-46, 1997), sorghum gamma- kafirin (PMB 32:1029-35, 1996)], embryo specific promoters [e.g., rice OSH1 (Sato et al, Proc. Nati. Acad. Sci. USA, 93: 8117-8122), KNOX (Postma-Haarsma ef al, Plant Mol. Biol. 39:257-71, 1999), rice oleosin (Wu et at, J. Biochem., 123:386, 1998)], and flower-specific promoters [e.g., AtPRP4, chalcone synthase (chsA) (Van der Meer, et al., Plant Mol. Biol. 15, 95-
 20 109, 1990), LAT52 (Twell et al Mol. Gen Genet. 217:240-245; 1989), apetala- 3].

Suitable abiotic stress-inducible promoters include, but not limited to, salt-inducible promoters such as RD29A (Yamaguchi-Shinozaki et al., Mol. Gen. Genet. 236:331-340, 1993); drought-inducible promoters such as maize rab17 gene promoter (Pla et. al., Plant Mol. Biol. 21:259-266, 1993), maize rab28 gene promoter (Busk et.
 25 al., Plant J. 11:1285-1295, 1997) and maize lvr2 gene promoter (Pelleschi et. al., Plant Mol. Biol. 39:373-380, 1999); heat-inducible promoters such as heat tomato hsp80-promoter from tomato (U.S. Pat. No. 5,187,267).

The nucleic acid construct of some embodiments of the invention can further include an appropriate selectable marker and/or an origin of replication. According to
 30 some embodiments of the invention, the nucleic acid construct utilized is a shuttle vector, which can propagate both in E. coli (wherein the construct comprises an appropriate selectable marker and origin of replication) and be compatible with

propagation in cells. The construct according to the present invention can be, for example, a plasmid, a bacmid, a phagemid, a cosmid, a phage, a virus or an artificial chromosome.

The nucleic acid construct of some embodiments of the invention can be utilized to stably or transiently transform plant cells. In stable transformation, the exogenous polynucleotide is integrated into the plant genome and as such it represents a stable and inherited trait. In transient transformation, the exogenous polynucleotide is expressed by the cell transformed but it is not integrated into the genome and as such it represents a transient trait.

There are various methods of introducing foreign genes into both monocotyledonous and dicotyledonous plants (Potrykus, I., *Annu. Rev. Plant. Physiol., Plant. Mol. Biol.* (1991) 42:205-225; Shimamoto et al., *Nature* (1989) 338:274-276).

The principle methods of causing stable integration of exogenous DNA into plant genomic DNA include two main approaches:

(i) *Agrobacterium*-mediated gene transfer: Klee et al. (1987) *Annu. Rev. Plant Physiol.* 38:467-486; Klee and Rogers in *Cell Culture and Somatic Cell Genetics of Plants*, Vol. 6, *Molecular Biology of Plant Nuclear Genes*, eds. Schell, J., and Vasil, L. K., Academic Publishers, San Diego, Calif. (1989) p. 2-25; Gatenby, in *Plant Biotechnology*, eds. Kung, S. and Arntzen, C. J., Butterworth Publishers, Boston, Mass. (1989) p. 93-112.

(ii) Direct DNA uptake: Paszkowski et al., in *Cell Culture and Somatic Cell Genetics of Plants*, Vol. 6, *Molecular Biology of Plant Nuclear Genes* eds. Schell, J., and Vasil, L. K., Academic Publishers, San Diego, Calif. (1989) p. 52-68; including methods for direct uptake of DNA into protoplasts, Toriyama, K. et al. (1988) *Bio/Technology* 6:1072-1074. DNA uptake induced by brief electric shock of plant cells: Zhang et al. *Plant Cell Rep.* (1988) 7:379-384. Fromm et al. *Nature* (1986) 319:791-793. DNA injection into plant cells or tissues by particle bombardment, Klein et al. *Bio/Technology* (1988) 6:559-563; McCabe et al. *Bio/Technology* (1988) 6:923-926; Sanford, *Physiol. Plant.* (1990) 79:206-209; by the use of micropipette systems: Neuhaus et al., *Theor. Appl. Genet.* (1987) 75:30-36; Neuhaus and Spangenberg, *Physiol. Plant.* (1990) 79:213-217; glass fibers or silicon carbide whisker transformation of cell cultures, embryos or callus tissue, U.S. Pat. No. 5,464,765 or by the direct

incubation of DNA with germinating pollen, DeWet et al. in *Experimental Manipulation of Ovule Tissue*, eds. Chapman, G. P. and Mantell, S. H. and Daniels, W. Longman, London, (1985) p. 197-209; and Ohta, *Proc. Natl. Acad. Sci. USA* (1986) 83:715-719.

5 The *Agrobacterium* system includes the use of plasmid vectors that contain defined DNA segments that integrate into the plant genomic DNA. Methods of inoculation of the plant tissue vary depending upon the plant species and the *Agrobacterium* delivery system. A widely used approach is the leaf disc procedure which can be performed with any tissue explant that provides a good source for
10 initiation of whole plant differentiation. See, e.g., Horsch et al. in *Plant Molecular Biology Manual A5*, Kluwer Academic Publishers, Dordrecht (1988) p. 1-9. A supplementary approach employs the *Agrobacterium* delivery system in combination with vacuum infiltration. The *Agrobacterium* system is especially viable in the creation of transgenic dicotyledonous plants.

15 There are various methods of direct DNA transfer into plant cells. In electroporation, the protoplasts are briefly exposed to a strong electric field. In microinjection, the DNA is mechanically injected directly into the cells using very small micropipettes. In microparticle bombardment, the DNA is adsorbed on microprojectiles such as magnesium sulfate crystals or tungsten particles, and the microprojectiles are
20 physically accelerated into cells or plant tissues.

 Following stable transformation plant propagation is exercised. The most common method of plant propagation is by seed. Regeneration by seed propagation, however, has the deficiency that due to heterozygosity there is a lack of uniformity in the crop, since seeds are produced by plants according to the genetic variances governed
25 by Mendelian rules. Basically, each seed is genetically different and each will grow with its own specific traits. Therefore, it is preferred that the transformed plant be produced such that the regenerated plant has the identical traits and characteristics of the parent transgenic plant. Therefore, it is preferred that the transformed plant be regenerated by micropropagation which provides a rapid, consistent reproduction of the
30 transformed plants.

 Micropropagation is a process of growing new generation plants from a single piece of tissue that has been excised from a selected parent plant or cultivar. This

process permits the mass reproduction of plants having the preferred tissue expressing the fusion protein. The new generation plants which are produced are genetically identical to, and have all of the characteristics of, the original plant. Micropropagation allows mass production of quality plant material in a short period of time and offers a rapid multiplication of selected cultivars in the preservation of the characteristics of the original transgenic or transformed plant. The advantages of cloning plants are the speed of plant multiplication and the quality and uniformity of plants produced.

Micropropagation is a multi-stage procedure that requires alteration of culture medium or growth conditions between stages. Thus, the micropropagation process involves four basic stages: Stage one, initial tissue culturing; stage two, tissue culture multiplication; stage three, differentiation and plant formation; and stage four, greenhouse culturing and hardening. During stage one, initial tissue culturing, the tissue culture is established and certified contaminant-free. During stage two, the initial tissue culture is multiplied until a sufficient number of tissue samples are produced to meet production goals. During stage three, the tissue samples grown in stage two are divided and grown into individual plantlets. At stage four, the transformed plantlets are transferred to a greenhouse for hardening where the plants' tolerance to light is gradually increased so that it can be grown in the natural environment.

According to some embodiments of the invention, the transgenic plants are generated by transient transformation of leaf cells, meristematic cells or the whole plant.

Transient transformation can be effected by any of the direct DNA transfer methods described above or by viral infection using modified plant viruses.

Viruses that have been shown to be useful for the transformation of plant hosts include CaMV, Tobacco mosaic virus (TMV), brome mosaic virus (BMV) and Bean Common Mosaic Virus (BV or BCMV). Transformation of plants using plant viruses is described in U.S. Pat. No. 4,855,237 (bean golden mosaic virus; BGV), EP-A 67,553 (TMV), Japanese Published Application No. 63-14693 (TMV), EPA 194,809 (BV), EPA 278,667 (BV); and Gluzman, Y. et al., Communications in Molecular Biology: Viral Vectors, Cold Spring Harbor Laboratory, New York, pp. 172-189 (1988). Pseudovirus particles for use in expressing foreign DNA in many hosts, including plants are described in WO 87/06261.

According to some embodiments of the invention, the virus used for transient transformations is avirulent and thus is incapable of causing severe symptoms such as reduced growth rate, mosaic, ring spots, leaf roll, yellowing, streaking, pox formation, tumor formation and pitting. A suitable avirulent virus may be a naturally occurring
5 avirulent virus or an artificially attenuated virus. Virus attenuation may be effected by using methods well known in the art including, but not limited to, sub-lethal heating, chemical treatment or by directed mutagenesis techniques such as described, for example, by Kurihara and Watanabe (*Molecular Plant Pathology* 4:259-269, 2003), Gal-
on et al. (1992), Atreya et al. (1992) and Huet et al. (1994).

10 Suitable virus strains can be obtained from available sources such as, for example, the American Type culture Collection (ATCC) or by isolation from infected plants. Isolation of viruses from infected plant tissues can be effected by techniques well known in the art such as described, for example by Foster and Tatlor, Eds. "Plant Virology Protocols: From Virus Isolation to Transgenic Resistance (Methods in
15 Molecular Biology (Humana Pr), Vol 81)", Humana Press, 1998. Briefly, tissues of an infected plant believed to contain a high concentration of a suitable virus, preferably young leaves and flower petals, are ground in a buffer solution (e.g., phosphate buffer solution) to produce a virus infected sap which can be used in subsequent inoculations.

Construction of plant RNA viruses for the introduction and expression of non-
20 viral exogenous polynucleotide sequences in plants is demonstrated by the above references as well as by Dawson, W. O. et al., *Virology* (1989) 172:285-292; Takamatsu et al. *EMBO J.* (1987) 6:307-311; French et al. *Science* (1986) 231:1294-1297; Takamatsu et al. *FEBS Letters* (1990) 269:73-76; and U.S. Pat. No. 5,316,931.

When the virus is a DNA virus, suitable modifications can be made to the virus
25 itself. Alternatively, the virus can first be cloned into a bacterial plasmid for ease of constructing the desired viral vector with the foreign DNA. The virus can then be excised from the plasmid. If the virus is a DNA virus, a bacterial origin of replication can be attached to the viral DNA, which is then replicated by the bacteria. Transcription and translation of this DNA will produce the coat protein which will
30 encapsidate the viral DNA. If the virus is an RNA virus, the virus is generally cloned as a cDNA and inserted into a plasmid. The plasmid is then used to make all of the constructions. The RNA virus is then produced by transcribing the viral sequence of the

plasmid and translation of the viral genes to produce the coat protein(s) which encapsidate the viral RNA.

In one embodiment, a plant viral polynucleotide is provided in which the native coat protein coding sequence has been deleted from a viral polynucleotide, a non-native plant viral coat protein coding sequence and a non-native promoter, preferably the subgenomic promoter of the non-native coat protein coding sequence, capable of expression in the plant host, packaging of the recombinant plant viral polynucleotide, and ensuring a systemic infection of the host by the recombinant plant viral polynucleotide, has been inserted. Alternatively, the coat protein gene may be inactivated by insertion of the non-native polynucleotide sequence within it, such that a protein is produced. The recombinant plant viral polynucleotide may contain one or more additional non-native subgenomic promoters. Each non-native subgenomic promoter is capable of transcribing or expressing adjacent genes or polynucleotide sequences in the plant host and incapable of recombination with each other and with native subgenomic promoters. Non-native (foreign) polynucleotide sequences may be inserted adjacent the native plant viral subgenomic promoter or the native and a non-native plant viral subgenomic promoters if more than one polynucleotide sequence is included. The non-native polynucleotide sequences are transcribed or expressed in the host plant under control of the subgenomic promoter to produce the desired products.

In a second embodiment, a recombinant plant viral polynucleotide is provided as in the first embodiment except that the native coat protein coding sequence is placed adjacent one of the non-native coat protein subgenomic promoters instead of a non-native coat protein coding sequence.

In a third embodiment, a recombinant plant viral polynucleotide is provided in which the native coat protein gene is adjacent its subgenomic promoter and one or more non-native subgenomic promoters have been inserted into the viral polynucleotide. The inserted non-native subgenomic promoters are capable of transcribing or expressing adjacent genes in a plant host and are incapable of recombination with each other and with native subgenomic promoters. Non-native polynucleotide sequences may be inserted adjacent the non-native subgenomic plant viral promoters such that the sequences are transcribed or expressed in the host plant under control of the subgenomic promoters to produce the desired product.

In a fourth embodiment, a recombinant plant viral polynucleotide is provided as in the third embodiment except that the native coat protein coding sequence is replaced by a non-native coat protein coding sequence.

The viral vectors are encapsidated by the coat proteins encoded by the recombinant plant viral polynucleotide to produce a recombinant plant virus. The recombinant plant viral polynucleotide or recombinant plant virus is used to infect appropriate host plants. The recombinant plant viral polynucleotide is capable of replication in the host, systemic spread in the host, and transcription or expression of foreign gene(s) (exogenous polynucleotide) in the host to produce the desired protein.

Techniques for inoculation of viruses to plants may be found in Foster and Taylor, eds. "Plant Virology Protocols: From Virus Isolation to Transgenic Resistance (Methods in Molecular Biology (Humana Pr), Vol 81)", Humana Press, 1998; Maramorosh and Koprowski, eds. "Methods in Virology" 7 vols, Academic Press, New York 1967-1984; Hill, S.A. "Methods in Plant Virology", Blackwell, Oxford, 1984; Walkey, D.G.A. "Applied Plant Virology", Wiley, New York, 1985; and Kado and Agrawa, eds. "Principles and Techniques in Plant Virology", Van Nostrand-Reinhold, New York.

In addition to the above, the polynucleotide of the present invention can also be introduced into a chloroplast genome thereby enabling chloroplast expression.

A technique for introducing exogenous polynucleotide sequences to the genome of the chloroplasts is known. This technique involves the following procedures. First, plant cells are chemically treated so as to reduce the number of chloroplasts per cell to about one. Then, the exogenous polynucleotide is introduced via particle bombardment into the cells with the aim of introducing at least one exogenous polynucleotide molecule into the chloroplasts. The exogenous polynucleotides selected such that it is integratable into the chloroplast's genome via homologous recombination which is readily effected by enzymes inherent to the chloroplast. To this end, the exogenous polynucleotide includes, in addition to a gene of interest, at least one polynucleotide stretch which is derived from the chloroplast's genome. In addition, the exogenous polynucleotide includes a selectable marker, which serves by sequential selection procedures to ascertain that all or substantially all of the copies of the chloroplast genomes following such selection will include the exogenous polynucleotide. Further

details relating to this technique are found in U.S. Pat. Nos. 4,945,050; and 5,693,507 which are incorporated herein by reference. A polypeptide can thus be produced by the protein expression system of the chloroplast and become integrated into the chloroplast's inner membrane.

5 Since abiotic stress tolerance, water use efficiency, fertilizer use efficiency, growth, biomass, yield and/or vigor in plants can involve multiple genes acting additively or in synergy (see, for example, in Quesda et al., Plant Physiol. 130:951-063, 2002), the present invention also envisages expressing a plurality of exogenous polynucleotides in a single host plant to thereby achieve superior effect on abiotic stress
10 tolerance, water use efficiency, fertilizer use efficiency, growth, biomass, yield and/or vigor.

Expressing a plurality of exogenous polynucleotides in a single host plant can be effected by co-introducing multiple nucleic acid constructs, each including a different exogenous polynucleotide, into a single plant cell. The transformed cell can then be
15 regenerated into a mature plant using the methods described hereinabove.

Alternatively, expressing a plurality of exogenous polynucleotides in a single host plant can be effected by co-introducing into a single plant-cell a single nucleic-acid construct including a plurality of different exogenous polynucleotides. Such a construct can be designed with a single promoter sequence which can transcribe a polycistronic
20 messenger RNA including all the different exogenous polynucleotide sequences. To enable co-translation of the different polypeptides encoded by the polycistronic messenger RNA, the polynucleotide sequences can be inter-linked via an internal ribosome entry site (IRES) sequence which facilitates translation of polynucleotide sequences positioned downstream of the IRES sequence. In this case, a transcribed
25 polycistronic RNA molecule encoding the different polypeptides described above will be translated from both the capped 5' end and the two internal IRES sequences of the polycistronic RNA molecule to thereby produce in the cell all different polypeptides. Alternatively, the construct can include several promoter sequences each linked to a different exogenous polynucleotide sequence.

30 The plant cell transformed with the construct including a plurality of different exogenous polynucleotides, can be regenerated into a mature plant, using the methods described hereinabove.

Alternatively, expressing a plurality of exogenous polynucleotides in a single host plant can be effected by introducing different nucleic acid constructs, including different exogenous polynucleotides, into a plurality of plants. The regenerated transformed plants can then be cross-bred and resultant progeny selected for superior
5 abiotic stress tolerance, water use efficiency, fertilizer use efficiency, growth, biomass, yield and/or vigor traits, using conventional plant breeding techniques.

Thus, the invention encompasses plants exogenously expressing (as described above) the polynucleotide(s) and/or polypeptide(s) of the invention. Once expressed within the plant cell or the entire plant, the level of the polypeptide encoded by the
10 exogenous polynucleotide can be determined by methods well known in the art such as, activity assays, Western blots using antibodies capable of specifically binding the polypeptide, Enzyme-Linked ImmunoSorbent Assay (ELISA), radio-immuno-assays (RIA), immunohistochemistry, immunocytochemistry, immunofluorescence and the like.

15 Methods of determining the level in the plant of the RNA transcribed from the exogenous polynucleotide are well known in the art and include, for example, Northern blot analysis, reverse transcription polymerase chain reaction (RT-PCR) analysis (including quantitative, semi-quantitative or real-time RT-PCR) and RNA-*in situ* hybridization.

20 As mentioned, the polypeptide according to some embodiments of the invention, functions as a water channel. Thus, the invention according to some embodiments encompasses functional equivalents of the polypeptide (e.g., polypeptides capable of the biological activity of a water channel) which can be identified by functional assays (e.g., being capable of transporting water in a plant) using e.g., a cell-swelling assay
25 (Meng, Q. X. et al. 2008. Cell Physiol Biochem, 21. pp. 123-128).

The polynucleotides and polypeptides described hereinabove can be used in a wide range of economical plants, in a safe and cost effective manner.

The effect of the transgene (the exogenous polynucleotide encoding the polypeptide) on abiotic stress tolerance, water use efficiency, fertilizer use efficiency,
30 growth, biomass, yield and/or vigor can be determined using known methods.

Abiotic stress tolerance - Transformed (*i.e.*, expressing the transgene) and non-transformed (wild type) plants are exposed to an abiotic stress condition, such as water

deprivation, suboptimal temperature (low temperature, high temperature), nutrient deficiency, nutrient excess, a salt stress condition, osmotic stress, heavy metal toxicity, anaerobiosis, atmospheric pollution and UV irradiation.

Salinity tolerance assay – Transgenic plants with tolerance to high salt concentrations are expected to exhibit better germination, seedling vigor or growth in high salt. Salt stress can be effected in many ways such as, for example, by irrigating the plants with a hyperosmotic solution, by cultivating the plants hydroponically in a hyperosmotic growth solution (e.g., Hoagland solution), or by culturing the plants in a hyperosmotic growth medium [e.g., 50 % Murashige-Skoog medium (MS medium)]. Since different plants vary considerably in their tolerance to salinity, the salt concentration in the irrigation water, growth solution, or growth medium can be adjusted according to the specific characteristics of the specific plant cultivar or variety, so as to inflict a mild or moderate effect on the physiology and/or morphology of the plants (for guidelines as to appropriate concentration see, Bernstein and Kafkafi, Root Growth Under Salinity Stress In: Plant Roots, The Hidden Half 3rd ed. Waisel Y, Eshel A and Kafkafi U. (editors) Marcel Dekker Inc., New York, 2002, and reference therein).

For example, a salinity tolerance test can be performed by irrigating plants at different developmental stages with increasing concentrations of sodium chloride (for example 50 mM, 100 mM, 200 mM, 400 mM NaCl) applied from the bottom and from above to ensure even dispersal of salt. Following exposure to the stress condition the plants are frequently monitored until substantial physiological and/or morphological effects appear in wild type plants. Thus, the external phenotypic appearance, degree of wilting and overall success to reach maturity and yield progeny are compared between control and transgenic plants. Quantitative parameters of tolerance measured include, but are not limited to, the average wet and dry weight, the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher biomass than wild-type plants, are identified as abiotic stress tolerant plants.

Osmotic tolerance test - Osmotic stress assays (including sodium chloride and mannitol assays) are conducted to determine if an osmotic stress phenotype was sodium chloride-specific or if it was a general osmotic stress related phenotype. Plants which are tolerant to osmotic stress may have more tolerance to drought and/or freezing. For

salt and osmotic stress germination experiments, the medium is supplemented for example with 50 mM, 100 mM, 200 mM NaCl or 100 mM, 200 mM NaCl, 400 mM mannitol. See also Example 5 of the Examples section which follows.

Drought tolerance assay/Osmoticum assay - Tolerance to drought is performed to identify the genes conferring better plant survival after acute water deprivation. To analyze whether the transgenic plants are more tolerant to drought, an osmotic stress produced by the non-ionic osmolyte sorbitol in the medium can be performed. Control and transgenic plants are germinated and grown in plant-agar plates for 4 days, after which they are transferred to plates containing 500 mM sorbitol. The treatment causes growth retardation, then both control and transgenic plants are compared, by measuring plant weight (wet and dry), yield, and by growth rates measured as time to flowering.

Conversely, soil-based drought screens are performed with plants overexpressing the polynucleotides detailed above. Seeds from control Arabidopsis plants, or other transgenic plants overexpressing the polypeptide of the invention are germinated and transferred to pots. Drought stress is obtained after irrigation is ceased accompanied by placing the pots on absorbent paper to enhance the soil-drying rate. Transgenic and control plants are compared to each other when the majority of the control plants develop severe wilting. Plants are re-watered after obtaining a significant fraction of the control plants displaying a severe wilting. Plants are ranked comparing to controls for each of two criteria: tolerance to the drought conditions and recovery (survival) following re-watering.

Cold stress tolerance - To analyze cold stress, mature (25 day old) plants are transferred to 4 °C chambers for 1 or 2 weeks, with constitutive light. Later on plants are moved back to greenhouse. Two weeks later damages from chilling period, resulting in growth retardation and other phenotypes, are compared between both control and transgenic plants, by measuring plant weight (wet and dry), and by comparing growth rates measured as time to flowering, plant size, yield, and the like.

Heat stress tolerance - Heat stress tolerance is achieved by exposing the plants to temperatures above 34 °C for a certain period. Plant tolerance is examined after transferring the plants back to 22 °C for recovery and evaluation after 5 days relative to internal controls (non-transgenic plants) or plants not exposed to neither cold or heat stress.

Germination tests - Germination tests compare the percentage of seeds from transgenic plants that could complete the germination process to the percentage of seeds from control plants that are treated in the same manner. Normal conditions are considered for example, incubations at 22 °C under 22-hour light 2-hour dark daily cycles. Evaluation of germination and seedling vigor is conducted between 4 and 14 days after planting. The basal media is 50 % MS medium (Murashige and Skoog, 1962 Plant Physiology 15, 473-497).

Germination is checked also at unfavorable conditions such as cold (incubating at temperatures lower than 10 °C instead of 22 °C) or using seed inhibition solutions that contain high concentrations of an osmolyte such as sorbitol (at concentrations of 50 mM, 100 mM, 200 mM, 300 mM, 500 mM, and up to 1000 mM) or applying increasing concentrations of salt (of 50 mM, 100 mM, 200 mM, 300 mM, 500 mM NaCl).

Water use efficiency – can be determined as the biomass produced per unit transpiration. To analyze WUE, leaf relative water content can be measured in control and transgenic plants. Fresh weight (FW) is immediately recorded; then leaves are soaked for 8 hours in distilled water at room temperature in the dark, and the turgid weight (TW) is recorded. Total dry weight (DW) is recorded after drying the leaves at 60 °C to a constant weight. Relative water content (RWC) is calculated according to the following Formula I:

Formula I
$$(FW - DW / TW - DW) \times 100$$

Fertilizer use efficiency - To analyze whether the transgenic plants are more responsive to fertilizers, plants are grown in agar plates or pots with a limited amount of fertilizer, as described, for example, in Example 6, hereinbelow and in Yanagisawa et al (Proc Natl Acad Sci U S A. 2004; 101:7833-8). The plants are analyzed for their overall size, time to flowering, yield, protein content of shoot and/or grain. The parameters checked are the overall size of the mature plant, its wet and dry weight, the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Other parameters that may be tested are: the chlorophyll content of leaves (as nitrogen plant status and the degree of leaf verdure is highly correlated), amino acid and the total protein content of the seeds or other plant parts such as leaves or shoots, oil content, etc. Similarly, instead of providing nitrogen at limiting amounts, phosphate or

potassium can be added at increasing concentrations. Again, the same parameters measured are the same as listed above. In this way, nitrogen use efficiency (NUE), phosphate use efficiency (PUE) and potassium use efficiency (KUE) are assessed, checking the ability of the transgenic plants to thrive under nutrient restraining
5 conditions.

Nitrogen determination – The procedure for N (nitrogen) concentration determination in the structural parts of the plants involves the potassium persulfate digestion method to convert organic N to NO_3^- (Purcell and King 1996 Argon. J. 88:111-113, the modified Cd^{2+} mediated reduction of NO_3^- to NO_2^- (Vodovotz 1996
10 Biotechniques 20:390-394) and the measurement of nitrite by the Griess assay (Vodovotz 1996, supra). The absorbance values are measured at 550 nm against a standard curve of NaNO_2 . The procedure is described in details in Samonte et al. 2006 Agron. J. 98:168-176.

Grain protein concentration - Grain protein content ($\text{g grain protein m}^{-2}$) is
15 estimated as the product of the mass of grain N (g grain N m^{-2}) multiplied by the N/protein conversion ratio of k-5.13 (Mosse 1990, supra). The grain protein concentration is estimated as the ratio of grain protein content per unit mass of the grain ($\text{g grain protein kg}^{-1}$ grain).

Oil content - The oil content of a plant can be determined by extraction of the oil
20 from the seed or the vegetative portion of the plant. Briefly, lipids (oil) can be removed from the plant (e.g., seed) by grinding the plant tissue in the presence of specific solvents (e.g., hexane or petroleum ether) and extracting the oil in a continuous extractor. Indirect oil content analysis can be carried out using various known methods such as Nuclear Magnetic Resonance (NMR) Spectroscopy, which measures the resonance
25 energy absorbed by hydrogen atoms in the liquid state of the sample [See for example, Conway TF. and Earle FR., 1963, Journal of the American Oil Chemists' Society; Springer Berlin / Heidelberg, ISSN: 0003-021X (Print) 1558-9331 (Online)]; the Near Infrared (NI) Spectroscopy, which utilizes the absorption of near infrared energy (1100-2500 nm) by the sample; and a method described in WO/2001/023884, which is based
30 on extracting oil a solvent, evaporating the solvent in a gas stream which forms oil particles, and directing a light into the gas stream and oil particles which forms a detectable reflected light.

The plant vigor can be calculated by the increase in growth parameters such as leaf area, fiber length, rosette diameter, plant fresh weight and the like per time.

The growth rate can be measured using digital analysis of growing plants. For example, images of plants growing in greenhouse on plot basis can be captured every 3
5 days and the rosette area can be calculated by digital analysis. Rosette area growth is calculated using the difference of rosette area between days of sampling divided by the difference in days between samples.

Measurements of seed yield can be done by collecting the total seeds from 8-16 plants together, weighting them using analytical balance and dividing the total weight
10 by the number of plants. Seed per growing area can be calculated in the same manner while taking into account the growing area given to a single plant. Increase seed yield per growing area could be achieved by increasing seed yield per plant, and/or by increasing number of plants capable of growing in a given area.

Evaluation of the seed yield per plant can be done by measuring the amount
15 (weight or size) or quantity (*i.e.*, number) of dry seeds produced and harvested from 8-16 plants and divided by the number of plants.

Evaluation of growth rate can be done by measuring plant biomass produced, rosette area, leaf size or root length per time (can be measured in cm² per day of leaf area).

20 Fiber length can be measured using fibrograph. The fibrograph system was used to compute length in terms of "Upper Half Mean" length. The upper half mean (UHM) is the average length of longer half of the fiber distribution. The fibrograph measures length in span lengths at a given percentage point (Hypertext Transfer Protocol://World Wide Web (dot) cottoninc (dot) com/ClassificationofCotton/?Pg=4#Length).

25 Thus, the present invention is of high agricultural value for promoting the yield of commercially desired crops (e.g., biomass of vegetative organ such as poplar wood, or reproductive organ such as number of seeds or seed biomass).

As used herein the term "about" refers to $\pm 10\%$.

The terms "comprises", "comprising", "includes", "including", "having" and
30 their conjugates mean "including but not limited to".

The term "consisting of" means "including and limited to".

The term "consisting essentially of" means that the composition, method or structure may include additional ingredients, steps and/or parts, but only if the additional ingredients, steps and/or parts do not materially alter the basic and novel characteristics of the claimed composition, method or structure.

5 As used herein, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a compound" or "at least one compound" may include a plurality of compounds, including mixtures thereof.

10 Throughout this application, various embodiments of this invention may be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

20 Whenever a numerical range is indicated herein, it is meant to include any cited numeral (fractional or integral) within the indicated range. The phrases "ranging/ranges between" a first indicate number and a second indicate number and "ranging/ranges from" a first indicate number "to" a second indicate number are used herein interchangeably and are meant to include the first and second indicated numbers and all the fractional and integral numerals therebetween.

25 As used herein the term "method" refers to manners, means, techniques and procedures for accomplishing a given task including, but not limited to, those manners, means, techniques and procedures either known to, or readily developed from known manners, means, techniques and procedures by practitioners of the chemical, pharmacological, biological, biochemical and medical arts.

30 It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for

brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination or as suitable in any other described embodiment of the invention. Certain features described in the context of various embodiments are not to be considered essential features of those embodiments, unless
5 the embodiment is inoperative without those elements.

Various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below find experimental support in the following examples.

10

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions illustrate some embodiments of the invention in a non limiting fashion.

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and
15 recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John
20 Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed.
25 (1994); "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat.
30 Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); "Nucleic

Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., Eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

EXAMPLE 1

IDENTIFICATION OF AQP GENES USING DIGITAL EXPRESSION ANALYSIS AND CROSS-SPECIES COMPARATIVE GENOMIC

The large number of AQPs in plants and the contradictory results obtained when AQPs were overexpressed in plants demonstrate the need to selectively identify the AQP genes which can improve water use efficiency (WUE) in plants, lead to increased yield and biomass under abiotic stress as well as under favorable conditions.

Under unfavorable stress conditions, some biological activities of the plant are stopped or reduced, while others, not earlier active, initiate. Still, some of the activities, which are vital for plant survival, are maintained. One hypothesis is that key genes needed for plants to maintain vital activities under unfavorable conditions would be active under broad spectrum of biotic and abiotic stresses.

To test this hypothesis and to identify the key AQP genes having the potential to improve plant performance under different biotic and/or abiotic stress conditions (e.g., salt or drought stress) a combination of digital expression analysis (also known as Electronic Northern blot) and cross-species comparative genomics was performed. The database used was available from NCBI (Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov/dbEST/) and included 7.2 million expressed sequence tags (ESTs) from 1,195 relevant EST's libraries originated from 15 different species, including both monocot and dicot species, namely: Arabidopsis, barley,

Brassica rapa, cotton, grape, maize, medicago, poplar, potato, rice, sorghum, soybean, sugarcane, tomato and wheat.

Tomato plants were selected as a model plant based on the high quality tomato database from several tomato species which can be used for data-mining and the present inventors' experience in using the tomato genome as a model plant. In addition, the relatively high salt tolerance exhibited by various tomato species makes the tomato genome an excellent candidate for identifying new stress tolerance mechanisms. Moreover, tomato is not only used as a model plant for genetic studies, it is also used as an important crop with well-defined yield parameters, which can be used to distinguish between genes affecting abiotic-stress tolerance and genes preventing yield loss under abiotic-stress conditions.

Gene analysis and data mining – For gene analysis and data mining the bioinformatic filtering approach used had three phases:

1. Clustering and assembly: EST and mRNA sequences of each of the 15 species were extracted from GenBank versions 157, 160, 161, 162, 164, 165, 166, clustered and assembled using Compugen's LEADS clustering and assembly platform (Compugen Ltd., Tel Aviv, Israel; Yelin et. al. 2003, Nature Biotechnology 21, 379-85). Automatically extracted EST library annotations were manually accurated and classified by anatomy, developmental stage, abiotic/biotic stress treatment and cultivars. The results were loaded into Oracle database. The predicted proteins were then annotated using InterPro(2) (Hypertext Transfer Protocol://World Wide Web (dot) ebi (dot) ac (dot) uk/interpro/).

2. Selection of clusters - All clusters that contained the Major intrinsic protein domain (IPR000425) were selected for further analysis (n = 1,114).

3. Obtaining expression profile of the clusters - By digital expression approach the expression profile of all clusters was obtained in terms of plant anatomy (*i.e.*, in what tissues/organs the gene was expressed), developmental stage (*i.e.*, the developmental stages at which a gene can be found) and profile of treatment (provides the physiological conditions under which a gene is expressed such as drought, cold, pathogen infection, etc).

Digital expression computations was calculated as follows: over-expression fold was computed as $m / (n * M/N)$, where "N" is total number of ESTs of specific organism;

“M is number of ESTs in a given library/tissue/category; “n” is total number of ESTs in a given contig; “m” is the number of ESTs from the library/tissue/category in the contig; P-value was computed using Exact Fisher Test statistic. The combined P-value for over-expression in both Root and Abiotic stresses conditions was computed as $1 - (1-p_1) \times (1-p_2)$. 1,114 different AQP genes were identified in the inter species transcriptional databases. For the data mining process, the present inventors used a combination of two approaches: selection of AQP clusters showing significant over expression (EST distribution versus normal is more than two folds; statistical significance of over-expression - p Value < 0.05) either in roots compared to shoots or under various abiotic stresses (including drought, cold, salinity, heat, chemical treatments, etc.), compared to non stress control. It was found that ESTs of about 9 % of the AQP genes were significantly overrepresented in roots and 3.5 % of them were induced under different abiotic stresses. AQP genes which are highly overrepresented in roots were selected since plants with an efficient root system are expected to capture more water from a drying soil. In addition, AQP genes which are overrepresented in various abiotic stresses such as nutrient deficiency, heat, salinity and heavy metal stresses and biotic stresses such as application of elicitors and pathogens were selected considering that they can provide high tolerance to a wide spectrum of stresses.

The same set of 1,114 AQPs was classified according to the accepted groups known in the literature: first into the four major sub-groups: PIPs, TIPs, NIPs and SIPs, and a second classification divided these four sub-groups into eleven sub-groups according to their homology in amino acid sequences. A Fisher's exact test was then used to identify subgroups having significant EST over-presentation both in roots and upon exposure to different abiotic stresses. As shown in Table 1, hereinbelow, from the eleven subgroups, only the TIP2 subgroup showed a significant EST overrepresentation both in roots and upon exposure to abiotic stresses (P-value 1.7×10^{-5} and 1.6×10^{-3} , respectively).

Table 1
AQP type distribution and over-expression in roots and abiotic stresses

AQP type	Total No. of genes in database	Roots			Exposure to abiotic stresses		
		No. of over-expressed genes	% over-expressed/all	P-value	No. of over-expressed genes	% over-expressed/all	P-value
PIP1	243	26	10.7	0.13	10	4.1	0.34
PIP2	336	25	7.4	0.87	12	3.6	0.53
PIP3	11	0	0.0	1	0	0	1
SIP1	39	0	0.0	1	0	0	1
SIP2	16	0	0.0	1	0	0	1
TIP1	152	11	7.2	0.8	3	2	0.92
TIP2	101	22	21.8	1.70E-05	10	9.9	1.6E-03
TIP3	29	0	0.0	1	0	0	1
TIP4	48	5	10.4	0.41	1	2.1	0.83
TIP5	3	0	0.0	1	0	0	1
NIP	136	8	5.9	0.93	3	2.2	0.88
Total	1114	97			39		

Table 1.

5 These results suggest that over-expression and/or protein over-accumulation of the Tip2 subgroup can improve plant water use efficiency, ABST and yield.

10 ***Genes of the Tip2 subgroup are highly expressed in roots and in abiotic stresses*** – As shown in Table 1, hereinabove, the TIP2 subgroup (or subfamily) is highly expressed in roots and in abiotic stresses. The TIP2 subgroup is found in 38 plant species and other organisms (nucleic acid SEQ ID NOs: 1, 2, 19, 20-22; Table 2), available in public databases [Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov/dbEST/]. In tomato, the TIP2 gene was highly expressed in roots (6 fold, $p \leq 1.01 \text{ E-}24$) and in both biotic (2 fold, $p \leq 4.6 \text{ E-}02$) and abiotic stresses (4.5 fold, $p \leq \text{E-}02$) (data not shown).

15 ***Identification of a short consensus sequence of the Tip2 sub-family*** - While comparing the consensus amino-acid sequences of Aquaporins, a short consensus sequence was identified which is unique to proteins of the Tip2 sub-family. The present inventors have suggested that this motif has an important role in managing water use efficiency (WUE), and when over-expressed in a plant can confer ABST and improved yield. The amino-acid consensus sequence identified is TLXFXFAGVGS (SEQ ID NO:2826), wherein X stands for any amino acid.

20 In addition, other genes of the aquaporin gene family were identified by bioinformatics tools as improving ABST and yield, based on combined digital gene

expression profile in roots, tissues with low water levels (such as seed and pollen) and under abiotic stress conditions. These include SEQ ID NOs: 3-18, 23-26 (Table 2).

Table 2
Identified Aquaporin Genes

SEQ ID NO: (Polynucleotide)	Gene name	Cluster name	Organism	SEQ ID NO: (Polypeptide)
1	MAB54	tomato gb164 BG125449	tomato	27
2	MAB55	tomato gb164 BG134896	tomato	28
3	MAB56	tomato gb164 AW218990	tomato	29
4	MAB57	tomato gb164 AA824812	tomato	30
5	MAB58	tomato gb164 BP881534	tomato	31
7	MAB69	tomato gb164 AI637360	tomato	33
8	MAB70	tomato gb164 BG133531	tomato	34
9	MAB71	tomato gb164 BG629975	tomato	35
10	MAB72	tomato gb164 BG136017	tomato	36
11	MAB73	tomato gb164 BG131871	tomato	37
12	MAB74	tomato gb164 AI775489	tomato	38
13	MAB75	tomato gb164 BG136239	tomato	39
14	MAB76	tomato gb164 BG134058	tomato	40
15	MAB77	tomato gb164 BG629900	tomato	41
16	MAB78	tomato gb164 BG130774	tomato	42
17	MAB79	tomato gb164 BG124486	tomato	43
18	MAB80	tomato gb164 AI483521	tomato	44
19	MAB81	tomato gb164 CO751453	tomato	45
20	MAB115	barley gb157.2 BF626376	barley	46
22	MAB117	barley gb157.2 BE412516	barley	48
23	MAB119	tomato gb164 BG134199	tomato	49
24	MAB176	tomato gb164 CO635830	tomato	50
25	MAB177	tomato gb164 CO751496	tomato	51
26	MAB178	tomato gb164 CO751374	tomato	52

Table 2.

Sequences which are homologous [showing at least 80 % protein sequence identity on 80 % of the global hit or query length, as calculated using BlastP and tBlastN algorithms of the National Center of Biotechnology Information (NCBI)] or orthologues of the AQP genes described in Table 2, and are expected to possess the same role in ABST and yield improvement in plants, are disclosed in Table 3 hereinbelow (SEQ ID NOs:6, 215-1101 and 1138-1400; Table 3). In addition, Table 3 also includes homologous and orthologues of the AQP TIP2 subfamily (SEQ ID NOs:21, 53-214, 1102-1137) and additional homologous and orthologues (SEQ ID NOs:2844-3051).

Table 3

Polynucleotide and polypeptide sequences of AQP homologous and orthologous

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
53	apple gb157.3 C N883304 T1	apple	1401	27	84	92.3387 097	100	blastp
54	apple gb157.3 C N489003 T1	apple	1402	27	83	100	100	blastp
55	aquilegia gb157. 3 DR915168 T1	aquilegia	1403	27	85	100	100	blastp
56	arabidopsis gb16 5 AT3G16240_T 1	arabidop sis	1404	27	81	99.1935 484	98.8	blastp
57	artemisia gb164 EY035829 T1	artemisia	1405	27	80	98.7903 226	99.1902 834	blastp
58	artemisia gb164 EY113320 T1	artemisia	1406	27	85	62.9032 258	100	blastp
59	artemisia gb164 EY070770 T1	artemisia	1407	27	81	98.7903 226	99.1902 834	blastp
60	avocado gb164 C V002132 T1	avocado	1408	27	84	50	100	blastp
61	b_juncea gb164 EVGN00333108 491419 T1	b_juncea	1409	27	83	100	100	blastp
62	b_juncea gb164 EVGN00503709 641655 T1	b_juncea	1410	27	82	53.6290 323	97.0588 235	blastp
63	b_juncea gb164 EVGN01003711 220829 T1	b_juncea	1411	27	84	63.7096 774	100	blastp
64	b_oleracea gb16 1 AM059585 T1	b_olerac ea	1412	27	84	100	100	blastp
65	b_oleracea gb16 1 AM385334 T1	b_olerac ea	1413	27	82	100	100	blastp
66	b_oleracea gb16 1 AM385915 T1	b_olerac ea	1414	27	81	100	100	blastp
67	b_rapa gb162 B G543171 T1	b_rapa	1415	27	82	100	100	blastp
68	b_rapa gb162 B G543223 T1	b_rapa	1416	27	83	100	100	blastp
69	b_rapa gb162 L3 7478 T1	b_rapa	1417	27	81	100	100	blastp
70	banana gb160 D N238689 T1	banana	1418	27	83	76.6129 032	100	blastp
71	bean gb164 CB5 40614 T1	bean	1419	27	83	98.7903 226	98.7903 226	blastp
72	canola gb161 EV 092237 T1	canola	1420	27	84	100	100	blastp
73	canola gb161 CN 828178 T1	canola	1421	27	81	100	100	blastp
74	canola gb161 CX 188169 T1	canola	1422	27	82	100	100	blastp
75	canola gb161 CD 840590 T1	canola	1423	27	81	100	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
76	cassava gb164 C K650415 T1	cassava	1424	27	85	100	100	blastp
77	castorbean gb16 0 EE254645 T1	castorbea n	1425	27	87	100	100	blastp
78	centaurea gb161 EH725826 T1	centaure a	1426	27	84	95.9677 419	84.3971 631	blastp
79	centaurea gb161 EL932474 T1	centaure a	1427	27	88	89.1129 032	97.7876 106	blastp
80	cherry gb157.2 E E488049 T1	cherry	1428	27	80	69.3548 387	100	blastp
81	cichorium gb161 DT211633 T1	cichorium m	1429	27	80	100	92.8571 429	blastp
82	cichorium gb161 EH672622 T1	cichorium m	1430	27	87	100	100	blastp
83	citrus gb157.2 C X663669 T1	citrus	1431	27	88	98.7903 226	99.1902 834	blastp
84	citrus gb157.2 C F417983 T1	citrus	1432	27	88	98.7903 226	99.1902 834	blastp
85	citrus gb157.2 C K665344 T1	citrus	1433	27	88	98.7903 226	99.1902 834	blastp
86	citrus gb157.2 C K665344 T2	citrus	1434	27	87	82.2580 645	100	blastp
87	clover gb162 BB 908328 T1	clover	1435	27	81	69.7580 645	100	blastp
88	cotton gb164 AF 009567 T1	cotton	1436	27	87	100	100	blastp
89	cowpea gb166 F F397761 T1	cowpea	1437	27	84	100	100	blastp
90	cowpea gb166 F C457059 T1	cowpea	1438	27	83	98.7903 226	98.7903 226	blastp
91	dandelion gb161 DY818755 T1	dandelio n	1439	27	85	100	100	blastp
92	ginger gb164 DY 358186 T1	ginger	1440	27	80	98.3870 968	99.1836 735	blastp
93	ginger gb164 DY 351866 T1	ginger	1441	27	80	98.3870 968	99.1836 735	blastp
94	iceplant gb164 A F133532 T1	iceplant	1442	27	81	100	100	blastp
95	ipomoea gb157.2 BJ576630 T1	ipomoea	1443	27	87	100	100	blastp
96	lettuce gb157.2 DW074363 T1	lettuce	1444	27	87	100	100	blastp
97	lettuce gb157.2 DW074363 T2	lettuce	1445	27	85	50.8064 516	90.6474 82	blastp
98	lettuce gb157.2 DW145132 T1	lettuce	1446	27	87	100	100	blastp
99	lettuce gb157.2 DW043760 T1	lettuce	1447	27	87	100	100	blastp
100	lettuce gb157.2 DW104999 T1	lettuce	1448	27	87	100	100	blastp
101	lotus gb157.2 BI 420407 T1	lotus	1449	27	84	100	100	blastp

Polynuc. SEQ ID NO:	Cluster name	Organis m	Polypep. SEQ ID NO:	Hom. of SEQ ID NO:	% Ident.	Query cover.	% Subject cover.	Algorith m
102	lotus gb157.2 BF177457_T1	lotus	1450	27	86	98.7903226	98.7951807	blastp
103	medicago gb157.2 AI974300_T1	medicag o	1451	27	83	89.1129032	94.8497854	blastp
104	medicago gb157.2 AA660400_T1	medicag o	1452	27	84	100	100	blastp
105	nicotiana_benth miana gb162 CN741988_T1	nicotiana _benth miana	1453	27	86	98.7903226	98.7903226	blastp
106	nicotiana_benth miana gb162 CN655366_T1	nicotiana _benth miana	1454	27	92	100	100	blastp
107	nicotiana_benth miana gb162 CN741998_T1	nicotiana _benth miana	1455	27	89	98.7903226	98.7903226	blastp
108	nicotiana_benth miana gb162 CN742343_T1	nicotiana _benth miana	1456	27	93	100	100	blastp
109	peach gb157.2 BU045214_T1	peach	1457	27	82	100	100	blastp
110	pepper gb157.2 CO776446_T1	pepper	1458	27	84	61.6935484	100	blastp
111	pepper gb157.2 CA518313_T1	pepper	1459	27	86	63.3064516	100	blastp
112	periwinkle gb164 EG555051_T1	periwink le	1460	27	88	99.1935484	99.1935484	blastp
113	petunia gb157.2 CV296219_T1	petunia	1461	27	84	63.7096774	85.2517986	tblastn
114	poplar gb157.2 BI129443_T1	poplar	1462	27	86	100	100	blastp
115	poplar gb157.2 AI166943_T2	poplar	1463	27	83	61.6935484	100	blastp
116	poplar gb157.2 AI166943_T1	poplar	1464	27	85	100	100	blastp
117	poplar gb157.2 BI127662_T1	poplar	1465	27	89	79.0322581	100	blastp
118	potato gb157.2 BQ513382_T1	potato	1466	27	97	100	100	blastp
119	potato gb157.2 BQ513382_T2	potato	1467	27	97	50.8064516	96.1832061	blastp
120	radish gb164 EV538411_T1	radish	1468	27	82	92.3387097	100	blastp
121	radish gb164 AB010416_T1	radish	1469	27	81	100	100	blastp
122	radish gb164 EW725945_T1	radish	1470	27	82	100	100	blastp
123	radish gb164 EV527946_T1	radish	1471	27	81	100	100	blastp
124	rose gb157.2 BQ104096_T1	rose	1472	27	85	85.0806452	95.045045	blastp
125	safflower gb162 EL374001_T1	safflower	1473	27	87	100	100	blastp

Polynuc. SEQ ID NO:	Cluster name	Organism	Polypep. SEQ ID NO:	Hom. of SEQ ID NO:	% Ident.	Query cover.	% Subject cover.	Algorith m
126	safflower gb162 EL406178_T1	safflower	1474	27	83	100	100	blastp
127	sesame gb157.2 BU668161_T1	sesame	1475	27	81	61.2903 226	86.3636 364	tblastn
128	soybean gb166 A W349399_T1	soybean	1476	27	84	98.7903 226	98.7903 226	blastp
129	soybean gb166 C D416937_T1	soybean	1477	27	85	75.4032 258	100	blastp
130	soybean gb166 C A786095_T1	soybean	1478	27	84	98.7903 226	98.7903 226	blastp
131	soybean gb166 A W350817_T1	soybean	1479	27	81	100	100	blastp
132	spruce gb162 CO 216479_T1	spruce	1480	27	80	98.7903 226	98.4	blastp
133	strawberry gb16 4 DV438565_T1	strawberr y	1481	27	82	100	100	blastp
134	sunflower gb162 X95952_T1	sunflowe r	1482	27	82	100	100	blastp
135	sunflower gb162 CD847513_T1	sunflowe r	1483	27	83	100	100	blastp
136	sunflower gb162 CD845750_T1	sunflowe r	1484	27	84	100	100	blastp
137	sunflower gb162 CD848081_T1	sunflowe r	1485	27	86	100	100	blastp
138	sunflower gb162 CD849577_T1	sunflowe r	1486	27	83	100	100	blastp
139	tobacco gb162 C V016921_T1	tobacco	1487	27	88	100	100	blastp
140	tobacco gb162 C V018684_T1	tobacco	1488	27	93	100	100	blastp
141	tobacco gb162 C V019641_T1	tobacco	1489	27	91	100	100	blastp
142	tomato gb164 A W626247_T1	tomato	No predicted protein	27	83	50	88.3610 451	tblastn
143	triphysaria gb16 4 EX999390_T1	triphysar ia	1490	27	81	100	100	blastp
144	triphysaria gb16 4 BM356478_T1	triphysar ia	1491	27	80	100	100	blastp
145	triphysaria gb16 4 BM356478_T2	triphysar ia	1492	27	81	81.0483 871	98.0487 805	blastp
146	aquilegia gb157. 3 DR922172_T1	aquilegia	1493	28	86	100	100	blastp
147	arabidopsis gb16 5 AT5G47450_T 1	arabidop sis	1494	28	82	98.8	98.8	blastp
148	arabidopsis gb16 5 AT4G17340_T 1	arabidop sis	1495	28	85	99.6	99.6	blastp
149	artemisia gb164 EY080612_T1	artemisia	1496	28	83	69.2	100	blastp
150	b_rapa gb162 E X104899_T1	b_rapa	1497	28	84	95.2	99.1666 667	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
151	canola gb161 EE 430505 T1	canola	1498	28	85	95.2	94.8207 171	blastp
152	canola gb161 D Y017904 T1	canola	1499	28	82	98.8	98.8	blastp
153	canola gb161 EL 590702 T1	canola	1500	28	84	99.6	99.6	blastp
154	canola gb161 CD 818320 T1	canola	1501	28	85	99.6	99.6	blastp
155	cassava gb164 D B923860 T1	cassava	1502	28	81	100	100	blastp
156	centaurea gb161 EL932179 T1	centaure a	1503	28	84	98.8	99.1935 484	blastp
157	centaurea gb161 EH718862 T1	centaure a	1504	28	82	87.6	88.9795 918	blastp
158	cichorium gb161 EH689841 T1	cichoriu m	1505	28	86	88.8	64.7230 321	tblastn
159	citrus gb157.2 C O913277 T1	citrus	1506	28	84	100	100	blastp
160	citrus gb157.2 C O912449 T1	citrus	1507	28	82	95.6	75.2360 965	tblastn
161	cotton gb164 DV 437956 T1	cotton	1508	28	88	50.8	100	blastp
162	cotton gb164 CD 486503 T1	cotton	1509	28	86	100	100	blastp
163	dandelion gb161 DY827614 T1	dandelio n	1510	28	84	100	100	blastp
164	dandelion gb161 DY822865 T1	dandelio n	1511	28	86	100	100	blastp
165	dandelion gb161 DY819043 T1	dandelio n	1512	28	86	100	100	blastp
166	iceplant gb164 A F133533 T1	iceplant	1513	28	82	82	99.5145 631	blastp
167	lettuce gb157.2 DW057721 T1	lettuce	1514	28	85	100	100	blastp
168	lettuce gb157.2 DW045203 T1	lettuce	1515	28	85	100	100	blastp
169	lettuce gb157.2 DW046133 T1	lettuce	1516	28	84	100	100	blastp
170	lettuce gb157.2 DW080742 T1	lettuce	1517	28	85	85.6	100	blastp
171	lettuce gb157.2 DW075611 T1	lettuce	1518	28	86	100	100	blastp
172	lettuce gb157.2 DW123899 T1	lettuce	1519	28	86	100	100	blastp
173	lettuce gb157.2 DW103468 T1	lettuce	1520	28	84	100	100	blastp
174	lettuce gb157.2 DW161237 T1	lettuce	1521	28	85	100	100	blastp
175	lettuce gb157.2 DW079798 T1	lettuce	1522	28	85	100	100	blastp
176	lettuce gb157.2 DW079554 T1	lettuce	1523	28	85	100	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
177	lettuce gb157.2 DW147378 T1	lettuce	1524	28	85	100	100	blastp
178	lettuce gb157.2 DW052373 T1	lettuce	1525	28	83	100	100	blastp
179	lettuce gb157.2 DW105592 T1	lettuce	1526	28	86	100	100	blastp
180	lettuce gb157.2 DW075384 T1	lettuce	1527	28	85	100	100	blastp
181	lettuce gb157.2 DW155153 T1	lettuce	1528	28	86	100	100	blastp
182	lettuce gb157.2 CV699993 T1	lettuce	1529	28	85	100	100	blastp
183	lettuce gb157.2 DW078166 T1	lettuce	1530	28	84	100	100	blastp
184	lotus gb157.2 A V409092 T1	lotus	1531	28	80	53.2	100	blastp
185	medicago gb157. 2 AI974377 T1	medicag o	1532	28	81	98.8	99.5951 417	blastp
186	melon gb165 A M725511 T1	melon	1533	28	84	100	100	blastp
187	nicotiana_bentha miana gb162 EH 370474 T1	nicotiana _bentha miana	1534	28	90	70.4	100	blastp
188	onion gb162 BE 205571 T1	onion	1535	28	83	99.6	99.5967 742	blastp
189	onion gb162 AA 601764 T1	onion	1536	28	86	95.2	96.3414 634	blastp
190	papaya gb165 E X255759 T1	papaya	1537	28	82	99.6	99.5983 936	blastp
191	peanut gb161 EH 043676 T1	peanut	1538	28	82	99.6	99.5967 742	blastp
192	pepper gb157.2 CK901741 T1	pepper	1539	28	94	86.4	100	blastp
193	periwinkle gb16 4 FD423620 T1	periwink le	1540	28	86	64.4	96.4071 856	blastp
194	poplar gb157.2 B U886993 T1	poplar	1541	28	84	100	100	blastp
195	poplar gb157.2 C A826065 T1	poplar	1542	28	85	86.8	100	blastp
196	potato gb157.2 B G591546 T2	potato	1543	28	81	100	100	blastp
197	radish gb164 EV 531940 T1	radish	1544	28	83	94.8	94.8	blastp
198	radish gb164 EV 527785 T1	radish	1545	28	84	92.8	95.4732 51	blastp
199	radish gb164 EV 550763 T1	radish	1546	28	84	95.2	94.8207 171	blastp
200	radish gb164 EX 902593 T1	radish	1547	28	85	95.2	99.5815 9	blastp
201	radish gb164 EV 535199 T1	radish	1548	28	84	96	98.7654 321	blastp
202	radish gb164 EV 525705 T1	radish	1549	28	85	96	98.7654 321	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
203	safflower gb162 EL399548 T1	safflower	1550	28	86	86.8	100	blastp
204	safflower gb162 EL376421 T1	safflower	1551	28	87	100	100	blastp
205	spurge gb161 D V127241 T1	spurge	1552	28	85	88.4	99.1031 39	blastp
206	strawberry gb16 4 GFXDQ17802 2X1 T1	strawberr y	1553	28	82	100	100	blastp
207	sunflower gb162 X95953 T1	sunflowe r	1554	28	86	100	100	blastp
208	sunflower gb162 DY911049 T1	sunflowe r	1555	28	85	100	100	blastp
209	sunflower gb162 DY921796 T1	sunflowe r	1556	28	81	88.8	98.2300 885	blastp
210	sunflower gb162 DY918762 T1	sunflowe r	1557	28	85	100	100	blastp
211	sunflower gb162 DY906198 T1	sunflowe r	1558	28	81	100	100	blastp
212	sunflower gb162 DY932268 T1	sunflowe r	1559	28	81	100	100	blastp
213	tobacco gb162 G FXS45406X1_T 1	tobacco	1560	28	93	100	100	blastp
214	tobacco gb162 E B445911 T1	tobacco	1561	28	89	100	100	blastp
215	apricot gb157.2 CB818493 T1	apricot	1562	29	81	54.5454 545	95.8333 333	blastp
216	arabidopsis gb16 5 AT4G01470_T 1	arabidop sis	1563	29	80	99.2094 862	99.6031 746	blastp
217	avocado gb164 C K760396 T1	avocado	1564	29	81	54.5454 545	93.8775 51	blastp
218	b_rapa gb162 E X017183 T1	b_rapa	1565	29	83	69.5652 174	94.1176 471	blastp
219	barley gb157.3 B E413237 T1	barley	1566	29	81	99.2094 862	99.6031 746	blastp
220	cassava gb164 C K644827 T1	cassava	1567	29	90	57.3122 53	99.3150 685	blastp
221	cassava gb164 B M259770 T1	cassava	1568	29	82	99.2094 862	99.6031 746	blastp
222	cassava gb164 C K645124 T1	cassava	1569	29	80	99.2094 862	99.6031 746	blastp
223	castorbean gb16 0 EG666198 T1	castorbea n	1570	29	84	99.2094 862	99.6031 746	blastp
224	castorbean gb16 0 AJ605571 T1	castorbea n	1571	29	82	99.2094 862	99.6015 936	blastp
225	castorbean gb16 0 AJ605570 T1	castorbea n	1572	29	83	99.2094 862	99.6031 746	blastp
226	centaurea gb161 EL931525 T1	centaure a	1573	29	88	74.7035 573	97.9274 611	blastp
227	cichorium gb161 EH707617 T1	cichoriu m	1574	29	87	65.6126 482	99.4011 976	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
228	citrus gb157.2 C F834233 T1	citrus	1575	29	80	94.4664 032	94.4444 444	blastp
229	citrus gb157.2 B Q624227 T1	citrus	1576	29	87	99.2094 862	99.6031 746	blastp
230	citrus gb157.2 B Q623056 T1	citrus	1577	29	87	97.2332 016	98.4	blastp
231	citrus gb157.2 B Q624617 T1	citrus	1578	29	87	99.2094 862	99.6031 746	blastp
232	cotton gb164 CD 486523 T1	cotton	1579	29	81	99.2094 862	99.6031 746	blastp
233	cotton gb164 AI 729919 T1	cotton	1580	29	82	99.2094 862	99.6031 746	blastp
234	cotton gb164 BG 442315 T1	cotton	1581	29	86	99.2094 862	99.6031 746	blastp
235	cotton gb164 EX 167179 T1	cotton	1582	29	84	56.9169 96	100	blastp
236	cotton gb164 AI 726375 T1	cotton	1583	29	82	99.2094 862	99.6031 746	blastp
237	cowpea gb166 F F384697 T1	cowpea	1584	29	84	99.2094 862	99.6031 746	blastp
238	dandelion gb161 DY825779 T1	dandelio n	1585	29	88	99.2094 862	99.6031 746	blastp
239	fescue gb161 CK 802772 T1	fescue	1586	29	80	99.2094 862	99.6031 746	blastp
240	grape gb160 BQ 796848 T1	grape	1587	29	84	99.2094 862	99.6015 936	blastp
241	grape gb160 CF6 05030 T1	grape	1588	29	82	99.2094 862	99.6031 746	blastp
242	ipomoea gb157.2 EE883704 T1	ipomoea	1589	29	85	53.7549 407	100	blastp
243	ipomoea gb157.2 BJ554617 T1	ipomoea	1590	29	85	99.2094 862	99.6031 746	blastp
244	lettuce gb157.2 DW074608 T1	lettuce	1591	29	87	99.2094 862	99.6031 746	blastp
245	lettuce gb157.2 DY977540 T1	lettuce	1592	29	87	99.2094 862	99.6031 746	blastp
246	lotus gb157.2 B W615882 T1	lotus	1593	29	80	50.1976 285	100	blastp
247	maize gb164 DQ 245749 T1	maize	1594	29	81	99.2094 862	99.6031 746	blastp
248	medicago gb157. 2 BI266516 T1	medicag o	1595	29	82	99.2094 862	99.6031 746	blastp
249	nicotiana_bentha miana gb162 CN 743053 T1	nicotiana _bentha miana	1596	29	94	83.0039 526	99.5260 664	blastp
250	papaya gb165 E X256526 T1	papaya	1597	29	80	99.2094 862	99.6031 746	blastp
251	papaya gb165 E X255270 T1	papaya	1598	29	86	99.2094 862	99.6031 746	blastp
252	peach gb157.2 A F367456 T1	peach	1599	29	84	53.7549 407	100	blastp
253	pepper gb157.2 CK902019 T1	pepper	1600	29	81	73.1225 296	98.9304 813	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
254	poplar gb157.2 A I163470 T1	poplar	1601	29	81	99.2094 862	99.6031 746	blastp
255	poplar gb157.2 A I166549 T1	poplar	1602	29	82	99.2094 862	99.6031 746	blastp
256	poplar gb157.2 B U887722 T1	poplar	1603	29	81	99.2094 862	99.6031 746	blastp
257	poplar gb157.2 B U875073 T1	poplar	1604	29	83	99.2094 862	99.6031 746	blastp
258	poplar gb157.2 C A823737 T1	poplar	1605	29	88	53.3596 838	99.2647 059	blastp
259	poplar gb157.2 A I166136 T1	poplar	1606	29	80	99.2094 862	99.6031 746	blastp
260	radish gb164 EV 544876 T1	radish	1607	29	80	99.2094 862	99.6031 746	blastp
261	rice gb157.2 AA 752956 T1	rice	1608	29	80	99.2094 862	99.6031 746	blastp
262	soybean gb166 C X703984 T1	soybean	1609	29	80	99.2094 862	99.6031 746	blastp
263	soybean gb166 S OYNODB T1	soybean	1610	29	86	99.2094 862	99.6031 746	blastp
264	spurge gb161 D V146067 T1	spurge	1611	29	84	87.3517 787	100	blastp
265	spurge gb161 A W990927 T1	spurge	1612	29	80	99.2094 862	99.6031 746	blastp
266	sunflower gb162 DY919534 T1	sunflower	1613	29	86	99.2094 862	99.6031 746	blastp
267	tobacco gb162 E B443312 T1	tobacco	1614	29	92	99.2094 862	99.6031 746	blastp
268	tobacco gb162 C V019217 T1	tobacco	1615	29	81	98.0237 154	99.5967 742	blastp
269	tobacco gb162 E B443618 T1	tobacco	1616	29	92	99.2094 862	99.6031 746	blastp
270	tobacco gb162 C V018899 T1	tobacco	1617	29	81	98.0237 154	99.5967 742	blastp
271	wheat gb164 BE 418306 T1	wheat	1618	29	80	99.2094 862	99.6031 746	blastp
272	wheat gb164 BE 404792 T1	wheat	1619	29	82	52.9644 269	99.2592 593	blastp
273	wheat gb164 BE 216922 T1	wheat	1620	29	81	99.2094 862	99.6031 746	blastp
274	artemisia gb164 EY083433 T1	artemisia	1621	30	80	79.6	100	blastp
275	banana gb160 ES 432704 T1	banana	1622	30	81	88.8	93.6708 861	blastp
276	banana gb160 D N238541 T1	banana	1623	30	80	100	100	blastp
277	barley gb157.3 B E412510 T1	barley	1624	30	80	100	100	blastp
278	cotton gb164 AI 726168 T1	cotton	1625	30	80	98.8	99.5983 936	blastp
279	cotton gb164 AI 731742 T1	cotton	1626	30	80	100	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
280	cotton gb164 AI 055329 T1	cotton	1627	30	80	100	100	blastp
281	grape gb160 BQ 794219 T1	grape	1628	30	81	100	100	blastp
282	ipomoea gb157.2 BJ554855 T1	ipomoea	1629	30	81	98	100	blastp
283	ipomoea gb157.2 BM878761 T1	ipomoea	1630	30	84	100	100	blastp
284	lettuce gb157.2 DW045084 T1	lettuce	1631	30	80	86.8	98.1981 982	blastp
285	lettuce gb157.2 DW114621 T1	lettuce	1632	30	80	88	99.1031 39	blastp
286	lettuce gb157.2 DW078778 T1	lettuce	1633	30	81	50.8	100	blastp
287	maize gb164 CO 528320 T1	maize	1634	30	82	69.6	100	blastp
288	maize gb164 A W257922 T1	maize	1635	30	80	52.4	100	blastp
289	maize gb164 BI6 75058 T1	maize	1636	30	80	54	99.2592 593	blastp
290	maize gb164 A W352518 T1	maize	1637	30	80	51.2	100	blastp
291	maize gb164 AF 037061 T1	maize	1638	30	81	100	100	blastp
292	nicotiana_bentha miana gb162 CN 655062 T1	nicotiana _bentha miana	1639	30	90	100	100	blastp
293	nicotiana_bentha miana gb162 CN 741621 T1	nicotiana _bentha miana	1640	30	90	100	100	blastp
294	oil_palm gb166 CN599861 T1	oil_palm	1641	30	80	100	100	blastp
295	papaya gb165 E X246150 T1	papaya	1642	30	82	100	100	blastp
296	pepper gb157.2 BM060520 T1	pepper	1643	30	91	99.2	98.8	blastp
297	periwinkle gb16 4 EG554262 T1	periwink le	1644	30	82	100	100	blastp
298	petunia gb157.2 AF452015 T1	petunia	1645	30	89	100	100	blastp
299	potato gb157.2 C K853059 T1	potato	1646	30	96	92	91.3043 478	blastp
300	potato gb157.2 C K852742 T1	potato	1647	30	82	60.4	100	blastp
301	potato gb157.2 B M407759 T1	potato	1648	30	99	81.2	97.5961 538	blastp
302	potato gb157.2 C K718033 T1	potato	1649	30	98	65.2	92.0903 955	blastp
303	potato gb157.2 C K717899 T1	potato	1650	30	100	62	95.0920 245	blastp
304	potato gb157.2 C V472240 T1	potato	1651	30	97	79.6	95.2153 11	blastp

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305	potato gb157.2 B G098199 T1	potato	1652	30	95	93.2	99.5726 496	blastp
306	rice gb157.2 U37 925 T1	rice	1653	30	81	100	100	blastp
307	rye gb164 BE49 4266 T1	rye	1654	30	80	100	100	blastp
308	sorghum gb161. xeno AF037061_ T1	sorghum	1655	30	80	100	100	blastp
309	sugarcane gb157 .2 BQ535365_T 1	sugarcane	1656	30	80	80.4	100	blastp
310	switchgrass gb16 5 DN141449 T1	switchgrass	1657	30	81	100	100	blastp
311	switchgrass gb16 5 DN142089 T1	switchgrass	1658	30	81	100	100	blastp
312	tobacco gb162 C N824866 T1	tobacco	1659	30	90	100	100	blastp
313	tobacco gb162 C V017118 T1	tobacco	1660	30	90	100	100	blastp
314	wheat gb164 TA U86762 T1	wheat	1661	30	80	100	100	blastp
315	wheat gb164 BE 499589 T1	wheat	1662	30	80	72	100	blastp
316	lettuce gb157.2 DW087170 T1	lettuce	1663	31	80	100	100	blastp
317	tobacco gb162 E H616288 T1	tobacco	1664	32	87	50.7692 308	85.1612 903	blastp
318	apple gb157.3 C O068608 T1	apple	1665	33	86	98.2638 889	98.9510 49	blastp
319	apple gb157.3 A B100869 T1	apple	1666	33	83	98.2638 889	99.3079 585	blastp
320	apple gb157.3 A B100870 T1	apple	1667	33	83	98.2638 889	99.3079 585	blastp
321	apple gb157.3 C N860225 T1	apple	1668	33	86	54.8611 111	90.2857 143	blastp
322	apple gb157.3 C K900645 T1	apple	1669	33	85	98.2638 889	98.9510 49	blastp
323	apricot gb157.2 CB822297 T1	apricot	1670	33	89	51.0416 667	98.6577 181	blastp
324	apricot gb157.2 CB819647 T1	apricot	1671	33	83	98.2638 889	98.9655 172	blastp
325	aquilegia gb157. 3 DR917005 T1	aquilegia	1672	33	86	98.2638 889	98.9547 038	blastp
326	arabidopsis gb16 5 AT4G00430_T 2	arabidopsis	1673	33	84	73.6111 111	97.2602 74	blastp
327	arabidopsis gb16 5 AT2G45960_T 3	arabidopsis	1674	33	86	88.1944 444	84.3853 821	blastp
328	arabidopsis gb16 5 AT4G23400_T 1	arabidopsis	1675	33	87	98.2638 889	98.9547 038	blastp

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329	arabidopsis gb165 AT2G45960_T1	arabidop sis	1676	33	86	98.2638 889	98.9510 49	blastp
330	arabidopsis gb165 AT4G00430_T1	arabidop sis	1677	33	87	98.2638 889	98.9547 038	blastp
331	arabidopsis gb165 AT1G01620_T1	arabidop sis	1678	33	88	98.2638 889	98.9510 49	blastp
332	arabidopsis gb165 AT3G61430_T1	arabidop sis	1679	33	85	98.2638 889	98.9510 49	blastp
333	arabidopsis gb165 AT2G45960_T4	arabidop sis	1680	33	86	88.1944 444	92.7007 299	blastp
334	artemisia gb164 EY046087_T1	artemisia	1681	33	86	98.2638 889	98.9547 038	blastp
335	artemisia gb164 EY046310_T1	artemisia	1682	33	87	73.6111 111	99.0697 674	blastp
336	artemisia gb164 EY032836_T1	artemisia	1683	33	84	97.5694 444	98.2758 621	blastp
337	artemisia gb164 EY031810_T1	artemisia	1684	33	84	89.2361 111	99.2307 692	blastp
338	avocado gb164 CK751385_T1	avocado	1685	33	86	98.2638 889	98.9547 038	blastp
339	avocado gb164 CK745633_T1	avocado	1686	33	91	73.6111 111	99.0654 206	blastp
340	b_juncea gb164 EVGN00081008450640_T1	b_juncea	1687	33	87	98.2638 889	98.9510 49	blastp
341	b_juncea gb164 EVGN00515811862066_T1	b_juncea	1688	33	90	60.4166 667	96.1325 967	blastp
342	b_juncea gb164 EVGN00230716760965_T1	b_juncea	1689	33	89	73.6111 111	99.0654 206	blastp
343	b_juncea gb164 EVGN01776308261252_T1	b_juncea	1690	33	84	66.3194 444	96.4646 465	blastp
344	b_juncea gb164 EVGN00910030360678_T1	b_juncea	1691	33	91	65.2777 778	98.9473 684	blastp
345	b_juncea gb164 EVGN03812526911787_T1	b_juncea	1692	33	88	51.0416 667	98.6577 181	blastp
346	b_juncea gb164 EVGN00227203510305_T1	b_juncea	1693	33	91	65.2777 778	98.9473 684	blastp
347	b_juncea gb164 EVGN00462518410866_T1	b_juncea	1694	33	87	98.2638 889	98.9510 49	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
348	b_juncea gb164 EVGN00248411 120906 T1	b_juncea	1695	33	89	73.2638 889	99.0610 329	blastp
349	b_juncea gb164 EF471211 T1	b_juncea	1696	33	86	98.2638 889	98.2638 889	blastp
350	b_juncea gb164 EVGN00440012 650683 T1	b_juncea	1697	33	86	98.2638 889	98.9510 49	blastp
351	b_juncea gb164 EVGN00452211 183349 T1	b_juncea	1698	33	86	98.2638 889	98.9510 49	blastp
352	b_juncea gb164 EVGN03595331 210044 T1	b_juncea	1699	33	89	57.6388 889	93.2584 27	blastp
353	b_juncea gb164 EVGN00088009 631302 T1	b_juncea	1700	33	87	98.2638 889	98.9510 49	blastp
354	b_juncea gb164 EVGN00512912 541009 T1	b_juncea	1701	33	85	51.7361 111	93.9075 63	tblastn
355	b_juncea gb164 EVGN00756014 550623 T1	b_juncea	1702	33	84	69.0972 222	90.3177 005	tblastn
356	b_oleracea gb16 1 AF299051 T1	b_olerac ea	1703	33	86	98.2638 889	98.9510 49	blastp
357	b_oleracea gb16 1 AM391520 T1	b_olerac ea	1704	33	87	75.3472 222	99.5412 844	blastp
358	b_oleracea gb16 1 AM058918 T1	b_olerac ea	1705	33	87	98.2638 889	98.9510 49	blastp
359	b_oleracea gb16 1 AF299050 T1	b_olerac ea	1706	33	86	98.2638 889	98.9510 49	blastp
360	b_oleracea gb16 1 DY029936 T1	b_olerac ea	1707	33	86	98.2638 889	98.9510 49	blastp
361	b_oleracea gb16 1 EH422530 T1	b_olerac ea	1708	33	87	78.4722 222	100	blastp
362	b_rapa gb162 C V546930 T1	b_rapa	1709	33	84	71.5277 778	99.5169 082	blastp
363	b_rapa gb162 B G544387 T1	b_rapa	1710	33	86	95.4861 111	99.2779 783	blastp
364	b_rapa gb162 C A992432 T1	b_rapa	1711	33	86	98.2638 889	98.9510 49	blastp
365	b_rapa gb162 C V546129 T2	b_rapa	1712	33	83	54.8611 111	99.3710 692	blastp
366	b_rapa gb162 EE 526280 T1	b_rapa	1713	33	87	98.2638 889	98.9510 49	blastp
367	b_rapa gb162 L3 3552 T1	b_rapa	1714	33	86	98.2638 889	98.9510 49	blastp
368	b_rapa gb162 B G543719 T1	b_rapa	1715	33	84	77.0833 333	99.5515 695	blastp
369	b_rapa gb162 AF 004293 T1	b_rapa	1716	33	87	98.2638 889	98.9510 49	blastp
370	b_rapa gb162 B G544086 T1	b_rapa	1717	33	87	98.2638 889	98.9510 49	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
371	b_rapa gb162 C X267412 T1	b_rapa	1718	33	86	98.2638 889	99.2982 456	blastp
372	b_rapa gb162 C V546129 T1	b_rapa	1719	33	86	98.2638 889	98.2638 889	blastp
373	b_rapa gb162 C V545634 T1	b_rapa	1720	33	83	56.5972 222	90.5555 556	blastp
374	banana gb160 D N238827 T1	banana	1721	33	84	60.7638 889	99.4285 714	blastp
375	banana gb160 ES 431094 T1	banana	1722	33	89	63.8888 889	98.9247 312	blastp
376	barley gb157.3 B E412959 T2	barley	1723	33	83	98.2638 889	98.9726 027	blastp
377	barley gb157.3 A L507831 T1	barley	1724	33	85	99.3055 556	99.6551 724	blastp
378	barley gb157.3 B E412959 T1	barley	1725	33	83	98.2638 889	98.9726 027	blastp
379	barley gb157.3 B E412959 T5	barley	1726	33	82	98.2638 889	98.9830 508	blastp
380	barley gb157.3 B E412959 T4	barley	1727	33	82	98.2638 889	98.9830 508	blastp
381	barley gb157.3 A L502020 T1	barley	1728	33	82	98.2638 889	98.9726 027	blastp
382	barley gb157.3 B E412972 T1	barley	1729	33	85	98.2638 889	98.9583 333	blastp
383	basilicum gb157. 3 DY340092 T1	basilicu m	1730	33	88	61.8055 556	99.4413 408	blastp
384	basilicum gb157. 3 DY332264 T1	basilicu m	1731	33	87	73.9583 333	99.5327 103	blastp
385	bean gb164 CB5 43592 T1	bean	1732	33	88	98.2638 889	98.9547 038	blastp
386	bean gb164 PVU 97023 T1	bean	1733	33	84	98.2638 889	99.3079 585	blastp
387	bean gb164 CB5 42193 T1	bean	1734	33	84	98.6111 111	99.6539 792	blastp
388	beet gb162 BVU 60149 T1	beet	1735	33	84	98.2638 889	98.9510 49	blastp
389	brachypodium g b161.xeno BE44 3278 T1	brachypo dium	1736	33	83	82.9861 111	95.6521 739	blastp
390	brachypodium g b161.xeno BE21 6990 T1	brachypo dium	1737	33	85	98.2638 889	98.9583 333	blastp
391	brachypodium g b161.xeno BE40 3307 T1	brachypo dium	1738	33	82	86.8055 556	72.7011 494	blastp
392	canola gb161 CN 731957 T1	canola	1739	33	86	98.2638 889	98.9510 49	blastp
393	canola gb161 CX 194503 T1	canola	1740	33	86	98.2638 889	98.9510 49	blastp
394	canola gb161 CD 814405 T1	canola	1741	33	87	98.2638 889	98.9510 49	blastp
395	canola gb161 EG 020906 T1	canola	1742	33	86	98.2638 889	98.9510 49	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
396	canola gb161 H7 4720 T1	canola	1743	33	86	98.2638 889	98.9510 49	blastp
397	canola gb161 CN 831315 T1	canola	1744	33	86	84.0277 778	93.4362 934	blastp
398	canola gb161 CD 817408 T1	canola	1745	33	87	98.2638 889	98.9510 49	blastp
399	canola gb161 EE 502121 T1	canola	1746	33	89	52.7777 778	98.7096 774	blastp
400	canola gb161 CX 187544 T1	canola	1747	33	87	98.2638 889	98.9510 49	blastp
401	canola gb161 CD 822064 T1	canola	1748	33	86	98.2638 889	98.9510 49	blastp
402	canola gb161 CD 824965 T1	canola	1749	33	81	92.0138 889	93.0313 589	blastp
403	canola gb161 EE 485551 T1	canola	1750	33	87	98.2638 889	98.9510 49	blastp
404	canola gb161 CB 686274 T1	canola	1751	33	86	98.2638 889	98.9510 49	blastp
405	canola gb161 CD 814573 T1	canola	1752	33	83	76.3888 889	94.0425 532	blastp
406	canola gb161 CX 193398 T1	canola	1753	33	86	98.2638 889	98.2638 889	blastp
407	canola gb161 CD 818853 T1	canola	1754	33	86	98.2638 889	98.9510 49	blastp
408	canola gb161 D Y005979 T1	canola	1755	33	85	78.4722 222	99.5594 714	blastp
409	canola gb161 EE 464964 T1	canola	1756	33	85	81.5972 222	99.5762 712	blastp
410	cassava gb164 B M260264 T1	cassava	1757	33	85	97.9166 667	99.3031 359	blastp
411	cassava gb164 C K901165 T1	cassava	1758	33	87	73.6111 111	99.0697 674	blastp
412	cassava gb164 C K642415 T1	cassava	1759	33	87	98.2638 889	98.9547 038	blastp
413	cassava gb164 D V455398 T1	cassava	1760	33	85	97.9166 667	99.3031 359	blastp
414	castorbean gb16 0 T14819 T1	castorbea n	1761	33	89	98.2638 889	98.9547 038	blastp
415	castorbean gb16 0 EG691229 T1	castorbea n	1762	33	86	98.2638 889	98.9510 49	blastp
416	castorbean gb16 0 AJ605566 T1	castorbea n	1763	33	87	97.9166 667	99.3031 359	blastp
417	castorbean gb16 0 MDL29969M0 00266 T1	castorbea n	1764	33	84	98.2638 889	99.3055 556	blastp
418	castorbean gb16 0 AJ605574 T1	castorbea n	1765	33	87	97.9166 667	98.9583 333	blastp
419	centaurea gb161 EH732068 T1	centaure a	1766	33	82	97.5694 444	98.6062 718	blastp
420	cichorium gb161 EH673032 T1	cichoriu m	1767	33	87	98.2638 889	98.9547 038	blastp
421	cichorium gb161 EH706808 T1	cichoriu m	1768	33	90	51.7361 111	98.6842 105	blastp

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422	cichorium gb161 EH701938 T1	cichoriu m	1769	33	86	64.9305 556	95.4314 721	blastp
423	citrus gb157.2 C O912471 T1	citrus	1770	33	82	69.4444 444	99.5098 039	blastp
424	citrus gb157.2 B Q624312 T1	citrus	1771	33	88	98.2638 889	98.9547 038	blastp
425	citrus gb157.2 C N182376 T1	citrus	1772	33	84	92.7083 333	94.0559 441	blastp
426	citrus gb157.2 C B291370 T1	citrus	1773	33	89	98.2638 889	98.9547 038	blastp
427	citrus gb157.2 C F833327 T1	citrus	1774	33	85	98.2638 889	99.3031 359	blastp
428	citrus gb157.2 B Q624860 T1	citrus	1775	33	85	97.9166 667	99.6503 497	blastp
429	citrus gb157.2 C F508404 T1	citrus	1776	33	81	97.9166 667	99.6503 497	blastp
430	citrus gb157.2 C B293694 T1	citrus	1777	33	84	98.2638 889	99.3031 359	blastp
431	citrus gb157.2 B Q622975 T1	citrus	1778	33	85	97.9166 667	99.6503 497	blastp
432	citrus gb157.2 B E213453 T1	citrus	1779	33	86	73.6111 111	99.5305 164	blastp
433	citrus gb157.2 C F828110 T1	citrus	1780	33	85	98.6111 111	99.6527 778	blastp
434	citrus gb157.2 B Q623397 T1	citrus	1781	33	86	93.4027 778	99.6336 996	blastp
435	clover gb162 BB 903117 T1	clover	1782	33	85	98.6111 111	99.6539 792	blastp
436	coffea gb157.2 B Q449035 T1	coffea	1783	33	88	98.9583 333	99.3055 556	blastp
437	coffea gb157.2 D V663743 T1	coffea	1784	33	85	98.2638 889	98.9473 684	blastp
438	cotton gb164 CD 486529 T1	cotton	1785	33	83	98.2638 889	99.3055 556	blastp
439	cotton gb164 BE 052445 T1	cotton	1786	33	87	98.2638 889	98.9547 038	blastp
440	cotton gb164 AI 726690 T1	cotton	1787	33	86	98.2638 889	98.9547 038	blastp
441	cotton gb164 DN 803576 T1	cotton	1788	33	83	87.8472 222	98.8281 25	blastp
442	cotton gb164 B M358242 T1	cotton	1789	33	81	98.2638 889	99.2882 562	blastp
443	cotton gb164 CO 085369 T1	cotton	1790	33	81	52.7777 778	99.3506 494	blastp
444	cotton gb164 CO 098674 T1	cotton	1791	33	84	98.2638 889	99.3055 556	blastp
445	cotton gb164 CO 070796 T1	cotton	1792	33	84	98.2638 889	99.3031 359	blastp
446	cotton gb164 AI 729945 T1	cotton	1793	33	85	98.2638 889	99.3079 585	blastp
447	cotton gb164 D W496760 T1	cotton	1794	33	86	80.5555 556	98.3122 363	blastp

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448	cowpea gb166 F384916_T1	cowpea	1795	33	82	98.2638889	99.3031359	blastp
449	cowpea gb166 F555791_T1	cowpea	1796	33	82	98.6111111	99.6539792	blastp
450	cowpea gb166 F457489_T1	cowpea	1797	33	87	98.2638889	98.9547038	blastp
451	cowpea gb166 A037241_T1	cowpea	1798	33	84	98.2638889	99.3079585	blastp
452	cryptomeria gb166 DC429824_T1	cryptome ria	1799	33	84	71.5277778	99.5215311	blastp
453	cryptomeria gb166 AU036730_T1	cryptome ria	1800	33	85	98.6111111	99.6515679	blastp
454	dandelion gb161 DY814032_T1	dandelio n	1801	33	84	82.2916667	93.7007874	blastp
455	dandelion gb161 DY802714_T1	dandelio n	1802	33	82	98.2638889	99.3031359	blastp
456	dandelion gb161 DY822683_T1	dandelio n	1803	33	84	95.8333333	99.6415771	blastp
457	dandelion gb161 DY806788_T1	dandelio n	1804	33	87	98.2638889	98.9583333	blastp
458	dandelion gb161 DY808781_T1	dandelio n	1805	33	84	84.0277778	99.5918367	blastp
459	dandelion gb161 DY810613_T1	dandelio n	1806	33	81	76.3888889	94.8497854	blastp
460	fescue gb161 CK803261_T1	fescue	1807	33	85	97.9166667	98.6111111	blastp
461	fescue gb161 DT682664_T1	fescue	1808	33	84	67.3611111	99.4923858	blastp
462	fescue gb161 DT677062_T1	fescue	1809	33	83	98.2638889	98.9655172	blastp
463	fescue gb161 DT679061_T1	fescue	1810	33	86	98.2638889	98.9619377	blastp
464	flax gb157.3 CV478314_T1	flax	1811	33	84	71.875	99.5260664	blastp
465	ginger gb164 DY345344_T1	ginger	1812	33	88	98.2638889	98.951049	blastp
466	ginger gb164 DY358322_T1	ginger	1813	33	85	98.2638889	98.9473684	blastp
467	ginger gb164 DY360757_T1	ginger	1814	33	84	98.6111111	99.6478873	blastp
468	ginger gb164 DY345596_T1	ginger	1815	33	86	98.2638889	98.9473684	blastp
469	grape gb160 AF188844_T1	grape	1816	33	87	98.2638889	98.9547038	blastp
470	grape gb160 AF188843_T1	grape	1817	33	85	98.2638889	98.951049	blastp
471	grape gb160 AF188843_T3	grape	1818	33	85	98.2638889	98.951049	blastp
472	grape gb160 CB971128_T1	grape	1819	33	87	98.2638889	99.3006993	blastp

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473	grape gb160 AF1 88843 T4	grape	1820	33	84	72.2222 222	86.3070 539	blastp
474	iceplant gb164 MCU26537 T1	iceplant	1821	33	85	98.2638 889	98.9473 684	blastp
475	iceplant gb164 C IPMIPA T1	iceplant	1822	33	85	98.2638 889	99.2957 746	blastp
476	iceplant gb164 C IPMIPB T1	iceplant	1823	33	87	98.2638 889	98.9473 684	blastp
477	ipomoea gb157.2 BM878883 T1	ipomoea	1824	33	87	98.9583 333	99.3031 359	blastp
478	ipomoea gb157.2 BJ553988 T1	ipomoea	1825	33	85	98.6111 111	99.6491 228	blastp
479	ipomoea gb157.2 BJ553369 T1	ipomoea	1826	33	84	98.6111 111	99.6478 873	blastp
480	ipomoea gb157.2 BJ553198 T1	ipomoea	1827	33	89	98.9583 333	99.3031 359	blastp
481	lettuce gb157.2 DW079915 T1	lettuce	1828	33	86	98.2638 889	97.9310 345	blastp
482	lettuce gb157.2 DW043941 T1	lettuce	1829	33	87	98.2638 889	98.9547 038	blastp
483	lettuce gb157.2 DW047538 T1	lettuce	1830	33	87	96.875	98.2456 14	blastp
484	lettuce gb157.2 DW104582 T1	lettuce	1831	33	84	98.2638 889	99.3031 359	blastp
485	lettuce gb157.2 DW044606 T1	lettuce	1832	33	84	98.2638 889	99.3031 359	blastp
486	lettuce gb157.2 DW148209 T1	lettuce	1833	33	85	89.2361 111	94.1605 839	blastp
487	lettuce gb157.2 DW148478 T1	lettuce	1834	33	83	98.6111 111	95.3333 333	blastp
488	lettuce gb157.2 DW108503 T1	lettuce	1835	33	86	98.2638 889	98.9547 038	blastp
489	lettuce gb157.2 DW046100 T1	lettuce	1836	33	86	96.875	99.6441 281	blastp
490	lettuce gb157.2 DW075079 T1	lettuce	1837	33	85	98.2638 889	99.3031 359	blastp
491	lettuce gb157.2 DW076402 T1	lettuce	1838	33	87	98.2638 889	98.9547 038	blastp
492	lettuce gb157.2 DW084041 T1	lettuce	1839	33	86	89.5833 333	92.8315 412	blastp
493	lettuce gb157.2 DW145601 T1	lettuce	1840	33	87	98.2638 889	98.9547 038	blastp
494	lettuce gb157.2 CV699980 T1	lettuce	1841	33	86	98.2638 889	98.9547 038	blastp
495	lettuce gb157.2 DW064849 T1	lettuce	1842	33	87	98.2638 889	98.9547 038	blastp
496	lettuce gb157.2 DW147179 T1	lettuce	1843	33	83	98.6111 111	89.0965 732	blastp
497	lettuce gb157.2 DW045991 T1	lettuce	1844	33	83	98.6111 111	97.2789 116	blastp
498	lotus gb157.2 AF 145707 T1	lotus	1845	33	84	98.2638 889	99.3079 585	blastp

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499	lotus gb157.2 AI 967594 T1	lotus	1846	33	86	96.875	98.2456 14	blastp
500	lotus gb157.2 AF 145708 T1	lotus	1847	33	87	66.6666 667	100	blastp
501	maize gb164 EC 881658 T1	maize	1848	33	86	54.5138 889	98.7421 384	blastp
502	maize gb164 AI3 72377 T1	maize	1849	33	85	98.2638 889	98.9583 333	blastp
503	maize gb164 AF 145706 T1	maize	1850	33	83	60.7638 889	100	blastp
504	maize gb164 AI8 55222 T1	maize	1851	33	84	98.2638 889	98.9726 027	blastp
505	maize gb164 AI6 19392 T1	maize	1852	33	86	98.2638 889	98.9619 377	blastp
506	maize gb164 AI8 61086 T1	maize	1853	33	84	98.2638 889	98.9583 333	blastp
507	medicago gb157. 2 AW684000_T 1	medicag o	1854	33	84	98.2638 889	99.3079 585	blastp
508	medicago gb157. 2 AI974398 T1	medicag o	1855	33	83	98.2638 889	99.3079 585	blastp
509	medicago gb157. 2 AL366983 T1	medicag o	1856	33	88	97.5694 444	98.6062 718	blastp
510	medicago gb157. 2 AI737528 T1	medicag o	1857	33	84	98.6111 111	99.3103 448	blastp
511	medicago gb157. 2 BQ151876 T1	medicag o	1858	33	84	82.2916 667	87.2262 774	blastp
512	melon gb165 DV 632745 T1	melon	1859	33	84	98.2638 889	99.3150 685	blastp
513	melon gb165 CF 674915 T1	melon	1860	33	83	98.2638 889	99.3150 685	blastp
514	melon gb165 DV 632772 T1	melon	1861	33	85	98.2638 889	98.9510 49	blastp
515	millet gb161 CD 724341 T1	millet	1862	33	83	57.2916 667	92.1787 709	blastp
516	nicotiana_bentha miana gb162 ES 885295 T1	nicotiana _bentha miana	1863	33	84	66.6666 667	97.9487 179	blastp
517	oil_palm gb166 CN600863 T1	oil_palm	1864	33	85	98.2638 889	98.9547 038	blastp
518	oil_palm gb166 CN600797 T1	oil_palm	1865	33	86	98.2638 889	98.9547 038	blastp
519	onion gb162 AF 255796 T1	onion	1866	33	86	98.2638 889	98.9583 333	blastp
520	papaya gb165 E X228092 T1	papaya	1867	33	84	72.2222 222	93.2735 426	blastp
521	papaya gb165 AJ 000031 T1	papaya	1868	33	85	98.2638 889	99.3079 585	blastp
522	papaya gb165 E X257869 T1	papaya	1869	33	83	98.2638 889	99.3031 359	blastp
523	papaya gb165 A M903842 T1	papaya	1870	33	90	98.2638 889	98.9510 49	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
524	peach gb157.2 B U039203 T1	peach	1871	33	84	98.2638 889	98.9655 172	blastp
525	peach gb157.2 B U040913 T1	peach	1872	33	90	51.3888 889	98.6666 667	blastp
526	peanut gb161 C D038184 T1	peanut	1873	33	83	98.6111 111	99.6539 792	blastp
527	peanut gb161 ES 490696 T1	peanut	1874	33	82	73.9583 333	99.5348 837	blastp
528	peanut gb161 C D038104 T1	peanut	1875	33	83	98.2638 889	99.3079 585	blastp
529	pepper gb157.2 CA523071 T1	pepper	1876	33	97	96.875	100	blastp
530	pepper gb157.2 BM063708 T1	pepper	1877	33	95	99.3055 556	100	blastp
531	periwinkle gb16 4 EG554502 T1	periwink le	1878	33	88	98.9583 333	99.3031 359	blastp
532	periwinkle gb16 4 EG554518 T1	periwink le	1879	33	87	98.9583 333	99.3031 359	blastp
533	periwinkle gb16 4 EG556773 T1	periwink le	1880	33	83	84.0277 778	96.8	blastp
534	petunia gb157.2 AF452010 T1	petunia	1881	33	93	99.3055 556	100	blastp
535	petunia gb157.2 CV292775 T1	petunia	1882	33	92	61.8055 556	100	blastp
536	petunia gb157.2 AF452011 T1	petunia	1883	33	86	98.2638 889	99.3006 993	blastp
537	pine gb157.2 AL 751335 T1	pine	1884	33	83	98.2638 889	98.9583 333	blastp
538	pine gb157.2 AA 556193 T1	pine	1885	33	85	98.2638 889	98.9583 333	blastp
539	pine gb157.2 AL 750485 T1	pine	1886	33	85	98.2638 889	98.9583 333	blastp
540	pineapple gb157. 2 DT335964 T1	pineappl e	1887	33	83	98.2638 889	97.9452 055	blastp
541	pineapple gb157. 2 DT338557 T1	pineappl e	1888	33	86	98.2638 889	98.9583 333	blastp
542	poplar gb157.2 B U817536 T1	poplar	1889	33	83	98.2638 889	99.3031 359	blastp
543	poplar gb157.2 A I162483 T1	poplar	1890	33	88	98.2638 889	98.9583 333	blastp
544	poplar gb157.2 B I122420 T1	poplar	1891	33	87	97.9166 667	99.3031 359	blastp
545	poplar gb157.2 A I165418 T1	poplar	1892	33	85	97.9166 667	99.3031 359	blastp
546	poplar gb157.2 B U817536 T3	poplar	1893	33	82	88.1944 444	92.0863 309	blastp
547	poplar gb157.2 B U881784 T1	poplar	1894	33	83	98.2638 889	99.3031 359	blastp
548	potato gb157.2 B E923816 T1	potato	1895	33	85	98.2638 889	99.3006 993	blastp
549	potato gb157.2 C K260061 T1	potato	1896	33	91	62.5	98.9010 989	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
550	potato gb157.2 B E924585 T1	potato	1897	33	86	98.2638 889	98.9473 684	blastp
551	potato gb157.2 B F153976 T1	potato	1898	33	86	61.1111 111	100	blastp
552	potato gb157.2 A J487323 T1	potato	1899	33	97	100	100	blastp
553	potato gb157.2 B F154021 T1	potato	1900	33	92	99.3055 556	100	blastp
554	potato gb157.2 B G599633 T1	potato	1901	33	95	98.9583 333	99.3031 359	blastp
555	potato gb157.2 B E922307 T1	potato	1902	33	85	98.2638 889	99.3006 993	blastp
556	radish gb164 EV 536875 T1	radish	1903	33	86	98.2638 889	98.9510 49	blastp
557	radish gb164 EW 726189 T1	radish	1904	33	83	60.0694 444	96.1111 111	blastp
558	radish gb164 EX 756217 T1	radish	1905	33	86	98.2638 889	98.9510 49	blastp
559	radish gb164 AB 030696 T1	radish	1906	33	86	98.2638 889	98.9510 49	blastp
560	radish gb164 AB 030695 T1	radish	1907	33	87	98.2638 889	98.9510 49	blastp
561	radish gb164 AB 012044 T1	radish	1908	33	85	98.2638 889	98.9510 49	blastp
562	radish gb164 EV 567230 T1	radish	1909	33	87	98.2638 889	98.9547 038	blastp
563	radish gb164 EY 936735 T1	radish	1910	33	86	98.2638 889	98.9510 49	blastp
564	rice gb157.2 U37 951 T1	rice	1911	33	86	98.2638 889	98.9619 377	blastp
565	rice gb157.2 U40 140 T1	rice	1912	33	86	98.2638 889	98.9583 333	blastp
566	rice gb157.2 BE0 39992 T1	rice	1913	33	82	98.2638 889	98.9583 333	blastp
567	rice gb157.2 U37 951 T2	rice	1914	33	86	73.6111 111	99.0654 206	blastp
568	rose gb157.2 BQ 104887 T1	rose	1915	33	83	97.5694 444	98.6206 897	blastp
569	rose gb157.2 BQ 103877 T1	rose	1916	33	85	98.2638 889	98.9547 038	blastp
570	rose gb157.2 EC 586734 T1	rose	1917	33	80	62.1527 778	99.4444 444	blastp
571	rye gb164 BE58 6240 T1	rye	1918	33	83	98.2638 889	98.9726 027	blastp
572	safflower gb162 EL407054 T1	safflower	1919	33	86	89.5833 333	94.5454 545	blastp
573	safflower gb162 EL400504 T1	safflower	1920	33	85	98.2638 889	92.5081 433	blastp
574	safflower gb162 EL400004 T1	safflower	1921	33	83	84.375	99.5934 959	blastp
575	sesame gb157.2 BU668587 T1	sesame	1922	33	91	57.2916 667	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
576	sesame gb157.2 BU669929 T1	sesame	1923	33	87	55.2083 333	99.375	blastp
577	sorghum gb161. xeno A1372377_ T1	sorghum	1924	33	85	98.2638 889	98.9583 333	blastp
578	sorghum gb161. xeno A1861086_ T1	sorghum	1925	33	82	98.2638 889	98.9655 172	blastp
579	sorghum gb161. xeno SBU87981 T1	sorghum	1926	33	86	98.2638 889	98.9619 377	blastp
580	soybean gb166 C D401115 T1	soybean	1927	33	82	98.2638 889	99.3031 359	blastp
581	soybean gb166 A W348556 T1	soybean	1928	33	84	98.6111 111	99.6539 792	blastp
582	soybean gb166 B E352670 T1	soybean	1929	33	86	98.2638 889	98.9547 038	blastp
583	soybean gb166 B I967765 T1	soybean	1930	33	86	98.2638 889	98.9619 377	blastp
584	soybean gb166 B E661219 T1	soybean	1931	33	82	98.2638 889	99.3079 585	blastp
585	soybean gb166 B E352747 T5	soybean	1932	33	81	88.1944 444	98.4732 824	blastp
586	soybean gb166 C D416359 T1	soybean	1933	33	85	97.5694 444	98.6013 986	blastp
587	soybean gb166 A W350352 T1	soybean	1934	33	84	97.5694 444	98.6013 986	blastp
588	soybean gb166 B E352747 T1	soybean	1935	33	82	98.2638 889	99.3079 585	blastp
589	soybean gb166 B E820629 T1	soybean	1936	33	85	98.2638 889	99.2957 746	blastp
590	spikemoss gb165 DN838148 T4	spikemos s	1937	33	82	51.0416 667	99.3243 243	blastp
591	spruce gb162 CO 224550 T1	spruce	1938	33	80	96.875	98.9473 684	blastp
592	spruce gb162 CO 216100 T1	spruce	1939	33	86	98.2638 889	98.9726 027	blastp
593	spruce gb162 CO 216028 T1	spruce	1940	33	85	98.2638 889	98.9583 333	blastp
594	spurge gb161 B G354070 T1	spurge	1941	33	87	97.9166 667	98.2638 889	blastp
595	strawberry gb16 4 CO378647 T1	strawberr y	1942	33	82	98.2638 889	99.3103 448	blastp
596	strawberry gb16 4 CX661400 T1	strawberr y	1943	33	84	98.2638 889	98.9547 038	blastp
597	strawberry gb16 4 DV438296 T1	strawberr y	1944	33	83	98.2638 889	98.9510 49	blastp
598	sugarcane gb157 .2 CA264801_T 1	sugarcan e	1945	33	80	60.0694 444	88.8888 889	blastp
599	sugarcane gb157 .2 CA086058_T 1	sugarcan e	1946	33	85	98.2638 889	98.9583 333	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
600	sugarcane gb157 .2 CA071197_T 1	sugarcane	1947	33	84	97.2222 222	98.2638 889	blastp
601	sugarcane gb157 .2 BQ530399_T 1	sugarcane	1948	33	84	91.6666 667	99.2537 313	blastp
602	sugarcane gb157 .2 CA085969_T 1	sugarcane	1949	33	82	74.3055 556	99.5391 705	blastp
603	sugarcane gb157 .2 CA074778_T 1	sugarcane	1950	33	84	71.1805 556	93.6936 937	blastp
604	sugarcane gb157 .2 CA130651_T 1	sugarcane	1951	33	81	62.1527 778	99.4505 495	blastp
605	sugarcane gb157 .2 AA525652_T 1	sugarcane	1952	33	88	53.4722 222	98.7179 487	blastp
606	sugarcane gb157 .2 BQ536359_T 1	sugarcane	1953	33	86	98.2638 889	98.9619 377	blastp
607	sunflower gb162 DY909123_T1	sunflower	1954	33	86	98.2638 889	98.9547 038	blastp
608	sunflower gb162 CD846367_T1	sunflower	1955	33	85	98.2638 889	98.9547 038	blastp
609	sunflower gb162 CD846084_T1	sunflower	1956	33	86	98.2638 889	98.9547 038	blastp
610	sunflower gb162 DY915760_T1	sunflower	1957	33	84	72.2222 222	100	blastp
611	sunflower gb162 CF080940_T1	sunflower	1958	33	83	73.6111 111	99.5327 103	blastp
612	sunflower gb162 CF087907_T1	sunflower	1959	33	83	96.875	97.5694 444	blastp
613	sunflower gb162 CX946986_T1	sunflower	1960	33	84	98.2638 889	98.6111 111	blastp
614	sunflower gb162 DY918780_T1	sunflower	1961	33	87	73.6111 111	99.0697 674	blastp
615	switchgrass gb16 5 FE619753_T1	switchgrass	1962	33	86	98.2638 889	98.9583 333	blastp
616	switchgrass gb16 5 DN142591_T1	switchgrass	1963	33	85	98.2638 889	98.9583 333	blastp
617	switchgrass gb16 5 DN141716_T1	switchgrass	1964	33	85	98.2638 889	98.9619 377	blastp
618	switchgrass gb16 5 DN141343_T1	switchgrass	1965	33	86	98.2638 889	98.9583 333	blastp
619	switchgrass gb16 5 DN142037_T1	switchgrass	1966	33	85	98.2638 889	98.9619 377	blastp
620	thellungiella gb1 57.2 DN774595_ T1	thellungiella	1967	33	85	98.2638 889	98.9510 49	blastp
621	thellungiella gb1 57.2 BM986095_ T1	thellungiella	1968	33	86	98.2638 889	98.9510 49	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Poly pep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
622	thellungiella gb157.2 B1698563_T1	thellungiella	1969	33	85	72.5694444	99.5238095	blastp
623	tobacco gb162 EB426225_T1	tobacco	1970	33	87	98.2638889	98.2578397	blastp
624	tobacco gb162 CK720591_T1	tobacco	1971	33	95	99.3055556	99.6515679	blastp
625	tobacco gb162 CK720595_T1	tobacco	1972	33	96	73.6111111	99.0654206	blastp
626	tobacco gb162 EB427872_T1	tobacco	1973	33	88	98.2638889	99.2982456	blastp
627	tobacco gb162 CK720593_T1	tobacco	1974	33	87	97.9166667	98.9473684	blastp
628	tobacco gb162 AF024511_T1	tobacco	1975	33	95	99.3055556	99.6515679	blastp
629	tobacco gb162 CK720596_T1	tobacco	1976	33	96	98.9583333	99.3031359	blastp
630	tobacco gb162 NTU62280_T1	tobacco	1977	33	96	98.9583333	99.3031359	blastp
631	tomato gb164 AW622243_T1	tomato	1978	33	94	98.9583333	99.3031359	blastp
632	tomato gb164 BG123213_T1	tomato	1979	33	94	99.3055556	100	blastp
633	tomato gb164 AI637363_T1	tomato	1980	33	87	98.2638889	98.9473684	blastp
634	tomato gb164 BG123955_T1	tomato	1981	33	85	98.2638889	99.3006993	blastp
635	tomato gb164 BP876517_T1	tomato	1982	33	80	55.9027778	86.8705036	tblastn
636	triphysaria gb164 BM357654_T1	triphysaria	1983	33	86	73.6111111	99.5305164	blastp
637	triphysaria gb164 EY141207_T1	triphysaria	1984	33	90	65.625	99.4736842	blastp
638	triphysaria gb164 DR174621_T1	triphysaria	1985	33	87	69.0972222	100	blastp
639	triphysaria gb164 BM356761_T1	triphysaria	1986	33	86	88.5416667	99.6108949	blastp
640	triphysaria gb164 DR169763_T1	triphysaria	1987	33	87	98.2638889	99.6466431	blastp
641	triphysaria gb164 BM356902_T1	triphysaria	1988	33	86	96.5277778	99.6428571	blastp
642	triphysaria gb164 DR174271_T1	triphysaria	1989	33	86	92.7083333	97.4545455	blastp
643	triphysaria gb164 DR171777_T1	triphysaria	1990	33	88	100	99.6539792	blastp
644	wheat gb164 BE406715_T1	wheat	1991	33	83	98.2638889	98.9726027	blastp
645	wheat gb164 BQ838456_T1	wheat	1992	33	83	98.2638889	98.9726027	blastp
646	wheat gb164 BE426386_T1	wheat	1993	33	82	98.2638889	98.9726027	blastp
647	wheat gb164 BE403388_T1	wheat	1994	33	88	51.0416667	98.6577181	blastp

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648	wheat gb164 BE 403307 T1	wheat	1995	33	83	98.2638 889	98.9726 027	blastp
649	wheat gb164 BE 498268 T1	wheat	1996	33	81	60.4166 667	96.7213 115	blastp
650	wheat gb164 AL 828763 T1	wheat	1997	33	84	84.7222 222	96.4705 882	blastp
651	wheat gb164 AF 139816 T1	wheat	1998	33	83	98.2638 889	98.9726 027	blastp
652	wheat gb164 BE 216990 T1	wheat	1999	33	86	98.2638 889	98.9583 333	blastp
653	wheat gb164 BE 403886 T1	wheat	2000	33	85	99.3055 556	99.6551 724	blastp
654	wheat gb164 BE 430165 T1	wheat	2001	33	85	99.3055 556	99.6551 724	blastp
655	wheat gb164 CA 484202 T1	wheat	2002	33	87	56.9444 444	97.6190 476	blastp
656	wheat gb164 BE 404199 T1	wheat	2003	33	86	98.2638 889	98.9583 333	blastp
657	wheat gb164 BE 406086 T1	wheat	2004	33	83	98.2638 889	98.9726 027	blastp
658	wheat gb164 BF 293776 T1	wheat	2005	33	83	98.2638 889	98.9655 172	blastp
659	wheat gb164 CK 193386 T1	wheat	2006	33	81	97.2222 222	96.6216 216	blastp
660	castorbean gb16 0 AJ605572 T1	castorbean	2007	34	80	99.1902 834	98.7854 251	blastp
661	citrus gb157.2 C K740163 T1	citrus	2008	34	80	99.1902 834	98.7854 251	blastp
662	coffea gb157.2 D V664793 T1	coffea	2009	34	80	100	100	blastp
663	lettuce gb157.2 DW074942 T1	lettuce	2010	34	80	99.1902 834	99.5934 959	blastp
664	pepper gb157.2 BM063938 T1	pepper	2011	34	95	76.1133 603	100	blastp
665	periwinkle gb16 4 EG558295 T1	periwinkle	2012	34	81	99.1902 834	98.7903 226	blastp
666	potato gb157.2 B M112462 T1	potato	2013	34	98	94.7368 421	99.5744 681	blastp
667	tobacco gb162 A J237751 T1	tobacco	2014	34	95	100	100	blastp
668	tobacco gb162 E B425012 T1	tobacco	2015	34	93	100	100	blastp
669	nicotiana_bentha miana gb162 CK 284579 T1	nicotiana _bentha miana	2016	35	86	74.6177 37	97.5903 614	blastp
670	potato gb157.2 B G594926 T1	potato	2017	35	96	100	96.4497 041	blastp
671	tomato gb164 D B679435 T1	tomato	2018	35	90	76.1467 89	100	blastp
672	tobacco gb162 C K720588 T1	tobacco	2019	36	81	53.5580 524	100	blastp
673	apple gb157.3 C N494715 T1	apple	2020	37	84	85.7142 857	94.7368 421	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
674	apple gb157.3 C O066689 T1	apple	2021	37	81	94.2857 143	76.1538 462	blastp
675	castorbean gb16 0 MDL30026M0 01488 T1	castorbea n	2022	37	90	95.2380 952	36.9003 69	blastp
676	citrus gb157.2 C X300349 T1	citrus	2023	37	83	99.0476 19	72.7272 727	blastp
677	coffea gb157.2 D V663640 T1	coffea	2024	37	80	93.3333 333	34.5070 423	blastp
678	cowpea gb166 F F395821 T1	cowpea	2025	37	82	93.3333 333	95.1456 311	blastp
679	cowpea gb166 F F395821 T2	cowpea	2026	37	82	94.2857 143	13.2450 331	tblastn
680	ipomoea gb157.2 CJ769054 T1	ipomoea	2027	37	87	100	59.3220 339	blastp
681	lettuce gb157.2 CV699989 T1	lettuce	2028	37	83	98.0952 381	36.5248 227	blastp
682	medicago gb157. 2 AW208262_T 1	medicag o	2029	37	80	95.2380 952	37.1747 212	blastp
683	melon gb165 A M727408 T1	melon	2030	37	82	97.1428 571	36.9565 217	blastp
684	poplar gb157.2 C N517706 T1	poplar	2031	37	84	96.1904 762	36.5942 029	blastp
685	poplar gb157.2 B U813630 T1	poplar	2032	37	84	99.0476 19	37.6811 594	blastp
686	potato gb157.2 D N587628 T1	potato	2033	37	90	96.1904 762	93.5185 185	blastp
687	rice gb157.2 B18 05522 T1	rice	2034	37	80	97.1428 571	35.9154 93	blastp
688	soybean gb166 F K397604 T1	soybean	2035	37	82	54.2857 143	98.2758 621	blastp
689	sunflower gb162 DY951259 T1	sunflowe r	2036	37	82	98.0952 381	39.0151 515	blastp
690	sunflower gb162 DY942645 T1	sunflowe r	2037	37	83	98.0952 381	37.3188 406	blastp
691	triphysaria gb16 4 EY130232 T1	triphysar ia	2038	37	85	99.0476 19	37.6811 594	blastp
692	arabidopsis gb16 5 AT4G10380_T 1	arabidop sis	2039	38	80	97.6271 186	96.0526 316	blastp
693	artemisia gb164 EY089420 T1	artemisia	2040	38	87	55.5932 203	100	blastp
694	artemisia gb164 EY113317 T1	artemisia	2041	38	89	51.8644 068	100	blastp
695	b_oleracea gb16 1 AM391026 T1	b_olerac ea	2042	38	81	93.8983 051	95.8620 69	blastp
696	b_rapa gb162 C V545128 T1	b_rapa	2043	38	81	97.6271 186	96.0132 89	blastp
697	canola gb161 ES 903871 T1	canola	2044	38	85	52.2033 898	100	blastp
698	cassava gb164 C K641734 T1	cassava	2045	38	89	93.8983 051	98.9247 312	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
699	castorbean gb160 EG668085 T1	castorbea n	2046	38	85	100	100	blastp
700	castorbean gb160 EG668085 T2	castorbea n	2047	38	90	62.0338 983	100	blastp
701	centaurea gb161 EH739099 T1	centaure a	2048	38	83	69.1525 424	98.0487 805	blastp
702	centaurea gb161 EH710762 T1	centaure a	2049	38	89	80.6779 661	95.9677 419	blastp
703	citrus gb157.2 CX299695 T1	citrus	2050	38	98	62.0338 983	100	blastp
704	citrus gb157.2 CO912981 T1	citrus	2051	38	80	100	100	blastp
705	citrus gb157.2 CO912981 T2	citrus	2052	38	81	78.3050 847	95.5465 587	blastp
706	cotton gb164 CO071578 T1	cotton	2053	38	90	77.9661 017	95.4356 846	blastp
707	cotton gb164 BE052767 T1	cotton	2054	38	88	86.4406 78	100	blastp
708	grape gb160 CB350030 T1	grape	2055	38	86	100	100	blastp
709	lettuce gb157.2 DW123895 T1	lettuce	2056	38	86	97.6271 186	96.6555 184	blastp
710	melon gb165 AM726471 T1	melon	2057	38	80	78.6440 678	92.8	blastp
711	nicotiana_benth miana gb162 CK281387 T1	nicotiana _benth miana	2058	38	94	100	100	blastp
712	onion gb162 CF436356 T1	onion	2059	38	83	86.1016 949	98.0988 593	blastp
713	poplar gb157.2 BU895174 T1	poplar	2060	38	84	97.6271 186	96.3333 333	blastp
714	poplar gb157.2 BI126692 T1	poplar	2061	38	85	100	100	blastp
715	radish gb164 EX772276 T1	radish	2062	38	87	62.0338 983	100	blastp
716	safflower gb162 EL376221 T1	safflower	2063	38	87	55.5932 203	94.2528 736	blastp
717	soybean gb166 AW351195 T1	soybean	2064	38	83	57.2881 356	100	blastp
718	spurge gb161 DV120704 T1	spurge	2065	38	81	66.1016 949	100	blastp
719	strawberry gb164 EX663538 T1	strawberr y	2066	38	87	73.5593 22	100	blastp
720	sunflower gb162 BQ915292 T1	sunflowe r	2067	38	83	69.8305 085	95.0636 943	tblastn
721	tobacco gb162 EB426773 T1	tobacco	2068	38	94	100	100	blastp
722	triphysaria gb164 EY008469 T1	triphysar ia	2069	38	90	67.7966 102	100	blastp
723	pepper gb157.2 BM066463 T1	pepper	2070	39	91	60	100	blastp
724	tobacco gb162 EB445778 T1	tobacco	2071	39	88	85.8333 333	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
725	pepper gb157.2 CA515996_T1	pepper	2072	40	82	64.4628 099	100	blastp
726	potato gb157.2 B E341068_T1	potato	2073	40	92	100	100	blastp
727	potato gb157.2 B G887984_T1	potato	2074	41	100	79.4238 683	91.4691 943	blastp
728	apple gb157.3 C N898142_T1	apple	2075	42	86	70.9677 419	98.0582 524	blastp
729	apple gb157.3 C N492544_T1	apple	2076	42	82	99.6415 771	98.9399 293	blastp
730	apple gb157.3 C N495819_T1	apple	2077	42	84	99.6415 771	98.9547 038	blastp
731	apple gb157.3 C N869175_T1	apple	2078	42	86	100	100	blastp
732	apple gb157.3 C N488973_T1	apple	2079	42	87	100	100	blastp
733	apricot gb157.2 CB820380_T1	apricot	2080	42	88	69.8924 731	98.4848 485	blastp
734	aquilegia gb157. 3 DR921860_T1	aquilegia	2081	42	85	94.9820 789	100	blastp
735	arabidopsis gb16 5 AT2G37170_T 1	arabidop sis	2082	42	80	100	99.2982 456	blastp
736	arabidopsis gb16 5 AT3G54820_T 1	arabidop sis	2083	42	81	95.6989 247	94.7552 448	blastp
737	arabidopsis gb16 5 AT3G53420_T 1	arabidop sis	2084	42	81	100	99.3031 359	blastp
738	arabidopsis gb16 5 AT5G60660_T 1	arabidop sis	2085	42	80	99.2831 541	97.2508 591	blastp
739	artemisia gb164 EY056827_T1	artemisia	2086	42	89	79.5698 925	100	blastp
740	artemisia gb164 EY033689_T1	artemisia	2087	42	83	100	100	blastp
741	artemisia gb164 EY032199_T1	artemisia	2088	42	81	100	100	blastp
742	artemisia gb164 EY042731_T1	artemisia	2089	42	88	100	100	blastp
743	artemisia gb164 EX980079_T1	artemisia	2090	42	82	99.6415 771	98.9473 684	blastp
744	avocado gb164 C K754546_T1	avocado	2091	42	86	51.6129 032	97.2972 973	blastp
745	b_juncea gb164 EVGN00454408 761136_T1	b_juncea	2092	42	81	100	99.2982 456	blastp
746	b_juncea gb164 EVGN00454408 761136_T2	b_juncea	2093	42	81	98.9247 312	97.9020 979	blastp
747	b_juncea gb164 EVGN00748222 952488_T2	b_juncea	2094	42	80	100	88.7850 467	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
748	b_juncea gb164 EVGN00204411 253360 T1	b_juncea	2095	42	84	82.0788 53	97.8991 597	blastp
749	b_juncea gb164 EVGN00054208 600715 T1	b_juncea	2096	42	80	100	99.2982 456	blastp
750	b_juncea gb164 EVGN00049614 332152 T1	b_juncea	2097	42	83	64.5161 29	96.2566 845	blastp
751	b_juncea gb164 EVGN01023711 071914 T1	b_juncea	2098	42	85	58.4229 391	100	blastp
752	b_juncea gb164 EVGN00247216 171316 T1	b_juncea	2099	42	81	100	99.3031 359	blastp
753	b_juncea gb164 EVGN00778009 020884 T1	b_juncea	2100	42	88	64.1577 061	100	blastp
754	b_juncea gb164 EVGN02648808 940517 T1	b_juncea	2101	42	85	53.4050 179	98.6754 967	blastp
755	b_juncea gb164 EVGN00316414 413452 T1	b_juncea	2102	42	82	82.7956 989	100	blastp
756	b_juncea gb164 DT317706 T1	b_juncea	2103	42	81	100	99.3031 359	blastp
757	b_juncea gb164 EVGN00748222 952488 T1	b_juncea	2104	42	81	100	99.3031 359	blastp
758	b_oleracea gb16 1 AM386520 T1	b_olerac ea	2105	42	80	100	100	blastp
759	b_oleracea gb16 1 AM058395 T1	b_olerac ea	2106	42	83	57.3476 703	91.9540 23	blastp
760	b_oleracea gb16 1 AM385504 T1	b_olerac ea	2107	42	81	100	99.2982 456	blastp
761	b_rapa gb162 B G544498 T1	b_rapa	2108	42	81	100	100	blastp
762	b_rapa gb162 B Q791962 T2	b_rapa	2109	42	81	100	99.2982 456	blastp
763	b_rapa gb162 B Q791962 T1	b_rapa	2110	42	81	100	99.2982 456	blastp
764	b_rapa gb162 E X065729 T1	b_rapa	2111	42	81	92.1146 953	100	blastp
765	b_rapa gb162 C A992278 T1	b_rapa	2112	42	83	89.9641 577	98.8372 093	blastp
766	b_rapa gb162 C O749284 T1	b_rapa	2113	42	81	100	99.2982 456	blastp
767	barley gb157.3 B E412486 T1	barley	2114	42	81	100	100	blastp
768	bean gb164 CB5 42746 T1	bean	2115	42	80	100	100	blastp
769	bean gb164 CB2 80567 T1	bean	2116	42	86	99.6415 771	98.9473 684	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
770	bean gb164 BQ481649 T1	bean	2117	42	82	100	100	blastp
771	bean gb164 CV532291 T1	bean	2118	42	86	99.6415771	98.9547038	blastp
772	brachypodium gb161.xeno BE416137 T1	brachypodium	2119	42	80	94.9820789	100	blastp
773	brachypodium gb161.xeno AF139814 T1	brachypodium	2120	42	80	100	100	blastp
774	canola gb161 CN729066 T1	canola	2121	42	81	100	99.3031359	blastp
775	canola gb161 DQ068169 T1	canola	2122	42	81	100	99.2982456	blastp
776	canola gb161 AF118382 T1	canola	2123	42	81	100	99.3031359	blastp
777	canola gb161 AF118383 T1	canola	2124	42	81	100	100	blastp
778	canola gb161 CD819509 T1	canola	2125	42	80	100	99.2982456	blastp
779	canola gb161 EE419467 T1	canola	2126	42	81	100	100	blastp
780	canola gb161 EE459735 T1	canola	2127	42	81	100	99.2982456	blastp
781	canola gb161 CX192356 T1	canola	2128	42	80	100	100	blastp
782	canola gb161 CN827413 T1	canola	2129	42	81	100	99.2982456	blastp
783	canola gb161 EE432011 T1	canola	2130	42	81	100	99.2982456	blastp
784	cassava gb164 DB922106 T1	cassava	2131	42	81	93.90681	92.5266904	blastp
785	cassava gb164 CK640888 T1	cassava	2132	42	83	100	100	blastp
786	cassava gb164 CK642866 T1	cassava	2133	42	84	99.6415771	98.951049	blastp
787	cassava gb164 CK642551 T1	cassava	2134	42	86	100	99.3055556	blastp
788	castorbean gb160 AJ605565 T1	castorbean	2135	42	86	100	99.3055556	blastp
789	castorbean gb160 AJ605568 T1	castorbean	2136	42	87	99.6415771	98.9399293	blastp
790	castorbean gb160 EE259660 T1	castorbean	2137	42	85	100	100	blastp
791	centaurea gb161 EL933765 T1	centaurea	2138	42	84	87.0967742	92.8571429	blastp
792	centaurea gb161 EL931761 T1	centaurea	2139	42	82	75.9856631	89.2561983	blastp
793	cichorium gb161 DT212328 T1	cichorium	2140	42	86	100	100	blastp
794	citrus gb157.2 BQ625054 T1	citrus	2141	42	83	100	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
795	citrus gb157.2 C F509045_T1	citrus	2142	42	86	100	99.3031 359	blastp
796	citrus gb157.2 C B291797_T1	citrus	2143	42	80	100	84.0707 965	blastp
797	citrus gb157.2 B Q623325_T1	citrus	2144	42	86	100	99.3031 359	blastp
798	citrus gb157.2 B Q623742_T1	citrus	2145	42	88	94.9820 789	99.2619 926	blastp
799	citrus gb157.2 C F417769_T1	citrus	2146	42	83	100	99.3031 359	blastp
800	citrus gb157.2 B Q623128_T1	citrus	2147	42	88	68.4587 814	98.9637 306	blastp
801	citrus gb157.2 C B293000_T1	citrus	2148	42	82	93.1899 642	98.8847 584	blastp
802	citrus gb157.2 B Q622991_T1	citrus	2149	42	84	96.4157 706	98.5559 567	blastp
803	citrus gb157.2 C F503882_T1	citrus	2150	42	83	100	100	blastp
804	cotton gb164 BE 052942_T1	cotton	2151	42	84	99.2831 541	98.5815 603	blastp
805	cotton gb164 AF 064467_T1	cotton	2152	42	80	100	100	blastp
806	cotton gb164 BG 443494_T1	cotton	2153	42	85	100	99.2982 456	blastp
807	cotton gb164 CO 086106_T1	cotton	2154	42	88	70.2508 961	100	blastp
808	cotton gb164 BQ 406033_T1	cotton	2155	42	82	100	99.2982 456	blastp
809	cotton gb164 CO 109551_T1	cotton	2156	42	82	100	100	blastp
810	cotton gb164 DV 437970_T1	cotton	2157	42	80	64.1577 061	95.3608 247	blastp
811	cotton gb164 AI 725803_T1	cotton	2158	42	84	100	99.2982 456	blastp
812	cotton gb164 CD 486305_T1	cotton	2159	42	81	98.9247 312	94.0199 336	blastp
813	cowpea gb166 E S884222_T2	cowpea	2160	42	85	86.3799 283	93.5606 061	blastp
814	cowpea gb166 E S884222_T1	cowpea	2161	42	86	99.6415 771	98.9547 038	blastp
815	cowpea gb166 F F538675_T1	cowpea	2162	42	89	52.6881 72	98	blastp
816	cowpea gb166 F C458151_T1	cowpea	2163	42	80	100	100	blastp
817	cowpea gb166 F C458381_T1	cowpea	2164	42	85	99.6415 771	98.9473 684	blastp
818	cryptomeria gb1 66 AU036821_T 1	cryptome ria	2165	42	83	95.6989 247	93.6395 76	blastp
819	cryptomeria gb1 66 BW995927_T 1	cryptome ria	2166	42	81	53.0465 95	98.0132 45	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
820	dandelion gb161 DY827637 T1	dandelio n	2167	42	87	93.9068 1	88.9632 107	blastp
821	dandelion gb161 DY814583 T1	dandelio n	2168	42	85	93.5483 871	93.2862 191	blastp
822	dandelion gb161 DY828216 T1	dandelio n	2169	42	85	100	100	blastp
823	dandelion gb161 DY818322 T1	dandelio n	2170	42	80	85.3046 595	98.7654 321	blastp
824	dandelion gb161 DY805523 T1	dandelio n	2171	42	82	98.9247 312	98.2456 14	blastp
825	fescue gb161 DT 675934 T1	fescue	2172	42	82	61.2903 226	93.9226 519	blastp
826	ginger gb164 DY 345807 T1	ginger	2173	42	81	100	100	blastp
827	ginger gb164 DY 373920 T1	ginger	2174	42	88	69.5340 502	100	blastp
828	grape gb160 BQ 792080 T1	grape	2175	42	81	100	99.3031 359	blastp
829	grape gb160 CB 973593 T1	grape	2176	42	84	100	100	blastp
830	grape gb160 BM 437196 T1	grape	2177	42	84	100	99.2957 746	blastp
831	iceplant gb164 C IPMIPC T1	iceplant	2178	42	83	100	100	blastp
832	iceplant gb164 B E035661 T1	iceplant	2179	42	82	99.6415 771	98.6254 296	blastp
833	ipomoea gb157.2 BM878800 T1	ipomoea	2180	42	80	99.6415 771	100	blastp
834	ipomoea gb157.2 AU224434 T2	ipomoea	2181	42	90	86.7383 513	93.2330 827	blastp
835	ipomoea gb157.2 BJ553793 T1	ipomoea	2182	42	82	100	99.2957 746	blastp
836	ipomoea gb157.2 AU224434 T1	ipomoea	2183	42	89	100	100	blastp
837	lettuce gb157.2 DW115660 T1	lettuce	2184	42	85	99.2831 541	98.5964 912	blastp
838	lettuce gb157.2 DW113963 T1	lettuce	2185	42	80	97.8494 624	95.7894 737	blastp
839	lettuce gb157.2 DW110249 T1	lettuce	2186	42	84	99.6415 771	98.9399 293	blastp
840	lettuce gb157.2 DW051453 T1	lettuce	2187	42	86	100	100	blastp
841	lettuce gb157.2 DW076507 T1	lettuce	2188	42	84	100	100	blastp
842	lettuce gb157.2 DW127617 T1	lettuce	2189	42	84	100	100	blastp
843	lettuce gb157.2 AJ937963 T1	lettuce	2190	42	80	100	100	blastp
844	lettuce gb157.2 DW049421 T1	lettuce	2191	42	83	92.8315 412	98.5018 727	blastp
845	lettuce gb157.2 DW114305 T1	lettuce	2192	42	87	99.2831 541	98.9473 684	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
846	lettuce gb157.2 DW053722 T1	lettuce	2193	42	80	100	100	blastp
847	lettuce gb157.2 DW146178 T1	lettuce	2194	42	81	100	100	blastp
848	lettuce gb157.2 DW077710 T1	lettuce	2195	42	85	99.2831 541	98.5964 912	blastp
849	lettuce gb157.2 DW070566 T1	lettuce	2196	42	84	100	100	blastp
850	lettuce gb157.2 DW093078 T1	lettuce	2197	42	85	94.9820 789	100	blastp
851	lettuce gb157.2 DW074446 T1	lettuce	2198	42	84	97.4910 394	96.1672 474	blastp
852	lettuce gb157.2 DW153482 T1	lettuce	2199	42	83	99.6415 771	98.9399 293	blastp
853	lettuce gb157.2 DW080306 T1	lettuce	2200	42	86	100	100	blastp
854	lettuce gb157.2 DW043674 T1	lettuce	2201	42	84	99.6415 771	98.9399 293	blastp
855	lettuce gb157.2 DW095979 T1	lettuce	2202	42	83	97.1326 165	98.5559 567	blastp
856	lettuce gb157.2 DW077206 T1	lettuce	2203	42	84	100	100	blastp
857	lettuce gb157.2 DW047573 T1	lettuce	2204	42	86	98.9247 312	99.6453 901	blastp
858	lettuce gb157.2 DW096304 T1	lettuce	2205	42	87	100	100	blastp
859	lettuce gb157.2 DW075191 T1	lettuce	2206	42	81	100	100	blastp
860	lotus gb157.2 AI 967757 T1	lotus	2207	42	85	99.6415 771	98.9547 038	blastp
861	lotus gb157.2 AI 967387 T2	lotus	2208	42	80	99.6415 771	99.6515 679	blastp
862	lotus gb157.2 B G662315 T1	lotus	2209	42	82	99.6415 771	98.9619 377	blastp
863	maize gb164 BE 552783 T1	maize	2210	42	80	97.4910 394	95.8904 11	blastp
864	maize gb164 AI6 22334 T1	maize	2211	42	83	97.4910 394	95.8620 69	blastp
865	maize gb164 AI8 55280 T1	maize	2212	42	81	96.7741 935	95.1557 093	blastp
866	medicago gb157. 2 AW981259_T 1	medicag o	2213	42	80	100	99.3031 359	blastp
867	medicago gb157. 2 AA660788 T1	medicag o	2214	42	83	99.6415 771	98.9547 038	blastp
868	melon gb165 DV 631824 T1	melon	2215	42	84	100	100	blastp
869	melon gb165 DV 633977 T1	melon	2216	42	83	64.5161 29	100	blastp
870	melon gb165 A M720039 T1	melon	2217	42	81	86.0215 054	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Poly pep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
871	nicotiana_benthamiana gb162 CN743200 T1	nicotiana_benthamiana	2218	42	80	100	100	blastp
872	nicotiana_benthamiana gb162 CK294539 T1	nicotiana_benthamiana	2219	42	80	98.2078853	96.8641115	blastp
873	onion gb162 AF255795 T1	onion	2220	42	82	97.1326165	95.532646	blastp
874	onion gb162 CF434704 T1	onion	2221	42	80	99.2831541	99.2957746	blastp
875	papaya gb165 EL784273 T1	papaya	2222	42	82	82.078853	97.5206612	blastp
876	papaya gb165 AM904340 T1	papaya	2223	42	84	100	99.2882562	blastp
877	peach gb157.2 AF367458 T1	peach	2224	42	84	87.0967742	100	blastp
878	peach gb157.2 BU040116 T1	peach	2225	42	83	99.6415771	98.9547038	blastp
879	peach gb157.2 AF367460 T1	peach	2226	42	86	87.0967742	100	blastp
880	peanut gb161 CD037924 T1	peanut	2227	42	86	99.6415771	98.9547038	blastp
881	peanut gb161 CD038296 T1	peanut	2228	42	85	99.6415771	98.9547038	blastp
882	peanut gb161 CD037924 T2	peanut	2229	42	86	99.6415771	98.9547038	blastp
883	peanut gb161 CD037884 T1	peanut	2230	42	88	51.2544803	97.9452055	blastp
884	pepper gb157.2 BM061612 T1	pepper	2231	42	96	100	100	blastp
885	pepper gb157.2 BM061611 T1	pepper	2232	42	97	100	100	blastp
886	pepper gb157.2 BM061005 T1	pepper	2233	42	81	92.4731183	97.3977695	blastp
887	petunia gb157.2 AF452014 T1	petunia	2234	42	83	97.4910394	98.2332155	blastp
888	petunia gb157.2 CV295523 T1	petunia	2235	42	95	53.046595	93.6708861	blastp
889	petunia gb157.2 CV293001 T1	petunia	2236	42	83	55.5555556	100	blastp
890	pine gb157.2 AI813221 T1	pine	2237	42	81	96.0573477	94.3262411	blastp
891	pine gb157.2 CA844411 T1	pine	2238	42	81	56.6308244	98.75	blastp
892	poplar gb157.2 BI130501 T3	poplar	2239	42	85	100	99.2982456	blastp
893	poplar gb157.2 AI165755 T1	poplar	2240	42	86	99.6415771	98.9473684	blastp
894	poplar gb157.2 BU835712 T1	poplar	2241	42	85	99.6415771	98.9473684	blastp
895	poplar gb157.2 BI130501 T1	poplar	2242	42	85	100	99.2982456	blastp

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896	poplar gb157.2 B I130501 T4	poplar	2243	42	85	100	99.2982 456	blastp
897	poplar gb157.2 A I162288 T1	poplar	2244	42	86	99.2831 541	98.5964 912	blastp
898	poplar gb157.2 A J534524 T1	poplar	2245	42	84	100	100	blastp
899	potato gb157.2 B G096672 T1	potato	2246	42	96	100	100	blastp
900	potato gb157.2 B M109370 T1	potato	2247	42	80	98.2078 853	96.8641 115	blastp
901	potato gb157.2 B G589618 T1	potato	2248	42	80	98.2078 853	96.8641 115	blastp
902	potato gb157.2 C K261080 T1	potato	2249	42	83	70.2508 961	100	blastp
903	potato gb157.2 B G098124 T1	potato	2250	42	97	99.2831 541	100	blastp
904	potato gb157.2 B I406400 T1	potato	2251	42	80	98.2078 853	96.8641 115	blastp
905	potato gb157.2 B E920139 T1	potato	2252	42	90	100	100	blastp
906	potato gb157.2 B M112017 T1	potato	2253	42	80	98.2078 853	96.8641 115	blastp
907	potato gb157.2 B E921679 T1	potato	2254	42	96	100	100	blastp
908	potato gb157.2 B G600158 T1	potato	2255	42	80	98.2078 853	96.8641 115	blastp
909	potato gb157.2 B I406047 T1	potato	2256	42	80	100	100	blastp
910	potato gb157.2 C K719282 T1	potato	2257	42	80	98.2078 853	96.8641 115	blastp
911	radish gb164 EV 545956 T1	radish	2258	42	81	100	99.2982 456	blastp
912	radish gb164 EX 904869 T1	radish	2259	42	80	100	100	blastp
913	radish gb164 EV 545247 T1	radish	2260	42	80	100	100	blastp
914	radish gb164 EX 756889 T1	radish	2261	42	80	100	100	blastp
915	radish gb164 EV 539533 T1	radish	2262	42	81	100	99.3031 359	blastp
916	radish gb164 EV 546186 T1	radish	2263	42	82	55.5555 556	95.6790 123	blastp
917	radish gb164 AB 012045 T1	radish	2264	42	81	100	99.3031 359	blastp
918	radish gb164 EV 573001 T1	radish	2265	42	83	62.0071 685	98.8571 429	blastp
919	radish gb164 AB 030698 T1	radish	2266	42	81	100	100	blastp
920	radish gb164 EX 749049 T1	radish	2267	42	83	78.4946 237	100	blastp
921	radish gb164 AB 030697 T1	radish	2268	42	80	100	100	blastp

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922	radish gb164 EW 735060 T1	radish	2269	42	80	96.4157 706	95.4545 455	blastp
923	radish gb164 FD 936119 T1	radish	2270	42	83	50.5376 344	100	blastp
924	radish gb164 EV 543747 T1	radish	2271	42	81	100	99.3031 359	blastp
925	rice gb157.2 BE0 40651 T2	rice	2272	42	80	86.7383 513	94.3820 225	blastp
926	rice gb157.2 BE0 40651 T1	rice	2273	42	80	100	100	blastp
927	rice gb157.2 AA 754435 T5	rice	2274	42	80	85.6630 824	87.7192 982	blastp
928	rice gb157.2 AA 754435 T1	rice	2275	42	81	100	100	blastp
929	rose gb157.2 BI9 77420 T1	rose	2276	42	84	69.8924 731	91.6279 07	blastp
930	rose gb157.2 BI9 77750 T1	rose	2277	42	84	77.7777 778	100	blastp
931	rose gb157.2 BI9 78110 T1	rose	2278	42	83	64.5161 29	98.3783 784	blastp
932	safflower gb162 EL406648 T1	safflower	2279	42	81	98.5663 082	100	blastp
933	safflower gb162 EL411110 T1	safflower	2280	42	86	92.4731 183	97.7611 94	blastp
934	safflower gb162 EL401452 T1	safflower	2281	42	85	100	100	blastp
935	safflower gb162 EL402424 T1	safflower	2282	42	83	97.1326 165	100	blastp
936	safflower gb162 EL400227 T1	safflower	2283	42	85	86.7383 513	67.9193 401	tblastn
937	sorghum gb161. xeno AI622334_ T1	sorghum	2284	42	83	97.4910 394	95.8620 69	blastp
938	soybean gb166 C D393286 T1	soybean	2285	42	80	99.6415 771	99.6515 679	blastp
939	soybean gb166 G MU27347 T1	soybean	2286	42	86	99.6415 771	98.9473 684	blastp
940	soybean gb166 A W349289 T1	soybean	2287	42	85	99.6415 771	98.9473 684	blastp
941	soybean gb166 B E823946 T1	soybean	2288	42	87	99.6415 771	98.9436 62	blastp
942	soybean gb166 B E352729 T2	soybean	2289	42	80	56.2724 014	100	blastp
943	soybean gb166 A W350475 T1	soybean	2290	42	85	99.6415 771	98.9547 038	blastp
944	soybean gb166 B I119558 T1	soybean	2291	42	80	100	100	blastp
945	soybean gb166 A W349392 T1	soybean	2292	42	80	100	100	blastp
946	spruce gb162 AF 051202 T1	spruce	2293	42	81	96.0573 477	94.3262 411	blastp
947	spruce gb162 CO 227554 T1	spruce	2294	42	80	96.0573 477	93.6619 718	blastp

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948	spruce gb162 CO 220480 T1	spruce	2295	42	80	96.4157 706	94.6808 511	blastp
949	spruce gb162 CO 217151 T1	spruce	2296	42	80	96.0573 477	94.3262 411	blastp
950	spurge gb161 A W990929 T1	spurge	2297	42	80	59.8566 308	91.5343 915	blastp
951	spurge gb161 B G354126 T1	spurge	2298	42	83	100	100	blastp
952	spurge gb161 D V125170 T1	spurge	2299	42	87	83.5125 448	99.5780 591	blastp
953	strawberry gb16 4 DV438166 T1	strawberr y	2300	42	85	99.6415 771	98.9473 684	blastp
954	strawberry gb16 4 EX665494 T1	strawberr y	2301	42	86	100	99.2957 746	blastp
955	strawberry gb16 4 CO817390 T1	strawberr y	2302	42	85	100	100	blastp
956	sugarcane gb157 .2 BQ536871_T 2	sugarcane	2303	42	85	70.2508 961	100	blastp
957	sugarcane gb157 .2 BU103568_T 1	sugarcane	2304	42	83	97.4910 394	92.6666 667	blastp
958	sugarcane gb157 .2 BQ536871_T 1	sugarcane	2305	42	81	97.4910 394	95.8620 69	blastp
959	sugarcane gb157 .2 BQ535332_T 1	sugarcane	2306	42	84	97.4910 394	95.8620 69	blastp
960	sunflower gb162 CD849689 T1	sunflowe r	2307	42	83	100	100	blastp
961	sunflower gb162 CD849494 T1	sunflowe r	2308	42	83	94.9820 789	95.0704 225	blastp
962	sunflower gb162 CF091932 T1	sunflowe r	2309	42	81	83.5125 448	98.75	blastp
963	sunflower gb162 DY915644 T1	sunflowe r	2310	42	81	100	100	blastp
964	sunflower gb162 EL462160 T1	sunflowe r	2311	42	81	78.4946 237	88.8446 215	blastp
965	sunflower gb162 DY918039 T1	sunflowe r	2312	42	87	95.6989 247	100	blastp
966	sunflower gb162 DY951506 T1	sunflowe r	2313	42	87	89.9641 577	95.5223 881	blastp
967	sunflower gb162 DY933519 T1	sunflowe r	2314	42	84	99.6415 771	98.9473 684	blastp
968	sunflower gb162 DY917102 T1	sunflowe r	2315	42	82	100	100	blastp
969	sunflower gb162 DY932916 T1	sunflowe r	2316	42	86	58.0645 161	100	blastp
970	sunflower gb162 CD857425 T1	sunflowe r	2317	42	84	100	100	blastp
971	sunflower gb162 CD846314 T1	sunflowe r	2318	42	85	53.4050 179	97.4683 544	blastp

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972	sunflower gb162 CX944368_T1	sunflowe r	2319	42	88	68.1003 584	89.6226 415	blastp
973	sunflower gb162 DY908592_T1	sunflowe r	2320	42	80	100	100	blastp
974	switchgrass gb16 5 DN141399_T1	switchgr ass	2321	42	81	96.7741 935	98.9208 633	blastp
975	switchgrass gb16 5 FE621421_T1	switchgr ass	2322	42	86	51.9713 262	99.3150 685	blastp
976	switchgrass gb16 5 DN145656_T1	switchgr ass	2323	42	83	97.4910 394	95.8620 69	blastp
977	switchgrass gb16 5 FE637674_T1	switchgr ass	2324	42	81	82.4372 76	100	blastp
978	switchgrass gb16 5 DN141334_T1	switchgr ass	2325	42	83	77.0609 319	94.8497 854	blastp
979	switchgrass gb16 5 FE621578_T1	switchgr ass	2326	42	83	85.6630 824	100	blastp
980	thellungiella gb1 57.2 DN775526_ T1	thellungi ella	2327	42	81	72.4014 337	100	blastp
981	tobacco gb162 C K720599_T1	tobacco	2328	42	95	100	100	blastp
982	tobacco gb162 C K720599_T2	tobacco	2329	42	94	100	100	blastp
983	tobacco gb162 E B445427_T1	tobacco	2330	42	81	100	100	blastp
984	tobacco gb162 E B443112_T1	tobacco	2331	42	89	100	100	blastp
985	tobacco gb162 A F154641_T1	tobacco	2332	42	80	100	100	blastp
986	tobacco gb162 E B425288_T1	tobacco	2333	42	94	98.2078 853	100	blastp
987	tomato gb164 B G123951_T2	tomato	2334	42	81	92.8315 412	97.4074 074	blastp
988	tomato gb164 B G123951_T1	tomato	2335	42	80	98.2078 853	96.8641 115	blastp
989	tomato gb164 B G713781_T1	tomato	2336	42	92	53.4050 179	98.0519 481	blastp
990	tomato gb164 A W219533_T1	tomato	2337	42	81	97.1326 165	98.2142 857	blastp
991	triphysaria gb16 4 DR170852_T1	triphysar ia	2338	42	88	99.2831 541	99.2857 143	blastp
992	triphysaria gb16 4 BM356582_T1	triphysar ia	2339	42	88	64.8745 52	100	blastp
993	triphysaria gb16 4 BE574767_T1	triphysar ia	2340	42	80	100	100	blastp
994	wheat gb164 BE 444481_T1	wheat	2341	42	82	55.5555 556	100	blastp
995	wheat gb164 BE 398316_T1	wheat	2342	42	81	100	100	blastp
996	wheat gb164 BE 404002_T1	wheat	2343	42	82	51.6129 032	99.3055 556	blastp
997	apple gb157.3 C N892655_T1	apple	2344	43	84	100	100	blastp

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998	apple gb157.3 AU223658_T1	apple	2345	43	85	100	100	blastp
999	aquilegia gb157.3 DR914359_T1	aquilegia	2346	43	84	100	100	blastp
1000	arabidopsis gb165 AT2G16850_T1	arabidop sis	2347	43	84	100	100	blastp
1001	arabidopsis gb165 AT4G35100_T1	arabidop sis	2348	43	86	100	100	blastp
1002	avocado gb164 CK753629_T1	avocado	2349	43	85	66.4310954	92.6108374	blastp
1003	avocado gb164 CK752541_T1	avocado	2350	43	84	62.1908127	100	blastp
1004	b_juncea gb164 EVGN01060535361904_T1	b_juncea	2351	43	86	67.1378092	100	blastp
1005	b_juncea gb164 EVGN00138211060167_T1	b_juncea	2352	43	86	85.1590106	100	blastp
1006	b_juncea gb164 EVGN01177009332048_T1	b_juncea	2353	43	86	66.0777385	100	blastp
1007	b_juncea gb164 EVGN00071418640425_T1	b_juncea	2354	43	86	90.459364	100	blastp
1008	b_juncea gb164 EVGN01391814101746_T1	b_juncea	2355	43	92	53.0035336	100	blastp
1009	b_juncea gb164 EVGN00206114600060_T1	b_juncea	2356	43	85	100	100	blastp
1010	b_oleracea gb161 AF314656_T1	b_olerac ea	2357	43	85	100	100	blastp
1011	b_oleracea gb161 DY029187_T1	b_olerac ea	2358	43	86	100	100	blastp
1012	b_oleracea gb161 DY014978_T1	b_olerac ea	2359	43	87	54.770318	100	blastp
1013	b_rapa gb162 BQ791230_T1	b_rapa	2360	43	86	77.0318021	97.7375566	blastp
1014	b_rapa gb162 EX033370_T1	b_rapa	2361	43	87	100	100	blastp
1015	b_rapa gb162 CV432651_T1	b_rapa	2362	43	86	100	100	blastp
1016	b_rapa gb162 BG543906_T1	b_rapa	2363	43	85	100	100	blastp
1017	bean gb164 CB539790_T1	bean	2364	43	83	100	100	blastp
1018	beet gb162 BVU60148_T1	beet	2365	43	80	100	100	blastp
1019	canola gb161 DY007064_T1	canola	2366	43	86	100	100	blastp

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1020	canola gb161 CD 815284 T1	canola	2367	43	85	100	100	blastp
1021	canola gb161 CD 817684 T1	canola	2368	43	85	100	100	blastp
1022	canola gb161 CD 821191 T1	canola	2369	43	86	100	100	blastp
1023	canola gb161 CD 820375 T1	canola	2370	43	87	100	100	blastp
1024	cassava gb164 B M259748 T1	cassava	2371	43	84	100	100	blastp
1025	castorbean gb16 0 AJ605569 T1	castorbea n	2372	43	84	100	100	blastp
1026	castorbean gb16 0 AJ605569 T2	castorbea n	2373	43	84	69.9646 643	95.1219 512	blastp
1027	cichorium gb161 EH704748 T1	cichoriu m	2374	43	89	67.1378 092	100	blastp
1028	citrus gb157.2 B Q623127 T1	citrus	2375	43	85	100	100	blastp
1029	citrus gb157.2 C X664964 T1	citrus	2376	43	84	100	100	blastp
1030	clover gb162 BB 911260 T1	clover	2377	43	82	54.0636 042	100	blastp
1031	coffea gb157.2 B Q448890 T1	coffea	2378	43	86	100	100	blastp
1032	cotton gb164 AI 726086 T1	cotton	2379	43	84	97.8798 587	88.0258 9	blastp
1033	cotton gb164 CO 098535 T1	cotton	2380	43	82	92.2261 484	95.5719 557	blastp
1034	cotton gb164 BE 051956 T1	cotton	2381	43	83	100	100	blastp
1035	cotton gb164 BQ 414250 T1	cotton	2382	43	85	59.0106 007	100	blastp
1036	cotton gb164 BF 268907 T1	cotton	2383	43	87	90.1060 071	100	blastp
1037	cotton gb164 CO 075847 T1	cotton	2384	43	84	62.5441 696	100	blastp
1038	cotton gb164 BQ 405584 T1	cotton	2385	43	82	95.4063 604	95.7142 857	blastp
1039	cotton gb164 AI 055551 T1	cotton	2386	43	85	100	100	blastp
1040	cowpea gb166 F C456786 T1	cowpea	2387	43	84	100	100	blastp
1041	dandelion gb161 DY803814 T1	dandelio n	2388	43	85	100	100	blastp
1042	ginger gb164 DY 347270 T1	ginger	2389	43	80	100	100	blastp
1043	ginger gb164 DY 347296 T1	ginger	2390	43	84	94.6996 466	92.7335 64	blastp
1044	ginger gb164 DY 358056 T1	ginger	2391	43	81	100	100	blastp
1045	ginger gb164 DY 347277 T1	ginger	2392	43	81	100	100	blastp

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1046	ginger gb164 DY 360032 T1	ginger	2393	43	81	81.9787 986	93.9024 39	blastp
1047	grape gb160 BM 437910 T1	grape	2394	43	84	100	100	blastp
1048	iceplant gb164 MCU26538 T1	iceplant	2395	43	82	100	100	blastp
1049	ipomoea gb157.2 BJ553491 T1	ipomoea	2396	43	83	100	100	blastp
1050	lettuce gb157.2 DW046509 T1	lettuce	2397	43	84	100	100	blastp
1051	lettuce gb157.2 DW106553 T1	lettuce	2398	43	84	97.8798 587	100	blastp
1052	lettuce gb157.2 DW146059 T1	lettuce	2399	43	84	100	100	blastp
1053	lettuce gb157.2 DW110223 T1	lettuce	2400	43	83	97.1731 449	100	blastp
1054	lettuce gb157.2 DW079482 T1	lettuce	2401	43	84	100	100	blastp
1055	lettuce gb157.2 DW094572 T1	lettuce	2402	43	83	97.5265 018	92.8327 645	blastp
1056	lotus gb157.2 A W163949 T1	lotus	2403	43	85	54.4169 611	93.9024 39	blastp
1057	lotus gb157.2 AI 967574 T1	lotus	2404	43	82	98.5865 724	97.5352 113	blastp
1058	melon gb165 DV 632217 T1	melon	2405	43	83	100	100	blastp
1059	oil_palm gb166 CN600073 T1	oil_palm	2406	43	80	100	100	blastp
1060	papaya gb165 E X227970 T1	papaya	2407	43	85	100	100	blastp
1061	peach gb157.2 A F367457 T1	peach	2408	43	85	85.1590 106	99.5833 333	blastp
1062	pepper gb157.2 BM066074 T1	pepper	2409	43	96	67.4911 661	98.9637 306	blastp
1063	pepper gb157.2 CA518686 T1	pepper	2410	43	88	53.7102 473	100	blastp
1064	periwinkle gb16 4 AM232518 T1	periwink le	2411	43	90	100	100	blastp
1065	petunia gb157.2 AF452013 T1	petunia	2412	43	89	100	100	blastp
1066	poplar gb157.2 A I163573 T1	poplar	2413	43	84	100	100	blastp
1067	poplar gb157.2 A I162424 T1	poplar	2414	43	83	100	100	blastp
1068	potato gb157.2 B F053675 T1	potato	2415	43	89	83.7455 83	100	blastp
1069	potato gb157.2 B F459952 T1	potato	2416	43	97	100	100	blastp
1070	radish gb164 EV 526465 T1	radish	2417	43	86	100	100	blastp
1071	radish gb164 EV 539317 T1	radish	2418	43	85	100	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1072	radish gb164 EV 525026 T1	radish	2419	43	85	100	100	blastp
1073	rose gb157.2 BQ 103996 T1	rose	2420	43	82	100	100	blastp
1074	safflower gb162 EL372747 T1	safflower	2421	43	83	100	100	blastp
1075	sesame gb157.2 BU669158 T1	sesame	2422	43	88	50.8833 922	100	blastp
1076	sesame gb157.2 BU668646 T1	sesame	2423	43	87	51.9434 629	100	blastp
1077	soybean gb166 B E823128 T1	soybean	2424	43	82	100	100	blastp
1078	soybean gb166 B E352716 T1	soybean	2425	43	82	100	100	blastp
1079	spruce gb162 CO 217407 T1	spruce	2426	43	80	93.2862 191	93.5714 286	blastp
1080	spurge gb161 A W821924 T1	spurge	2427	43	84	100	97.2125 436	blastp
1081	strawberry gb16 4 CX661107 T1	strawberr y	2428	43	82	100	100	blastp
1082	sunflower gb162 CD853582 T1	sunflowe r	2429	43	85	100	100	blastp
1083	sunflower gb162 DY939653 T1	sunflowe r	2430	43	80	97.1731 449	97.8339 35	blastp
1084	sunflower gb162 CD849663 T1	sunflowe r	2431	43	81	100	100	blastp
1085	thellungiella gb1 57.2 DN777165_ T1	thellungi ella	2432	43	86	72.0848 057	90.5829 596	blastp
1086	tobacco gb162 C K720587 T1	tobacco	2433	43	90	99.6466 431	100	blastp
1087	tobacco gb162 C K720585 T1	tobacco	2434	43	90	100	100	blastp
1088	tobacco gb162 C V016422 T1	tobacco	2435	43	96	59.7173 145	100	blastp
1089	tobacco gb162 C K720589 T1	tobacco	2436	43	94	100	100	blastp
1090	tomato gb164 B G124140 T1	tomato	2437	43	88	100	100	blastp
1091	triphysaria gb16 4 EY018490 T1	triphysar ia	2438	43	83	100	100	blastp
1092	triphysaria gb16 4 EY007858 T1	triphysar ia	2439	43	84	100	100	blastp
1093	apple gb157.3 C N494428 T1	apple	2440	44	80	79.1390 728	93.0232 558	blastp
1094	castorbean gb16 0 EG696741 T1	castorbea n	2441	44	82	99.0066 225	97.7272 727	blastp
1095	citrus gb157.2 C X074332 T1	citrus	2442	44	82	99.0066 225	97.6973 684	blastp
1096	citrus gb157.2 C X674035 T1	citrus	2443	44	80	86.7549 669	85.8085 809	blastp
1097	cotton gb164 D W234737 T1	cotton	2444	44	80	99.6688 742	98.3333 333	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1098	lettuce gb157.2 DW066284_T1	lettuce	2445	44	80	95.0331 126	100	blastp
1099	petunia gb157.2 CV298254_T1	petunia	2446	44	84	65.8940 397	100	blastp
1100	potato gb157.2 C V500020_T1	potato	2447	44	94	72.1854 305	99.5433 79	blastp
1101	tobacco gb162 E B426672_T1	tobacco	2448	44	89	99.0066 225	97.6897 69	blastp
1102	brachypodium g b161.xeno BE41 5047_T1	brachypo dium	2449	46	92	100	100	blastp
1103	maize gb164 CF 244342_T1	maize	2450	46	90	90.7630 522	100	blastp
1104	maize gb164 AF 057183_T1	maize	2451	46	89	100	100	blastp
1105	sorghum gb161. xeno AF057183_ T1	sorghum	2452	46	88	100	100	blastp
1106	sugarcane gb157 .2 CA132045_T 1	sugarcan e	2453	46	89	100	100	blastp
1107	switchgrass gb16 5 FE617713_T1	switchgr ass	2454	46	90	100	100	blastp
1108	wheat gb164 BE 430088_T1	wheat	2455	46	95	100	100	blastp
1109	apple gb157.3 D T001281_T1	apple	2456	47	81	87.9518 072	100	blastp
1110	brachypodium g b161.xeno BE40 2447_T1	brachypo dium	2457	47	95	100	100	blastp
1111	ginger gb164 DY 364894_T1	ginger	2458	47	88	64.2570 281	98.7654 321	blastp
1112	maize gb164 A18 55402_T1	maize	2459	47	89	100	100	blastp
1113	maize gb164 A W017703_T1	maize	2460	47	85	100	100	blastp
1114	onion gb162 AC U58207_T1	onion	2461	47	83	99.5983 936	99.5967 742	blastp
1115	onion gb162 CF4 37464_T1	onion	2462	47	85	95.9839 357	98.75	blastp
1116	onion gb162 CF4 35351_T1	onion	2463	47	84	100	100	blastp
1117	rice gb157.2 AU 031632_T1	rice	2464	47	91	100	100	blastp
1118	rice gb157.2 CA 756239_T1	rice	2465	47	87	97.5903 614	31.6406 25	blastp
1119	sorghum gb161. xeno A1855402_ T1	sorghum	2466	47	89	100	100	blastp
1120	sugarcane gb157 .2 CA132045_T 2	sugarcan e	2467	47	90	99.5983 936	99.5967 742	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1121	switchgrass gb165 FE624217_T1	switchgrass	2468	47	90	100	100	blastp
1122	wheat gb164 BE404100_T1	wheat	2469	47	97	100	100	blastp
1123	fescue gb161 DT700572_T1	fescue	2470	48	94	100	100	blastp
1124	ginger gb164 DY361836_T1	ginger	2471	48	80	95.1612903	96.7346939	blastp
1125	rice gb157.2 U37952_T1	rice	2472	48	90	100	100	blastp
1126	rice gb157.2 U37952_T3	rice	2473	48	89	51.6129032	89.5104895	blastp
1127	rye gb164 BE495605_T1	rye	2474	48	98	80.6451613	100	blastp
1128	sorghum gb161.xeno A1724211_T1	sorghum	2475	48	90	100	100	blastp
1129	sugarcane gb157.2 CA110414_T1	sugarcane	2476	48	82	92.3387097	100	blastp
1130	sugarcane gb157.2 CA065356_T1	sugarcane	2477	48	83	90.3225806	96.5517241	blastp
1131	sugarcane gb157.2 CA143208_T1	sugarcane	2478	48	83	71.3709677	95.6756757	blastp
1132	sugarcane gb157.2 CA101765_T1	sugarcane	2479	48	91	100	100	blastp
1133	sugarcane gb157.2 CA133231_T1	sugarcane	2480	48	90	83.4677419	95.8333333	blastp
1134	switchgrass gb165 FE605472_T1	switchgrass	2481	48	91	100	100	blastp
1135	wheat gb164 BE489764_T1	wheat	2482	48	95	100	100	blastp
1136	wheat gb164 TAU86763_T1	wheat	2483	48	95	100	100	blastp
1137	wheat gb164 BE415001_T1	wheat	2484	48	95	100	100	blastp
1138	b_juncea gb164 EVGN00504508791211_T1	b_juncea	2485	50	80	85.0931677	100	blastp
1139	b_juncea gb164 EVGN01684214261870_T1	b_juncea	2486	50	84	50.931677	91.954023	blastp
1140	banana gb160 DN239388_T1	banana	2487	50	84	80.1242236	91.9708029	blastp
1141	barley gb157.3 BF253694_T1	barley	2488	50	91	58.3850932	98.9690722	blastp
1142	barley gb157.3 BE412959_T3	barley	2489	50	95	100	62.6923077	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1143	bean gb164 FD7 93482 T1	bean	2490	50	82	100	91.9075 145	blastp
1144	canola gb161 CX 193398 T3	canola	2491	50	83	99.3788 82	66.9527 897	blastp
1145	canola gb161 EV 123336 T1	canola	2492	50	81	52.7950 311	91.2087 912	blastp
1146	centaurea gb161 EL931277 T1	centaure a	2493	50	81	98.1366 46	62.2489 96	blastp
1147	cichorium gb161 DT213939 T1	cichoriu m	2494	50	83	64.5962 733	95.3271 028	blastp
1148	fescue gb161 DT 703843 T1	fescue	2495	50	99	100	94.1520 468	blastp
1149	lotus gb157.2 BI 418499 T1	lotus	2496	50	86	98.1366 46	88.7005 65	blastp
1150	onion gb162 BQ 579939 T1	onion	2497	50	86	100	57.1942 446	blastp
1151	peach gb157.2 B U040795 T1	peach	2498	50	82	98.1366 46	56.2043 796	blastp
1152	peach gb157.2 D W351857 T1	peach	2499	50	83	98.1366 46	91.8128 655	blastp
1153	rye gb164 BF429 463 T1	rye	2500	50	88	93.1677 019	100	blastp
1154	soybean gb166 B E352747 T4	soybean	2501	50	81	98.1366 46	70.7207 207	blastp
1155	sugarcane gb157 .2 CA194640_T 1	sugarcan e	2502	50	81	98.1366 46	56.6787 004	blastp
1156	sugarcane gb157 .2 CA103332_T 1	sugarcan e	2503	50	84	96.2732 919	87.0056 497	blastp
1157	sugarcane gb157 .2 CA167616_T 1	sugarcan e	2504	50	82	93.7888 199	74.2574 257	blastp
1158	sugarcane gb157 .2 CA103740_T 1	sugarcan e	2505	50	90	100	68.5344 828	blastp
1159	sugarcane gb157 .2 CA184547_T 1	sugarcan e	2506	50	82	97.5155 28	77.4834 437	tblastn
1160	sunflower gb162 CF089373 T1	sunflowe r	2507	50	87	98.1366 46	87.5	blastp
1161	wheat gb164 CA 484201 T1	wheat	2508	50	89	96.8944 099	65.9574 468	blastp
1162	apricot gb157.2 CV049856 T1	apricot	2509	51	86	100	65.9574 468	blastp
1163	arabidopsis gb16 5 AT2G37180_T 1	arabidop sis	2510	51	89	100	32.6315 789	blastp
1164	arabidopsis gb16 5 AT2G39010_T 1	arabidop sis	2511	51	92	100	32.1799 308	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1165	b_juncea gb164 EVGN00130608 921231 T1	b_juncea	2512	51	87	100	86.9158 879	blastp
1166	b_juncea gb164 EVGN00605203 140273 T1	b_juncea	2513	51	86	90.3225 806	86.5979 381	blastp
1167	b_juncea gb164 EVGN21262514 941904 T1	b_juncea	2514	51	86	56.9892 473	91.3793 103	blastp
1168	b_juncea gb164 EVGN00733314 152324 T1	b_juncea	2515	51	86	100	85.3211 009	blastp
1169	b_juncea gb164 EVGN00041211 340240 T1	b_juncea	2516	51	86	89.2473 118	49.4047 619	blastp
1170	b_juncea gb164 DT317704 T1	b_juncea	2517	51	91	100	80.1724 138	blastp
1171	b_juncea gb164 EVGN00208014 701957 T1	b_juncea	2518	51	85	89.2473 118	79.8076 923	blastp
1172	b_juncea gb164 EVGN00550314 491066 T1	b_juncea	2519	51	90	100	36.3281 25	blastp
1173	b_juncea gb164 EVGN01267508 262672 T1	b_juncea	2520	51	90	90.3225 806	95.4545 455	blastp
1174	b_juncea gb164 EVGN01803715 320789 T1	b_juncea	2521	51	89	100	51.3812 155	blastp
1175	b_juncea gb164 EVGN00397011 681539 T1	b_juncea	2522	51	91	100	34.4019 729	tblastn
1176	b_rapa gb162 D N965016 T1	b_rapa	2523	51	88	100	69.4029 851	blastp
1177	b_rapa gb162 E X025548 T1	b_rapa	2524	51	87	100	32.5174 825	blastp
1178	b_rapa gb162 B G543764 T1	b_rapa	2525	51	92	100	32.2916 667	blastp
1179	banana gb160 D N238638 T1	banana	2526	51	89	100	27.8721 279	tblastn
1180	banana gb160 D N238638 T2	banana	2527	51	89	100	30.5921 053	tblastn
1181	barley gb157.3 B E421292 T1	barley	2528	51	87	100	32.7464 789	blastp
1182	barley gb157.3 B J446923 T1	barley	2529	51	83	100	64.5833 333	blastp
1183	beet gb162 BQ4 88455 T1	beet	2530	51	81	100	26.6862 17	blastp
1184	beet gb162 BVU 60147 T1	beet	2531	51	84	100	32.2916 667	blastp
1185	canola gb161 CX 189721 T1	canola	2532	51	87	100	32.5174 825	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1186	canola gb161 CB686155_T1	canola	2533	51	92	100	32.2916667	blastp
1187	canola gb161 DY007249_T1	canola	2534	51	87	100	32.5174825	blastp
1188	canola gb161 ES986486_T1	canola	2535	51	86	96.7741935	87.3786408	blastp
1189	canola gb161 EV203446_T1	canola	2536	51	82	100	38.0108992	tblastn
1190	cassava gb164 DN740353_T1	cassava	2537	51	93	100	62.8378378	blastp
1191	cassava gb164 DV449516_T1	cassava	2538	51	94	100	68.8888889	blastp
1192	cassava gb164 BM259717_T1	cassava	2539	51	81	100	32.8621908	blastp
1193	castorbean gb160 EE257493_T2	castorbean	2540	51	81	100	46.5	blastp
1194	castorbean gb160 EE257493_T1	castorbean	2541	51	81	100	34.4444444	blastp
1195	cichorium gb161 EH706421_T1	cichorium	2542	51	94	100	80.8695652	blastp
1196	cichorium gb161 EH708948_T1	cichorium	2543	51	90	100	32.5554259	tblastn
1197	cichorium gb161 EH692078_T1	cichorium	2544	51	90	100	24.668435	tblastn
1198	citrus gb157.2 CB291468_T1	citrus	2545	51	82	100	86.1111111	blastp
1199	citrus gb157.2 BQ624699_T1	citrus	2546	51	90	100	27.56917	tblastn
1200	clover gb162 BB903718_T1	clover	2547	51	91	100	32.6315789	blastp
1201	clover gb162 BB930902_T1	clover	2548	51	88	100	32.4041812	blastp
1202	clover gb162 BB911526_T1	clover	2549	51	91	92.4731183	80.3738318	blastp
1203	clover gb162 BB913405_T1	clover	2550	51	90	96.7741935	81.0810811	blastp
1204	cotton gb164 ES804497_T1	cotton	2551	51	86	100	58.490566	blastp
1205	cotton gb164 EX172153_T1	cotton	2552	51	89	90.3225806	41.5156507	tblastn
1206	cowpea gb166 FF384339_T1	cowpea	2553	51	89	90.3225806	80	blastp
1207	cowpea gb166 FF396241_T1	cowpea	2554	51	82	97.8494624	88.3495146	blastp
1208	cowpea gb166 ES884224_T1	cowpea	2555	51	88	100	32.4041812	blastp
1209	cowpea gb166 FG857474_T1	cowpea	2556	51	89	100	68.8888889	blastp
1210	cryptomeria gb166 BY902595_T1	cryptomeria	2557	51	81	100	78.8135593	blastp
1211	cryptomeria gb166 BJ937695_T1	cryptomeria	2558	51	83	100	31.7406143	blastp

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1212	cryptomeria gb166 BW993227_T1	cryptome ria	2559	51	82	88.1720 43	86.3157 895	blastp
1213	dandelion gb161 DY802675_T1	dandelio n	2560	51	87	91.3978 495	75.2212 389	blastp
1214	fescue gb161 DT674412_T1	fescue	2561	51	82	84.9462 366	85.8695 652	blastp
1215	fescue gb161 DT695652_T1	fescue	2562	51	84	100	76.8595 041	blastp
1216	fescue gb161 DT702501_T1	fescue	2563	51	83	95.6989 247	96.7391 304	blastp
1217	fescue gb161 DT688112_T1	fescue	2564	51	83	100	85.3211 009	blastp
1218	fescue gb161 DT688728_T1	fescue	2565	51	92	100	81.5789 474	blastp
1219	ginger gb164 DY358169_T1	ginger	2566	51	87	100	32.9787 234	blastp
1220	ginger gb164 DY366672_T1	ginger	2567	51	82	93.5483 871	87	blastp
1221	ginger gb164 DY360033_T1	ginger	2568	51	91	100	27.7888 446	tblastn
1222	grape gb160 AF188843_T5	grape	2569	51	82	100	32.5174 825	blastp
1223	ipomoea gb157.2 BJ556470_T1	ipomoea	2570	51	88	100	32.4041 812	blastp
1224	lettuce gb157.2 DW158018_T1	lettuce	2571	51	90	100	32.6315 789	blastp
1225	lettuce gb157.2 DW091407_T1	lettuce	2572	51	90	100	34.7014 925	blastp
1226	lettuce gb157.2 DW060777_T1	lettuce	2573	51	89	89.2473 118	32.6771 654	blastp
1227	lotus gb157.2 AV775277_T1	lotus	2574	51	83	100	88.5714 286	blastp
1228	lotus gb157.2 AI967387_T1	lotus	2575	51	84	100	32.4041 812	blastp
1229	lotus gb157.2 AV774377_T1	lotus	2576	51	81	100	88.5714 286	blastp
1230	lotus gb157.2 BP059122_T1	lotus	2577	51	80	73.1182 796	85	blastp
1231	lotus gb157.2 BI419853_T1	lotus	2578	51	81	94.6236 559	88	blastp
1232	lotus gb157.2 BP049219_T1	lotus	2579	51	81	100	76.2295 082	blastp
1233	lotus gb157.2 AV775053_T1	lotus	2580	51	82	84.9462 366	86.8131 868	blastp
1234	lotus gb157.2 AV775249_T1	lotus	2581	51	85	95.6989 247	80.9090 909	blastp
1235	maize gb164 AF326496_T1	maize	2582	51	88	100	32.4041 812	blastp
1236	maize gb164 AY107589_T1	maize	2583	51	84	100	32.8621 908	blastp
1237	medicago gb157.2 AI974409_T1	medicag o	2584	51	87	100	32.4041 812	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1238	medicago gb157.2 AI974231_T1	medicag o	2585	51	89	100	32.6315789	blastp
1239	melon gb165 EB715587_T1	melon	2586	51	86	100	23.4848485	tblastn
1240	oat gb164 CN816056_T1	oat	2587	51	82	100	84.5454545	blastp
1241	oil_palm gb166 CN601069_T1	oil_palm	2588	51	89	100	32.9787234	blastp
1242	oil_palm gb166 EL686181_T1	oil_palm	2589	51	84	100	32.9787234	blastp
1243	peanut gb161 CD037823_T1	peanut	2590	51	82	100	31.8493151	blastp
1244	peanut gb161 CD038014_T1	peanut	2591	51	88	100	32.1799308	blastp
1245	periwinkle gb164 AM232518_T2	periwink le	2592	51	87	100	65.9574468	blastp
1246	physcomitrella gb157 BI436955_T1	physcom itrella	2593	51	89	100	33.3333333	blastp
1247	physcomitrella gb157 BJ198543_T1	physcom itrella	2594	51	82	100	32.5174825	blastp
1248	physcomitrella gb157 AW476973_T3	physcom itrella	2595	51	90	100	33.2142857	blastp
1249	physcomitrella gb157 BJ962015_T1	physcom itrella	2596	51	82	100	32.5259516	blastp
1250	pine gb157.2 AW870138_T1	pine	2597	51	82	100	34.7014925	blastp
1251	pine gb157.2 AI813147_T1	pine	2598	51	87	100	33.0960854	blastp
1252	pine gb157.2 AA739836_T1	pine	2599	51	87	100	33.0960854	blastp
1253	pine gb157.2 AL750425_T1	pine	2600	51	88	100	33.0960854	blastp
1254	pine gb157.2 BG038984_T1	pine	2601	51	80	100	32.8621908	blastp
1255	pine gb157.2 AW225939_T1	pine	2602	51	80	100	34.1911765	blastp
1256	pine gb157.2 BQ696500_T1	pine	2603	51	81	100	32.8621908	blastp
1257	pine gb157.2 AL751198_T1	pine	2604	51	87	100	33.3333333	blastp
1258	pine gb157.2 BQ695693_T1	pine	2605	51	82	100	32.8621908	blastp
1259	pine gb157.2 BF517326_T1	pine	2606	51	80	100	60.3896104	blastp
1260	pine gb157.2 AA739625_T1	pine	2607	51	81	100	34.7014925	blastp
1261	pine gb157.2 BG317873_T1	pine	2608	51	82	100	32.8621908	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1262	pine gb157.2 AI8 13147 T2	pine	2609	51	87	100	32.9787 234	blastp
1263	pine gb157.2 CF 388120 T1	pine	2610	51	87	100	33.3333 333	blastp
1264	pine gb157.2 BE 662590 T1	pine	2611	51	81	100	35.7692 308	blastp
1265	pine gb157.2 BG 318657 T1	pine	2612	51	82	100	32.8621 908	blastp
1266	pine gb157.2 AA 557104 T1	pine	2613	51	88	100	33.3333 333	blastp
1267	pine gb157.2 A W870138 T2	pine	2614	51	82	100	32.8621 908	blastp
1268	pine gb157.2 A W289749 T1	pine	2615	51	82	100	32.8621 908	blastp
1269	pine gb157.2 H7 5016 T1	pine	2616	51	88	100	32.7464 789	blastp
1270	pine gb157.2 AA 740005 T1	pine	2617	51	80	100	35.0943 396	blastp
1271	pine gb157.2 CA 305579 T1	pine	2618	51	91	100	75.6097 561	blastp
1272	pine gb157.2 BE 187350 T1	pine	2619	51	83	100	32.8621 908	blastp
1273	pine gb157.2 CF 473539 T1	pine	2620	51	84	100	32.9787 234	blastp
1274	pine gb157.2 A W290370 T1	pine	2621	51	83	100	32.7464 789	blastp
1275	pine gb157.2 A W290691 T1	pine	2622	51	82	75.2688 172	88.6075 949	blastp
1276	pine gb157.2 BG 318695 T1	pine	2623	51	82	100	34.7014 925	blastp
1277	pineapple gb157. 2 DT339628 T1	pineappl e	2624	51	91	98.9247 312	78.6324 786	blastp
1278	poplar gb157.2 A I162483 T2	poplar	2625	51	86	100	24.3455 497	tblastn
1279	poplar gb157.2 B U817536 T4	poplar	2626	51	87	100	22.6094 003	tblastn
1280	potato gb157.2 B Q515617 T1	potato	2627	51	80	98.9247 312	36.6533 865	blastp
1281	potato gb157.2 B E920139 T2	potato	2628	51	90	100	41.5178 571	blastp
1282	radish gb164 EV 526963 T1	radish	2629	51	87	100	32.5174 825	blastp
1283	radish gb164 EV 567230 T2	radish	2630	51	84	100	46.0396 04	blastp
1284	radish gb164 EV 551004 T1	radish	2631	51	92	100	32.2916 667	blastp
1285	radish gb164 EX 756464 T1	radish	2632	51	86	100	48.1865 285	blastp
1286	radish gb164 EY 910551 T1	radish	2633	51	91	100	31.9587 629	blastp
1287	radish gb164 EW 730466 T1	radish	2634	51	84	98.9247 312	87.6190 476	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1288	radish gb164 AF 051128_T1	radish	2635	51	81	87.0967 742	48.6	tblastn
1289	radish gb164 EX 756028_T1	radish	No predicted Protein	51	86	100	40.0286 944	tblastn
1290	rice gb157.2 BE2 29418_T1	rice	2636	51	90	100	32.9787 234	blastp
1291	rice gb157.2 BE2 29418_T3	rice	2637	51	90	100	38.5892 116	blastp
1292	rice gb157.2 AK 107700_T1	rice	2638	51	91	100	68.8888 889	blastp
1293	rice gb157.2 BE2 29418_T4	rice	2639	51	90	100	54.0697 674	blastp
1294	rice gb157.2 NM 001066078_T1	rice	2640	51	92	100	41.7040 359	blastp
1295	rice gb157.2 AW 155505_T1	rice	2641	51	83	100	32.0689 655	blastp
1296	rice gb157.2 AW 155505_T2	rice	2642	51	83	98.9247 312	35.7976 654	blastp
1297	rice gb157.2 AK 106746_T1	rice	2643	51	83	100	22.6461 039	tblastn
1298	sorghum gb161. xeno AY107589 _T1	sorghum	2644	51	86	100	33.3333 333	blastp
1299	sorghum gb161. xeno AI947598_ _T1	sorghum	2645	51	92	100	32.5174 825	blastp
1300	sorghum gb161. xeno AI855413_ _T1	sorghum	2646	51	80	100	31.4189 189	blastp
1301	sorghum gb161. xeno AW565915 _T1	sorghum	2647	51	81	100	31.1418 685	blastp
1302	sorghum gb161. xeno CF481617_ _T1	sorghum	2648	51	90	100	79.6610 169	blastp
1303	soybean gb166 B U549322_T1	soybean	2649	51	89	100	32.5174 825	blastp
1304	soybean gb166 B E352729_T1	soybean	2650	51	88	100	32.4041 812	blastp
1305	soybean gb166 B I974981_T1	soybean	2651	51	91	100	71.5384 615	blastp
1306	soybean gb166 B E658685_T1	soybean	2652	51	89	100	32.6315 789	blastp
1307	soybean gb166 B E352747_T3	soybean	2653	51	81	100	20.5904 059	tblastn
1308	spikemoss gb165 DN838269_T1	spikemos s	2654	51	88	100	32.0689 655	blastp
1309	spikemoss gb165 FE434019_T1	spikemos s	2655	51	88	100	32.0689 655	blastp
1310	spruce gb162 CO 225164_T1	spruce	2656	51	89	100	32.8621 908	blastp

Polynuc. SEQ ID NO:	Cluster name	Organis m	Polypep. SEQ ID NO:	Hom. of SEQ ID NO:	% Ident.	Query cover.	% Subject cover.	Algorith m
1311	spruce gb162 CO 258147_T1	spruce	2657	51	81	100	33.8181 818	blastp
1312	spruce gb162 CO 230791_T1	spruce	2658	51	88	100	46.0396 04	blastp
1313	spruce gb162 DR 546674_T1	spruce	2659	51	82	100	32.5	blastp
1314	spruce gb162 DR 560237_T1	spruce	2660	51	81	100	34.1911 765	blastp
1315	spurge gb161 D V116550_T1	spurge	2661	51	83	100	86.1111 111	blastp
1316	sugarcane gb157 .2 CA088464_T 1	sugarcane	2662	51	87	88.1720 43	81.1881 188	blastp
1317	sugarcane gb157 .2 CA086583_T 1	sugarcane	2663	51	92	100	62.4161 074	blastp
1318	sugarcane gb157 .2 CA234165_T 1	sugarcane	2664	51	86	62.3655 914	100	blastp
1319	sugarcane gb157 .2 CA107998_T 1	sugarcane	2665	51	89	100	32.5174 825	blastp
1320	sugarcane gb157 .2 CA204327_T 1	sugarcane	2666	51	95	100	34.1911 765	tblastn
1321	sugarcane gb157 .2 CA067786_T 1	sugarcane	2667	51	92	86.0215 054	18.6480 186	tblastn
1322	sunflower gb162 DY944685_T1	sunflower	2668	51	81	100	31.9587 629	blastp
1323	sunflower gb162 BQ968590_T1	sunflower	2669	51	87	52.6881 72	100	blastp
1324	sunflower gb162 CD848850_T1	sunflower	2670	51	89	98.9247 312	41.3173 653	tblastn
1325	tobacco gb162 E B445876_T1	tobacco	2671	51	90	100	32.4041 812	blastp
1326	tobacco gb162 E B445188_T1	tobacco	2672	51	88	100	32.4041 812	blastp
1327	tobacco gb162 C K720586_T1	tobacco	2673	51	81	100	34.7014 925	blastp
1328	tomato gb164 C O750818_T1	tomato	2674	51	92	88.1720 43	82.8282 828	blastp
1329	tomato gb164 A 772191_T1	tomato	2675	51	81	98.9247 312	33.6996 337	blastp
1330	tomato gb164 A W219533_T2	tomato	2676	51	89	100	39.2405 063	tblastn
1331	triphysaria gb16 4 DR173305_T1	triphysaria	2677	51	88	95.6989 247	80.9090 909	blastp
1332	triphysaria gb16 4 EX984185_T1	triphysaria	2678	51	90	100	75.6097 561	blastp
1333	triphysaria gb16 4 DR174019_T1	triphysaria	2679	51	91	100	67.8832 117	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorithm</i>
1334	wheat gb164 CA 609068 T1	wheat	2680	51	94	100	67.3913 043	blastp
1335	wheat gb164 BE 430411 T1	wheat	2681	51	86	100	32.4041 812	blastp
1336	wheat gb164 CK 208980 T1	wheat	2682	51	80	100	30	blastp
1337	wheat gb164 CA 620158 T1	wheat	2683	51	96	95.6989 247	87.2549 02	blastp
1338	wheat gb164 BE 405395 T1	wheat	2684	51	88	100	32.7464 789	blastp
1339	wheat gb164 CA 647310 T1	wheat	2685	51	80	77.4193 548	93.5064 935	blastp
1340	wheat gb164 BE 492099 T1	wheat	2686	51	87	100	32.7464 789	blastp
1341	wheat gb164 BE 402029 T1	wheat	2687	51	87	100	32.7464 789	blastp
1342	wheat gb164 CA 618130 T1	wheat	2688	51	86	88.1720 43	73.2142 857	blastp
1343	wheat gb164 CJ6 05707 T1	wheat	2689	51	82	100	69.4029 851	blastp
1344	wheat gb164 CA 614209 T1	wheat	2690	51	98	59.1397 849	98.2142 857	blastp
1345	wheat gb164 CA 701714 T1	wheat	2691	51	82	100	77.5	blastp
1346	wheat gb164 BE 403921 T1	wheat	2692	51	93	96.7741 935	82.5688 073	blastp
1347	wheat gb164 BE 217049 T1	wheat	2693	51	83	100	31.9587 629	blastp
1348	wheat gb164 CA 602649 T1	wheat	2694	51	84	100	30.0322 928	tblastn
1349	wheat gb164 CA 486220 T1	wheat	2695	51	82	96.7741 935	33.3759 591	tblastn
1350	b_juncea gb164 EVGN00044413 933329 T1	b_juncea	2696	52	85	64.3835 616	99.2957 746	blastp
1351	b_juncea gb164 EVGN00137910 990746 T1	b_juncea	2697	52	90	53.4246 575	99.1525 424	blastp
1352	barley gb157.3 B E413268 T1	barley	2698	52	81	96.8036 53	73.4482 759	blastp
1353	barley gb157.3 A J433979 T1	barley	2699	52	81	96.8036 53	73.4482 759	blastp
1354	barley gb157.3 B E412979 T1	barley	2700	52	82	96.8036 53	74.1258 741	blastp
1355	brachypodium g b161.xeno AF13 9815 T1	brachypo dium	2701	52	83	96.8036 53	73.6111 111	blastp
1356	citrus gb157.2 C X052950 T1	citrus	2702	52	84	50.2283 105	100	blastp
1357	clover gb162 BB 913131 T1	clover	2703	52	93	52.5114 155	99.1379 31	blastp
1358	clover gb162 BB 918704 T1	clover	2704	52	82	63.9269 406	99.2957 746	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Poly pep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1359	cotton gb164 CO 103246 T1	cotton	2705	52	91	56.6210 046	93.9393 939	blastp
1360	cowpea gb166 F G883860 T1	cowpea	2706	52	83	51.1415 525	99.1150 442	blastp
1361	fescue gb161 DT 702489 T1	fescue	2707	52	96	57.0776 256	93.2835 821	blastp
1362	fescue gb161 DT 702846 T1	fescue	2708	52	96	57.0776 256	96.8992 248	blastp
1363	ipomoea gb157.2 BU691146 T1	ipomoea	2709	52	81	87.2146 119	74.7035 573	blastp
1364	maize gb164 AI9 39909 T1	maize	2710	52	80	96.8036 53	73.6111 111	blastp
1365	maize gb164 AF 130975 T1	maize	2711	52	83	96.8036 53	74.3859 649	blastp
1366	maize gb164 AI9 47831 T1	maize	2712	52	83	96.8036 53	73.6111 111	blastp
1367	oil_palm gb166 EL692065 T1	oil_palm	2713	52	80	96.8036 53	75.1773 05	blastp
1368	physcomitrella g b157 AW476973 T1	physcom itrella	2714	52	80	93.6073 059	73.4767 025	blastp
1369	physcomitrella g b157 BI894596_ T1	physcom itrella	2715	52	80	96.3470 32	73.0103 806	blastp
1370	physcomitrella g b157 AW476973 T2	physcom itrella	2716	52	80	93.6073 059	73.4767 025	blastp
1371	pine gb157.2 CF 387570 T1	pine	2717	52	88	51.1415 525	99.1150 442	blastp
1372	radish gb164 EY 904434 T2	radish	2718	52	88	54.3378 995	99.1666 667	blastp
1373	radish gb164 FD 960377 T1	radish	2719	52	84	63.0136 986	99.2805 755	blastp
1374	rice gb157.2 AU 093957 T1	rice	2720	52	81	96.8036 53	74.1258 741	blastp
1375	rice gb157.2 BE0 39992 T2	rice	2721	52	92	57.0776 256	97.6562 5	blastp
1376	rice gb157.2 BE5 30955 T1	rice	2722	52	80	96.8036 53	73.1034 483	blastp
1377	rye gb164 BE58 6469 T1	rye	2723	52	82	61.1872 146	97.8102 19	blastp
1378	sorghum gb161. xeno AW922622 T1	sorghum	2724	52	83	96.8036 53	72.6027 397	blastp
1379	sorghum gb161. xeno BE344582_ T1	sorghum	2725	52	80	85.3881 279	74.8	blastp
1380	sorghum gb161. xeno AI855280_ T1	sorghum	2726	52	82	96.8036 53	73.3564 014	blastp
1381	spikemoss gb165 DN838148 T1	spikemos s	2727	52	83	91.7808 219	71.5302 491	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Poly pep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
1382	spikemoss gb165 DN838057_T1	spikemos s	2728	52	83	91.7808 219	71.5302 491	blastp
1383	sugarcane gb157 .2 CA139573_T 1	sugarcane	2729	52	82	90.4109 589	71.8978 102	blastp
1384	sugarcane gb157 .2 CA145403_T 1	sugarcane	2730	52	90	57.0776 256	99.2063 492	blastp
1385	sunflower gb162 CF083179_T1	sunflower	2731	52	80	57.0776 256	93.2835 821	blastp
1386	sunflower gb162 BU035823_T1	sunflower	2732	52	86	56.6210 046	89.2086 331	blastp
1387	switchgrass gb16 5 DN140790_T1	switchgr ass	2733	52	83	61.6438 356	99.2647 059	blastp
1388	switchgrass gb16 5 FE631354_T1	switchgr ass	2734	52	81	66.2100 457	96.6666 667	blastp
1389	tobacco gb162 D V159802_T1	tobacco	2735	52	81	87.6712 329	48.7722 269	tblastn
1390	wheat gb164 AF 139815_T1	wheat	2736	52	82	96.8036 53	74.1258 741	blastp
1391	wheat gb164 BE 406301_T1	wheat	2737	52	81	96.8036 53	73.4482 759	blastp
1392	wheat gb164 BE 404904_T1	wheat	2738	52	81	96.8036 53	73.4482 759	blastp
1393	wheat gb164 BE 400219_T1	wheat	2739	52	81	96.8036 53	73.4482 759	blastp
1394	wheat gb164 CA 619093_T1	wheat	2740	52	81	54.7945 205	90.1515 152	blastp
1395	wheat gb164 BE 605056_T1	wheat	2741	52	88	56.6210 046	93.2330 827	blastp
1396	wheat gb164 BQ 245211_T1	wheat	2742	52	82	96.8036 53	74.1258 741	blastp
1397	wheat gb164 BE 497487_T1	wheat	2743	52	81	96.8036 53	73.4482 759	blastp
1398	wheat gb164 BQ 295206_T1	wheat	2744	52	89	64.8401 826	100	blastp
1399	wheat gb164 BE 499954_T1	wheat	2745	52	80	98.6301 37	74.8275 862	blastp
1400	wheat gb164 BE 405794_T1	wheat	2746	52	81	96.8036 53	73.4482 759	blastp
6	tomato gb164 A W934056_T1	tomato	32	31	82	100	100	blastp
21	barley gb157.3 A L501410_T1	barley	47	46	87	98.3935 743	98.7951 8072	blastp
2844	antirrhinum gb16 6 AJ559427_T1	antirrhin um	3052	25	88	100	100	blastp
2845	antirrhinum gb16 6 AJ791214_T1	antirrhin um	3053	25	85	100	100	blastp
2846	bruguiera gb166 BP939664_T1	bruguier a	3054	25	82	61.2903 2258	100	blastp
2847	centaurea gb166 EL931601_T1	centaure a	3055	25	84	98.7903 2258	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Poly pep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
2848	eucalyptus gb166 CD668425_T1	eucalyptus	3056	25	85	98.7903 2258	98.7903 2258	blastp
2849	kiwi gb166 FG409998_T1	kiwi	3057	25	85	100	100	blastp
2850	kiwi gb166 FG453166_T1	kiwi	3058	25	86	100	100	blastp
2851	kiwi gb166 FG401585_T1	kiwi	3059	25	87	99.5967 7419	100	blastp
2852	kiwi gb166 FG419790_T1	kiwi	3060	25	85	100	100	blastp
2853	liriodendron gb166 FD495170_T1	liriodendron	3061	25	82	99.1935 4839	98.7951 8072	blastp
2854	poppy gb166 FG607362_T1	poppy	3062	25	82	82.6612 9032	99.5145 6311	blastp
2855	soybean gb167 AA660186_T1	soybean	3063	25	83	100	100	blastp
2856	soybean gb167 CA990807_T1	soybean	3064	25	82	95.5645 1613	100	blastp
2857	walnuts gb166 CV196664_T1	walnuts	3065	25	83	100	100	blastp
2858	antirrhinum gb166 X70417_T1	antirrhinum	3066	26	90	100	100	blastp
2859	banana gb167 FF560721_T1	banana	3067	26	86	77.6	99.4871 7949	blastp
2860	centaurea gb166 EL932548_T1	centaurea	3068	26	86	100	100	blastp
2861	antirrhinum gb166 AJ789802_T1	antirrhinum	3069	27	86	90.9090 9091	100	blastp
2862	bruguiera gb166 BP938735_T1	bruguiera	3070	27	81	69.9604 7431	100	blastp
2863	eucalyptus gb166 ES589574_T1	eucalyptus	3071	27	82	90.9090 9091	100	blastp
2864	kiwi gb166 FG427735_T1	kiwi	3072	27	86	50.1976 2846	99.2187 5	blastp
2865	kiwi gb166 FG406415_T1	kiwi	3073	27	81	54.1501 9763	100	blastp
2866	kiwi gb166 FG406885_T1	kiwi	3074	27	84	99.2094 8617	99.6031 746	blastp
2867	liriodendron gb166 CK744430_T1	liriodendron	3075	27	81	99.2094 8617	99.6031 746	blastp
2868	poppy gb166 FG608493_T1	poppy	3076	27	84	83.0039 5257	99.5260 6635	blastp
2869	soybean gb167 EV269611_T1	soybean	3077	27	86	60.0790 5138	96.2025 3165	blastp
2870	amborella gb166 CD482678_T1	amborella	3078	28	82	100	100	blastp
2871	cenchrus gb166 BM084541_T1	cenchrus	3079	28	81	100	100	blastp
2872	leymus gb166 EG376267_T1	leymus	3080	28	80	100	100	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
2873	leymus gb166 E G386149_T1	leymus	3081	28	80	100	100	blastp
2874	walnuts gb166 E L895384_T1	walnuts	3082	28	83	82	94.4954 1284	blastp
2875	amborella gb166 CD481950_T1	amborella	3083	30	88	98.2638 8889	98.9547 0383	blastp
2876	antirrhinum gb16 6 AJ796874_T1	antirrhini um	3084	30	86	93.4027 7778	100	blastp
2877	antirrhinum gb16 6 AJ798039_T1	antirrhini um	3085	30	84	73.2638 8889	99.5260 6635	blastp
2878	antirrhinum gb16 6 AJ792331_T1	antirrhini um	3086	30	88	85.0694 4444	100	blastp
2879	antirrhinum gb16 6 AJ558770_T1	antirrhini um	3087	30	86	98.2638 8889	99.3006 993	blastp
2880	banana gb167 FF 558844_T1	banana	3088	30	88	98.2638 8889	98.9510 4895	blastp
2881	bean gb167 CA8 98412_T1	bean	3089	30	81	98.2638 8889	99.3031 3589	blastp
2882	bruguiera gb166 BP941115_T1	bruguiera	3090	30	86	52.7777 7778	95	blastp
2883	bruguiera gb166 BP939033_T1	bruguiera	3091	30	85	97.9166 6667	99.3031 3589	blastp
2884	cenchrus gb166 EB656428_T1	cenchrus	3092	30	85	98.2638 8889	98.9583 3333	blastp
2885	centaurea gb166 EH767475_T1	centaurea	3093	30	86	98.2638 8889	98.9547 0383	blastp
2886	centaurea gb166 EL935569_T1	centaurea	3094	30	86	98.2638 8889	98.9583 3333	blastp
2887	cycas gb166 CB 089724_T1	cycas	3095	30	84	98.2638 8889	98.9547 0383	blastp
2888	cycas gb166 CB 088798_T1	cycas	3096	30	83	98.2638 8889	98.2698 9619	blastp
2889	eucalyptus gb16 6 CD668044_T1	eucalypt us	3097	30	84	98.2638 8889	99.3055 5556	blastp
2890	eucalyptus gb16 6 AW191311_T 1	eucalypt us	3098	30	87	98.2638 8889	98.9547 0383	blastp
2891	kiwi gb166 FG4 03284_T1	kiwi	3099	30	85	98.2638 8889	99.3006 993	blastp
2892	kiwi gb166 FG4 04130_T1	kiwi	3100	30	86	98.2638 8889	99.3006 993	blastp
2893	kiwi gb166 FG3 96354_T1	kiwi	3101	30	90	98.2638 8889	98.9510 4895	blastp
2894	kiwi gb166 FG4 04890_T1	kiwi	3102	30	85	72.2222 2222	99.5215 311	blastp
2895	kiwi gb166 FG4 17962_T1	kiwi	3103	30	87	62.1527 7778	99.4444 4444	blastp
2896	kiwi gb166 FG4 03188_T1	kiwi	3104	30	89	98.2638 8889	96.9178 0822	blastp
2897	kiwi gb166 FG4 03647_T1	kiwi	3105	30	85	68.0555 5556	99.4923 8579	blastp
2898	kiwi gb166 FG3 97405_T1	kiwi	3106	30	85	98.2638 8889	99.3006 993	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
2899	leymus gb166 E G384635_T1	leymus	3107	30	85	99.3055 5556	99.6551 7241	blastp
2900	leymus gb166 C N466016_T1	leymus	3108	30	83	98.2638 8889	98.9726 0274	blastp
2901	leymus gb166 C N466006_T1	leymus	3109	30	83	98.2638 8889	98.9726 0274	blastp
2902	leymus gb166 E G376500_T1	leymus	3110	30	83	98.2638 8889	98.9726 0274	blastp
2903	liriodendron gb1 66 CK749885_T 1	liriodend ron	3111	30	89	98.2638 8889	98.9547 0383	blastp
2904	liriodendron gb1 66 CV002697_T 1	liriodend ron	3112	30	88	98.2638 8889	98.9547 0383	blastp
2905	lovegrass gb167 DN480914_T1	lovegrass	3113	30	85	98.2638 8889	98.9619 3772	blastp
2906	nuphar gb166 C D472824_T1	nuphar	3114	30	86	98.2638 8889	98.9473 6842	blastp
2907	nuphar gb166 C D472574_T1	nuphar	3115	30	86	98.2638 8889	98.9473 6842	blastp
2908	nuphar gb166 C D473614_T1	nuphar	3116	30	84	51.7361 1111	98.0263 1579	blastp
2909	peanut gb167 ES 759056_T1	peanut	3117	30	83	64.2361 1111	100	blastp
2910	poppy gb166 FE 966578_T1	poppy	3118	30	83	98.6111 1111	98.6206 8966	blastp
2911	pseudoroegneria gb167 FF344096 _T1	pseudoro egneria	3119	30	82	98.2638 8889	98.9726 0274	blastp
2912	pseudoroegneria gb167 FF346975 _T1	pseudoro egneria	3120	30	85	98.6111 1111	98.6254 2955	blastp
2913	pseudoroegneria gb167 FF342094 _T1	pseudoro egneria	3121	30	83	98.2638 8889	98.9726 0274	blastp
2914	soybean gb167 C A898412_T1	soybean	3122	30	84	94.4444 4444	95.0877 193	blastp
2915	switchgrass gb16 7 FE621985_T1	switchgr ass	3123	30	87	52.4305 5556	98.6928 1046	blastp
2916	switchgrass gb16 7 DN141371_T1	switchgr ass	3124	30	86	98.2638 8889	98.9583 3333	blastp
2917	tamarix gb166 C F199714_T1	tamarix	3125	30	88	78.4722 2222	99.1228 0702	blastp
2918	tamarix gb166 C F226851_T1	tamarix	3126	30	85	98.2638 8889	99.3031 3589	blastp
2919	walnuts gb166 C B303847_T1	walnuts	3127	30	84	98.2638 8889	99.3103 4483	blastp
2920	walnuts gb166 C V194951_T1	walnuts	3128	30	86	98.2638 8889	99.3031 3589	blastp
2921	walnuts gb166 C V196162_T1	walnuts	3129	30	85	98.2638 8889	99.3150 6849	blastp
2922	zamia gb166 FD 765004_T1	zamia	3130	30	84	98.2638 8889	98.9547 0383	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organism</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
2923	antirrhinum gb166 AJ799752_T1	antirrhinum	3131	31	80	98.7854 251	100	blastp
2924	kiwi gb166 FG400670_T1	kiwi	3132	31	82	74.0890 6883	100	blastp
2925	kiwi gb166 FG418275_T1	kiwi	3133	31	83	98.7854 251	98.3870 9677	blastp
2926	centaurea gb166 EL931588_T1	centaurea	3134	34	83	88.5714 2857	32.7402 1352	blastp
2927	soybean gb167 AW119586_T1	soybean	3135	34	83	94.2857 1429	36.2637 3626	blastp
2928	soybean gb167 AW573764_T1	soybean	3136	34	83	94.2857 1429	36.6666 6667	blastp
2929	amborella gb166 FD440187_T1	amborella	3137	35	81	65.7627 1186	100	blastp
2930	centaurea gb166 EL931433_T1	centaurea	3138	35	82	97.6271 1864	96.6101 6949	blastp
2931	eucalyptus gb166 CD668486_T1	eucalyptus	3139	35	85	73.8983 0508	100	blastp
2932	petunia gb166 D243166_T1	petunia	3140	36	86	100	100	blastp
2933	amborella gb166 CD482946_T1	amborella	3141	39	82	99.6415 7706	98.9399 2933	blastp
2934	antirrhinum gb166 AJ559435_T1	antirrhinum	3142	39	88	99.2831 5412	98.5765 1246	blastp
2935	antirrhinum gb166 AJ793990_T1	antirrhinum	3143	39	89	71.3261 6487	100	blastp
2936	antirrhinum gb166 AJ559760_T1	antirrhinum	3144	39	83	61.2903 2258	87.2448 9796	blastp
2937	antirrhinum gb166 AJ558545_T1	antirrhinum	3145	39	88	88.5304 6595	100	blastp
2938	bean gb167 FE682762_T1	bean	3146	39	86	100	100	blastp
2939	bean gb167 CV531088_T1	bean	3147	39	86	99.6415 7706	98.9473 6842	blastp
2940	bean gb167 CA907460_T1	bean	3148	39	86	99.6415 7706	98.9473 6842	blastp
2941	cenchrus gb166 EB655519_T1	cenchrus	3149	39	83	97.4910 3943	95.8620 6897	blastp
2942	centaurea gb166 EL934360_T1	centaurea	3150	39	88	53.7634 4086	96.1538 4615	blastp
2943	centaurea gb166 EH751120_T1	centaurea	3151	39	80	88.5304 6595	100	blastp
2944	centaurea gb166 EH752971_T1	centaurea	3152	39	87	83.5125 448	100	blastp
2945	centaurea gb166 EH768434_T1	centaurea	3153	39	80	91.7562 724	99.6168 5824	blastp
2946	centaurea gb166 EH767287_T1	centaurea	3154	39	83	83.1541 2186	100	blastp
2947	cichorium gb166 DT212008_T1	cichorium	3155	39	82	89.9641 5771	100	blastp
2948	cichorium gb166 EL354583_T1	cichorium	3156	39	84	86.7383 5125	97.6190 4762	blastp

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2949	eucalyptus gb166 CD668553_T1	eucalyptus	3157	39	87	83.8709 6774	100	blastp
2950	eucalyptus gb166 CD668534_T1	eucalyptus	3158	39	80	69.8924 7312	100	blastp
2951	eucalyptus gb166 CD668523_T1	eucalyptus	3159	39	88	100	99.3006 993	blastp
2952	eucalyptus gb166 CD669942_T1	eucalyptus	3160	39	83	100	100	blastp
2953	kiwi gb166 FG405216_T1	kiwi	3161	39	84	100	99.2932 8622	blastp
2954	kiwi gb166 FG495821_T1	kiwi	3162	39	86	50.1792 1147	100	blastp
2955	kiwi gb166 FG417997_T1	kiwi	3163	39	86	64.5161 2903	100	blastp
2956	kiwi gb166 FG403725_T1	kiwi	3164	39	83	73.1182 7957	100	blastp
2957	kiwi gb166 FG397310_T1	kiwi	3165	39	88	100	100	blastp
2958	kiwi gb166 FG408531_T1	kiwi	3166	39	83	100	99.3031 3589	blastp
2959	leymus gb166 EG381236_T1	leymus	3167	39	81	55.5555 5556	97.4683 5443	blastp
2960	leymus gb166 EG376087_T1	leymus	3168	39	80	96.7741 9355	96.5517 2414	blastp
2961	leymus gb166 CD808804_T1	leymus	3169	39	81	100	100	blastp
2962	leymus gb166 EG378918_T1	leymus	3170	39	86	51.2544 8029	100	blastp
2963	liriodendron gb166 CK761396_T1	liriodendron	3171	39	81	99.6415 7706	98.9619 3772	blastp
2964	nuphar gb166 ES730700_T1	nuphar	3172	39	81	61.2903 2258	98.2758 6207	blastp
2965	poppy gb166 FE965621_T1	poppy	3173	39	84	88.5304 6595	100	blastp
2966	pseudoroegneria gb167 FF340233_T1	pseudoroegneria	3174	39	81	100	100	blastp
2967	switchgrass gb167 FE638368_T1	switchgrass	3175	39	80	100	100	blastp
2968	switchgrass gb167 FE657460_T1	switchgrass	3176	39	80	99.2831 5412	98.9583 3333	blastp
2969	switchgrass gb167 FE641178_T1	switchgrass	3177	39	82	78.8530 4659	86.5900 3831	blastp
2970	switchgrass gb167 FE619224_T1	switchgrass	3178	39	82	94.2652 3297	95.7295 3737	blastp
2971	switchgrass gb167 FE657460_T2	switchgrass	3179	39	81	100	100	blastp
2972	tamarix gb166 EH051524_T1	tamarix	3180	39	82	56.2724 0143	98.7421 3836	blastp
2973	walnuts gb166 CB304207_T1	walnuts	3181	39	84	100	99.3031 3589	blastp

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2974	walnuts gb166 C B303561 T1	walnuts	3182	39	84	100	100	blastp
2975	walnuts gb166 E L892579 T1	walnuts	3183	39	84	89.6057 3477	98.8235 2941	blastp
2976	zamia gb166 DY 032141 T1	zamia	3184	39	80	96.0573 4767	94.3262 4113	blastp
2977	zamia gb166 FD 764669 T1	zamia	3185	39	80	99.6415 7706	98.9247 3118	blastp
2978	zamia gb166 DY 034152 T1	zamia	3186	39	80	94.6236 5591	92.2535 2113	blastp
2979	antirrhinum gb16 6 AJ568195 T1	antirrhin um	3187	40	87	100	100	blastp
2980	antirrhinum gb16 6 AJ568110 T1	antirrhin um	3188	40	87	100	100	blastp
2981	banana gb167 FL 657842 T1	banana	3189	40	81	83.0388 6926	92.4901 1858	blastp
2982	bruguiera gb166 EF126757 T1	bruguier a	3190	40	84	100	100	blastp
2983	centaurea gb166 EH765776 T1	centaure a	3191	40	84	92.5795 053	100	blastp
2984	eucalyptus gb16 6 AJ627837 T1	eucalypt us	3192	40	85	100	100	blastp
2985	kiwi gb166 FG4 11924 T1	kiwi	3193	40	86	100	100	blastp
2986	kiwi gb166 FG4 00706 T1	kiwi	3194	40	85	100	100	blastp
2987	kiwi gb166 FG4 18898 T1	kiwi	3195	40	84	71.0247 3498	98.5	blastp
2988	kiwi gb166 FG4 20187 T1	kiwi	3196	40	85	72.7915 1943	100	blastp
2989	kiwi gb166 FG3 98010 T1	kiwi	3197	40	86	100	100	blastp
2990	petunia gb166 A F452012 T1	petunia	3198	40	88	100	100	blastp
2991	tamarix gb166 C V121772 T1	tamarix	3199	40	83	100	100	blastp
2992	walnuts gb166 E L893208 T1	walnuts	3200	40	84	100	100	blastp
2993	bean gb167 FD7 86218 T1	bean	3201	41	83	58.6092 7152	100	blastp
2994	citrus gb166 CX 074333 T2	citrus	3202	41	81	72.5165 5629	99.5412 844	blastp
2995	citrus gb166 CX 074333 T1	citrus	3203	41	83	96.0264 9007	91.4285 7143	blastp
2996	kiwi gb166 FG4 20468 T2	kiwi	3204	41	84	87.0860 9272	97.0479 7048	blastp
2997	kiwi gb166 FG4 20468 T1	kiwi	3205	41	83	58.9403 9735	95.6989 2473	blastp
2998	tamarix gb166 E G972096 T1	tamarix	3206	42	82	60.9756 0976	95.2380 9524	blastp
2999	pseudoroegneria gb167 FF353501 T1	pseudoro egneria	3207	43	86	98.3935 743	98.7951 8072	blastp

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3000	switchgrass gb167 FE646459_T1	switchgrass	3208	43	86	98.7951 8072	99.1967 8715	blastp
3001	switchgrass gb167 FL887003_T1	switchgrass	3209	43	84	71.4859 4378	93.2291 6667	blastp
3002	wheat gb164 BE403397_T1	wheat	3210	43	86	98.3935 743	98.7951 8072	blastp
3003	leymus gb166 EG381168_T1	leymus	3211	44	96	52.0161 2903	100	blastp
3004	pseudoroegneria gb167 FF341567_T1	pseudoroegneria	3212	44	97	100	100	blastp
3005	switchgrass gb167 FE618822_T1	switchgrass	3213	44	91	100	100	blastp
3006	switchgrass gb167 FE633786_T1	switchgrass	3214	44	92	78.2258 0645	100	blastp
3007	eucalyptus gb166 CB967586_T1	eucalyptus	3215	46	84	97.5155 2795	60.7843 1373	blastp
3008	liriodendron gb166 CK762443_T1	liriodendron	3216	46	80	74.5341 6149	100	blastp
3009	switchgrass gb167 FE615387_T1	switchgrass	3217	46	90	100	61.3899 6139	blastp
3010	walnuts gb166 EL893973_T1	walnuts	3218	46	82	97.5155 2795	55.4744 5255	blastp
3011	bean gb167 FD782805_T1	bean	3219	47	91	88.1720 4301	79.6116 5049	blastp
3012	bean gb167 EY457935_T1	bean	3220	47	82	100	38.5892 1162	blastp
3013	cichorium gb166 EH685648_T2	cichorium	3221	47	80	100	67.3913 0435	blastp
3014	cichorium gb166 EH685648_T1	cichorium	3222	47	80	100	32.1799 308	blastp
3015	citrus gb166 CK701147_T1	citrus	3223	47	90	100	76.8595 0413	blastp
3016	citrus gb166 CX544905_T1	citrus	3224	47	81	79.5698 9247	88.0952 381	blastp
3017	cycas gb166 CB088978_T1	cycas	3225	47	82	87.0967 7419	30.6818 1818	blastp
3018	cycas gb166 EX920749_T1	cycas	3226	47	88	100	76.2295 082	blastp
3019	kiwi gb166 FG429765_T1	kiwi	3227	47	84	98.9247 3118	77.9661 0169	blastp
3020	leymus gb166 CN466394_T1	leymus	3228	47	87	100	79.4871 7949	blastp
3021	leymus gb166 EG376019_T1	leymus	3229	47	88	100	32.7464 7887	blastp
3022	leymus gb166 EG390723_T1	leymus	3230	47	81	100	31.9587 6289	blastp
3023	leymus gb166 EG387193_T1	leymus	3231	47	81	100	32.1799 308	blastp
3024	nuphar gb166 CD473277_T1	nuphar	3232	47	91	100	75.6097 561	blastp

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3025	nuphar gb166 F D384794_T1	nuphar	3233	47	86	96.7741 9355	81.0810 8108	blastp
3026	nuphar gb166 C D475538_T1	nuphar	3234	47	89	100	69.9248 1203	blastp
3027	nuphar gb166 C D472711_T1	nuphar	3235	47	91	100	48.9473 6842	blastp
3028	petunia gb166 D C240378_T1	petunia	3236	47	92	58.0645 1613	98.1818 1818	blastp
3029	pseudoroegneria gb167 FF344283 _T1	pseudoro egneria	3237	47	87	100	32.7464 7887	blastp
3030	sorghum gb161.c rp AI724931_T1	sorghum	3238	47	92	100	32.5174 8252	blastp
3031	switchgrass gb16 7 FL923354_T1	switchgr ass	3239	47	82	100	33.6956 5217	blastp
3032	switchgrass gb16 7 FE657461_T1	switchgr ass	3240	47	92	98.9247 3118	74.7967 4797	blastp
3033	switchgrass gb16 7 FL765830_T1	switchgr ass	3241	47	82	100	72.2222 2222	blastp
3034	switchgrass gb16 7 FL915169_T1	switchgr ass	3242	47	83	97.8494 6237	87.5	blastp
3035	tamarix gb166 E H054604_T1	tamarix	3243	47	83	100	65.6470 5882	tblastn
3036	walnuts gb166 C B303798_T1	walnuts	3244	47	91	100	80.1724 1379	blastp
3037	bruguiera gb166 BP942548_T1	bruguier a	3245	48	82	52.0547 9452	100	blastp
3038	bruguiera gb166 BP938825_T1	bruguier a	3246	48	89	56.6210 0457	91.1764 7059	blastp
3039	centaurea gb166 EH739326_T1	centaure a	3247	48	83	87.2146 1187	50	tblastn
3040	eucalyptus gb16 6 CD669176_T1	eucalypt us	3248	48	87	56.1643 8356	91.7910 4478	blastp
3041	leymus gb166 E G382428_T1	leymus	3249	48	80	52.0547 9452	90.4761 9048	blastp
3042	liriodendron gb1 66 CK743477_T 1	liriodend ron	3250	48	81	94.0639 2694	54.5454 5455	tblastn
3043	marchantia gb16 6 BJ840587_T1	marchant ia	3251	48	83	94.0639 2694	72.5352 1127	blastp
3044	marchantia gb16 6 C96070_T1	marchant ia	3252	48	83	93.1506 8493	71.5789 4737	blastp
3045	nuphar gb166 C K748374_T1	nuphar	3253	48	82	65.7534 2466	99.3103 4483	blastp
3046	pseudoroegneria gb167 FF340047 _T1	pseudoro egneria	3254	48	81	96.8036 5297	73.4482 7586	blastp
3047	pseudoroegneria gb167 FF340899 _T1	pseudoro egneria	3255	48	81	96.8036 5297	73.4482 7586	blastp
3048	pseudoroegneria gb167 FF352644 _T1	pseudoro egneria	3256	48	82	96.8036 5297	74.1258 7413	blastp

<i>Polynuc. SEQ ID NO:</i>	<i>Cluster name</i>	<i>Organis m</i>	<i>Polypep. SEQ ID NO:</i>	<i>Hom. of SEQ ID NO:</i>	<i>% Ident.</i>	<i>Query cover.</i>	<i>% Subject cover.</i>	<i>Algorith m</i>
3049	sorghum gb161.c rp SBGWP0301 88_T1	sorghum	3257	48	80	96.8036 5297	74.1258 7413	blastp
3050	switchgrass gb16 7 FL718379_T1	switchgr ass	3258	48	81	96.8036 5297	74.1258 7413	blastp
3051	switchgrass gb16 7 FE639195_T1	switchgr ass	3259	48	82	96.8036 5297	73.1034 4828	blastp

Table 3: Homologues and orthologues of the AQP proteins are provided. Homology was calculated as % of identity over the aligned sequences. Polynuc. = Polynucleotide; Polypep. = Polypeptide; Hom. = Homologues/Orthologues; % Ident. = percent identity; Cover. = coverage.

5

EXAMPLE 2

mRNA EXPRESSION OF IN-SILICO EXPRESSED POLYNUCLEOTIDES

Messenger RNA levels were determined using reverse transcription assay followed by quantitative Real-Time PCR (qRT-PCR) analysis. RNA levels were compared between leaves of 20 days old seedlings of tomato plants grown under salinity water. A correlation analysis between mRNA levels in different experimental conditions/genetic backgrounds was performed in order to determine the role of the gene in the plant.

Materials and Experimental Methods

Quantitative Real Time RT-PCR (qRT-PCR) - To verify the level of expression, specificity and trait-association, Reverse Transcription followed by quantitative Real-Time PCR (qRT-PCR) was performed on total RNA extracted from leaves of 2 tomato varieties namely YO361 (salt tolerant variety) and FA191 (salt sensitive variety). Messenger RNA (mRNA) levels were determined for AQP genes, expressed under normal and stressed conditions.

Twenty days-old tomato seedlings were grown in soil and soaked with 300 mM NaCl for 0, 1, 6, 24, 118 hours. Leaves were harvested and frozen in liquid nitrogen and then kept at -80 °C until RNA extraction. Total RNA was extracted from leaves using RNeasy plant mini kit (Qiagen, Hilden, Germany) and by using the protocol provided by the manufacturer. Reverse transcription was performed using 1 µg total RNA, using 200 U Super Script II Reverse Transcriptase enzyme (Invitrogen), 150 ng random deoxynucleotide hexamers (Invitrogen), 500 µM deoxynucleotide tri-phosphates (dNTPs) mix (Takara, Japan), 0.2 volume of x5 reverse transcriptase (RT) buffer

15

20

25

(Invitrogen), 0.01 M dithiothreitol (DTT), 40 U RNAsin (Promega), diethylpyrocarbonate (DEPC) treated double distilled water (DDW) was added up to 24 μ l.

Mix of RNA, random deoxynucleotide hexamers, dNTPs mix and DEPC treated DDW was incubated at 65 °C for 5 minutes, followed by 4 °C for 5 minutes. Mix of reverse transcriptase (RT) buffer, dithiothreitol (DTT) and RNAsin was added to the RT reactions followed by incubation at 25 °C for 10 minutes and at 42 °C for 2 minutes afterwards. Finally, Super Script II Reverse Transcriptase enzyme was added to the RT reactions that were further incubated for 50 minutes at 42 °C, followed by 70 °C for 15 minutes.

cDNA was diluted 1:20 in Tris EDTA, pH = 7.5 for MAB69 and housekeeping genes. For MAB58 and MAB59 cDNA was diluted 1:2 due to very weak expression and consequently for housekeeping genes cDNA was diluted 1:8 in order to insert the Ct values in calibration curve range. 5 μ L of the diluted cDNA was used for qPCR.

For qPCR amplification, primers of the AQP genes were designed, as summarized in Table 4 below. The expression level of the housekeeping genes: Actin (SEQ ID NO: 2841), GAPDH (SEQ ID NO: 2842) and RPL19 (SEQ ID NO: 2747) was determined in order to normalize the expression level between the different tissues.

20

Table 4
Primers for qPCR amplification

<i>Gene</i>	<i>Forward primer SEQ ID NO:</i>	<i>Forward primer sequence (5'→3')</i>	<i>Reverse primer SEQ ID NO:</i>	<i>Reverse primer sequence (5'→3')</i>
MAB58	2829	CTTTTGGTAGGGCCGATGA AG	2830	CGAAGATGAAGGTGG ATAAGAGCT
MAB59	2831	CAGTATGAACGTCTCCGGT GG	2832	CAACAGCACCTAGCAA CTGACC
MAB69	2833	TGTCTTGGATTCCATTGAG CACT	2834	GTTTGAGCTGCTGTCC CCA
Actin (SEQ ID NO: 2841)	2835	CCACATGCCATTCTCCGTC T	2836	GCTTTTCTTTCACGTCC CTGA
GAPD H (SEQ ID NO: 2842)	2837	TTGTTGTGGGTGTCAACGA GA	2838	ATGGCGTGGACAGTGG TCA

<i>Gene</i>	<i>Forward primer SEQ ID NO:</i>	<i>Forward primer sequence (5'→3')</i>	<i>Reverse primer SEQ ID NO:</i>	<i>Reverse primer sequence (5'→3')</i>
RPL19 (SEQ ID NO: 2747)	2839	CACTCTGGATATGGTAAGC GTAAGG	2840	TTCTTGGACTCCCTGTA CTTACGA

Table 4.

Experimental Results

Changes in mRNA levels of AQP genes in leaves of plants under salt tolerance

- 5 – Steady state levels of tomato AQP genes in leaves of tolerant versus sensitive lines, under salinity conditions are summarized in Table 5 below. In all 3 cases, aquaporin gene expression was increased after plant was exposed to salt stress. Gene peak expression was higher in the salt tolerance tomato line (YO361) versus the sensitive line (FA191). The elevated gene expression demonstrates the involvement of the tested AQP
- 10 genes in tomato plants tolerating high salinity.

Table 5
Expression levels of tomato AQP genes

Well name (cDNA)	MAB58	MAB59	MAB69*
leaf FA191 0 h	2.86	5.97	875
leaf FA191 1 h	4.56	5.73	597
leaf FA191 6 h	5.34	8.2	945
leaf FA191 24 h	42.7	62.4	613
leaf FA191 118 h	55.4	22.2	1800
leaf YO361 0 h	1.96	2.81	638
leaf YO361 1 h	2.33	0.517	583
leaf YO361 6 h	2.88	5.66	464
leaf YO361 24 h	75.4	139	513
leaf YO361 118 h	26.3	Not determined	2300

- 15 **Table 5:** Provided are the steady state levels of tomato AQP genes under salinity conditions [the incubation periods in the salt solution are provided in hours (h)]. Different dilutions of cDNA were used (1:20 for MAB69 and 1:2 for MAB58 and MAB59). Numbers are given after normalization for each sample.

EXAMPLE 3**GENE CLONING AND GENERATION OF BINARY VECTORS FOR PLANT
EXPRESSION**

To validate their role in improving ABST and yield, the AQP genes were over-
5 expressed in plants, as follows.

Cloning strategy

Selected genes from those presented in Example 1 were cloned into binary
vectors for the generation of transgenic plants. For cloning, the full-length open reading
frames (ORFs) were identified. EST clusters and in some cases mRNA sequences were
10 analyzed to identify the entire open reading frame by comparing the results of several
translation algorithms to known proteins from other plant species. In case where the
entire coding sequence is not found, RACE kits from Ambion or Clontech (RACE =
Rapid Access to cDNA Ends) were used to prepare RNA from the plant samples to
thereby access the full cDNA transcript of the gene.

15 In order to clone the full-length cDNAs, Reverse Transcription followed by PCR
(RT-PCR) was performed on total RNA extracted from leaves, roots or other plant
tissues, growing under either normal or nutrient deficient conditions. Total RNA
extraction, production of cDNA and PCR amplification was performed using standard
protocols described elsewhere (Sambrook J., E.F. Fritsch, and T. Maniatis. 1989.
20 Molecular Cloning. A Laboratory Manual., 2nd Ed. Cold Spring Harbor Laboratory
Press, New York.), and are basic for those skilled in the art. PCR products were purified
using PCR purification kit (Qiagen) and sequencing of the amplified PCR products was
performed, using ABI 377 sequencer (Applied Biosystems).

Usually, 2 sets of primers were ordered for the amplification of each gene, via
25 nested PCR (meaning first amplifying the gene using external primers and then using the
produced PCR product as a template for a second PCR reaction, where the internal set of
primers are used). Alternatively, one or two of the internal primers were used for gene
amplification, both in the first and the second PCR reactions (meaning only 2-3 primers
were designed for a gene). To facilitate further cloning of the cDNAs, a 8-12 bp
30 extension is added to the 5' primer end of each internal primer. The primer extension
includes an endonuclease restriction site. The restriction sites are selected using two
parameters: (a) The restriction site does not exist in the cDNA sequence; and (b) The

restriction sites in the forward and reverse primers are designed so the digested cDNA is inserted in the sense formation into the binary vector utilized for transformation. In Table 6 below, primers used for cloning tomato and barley AQPs are provided.

5

Table 6
Primers used for cloning tomato and barley AQP genes

MAB gene No.	Forward external primer sequence from 5'→3' (SEQ ID NO:)	Forward internal primer sequence from 5'→3' (SEQ ID NO:)	Reverse external primer sequence from 5'→3' (SEQ ID NO:)	Reverse internal primer sequence from 5'→3' (SEQ ID NO:)
55	GGAGTCGACGACCAT CAAGTTTAAAGTGAC TTC (2770)	GGAGTCGACTT AAGTACATTCTT TAGTGAGAGCC (2771)	TGAGCTCACTTC AAAACCATCCG TTGTC (2772)	TGAGCTCCCATCC GTTGTCAAAATGA AC (2773)
56		GGAGTCGACGT AAGAAACAATA ATGCCAATTTT (2774)	CGAGCTCGTAA AGCCAAGTTTTG AAAGAC (2775)	CGAGCTCAAGAC AAACAAAGAGAA GAGGG (2776)
57		GTAAAAATGC CGATCAACC (2777)	GCGATATCTAA ATAACAAAAGC CGTCCG (2778)	GCGATATCAGCCG TCCGAATAAACAA AG (2779)
58	AATGTCGACCGAATT GATCTCCTTCTTGATC (2780)	TATGTCGACTTC ATTTCTTGGGTC ACTCG (2781)	TTTCTAGAGGTC TGGGATTATCGT CTTG (2782)	TTTCTAGAGATGT GCAGGCAGCTAC ATAC (2783)
59	AATGTCGACTTTAAG CGGTGTGTTTTGTG (2784)	AATGTCGACTC ACAATTATGCA GCCACG (2785)		AATCTAGATTAGA CCCAAACATACAA ACTTCAC (2786))
69	TAAGTCGACACAAAC CTTATCCTGGTCTCAT C (2787)	AATGTCGACCTT GGATTCCATTGA GCACTC (2788)		TGAGCTCTGGAGA AAGAAAACCTTAG ATACA (2789)
70	AACTGCAGAGCTGTA CATGGTCCTCCTCC (2790)	AACTGCAGTGT ACATGGTCCTCC TCCG (2791)	TCCCGGGCCAG ACAAAACCTCA ATTTTCATC (2792)	TCCCGGGCTTCAA TTTCATCTTCTGA TTTC (2793)
71	AAAGTCGACGGAAAA TGCATTAAACCTTA AG (2794)	TTTGTGACCTT AGTTTTCTCCCA CATATGG (2795)	AATCTAGACAA GTAGAGGTACT AGGTAGGGAC (2796)	AATCTAGAGTACT AGGTAGGGACAA TATGATATG (2797)
72	AATGTCGACGTGGAG GAGGAGTCTTTGATA C (2798)	AATGTCGACCTC CAACACTCTTAT CAATTACCA (2799)		TATCTAGAGGATG CAACTACAAAGA AATTG (2800)
74		TTCTGCAGGTTT GGGAGTTATTG ATCTAAGATG (2801)		TCCCGGGGCATAG TTCACACAGAGCA AATC (2802)
76	AATGTCGACCTGTAT CCTCTTAAGTATGAA TCG (2803)	AATGTCGACGT CGTCTTGATGT ATTTGTACTACT G (2804)	TTTCTAGACTAG TGGTATAGATC ATTTTATGGTGA C (2805)	AATCTAGATTAGA GCTGGAGAATGA ACTGAAGC (2806)
77	AACTGCAGCTTCTTTC ACCGAGTGGGAG (2807)	AACTGCAGCTTT CACCGAGTGGG AGAG (2808)	ACCCGGGAATT CCAAGTAGCTGT TATGATTC (2809)	TCCCGGGTCCAAC TAGCTGTTATGAT TCTG (2810)

<i>MAB gene No.</i>	<i>Forward external primer sequence from 5'→3' (SEQ ID NO:)</i>	<i>Forward internal primer sequence from 5'→3' (SEQ ID NO:)</i>	<i>Reverse external primer sequence from 5'→3' (SEQ ID NO:)</i>	<i>Reverse internal primer sequence from 5'→3' (SEQ ID NO:)</i>
79	AAGATATCAAAAAA TGTCGAAGGACGTG (2811)	AAGATATCAAC AATGTCGAAGG ACGTGATTGA (2812)		AAGATATCGACCA CCAAGTCTAGTCT CATACC (2813)
115	AGATTCGAATCTTTA GCCTG (2814)	AATCTAGAGAA GTCACAGAGAA AACAGTCGAG (2815)		AGAGCTCTTAAGG GAAATTCATCACA CAAGG (2816)
116	AAAGTCGACCTCATC AGTGTAAAGCCATA AG (2817)	TTTGTGACCAT AAGCCCTCTTTG AGTGTG (2818)	TATCTAGAATTG AATCGAAAGGG AAACAC (2819)	TTTCTAGAGACCG TGACACACCATT GTAC (2820)
117		TTTCTAGACTCA GCGACAACATT TCATCTC (2821)		TGAGCTCCAGATA GAGAAGCATGCA TCATC (2822)

Table 6.

PCR products were purified (PCR Purification Kit, Qiagen, Germany) and digested with the restriction endonucleases (Roche, Switzerland) according to the sites design in the primers (Tables 8 and 9 below). Each of the digested PCR products was cloned first into high copy plasmid pBlue-script KS [Hypertext Transfer Protocol://World Wide Web (dot) stratagene (dot) com/manuals/212205 (dot) pdf] which was digested with the same restriction enzymes. In some cases (Table 8, below) the Nopaline Synthase (NOS) terminator originated from the binary vector pBI101.3 [nucleotide coordinates 4417-4693 in GenBank Accession No. U12640 (SEQ ID NO:2824)] was already cloned into the pBlue-script KS, between the restriction endonuclease sites *SacI* and *EcoRI*, so the gene is introduced upstream of the terminator. In other cases (Table 9, below) the At6669 promoter (SEQ ID NO: 2823) is already cloned into the pBlue-script KS, so the gene is introduced downstream of the promoter. The digested PCR products and the linearized plasmid vector were ligated using T4 DNA ligase enzyme (Roche, Switzerland). Sequencing of the inserted genes was conducted, using ABI 377 sequencer (Applied Biosystems). Sequences of few of the cloned AQP genes, as well as their encoded proteins are listed in Table 7, below.

Table 7: Cloned sequences

Serial No	Gene Name	Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:
1	MAB115	2748	2765
2	MAB116	2749	47
3	MAB117	2750	48
4	MAB54	2751	27
5	MAB55	2752	28
6	MAB56	2753	29
7	MAB57	2754	30
8	MAB58	2755	2766
9	MAB59	2756	2767
10	MAB69	2757	33
11	MAB70	2758	34
12	MAB71	2759	2768
13	MAB72	2760	2769
14	MAB72 (Optimized for expression in Arabidopsis, Tomato and Maize)	2843	2769
15	MAB74	2761	38
16	MAB76	2762	40
17	MAB77	2763	41
18	MAB79	2764	43

Table 7.

The genes were digested again and ligated into pPI or pGI binary plasmids, harboring the At6669 promoter (between the *HindIII* and *SalI* restriction endonucleases site) (Table 8). In other cases the At6669 promoter together with the gene are digested out of the pBlue-script KS plasmid and ligated into pPI or pGI binary plasmids, using restriction endonucleases as given in Table 8.

Table 8

Restriction enzyme sites used to clone the MAB AQP genes into pKS+NOS terminator high copy plasmid, followed by cloning into the binary vector pGI+At6669 promoter

MAB gene No. (SEQ ID NO:)	Restriction enzymes used for cloning into high copy plasmid-FORWARD	Restriction enzymes used for cloning into high copy plasmid-REVERSE	Restriction enzymes used for cloning into binary vector-FORWARD	Restriction enzymes used for cloning into binary vector-REVERSE	Restriction enzymes used for digesting the binary vector
54 (SEQ ID NO:2751)	XbaI	SacI	SalI	EcoRI	SalI/EcoRI
55 (SEQ ID NO:2752)	SalI	SacI	SalI	EcoRI	SalI/EcoRI

MAB gene No. (SEQ ID NO:)	Restriction enzymes used for cloning into high copy plasmid-FORWARD	Restriction enzymes used for cloning into high copy plasmid-REVERSE	Restriction enzymes used for cloning into binary vector-FORWARD	Restriction enzymes used for cloning into binary vector-REVERSE	Restriction enzymes used for digesting the binary vector
56 (SEQ ID NO:2753)	Sall	SacI	Sall	EcoRI	Sall/EcoRI
58 (SEQ ID NO:2755)	Sall	XbaI	Sall	EcoRI	Sall/EcoRI
59 (SEQ ID NO:2756)	Sall	XbaI	Sall	EcoRI	Sall/EcoRI
69 (SEQ ID NO:2757)	Sall	SacI	Sall	EcoRI	Sall/EcoRI
71 (SEQ ID NO:2759)	Sall	XbaI	Sall	EcoRI	Sall/EcoRI
72 (SEQ ID NO:2760)	Sall	XbaI	Sall	EcoRI	Sall/EcoRI
76 (SEQ ID NO:2762)	Sall	XbaI	Sall	EcoRI	Sall/EcoRI
115 (SEQ ID NO:2748)	XbaI	SacI	Sall	EcoRI	Sall/EcoRI
116 (SEQ ID NO:2749)	Sall	XbaI	Sall	EcoRI	Sall/EcoRI
117 (SEQ ID NO:2750)	XbaI	SacI	Sall	EcoRI	Sall/EcoRI

Table 8: MAB AQP genes cloned into pKS+NOS terminator high copy plasmid, followed by cloning into the binary vector pGI+At6669 promoter.

Table 9

5 **Restriction enzyme sites used to clone the MAB AQP genes into pKS+At6669 promoter high copy plasmid, followed by cloning promoter+gene into pGI binary vector**

MAB gene No. (SEQ ID NO:)	Restriction enzymes used for cloning into high copy plasmid-FORWARD	Restriction enzymes used for cloning into high copy plasmid-REVERSE	Restriction enzymes used for cloning into binary vector-FORWARD	Restriction enzymes used for cloning into binary vector-REVERSE	Restriction enzymes used for digesting the binary vector
57 (SEQ ID NO:2754)	Blunt	EcoRV	Sall	EcoRV	Sall /Ecl136 II

MAB gene No. (SEQ ID NO:)	<i>Restriction enzymes used for cloning into high copy plasmid- FORWARD</i>	<i>Restriction enzymes used for cloning into high copy plasmid- REVERSE</i>	<i>Restriction enzymes used for cloning into binary vector- FORWARD</i>	<i>Restriction enzymes used for cloning into binary vector- REVERSE</i>	<i>Restriction enzymes used for digesting the binary vector</i>
70 (SEQ ID NO:2758)	PstI	SmaI	BamHI	SmaI	BamHI /Ecl136II
74 (SEQ ID NO:2761)	PstI	SmaI	BamHI	SmaI	BamHI /Ecl136II
77 (SEQ ID NO:2763)	PstI	SmaI	BamHI	SmaI	BamHI /Ecl136II
79 (SEQ ID NO:2764)	EcoRI	EcoRV	Sall	SmaI	Sall /Ecl136 II

Table 9: MAB AQP genes cloned into pKS+At6669 promoter high copy plasmid, followed by cloning promoter+gene into pGI binary vector.

The pPI plasmid vector was constructed by inserting a synthetic poly-(A) signal
 5 sequence, originating from pGL3 basic plasmid vector (Promega, Acc. No. U47295; bp
 4658-4811) into the *Hind*III restriction site of the binary vector pBI101.3 (Clontech,
 Acc. No. U12640). pGI (Figure 1) is similar to pPI, but the original gene in the back
 bone is GUS-Intron, rather than GUS. The cloned genes were sequenced.

Synthetic sequences (such as of MAB54, nucleotide SEQ ID NO: 2751, which
 10 encodes protein SEQ ID NO: 27; or MAB72 SEQ ID NO:2843, which encodes SEQ ID
 NO:2769) of some of the cloned polynucleotides were ordered from a commercial
 supplier (GeneArt, GmbH). To optimize the coding sequence, codon-usage Tables
 calculated from plant transcriptomes were used [example of such Tables can be found in
 the Codon Usage Database available online at Hypertext Transfer Protocol://World
 15 Wide Web (dot) kazusa (dot) or (dot) jp/codon/]. The optimized coding sequences were
 designed in a way that no changes were introduced in the encoded amino acid sequence
 while using codons preferred for expression in dicotyledonous plants mainly tomato and
Arabidopsis; and monocotyledonous plants such as maize. Such optimized sequences
 promote better translation rate and therefore higher protein expression levels. To the

optimized sequences flanking additional unique restriction enzymes sites were added to facilitate cloning genes in binary vectors.

Promoters used: CaMV 35S promoter (SEQ ID NO: 2825) and Arabidopsis At6669 promoter (SEQ ID NO: 2823; which is SEQ ID NO:61 of WO04081173 to
5 Evogene Ltd.).

EXAMPLE 4

GENERATION OF TRANSGENIC PLANTS EXPRESSING THE AQP GENES

Experimental Results

10 ***Arabidopsis transformation-*** Arabidopsis transformation of the following MAB genes and orthologues: MAB115, MAB54, MAB55, MAB56, MAB57, MAB58, MAB59 (ortholog of MAB58), MAB69, MAB70, MAB71, MAB72, MAB74, MAB76, MAB77, MAB79, MAB116 (ortholog of MAB115 and MAB55), and MAB117 (the sequence identifiers of the cloned polynucleotides and their expressed polypeptides are
15 provided in Table 7 above) was performed according to Clough SJ, Bent AF. (1998) "Floral dip: a simplified method for Agrobacterium-mediated transformation of Arabidopsis thaliana." Plant J. 16(6): 735-43; and Desfeux C, Clough SJ, Bent AF. (2000) "Female reproductive tissues are the primary targets of Agrobacterium-mediated transformation by the Arabidopsis floral-dip method." Plant Physiol. 123(3): 895-904;
20 with minor modifications. Briefly, *Arabidopsis thaliana* Columbia (Col0) T₀ Plants were sown in 250 ml pots filled with wet peat-based growth mix. The pots were covered with aluminum foil and a plastic dome, kept at 4 °C for 3–4 days, then uncovered and incubated in a growth chamber at 18–24 °C under 16/8 hours light/dark cycles. The T₀ plants were ready for transformation six days prior to anthesis. Single colonies of
25 *Agrobacterium* carrying the binary vectors harboring the AQP genes are cultured in LB medium supplemented with kanamycin (50 mg/L) and gentamycin (50 mg/L). The cultures were incubated at 28 °C for 48 hours under vigorous shaking and centrifuged at 4000 rpm for 5 minutes. The pellets comprising *Agrobacterium* cells were resuspended in a transformation medium which contained half-strength (2.15 g/L) Murashige-Skoog
30 (Duchefa); 0.044 µM benzylamino purine (Sigma); 112 µg/L B5 Gambourg vitamins (Sigma); 5 % sucrose; and 0.2 ml/L Silwet L-77 (OSI Specialists, CT) in double-distilled water, at pH of 5.7.

Transformation of T₀ plants was performed by inverting each plant into an *Agrobacterium* suspension such that the flowering stem was submerged for 3-5 seconds. Each inoculated T₀ plant was immediately placed in a plastic tray, then covered with clear plastic dome to maintain humidity and kept in the dark at room temperature for 18 hours to facilitate infection and transformation. Transformed (transgenic) plants were then uncovered and transferred to a greenhouse for recovery and maturation. The transgenic T₀ plants were grown in the greenhouse for 3-5 weeks until siliques maturation, and then seeds were harvested and kept at room temperature until sowing.

For generating T₁ and T₂ transgenic plants harboring the genes, seeds collected from transgenic T₀ plants are surface-sterilized by soaking in 70 % ethanol for 1 minute, followed by soaking in 5 % sodium hypochlorite and 0.05 % Triton X-100 for 5 minutes. The surface-sterilized seeds are thoroughly washed in sterile distilled water then placed on culture plates containing half-strength Murashige-Skoog (Duchefa); 2 % sucrose; 0.8 % plant agar; 50 mM kanamycin; and 200 mM carbenicillin (Duchefa). The culture plates are incubated at 4 °C for 48 hours then transferred to a growth room at 25 °C for an additional week of incubation. Vital T₁ *Arabidopsis* plants are transferred to fresh culture plates for another week of incubation. Following incubation the T₁ plants are removed from culture plates and planted in growth mix contained in 250 ml pots. The transgenic plants were allowed to grow in a greenhouse to maturity. Seeds harvested from T₁ plants are cultured and grown to maturity as T₂ plants under the same conditions as used for culturing and growing the T₁ plants. At least 10 independent transformation events are created from each construct for which T₂ seeds are collected. The introduction of the gene is determined for each event by PCR performed on genomic DNA extracted from each event produced.

Transformation of tomato (Var M82) plants with putative cotton genes-
Tomato (*Solanum esculentum*, var M82) transformation and cultivation of transgenic plants is effected according to: "Curtis I.S, Davey M.R, and Power J.B. 1995. "Leaf disk transformation". Methods Mol. Biol. 44, 59-70 and Meissner R, Chague V, Zhu Q, Emmanuel E, Elkind Y, Levy A.A. 2000. "Technical advance: a high throughput system for transposon tagging and promoter trapping in tomato". Plant J. 22, 265-74; with slight modifications.

EXAMPLE 5**EVALUATING TRANSGENIC ARABIDOPSIS PLANT GROWTH UNDER ABIOTIC STRESS AS WELL AS UNDER FAVORABLE CONDITIONS IN TISSUE CULTURE ASSAY**

5 **Assay 1: plant growth under osmotic stress [poly (ethylene glycol) (PEG)] in tissue culture conditions** - One of the consequences of drought is the induction of osmotic stress in the area surrounding the roots; therefore, in many scientific studies, PEG (e.g., 25 % PEG8000) is used to simulate the osmotic stress conditions resembling the high osmolarity found during drought stress.

10 Surface sterilized seeds were sown in basal media [50 % Murashige-Skoog medium (MS) supplemented with 0.8 % plant agar as solidifying agent] in the presence of Kanamycin (for selecting only transgenic plants). After sowing, plates were transferred for 2-3 days for stratification at 4 °C and then grown at 25 °C under 12-hour light 12-hour dark daily cycles for 7 to 10 days. At this time point, seedlings randomly
15 chosen were carefully transferred to plates containing 25 % PEG: 0.5 MS media or Normal growth conditions (0.5 MS media). Each plate contained 5 seedlings of the same transgenic event, and 3-4 different plates (replicates) for each event. For each polynucleotide of the invention at least four independent transformation events were analyzed from each construct. Plants expressing the polynucleotides of the invention
20 were compared to the average measurement of the control plants (empty vector or GUS reporter gene under the same promoter) used in the same experiment.

25 **Digital imaging** - A laboratory image acquisition system, which consists of a digital reflex camera (Canon EOS 300D) attached with a 55 mm focal length lens (Canon EF-S series), mounted on a reproduction device (Kaiser RS), which included 4 light units (4x150 Watts light bulb) and located in a darkroom, was used for capturing images of plantlets sown in agar plates.

The image capturing process was repeated every 2-5 days starting at day 1 till day 10-15 (see for example the images in Figures 2A-B)

30 An image analysis system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.39 (Java based image processing program which was developed at the U.S. National Institutes of Health and freely available on the internet at Hypertext Transfer

Protocol://rsbweb (dot) nih (dot) gov/). Images were captured in resolution of 10 Mega Pixels (3888 x 2592 pixels) and stored in a low compression JPEG (Joint Photographic Experts Group standard) format. Next, analyzed data was saved to text files and processed using the JMP statistical analysis software (SAS institute).

- 5 **Seedling analysis** - Using the digital analysis seedling data was calculated, including leaf area, root coverage and root length.

The relative growth rate for the various seedling parameters was calculated according to the following formulas II, III and IV.

Formula II:

- 10 Relative growth rate of leaf area = $(\Delta \text{ rosette area} / \Delta t) * (1 / \text{ rosette area } t_1)$

Δ rosette area is the interval between the current rosette area (measured at t_2) and the rosette area measured at the previous day (Area t_1)

Δt is the time interval ($t_2 - t_1$, in days) between the current analyzed image day (t_2) and the previous day (t_1).

- 15 Thus, the relative growth rate of leaf area is in units of 1/day.

Formula III:

Relative growth rate of root coverage = $(\Delta \text{ root coverage area} / \Delta t) * (1 / \text{ root coverage area } t_1)$

- 20 Δ root coverage area is the interval between the current root coverage area (measured at t_2) and the root coverage area measured at the previous day (Area t_1)

Δt is the time interval ($t_2 - t_1$, in days) between the current analyzed image day (t_2) and the previous day (t_1).

Thus, the relative growth rate of root coverage area is in units of 1/day.

25

Formula IV:

Relative growth rate of root length = $(\Delta \text{ root length} / \Delta t) * (1 / \text{ root length } t_1)$

Δ root length is the interval between the current root length (measured at t_2) and the root length measured at the previous day (Area t_1)

- 30 Δt is the time interval ($t_2 - t_1$, in days) between the current analyzed image day (t_2) and the previous day (t_1).

Thus, the relative growth rate of root length is in units of 1/day.

At the end of the experiment, plantlets were removed from the media and weighed for the determination of plant fresh weight. Plantlets were then dried for 24 hours at 60 °C, and weighed again to measure plant dry weight for later statistical analysis. Growth rate was determined by comparing the leaf area coverage, root coverage and root length, between each couple of sequential photographs, and results were used to resolve the effect of the gene introduced on plant vigor, under osmotic stress, as well as under optimal conditions. Similarly, the effect of the gene introduced on biomass accumulation, under osmotic stress as well as under optimal conditions, was determined by comparing the plants' fresh and dry weight to that of control plants (containing an empty vector or the GUS reporter gene under the same promoter). From every construct created, 3-5 independent transformation events were examined in replicates.

Statistical analyses - To identify genes conferring significantly improved tolerance to abiotic stresses or enlarged root architecture, the results obtained from the transgenic plants were compared to those obtained from control plants. To identify outperforming genes and constructs, results from the independent transformation events tested were analyzed separately. To evaluate the effect of a gene event over a control the data was analyzed by Student's t-test and the p value was calculated. Results were considered significant if $p \leq 0.1$. The JMP statistics software package was used (Version 5.2.1, SAS Institute Inc., Cary, NC, USA).

Experimental Results - The polynucleotide sequences of the invention were assayed for a number of desired traits.

Tables 10-14 depict analyses of the above mentioned growth parameters of seedlings overexpressing the polynucleotides of the invention under the regulation of the At6669 promoter (SEQ ID NO:2823) when grown under osmotic stress (25 % PEG) conditions.

Table 10
MAB70 – 25 % PEG

<i>Event No.</i>	<i>Control</i>	<i>7971.3</i>		<i>7972.1</i>		<i>7974.1</i>	
		A	P	A	P	A	P
RGR of Roots Coverage between day 5 and 10	0.16	0.29	0.00	0.31	0.00	0.30	0.02
RGR of Roots Length between day 1 and 5	0.07	0.12	0.05	0.13	0.03		

Table 10: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under 25 % PEG. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 11
MAB76 – 25 % PEG

<i>Event No.</i>	<i>Control</i>	<i>7635.4</i>		<i>7635.1</i>	
		A	P	A	P
RGR of Roots Coverage between day 5 and 10	0.16	0.22	0.02	0.21	0.09

Table 11: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under 25 % PEG. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 12
MAB79 – 25 % PEG

<i>Event No.</i>	<i>Control</i>	<i>7324.1</i>		<i>7961.1</i>	
		A	P	A	P
Dry Weight [gr]	0.01	0.01	0.06		
Fresh Wight [gr]	0.08			0.13	0.07
Leaf Area on day 5	0.15			0.19	0.05
RGR of Roots Coverage between day 5 and 10	0.16			0.32	0.05
RGR of Roots Length between day 1 and 5	0.07			0.11	0.02

Table 12: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under 25 % PEG. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 13
MAB56 – 25 % PEG

<i>Event No.</i>	<i>Control</i>	<i>6802.10</i>	
		A	P
Roots Coverage on day 7	2.46	3.38	0.09
Roots Length on day 7	2.81	3.43	0.07

Table 13: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under 25 % PEG. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 14
MAB58 – 25 % PEG

<i>Event No.</i>	<i>Control</i>	<i>6783.30</i>	
		A	P
Leaf Area on day 7	0.31	0.41	0.03
Leaf Area on day 14	0.80	1.09	0.02
Fresh Weight	0.18	0.31	0.00
Dry Weight [gr]	0.01	0.013	0.01

Table 14: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under 25 % PEG. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

- 5 Tables 15-29 depict analyses of the above mentioned growth parameters of seedlings overexpressing the polynucleotides of the invention under the regulation of the At6669 promoter in *Normal Growth* conditions (0.5 MS medium).

Table 15
MAB70 – Normal Growth Conditions

Event No.	Control	7971.3		7972.1		7974.1		7974.3	
		A	P	A	P	A	P	A	P
Dry Weight [gr]	0.01	0.01	0.03	0.01	0.05	0.02	0.04	0.01	0.07
Fresh Wight [gr]	0.14					0.24	0.04	0.22	0.10
Leaf Area on day 10	0.46	0.59	0.00						
Leaf Area on day 5	0.21					0.30	0.10		
RGR of Roots Coverage between day 5 and 10	0.18	0.42	0.00	0.37	0.00	0.32	0.01		
RGR of Roots Length between day 1 and 5	0.06	0.15	0.01	0.16	0.00	0.15	0.00		
RGR of Roots Length between day 5 and 10	0.22			0.32	0.09				

Table 15: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 16
MAB71 – Normal Growth Conditions

Event No.	Control	7331.5		7332.2		7333.5	
		A	P	A	P	A	P
Dry Weight [gr]	0.01	0.01	0.05				
Fresh Wight [gr]	0.14	0.20	0.08				
RGR of Roots Coverage between day 5 and 10	0.18			0.28	0.04	0.26	0.07
RGR of Roots Length between day 1 and 5	0.06			0.11	0.02	0.11	0.01

Table 16: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 17
MAB74 – Normal Growth Conditions

Event No.	Control	7981.1		7982.4		7983.9	
		A	P	A	P	A	P
Dry Weight [gr]	0.01	0.01	0.09	0.02	0.05	0.01	0.06
Fresh Wight [gr]	0.14					0.21	0.01
Leaf Area on day 10	0.46	0.67	0.01				
Leaf Area on day 5	0.21	0.29	0.04	0.29	0.01	0.27	0.00
RGR of Roots Coverage between day 5 and 10	0.18			0.31	0.07		
RGR of Roots Coverage between day 1 and 5	0.73			1.70	0.07		
RGR of Roots Length between day 1 and 5	0.06			0.12	0.09	0.14	0.03
RGR of Roots Length between day 5 and 10	0.22	0.45	0.05	0.58	0.00		

Table 17: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

5

Table 18
MAB76 – Normal Growth Conditions

Event No.	Control	7633.3		7635.4		7635.1	
		A	P	A	P	A	P
RGR Leaf Area between day 5 and 10	0.24	0.34	0.04	0.33	0.07		
RGR of Roots Coverage between day 5 and 10	0.18					0.38	0.08
RGR of Roots Length between day 1 and 5	0.06					0.13	0.02

Table 18: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

10

Table 19
MAB77 – Normal Growth Conditions

Event No.	Control	7931.11		8211.2		8212.2	
		A	P	A	P	A	P
Dry Weight [gr]	0.01	0.01	0.08			0.01	0.10
Roots Coverage on day 10	2.77					4.33	0.07
RGR Leaf Area between day 5 and 10	0.24	0.38	0.10	0.35	0.04		
RGR of Roots Coverage between day 5 and 10	0.18	0.27	0.09	0.29	0.09		
RGR of Roots Length between day 1 and 5	0.06			0.10	0.03		

Table 19: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

15

Table 20
MAB79 – Normal Growth Conditions

Event No.	Control	7323.3		7324.1		7961.1		7962.2	
		A	P	A	P	A	P	A	P
Dry Weight [gr]	0.01	0.02	0.03	0.02	0.08	0.01	0.00		
Fresh Wight [gr]	0.14	0.34	0.04	0.31	0.09				
Leaf Area on day 10	0.46	0.92	0.01	0.90	0.01	0.81	0.00		
Leaf Area on day 5	0.21					0.29	0.02	0.28	0.00
Roots Coverage on day 10	2.77	5.31	0.02	4.59	0.07	3.81	0.00	3.71	0.01
RGR Leaf Area between day 5 and 10	0.24					0.36	0.02		
RGR Leaf Area between day 1 and 5	0.82					1.34	0.00		
RGR of Roots Coverage between day 5 and 10	0.18					0.45	0.06	0.39	0.02
RGR of Roots Length between day 1 and 5	0.06	0.12	0.02	0.17	0.06			0.14	0.00

Table 20: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

20

Table 21
MAB115 – Normal Growth Conditions

Event No.	Control	8561.2..		8564.1..		8564.2..		8565.1..	
		A	P	A	P	A	P	A	P
Dry Weight [gr]	0.005	0.006	0.00					0.009	0.00
Leaf Area on day 10	0.24							0.27	0.00
Leaf Area on day 5	0.35							0.38	0.01
Roots Coverage on day 10	1.67							2.13	0.02
Roots Coverage on day 5	3.38							4.80	0.03
Roots Length on day 10	2.39							2.74	0.00
Roots Length on day 5	3.46							4.22	0.02
RGR Leaf Area between day 5 and 10	0.37	0.43	0.00					0.48	0.00
RGR Leaf Area between day 1 and 5	0.16	0.19	0.00						
RGR of Roots Coverage between day 5 and 10	1.89	3.21	0.00	2.24	0.02	2.23	0.02	3.47	0.01
RGR of Roots Coverage between day 1 and 5	0.33	0.35	0.00	0.41	0.00	0.43	0.00	0.44	0.00
RGR of Roots Length between day 1 and 5	0.37	0.56	0.02			0.53	0.06	0.68	0.00
RGR of Roots Length between day 5 and 10	0.15			0.18	0.00	0.17	0.00	0.18	0.00

Table 21: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 22
MAB54 – Normal Growth Conditions

Event No.	Control	8181.2..		8182.2..		8184.3..		8185.3..	
		A	P	A	P	A	P	A	P
Dry Weight [gr]	0.005	0.009	0.00	0.008	0.00	0.008	0.00	0.007	0.00
Roots Coverage on day 10	1.67	1.80	0.04						
Roots Coverage on day 5	3.38	4.27	0.02	3.40	0.00				
Roots Length on day 10	2.39	2.52	0.01						
Roots Length on day 5	3.46	4.11	0.02	3.50	0.00				
RGR Leaf Area between day 5 and 10	0.37	0.45	0.00						
RGR Leaf Area between day 1 and 5	0.16	0.17	0.04					0.19	0.00
RGR of Roots Coverage between day 5 and 10	1.89	3.59	0.00	3.60	0.01	2.28	0.01	2.20	0.01
RGR of Roots Coverage between day 1 and 5	0.33	0.52	0.00	0.55	0.00	0.39	0.00	0.36	0.00
RGR of Roots Length between day 1 and 5	0.37	0.70	0.00	0.73	0.00	0.48	0.08	0.51	0.02
RGR of Roots Length between day 5 and 10	0.15	0.21	0.01	0.22	0.01	0.17	0.00	0.17	0.00

Table 22: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 23
MAB55 – Normal Growth Conditions

Event No.		6802.1		6802.11		6802.8		6805.3	
		A	P	A	P	A	P	A	P
Roots Coverage on day 7	3.67	5.93	0.04						
Roots Coverage on day 14	7.40	13.26	0.04						
Roots Length on day 7	3.99	5.32	0.01						
Roots Length on day 14	6.14	7.80	0.04					7.65	0.04
RGR of Roots Coverage between day 1 and 7	0.53	1.30	0.00	1.11	0.02	0.93	0.02		
RGR of Roots Length between day 1 and 7	0.29	0.48	0.00	0.45	0.03	0.43	0.02		
Fresh Weight	0.19					0.10	0.00	0.12	0.01
Dry Weight [gr]	0.01					0.01	0.00	0.01	0.00

5 **Table 23:** Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 24
MAB56 – Normal Growth Conditions

Event No.		6691.2		6691.3		6693.2		6693.5	
		A	P	A	P	A	P	A	P
Roots Coverage on day 7	3.67	5.81	0.00					5.67	0.01
Roots Length on day 7	3.99	6.21	0.00					5.39	0.00
Roots Length on day 14	6.14	8.32	0.01					8.01	0.02
RGR of Roots Length between day 7 and 14	0.09	0.05	0.01	0.05	0.06	0.06	0.08		
Fresh Weight	0.19	0.14	0.03	0.14	0.03				
Dry Weight [gr]	0.01	0.01	0.02	0.01	0.02	0.00	0.00		

10 **Table 24:** Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 25
MAB57 – Normal Growth Conditions

Event No.		6912.14		6912.2		6912.6		6914.1	
		A	P	A	P	A	P	A	P
Roots Coverage on day 7	3.67	6.40	0.00	6.71	0.00				
Roots Coverage on day 14	7.40	17.33	0.00	15.27	0.05	12.30	0.02		
Roots Length on day 7	3.99	5.54	0.00	6.12	0.00	6.34	0.00		
Roots Length on day 14	6.14	8.76	0.00	8.48	0.01	7.97	0.02	7.85	0.04
RGR of Roots Length between day 1 and 7	0.29	0.39	0.06						
RGR of Roots Length between day 7 and 14	0.09					0.04	0.09		
Fresh Weight	0.19	0.24	0.09			0.11	0.01	0.11	0.01
Dry Weight [gr]	0.01					0.01	0.01	0.01	0.01

15 **Table 25:** Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 26
MAB58 – Normal Growth Conditions

Event No.		6783.1		6783.2		6783.3	
		A	P	A	P	A	P
Roots Coverage on day 7	3.67					6.18	0.00
Roots Coverage on day 14	7.40			12.65	0.02	12.00	0.09
Roots Length on day 7	3.99					5.20	0.02
Roots Length on day 14	6.14	7.38	0.09	7.51	0.07	7.59	0.08
RGR of Roots Length between day 1 and 7	0.29	0.35	0.07				
Fresh Weight	0.19	0.13	0.03				
Dry Weight [gr]	0.01	0.01	0.00				

Table 26: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 27
MAB59 – Normal Growth Condition

Event No.		6791.4		6793.4		6794.4	
		A	P	A	P	A	P
Roots Coverage on day 7	3.67			5.61	0.04	5.23	0.09
Roots Coverage on day 14	7.40			9.65	0.09	10.28	0.09
Roots Length on day 7	3.99			5.47	0.08	4.95	0.09
Roots Length on day 14	6.14					7.70	0.07
RGR of Roots Coverage between day 1 and 7	0.53					0.80	0.09
RGR of Roots Length between day 7 and 14	0.09			0.05	0.10		
Fresh Weight	0.19	0.09	0.00				
Dry Weight [gr]	0.01	0.004	0.00	0.005	0.02		

Table 27: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 28
MAB69 – Normal Growth Conditions

Event No.		6651.1		6651.12		6651.13		6651.8	
		A	P	A	P	A	P	A	P
Roots Length on day 7	3.99	4.97	0.10						
Roots Length on day 14	6.14	8.01	0.02						
RGR of Roots Length between day 1 and 7	0.29							0.35	0.09
Fresh Weight	0.19					0.12	0.02	0.12	0.01
Dry Weight [gr]	0.01			0.007	0.09	0.005	0.00	0.006	0.00

Table 28: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 29
MAB72 – Normal Growth Conditions

Event No.	Control	8552.1..		8552.4..		8553.2..	
		A	P	A	P	A	P
Dry Weight [gr]	0.005	0.008	0.00	0.008	0.00	0.007	0.00
Leaf Area on day 10	0.24	0.24	0.01				
Roots Coverage on day 10	1.67	1.84	0.01	1.93	0.02	1.89	0.03
Roots Coverage on day 5	3.38	3.60	0.04	3.90	0.06	4.50	0.00

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Roots Length on day 10	2.39	2.48	0.01				
Roots Length on day 5	3.46	3.70	0.04	3.65	0.04	3.84	0.00
RGR Leaf Area between day 5 and 10	0.37	0.47	0.00	0.39	0.00		
RGR Leaf Area between day 1 and 5	0.16			0.20	0.09		
RGR of Roots Coverage between day 5 and 10	1.89	1.93	0.03	2.29	0.06	3.04	0.01
RGR of Roots Coverage between day 1 and 5	0.33			0.35	0.00	0.52	0.00
RGR of Roots Length between day 1 and 5	0.37					0.55	0.01
RGR of Roots Length between day 5 and 10	0.15	0.16	0.00	0.18	0.00	0.22	0.01

Table 29: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under normal growth conditions. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

5

EXAMPLE 6

EVALUATING TRANSGENIC ARABIDOPSIS PLANT GROWTH UNDER ABIOTIC STRESS AS WELL AS FAVORABLE CONDITIONS IN GREENHOUSE ASSAY

ABS tolerance: Yield and plant growth rate at high salinity concentration

10 ***under greenhouse conditions*** - This assay followed the rosette area growth of plants grown in the greenhouse as well as seed yield at high salinity irrigation. Seeds were sown in agar media supplemented only with a selection agent (Kanamycin) and Hoagland solution under nursery conditions. The T₂ transgenic seedlings were then transplanted to 1.7 trays filled with peat and perlite. The trays were irrigated with tap

15 water (provided from the pots' bottom). Half of the plants were irrigated with a salt solution (40-80 mM NaCl and 5 mM CaCl₂) so as to induce salinity stress (stress conditions). The other half of the plants was irrigated with tap water (normal conditions). All plants were grown in the greenhouse until mature seeds, then harvested (the above ground tissue) and weighted (immediately or following drying in oven at 50

20 °C for 24 hours). High salinity conditions were achieved by irrigating with a solution containing 40-80 mM NaCl ("ABS" growth conditions) and compared to regular growth conditions.

Each construct was validated at its T₂ generation. Transgenic plants transformed with a construct including the uidA reporter gene (GUS) under the AT6669 promoter or

25 with an empty vector including the AT6669 promoter were used as control.

The plants were analyzed for their overall size, growth rate, flowering, seed yield, weight of 1,000 seeds, dry matter and harvest index (HI- seed yield/dry matter). Transgenic plants performance was compared to control plants grown in parallel under

the same conditions. Mock- transgenic plants expressing the uidA reporter gene (GUS-Intron) or with no gene at all, under the same promoter were used as control.

The experiment was planned in nested randomized plot distribution. For each gene of the invention three to five independent transformation events were analyzed from each construct.

Digital imaging - A laboratory image acquisition system, which consists of a digital reflex camera (Canon EOS 300D) attached with a 55 mm focal length lens (Canon EF-S series), mounted on a reproduction device (Kaiser RS), which included 4 light units (4 x 150 Watts light bulb) was used for capturing images of plant samples.

The image capturing process was repeated every 2 days starting from day 1 after transplanting till day 16. Same camera, placed in a custom made iron mount, was used for capturing images of larger plants sawn in white tubs in an environmental controlled greenhouse. The tubs were square shape include 1.7 liter trays. During the capture process, the tubs were placed beneath the iron mount, while avoiding direct sun light and casting of shadows.

An image analysis system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.39 (Java based image processing program which was developed at the U.S National Institutes of Health and freely available on the internet at Hypertext Transfer Protocol://rsbweb (dot) nih (dot) gov/). Images were captured in resolution of 10 Mega Pixels (3888 x 2592 pixels) and stored in a low compression JPEG (Joint Photographic Experts Group standard) format. Next, analyzed data was saved to text files and processed using the JMP statistical analysis software (SAS institute).

Leaf analysis - Using the digital analysis leaves data was calculated, including leaf number, area, perimeter, length and width.

Vegetative growth rate: the relative growth rate (RGR) of leaf number and rosette area were calculated formulas V and VI, respectively.

Formula V:

Relative growth rate of leaf number = $(\Delta \text{ leaf number} / \Delta t) * (1 / \text{leaf number } t_1)$

Δ leaf number is the interval between the current leaf number (measured at t_2) and the leaf number measured at the previous day (Area t_1)

Δt is the time interval ($t_2 - t_1$, in days) between the current analyzed image day (t_2) and the previous day (t_1).

Thus, the relative growth rate of leaf number is in units of 1/day.

5 **Formula VI:**

Relative growth rate of rosette area = $(\Delta \text{ rosette area} / \Delta t) * (1 / \text{ rosette area } t_1)$

Δ rosette area is the interval between the current rosette area (measured at t_2) and the rosette area measured at the previous day (Area t_1)

10 Δt is the time interval ($t_2 - t_1$, in days) between the current analyzed image day (t_2) and the previous day (t_1).

Thus, the relative growth rate of rosette area is in units of 1/day.

15 **Seeds average weight** - At the end of the experiment all seeds were collected. The seeds were scattered on a glass tray and a picture was taken. Using the digital analysis, the number of seeds in each sample was calculated.

20 **Dry weight and seed yield** - On about day 80 from sowing, the plants were harvested and left to dry at 30 °C in a drying chamber. The biomass and seed weight of each plot were measured and divided by the number of plants in each plot. Dry weight = total weight of the vegetative portion above ground (excluding roots) after drying at 30 °C in a drying chamber; Seed yield per plant = total seed weight per plant (gr). 1000 seed weight (the weight of 1000 seeds) (gr.) .

Harvest Index (HI) - The harvest index was calculated using Formula VII.

Formula VII:

Harvest Index = Average seed yield per plant/ Average dry weight

25 **Statistical analyses** - To identify genes conferring significantly improved tolerance to abiotic stresses, the results obtained from the transgenic plants were compared to those obtained from control plants. To identify outperforming genes and constructs, results from the independent transformation events tested were analyzed separately. Data was analyzed using Student's t-test and results were considered significant if the p value was less than 0.1. The JMP statistics software package is used (Version 5.2.1, SAS Institute Inc., Cary, NC, USA).

Experimental Results

Tables 30-45 depict analyses of plant parameters as describe above overexpressing the polynucleotides of the invention under the regulation of the At6669 promoter under salinity irrigation conditions [NaCl 40-80 mM; NaCl Electrical conductivity (E.C.) of 7-10].

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Table 30
MAB115 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	8564.1		8565.1	
		A	P	A	P
Rosette Diameter on day 3*	1.70	1.80	0.09	1.75	0.04
Rosette Diameter on day 5	2.36				
Rosette Diameter on day 8	3.77			4.00	0.09
Rosette Area on day 3	0.90				
Rosette Area on day 5	1.56			1.70	0.09
Rosette Area on day 8	4.06			4.38	0.06
Plot Coverage on day 5	12.30			13.61	0.06
Plot Coverage on day 8	31.90			35.07	0.02
Leaf Number on day 3	5.08			5.94	0.00
Leaf Number on day 5	6.86			7.38	0.05
RGR of Leaf Number between day 3 and 5	0.18				
RGR of Leaf Number between day 5 and 8	0.09				
RGR of Rosette Area between day 5 and 8	0.53	0.62	0.01		
Biomass DW [gr]	3.24				
Harvest Index	0.11	0.15	0.07	0.16	0.03

Table 30: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 31
MAB54 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	8181.2		8182.2		8183.2		8185.4	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3*	1.70	1.95	0.04						
Rosette Diameter on day 5	2.36			2.70	0.02	2.64	0.00		
Rosette Diameter on day 8	3.77			4.00	0.08				
Rosette Area on day 3	0.90					1.19	0.04		
Plot Coverage on day 3	7.04					9.52	0.04	7.49	0.08
Leaf Number on day 3	5.08			6.19	0.06				
Leaf Number on day 8	8.66	9.31	0.00	9.38	0.00				
RGR of Leaf Number between day 3 and 5	0.18								
RGR of Rosette Area between day 1 and 3	0.45			0.52	0.01				
1000 Seeds weight [gr]	0.02					0.02	0.00	0.02	0.00
Yield [gr]/Plant	0.04	0.06	0.05						
Harvest Index	0.11	0.17	0.01						

Table 31: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 32
MAB55 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	6802.10		6805.3		6805.4	
		A	P	A	P	A	P
Rosette Diameter on day 5	2.36	2.81	0.03				
Rosette Diameter on day 8	3.77	4.29	0.05				
Rosette Area on day 3	0.90	1.35	0.01				
Rosette Area on day 5	1.56			1.70	0.03		
Rosette Area on day 8	4.06	5.91	0.05				
Plot Coverage on day 3	7.04	10.76	0.01				
Plot Coverage on day 5	12.30			13.60	0.02		
Plot Coverage on day 8	31.90	47.28	0.06				
Leaf Number on day 3	5.08	6.25	0.00				
Leaf Number on day 5	6.86	7.94	0.03				
Leaf Number on day 8	8.66	9.50	0.01				
RGR of Rosette Area between day 1 and 3	0.45	0.51	0.05				
Yield [gr]/Plant	0.04					0.06	0.03
Harvest Index	0.11			0.15	0.05		

Table 32: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 33
MAB56 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	6691.2		6691.3		6693.2		6695.6	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.70					1.89	0.05	1.97	0.07
Rosette Diameter on day 5	2.36					2.55	0.09	2.58	0.01
Rosette Area on day 3	0.90			1.06	0.00	1.15	0.02	1.23	0.08
Rosette Area on day 5	1.56					1.94	0.02	1.94	0.03
Rosette Area on day 8	4.06	4.63	0.02						
Plot Coverage on day 3	7.04			8.45	0.00	9.21	0.01	9.82	0.07
Plot Coverage on day 5	12.30					15.49	0.01	15.53	0.02
Plot Coverage on day 8	31.90	37.03	0.01					34.82	0.05
Leaf Number on day 3	5.08			5.50	0.00	5.81	0.00	6.00	0.02
Leaf Number on day 5	6.86					7.38	0.01	7.50	0.02
1000 Seeds weight [gr]	0.02			0.02	0.08				
Harvest Index	0.11			0.18	0.01				

Table 33: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 34
MAB57 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	6912.1		6912.13		6914.5	
		A	P	A	P	A	P
Leaf Number on day 3	5.08					5.69	0.00
Leaf Number on day 5	6.86			8.13	0.06		
Leaf Number on day 8	8.66					9.56	0.06
RGR of Leaf Number between day 5 and 8	0.09	0.14	0.01				
RGR of Rosette Area between day 5 and 8	0.53	0.62	0.02			0.58	0.10
1000 Seeds weight [gr]	0.02					0.02	0.00
Yield [gr]/Plant	0.04	0.06	0.01	0.06	0.03	0.06	0.01

Harvest Index	0.11			0.19	0.06	0.23	0.00
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Table 34: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 35
MAB58 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	6783.3		7522.10		7522.3		7523.6	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.70							2.11	0.00
Rosette Diameter on day 5	2.36	2.57	0.00						
Rosette Diameter on day 8	3.77					4.06	0.07	4.54	0.00
Rosette Area on day 3	0.90							1.36	0.00
Rosette Area on day 5	1.56							2.29	0.00
Rosette Area on day 8	4.06							5.98	0.00
Plot Coverage on day 3	7.04							10.90	0.00
Plot Coverage on day 5	12.30							18.32	0.00
Plot Coverage on day 8	31.90							47.88	0.00
Leaf Number on day 3	5.08			5.63	0.06			6.06	0.00
Leaf Number on day 8	8.66	9.25	0.04					9.81	0.04
RGR of Leaf Number between day 5 and 8	0.09	0.12	0.03						
1000 Seeds weight [gr]	0.02	0.02	0.08						
Yield [gr]/Plant	0.04	0.06	0.09						

Table 35: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 36
MAB59 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	6791.6		6794.4		6794.5	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.70					2.38	0.05
Rosette Diameter on day 5	2.36			2.73	0.06		
Rosette Area on day 3	0.90			1.27	0.06	1.65	0.03
Plot Coverage on day 3	7.04			10.15	0.06	13.19	0.03
Leaf Number on day 3	5.08	6.44	0.05	6.00	0.02	6.75	0.01
Leaf Number on day 5	6.86	8.38	0.00	7.69	0.05	8.00	0.07
Leaf Number on day 8	8.66					9.38	0.02
Yield [gr]/Plant	0.04	0.06	0.06				
Harvest Index	0.11	0.16	0.04				

Table 36: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 37
MAB69 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	6651.11		6651.12		6651.2		8342.1	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.70			1.92	0.01				
Rosette Area on day 3	0.90			1.09	0.00				
Rosette Area on day 8	4.06			5.05	0.04				

Plot Coverage on day 3	7.04			8.74	0.00				
Plot Coverage on day 8	31.90			40.41	0.04				
Leaf Number on day 3	5.08			5.69	0.00				
Leaf Number on day 8	8.66							8.94	0.08
RGR of Rosette Area between day 1 and 3	0.45	0.49	0.02	0.51	0.04				
1000 Seeds weight [gr]	0.02	0.02	0.00			0.02	0.01		
Yield [gr]/Plant	0.04	0.05	0.09	0.06	0.02			0.07	0.01
Harvest Index	0.11			0.17	0.09	0.22	0.01		

Table 38: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 39
MAB70 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	7971.3		7972.1		7972.3	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.70					1.94	0.00
Rosette Diameter on day 5	2.36					2.62	0.04
Rosette Diameter on day 8	3.77			4.40	0.00		
Rosette Area on day 3	0.90			1.20	0.07	1.12	0.01
Rosette Area on day 5	1.56			2.06	0.05	1.87	0.00
Rosette Area on day 8	4.06			5.86	0.06		
Plot Coverage on day 3	7.04			9.61	0.06	9.00	0.01
Plot Coverage on day 5	12.30			16.46	0.04	14.93	0.00
Plot Coverage on day 8	31.90			46.87	0.06		
Leaf Number on day 3	5.08	5.94	0.09				
Leaf Number on day 8	8.66	9.31	0.00			9.75	0.09
RGR of Rosette Area between day 5 and 8	0.53			0.62	0.01		
Yield [gr]/Plant	0.04	0.08	0.00	0.07	0.01		
Harvest Index	0.11	0.25	0.00				

Table 39: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 40
MAB71 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	7331.4		7331.5		7333.5		7334.5	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 5	2.36	3.03	0.00			2.52	0.02		
Rosette Diameter on day 8	3.77	5.01	0.05	4.33	0.01				
Plot Coverage on day 5	12.30	19.90	0.09			14.25	0.08		
Leaf Number on day 3	5.08	6.44	0.05			5.47	0.06		
Leaf Number on day 5	6.86	8.13	0.00	7.56	0.00				
Leaf Number on day 8	8.66	10.38	0.05						
RGR of Leaf Number between day 5 and 8	0.09							0.12	0.01
RGR of Rosette Area between day 5 and 8	0.53	0.61	0.03					0.61	0.04
Yield [gr]/Plant	0.04							0.05	0.10
Harvest Index	0.11	0.21	0.06						

Table 40: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 41
MAB72 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	8552.1		8553.2		8553.3		8555.3	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.70			1.90	0.05			1.83	0.00
Rosette Diameter on day 5	2.36			2.67	0.00			2.55	0.01
Rosette Diameter on day 8	3.77			4.06	0.08	4.15	0.10		
Rosette Area on day 3	0.90			1.20	0.00	1.02	0.00	1.08	0.02
Rosette Area on day 5	1.56	1.88	0.07	2.00	0.00			1.87	0.00
Rosette Area on day 8	4.06	4.68	0.00	5.05	0.00			4.82	0.00
Plot Coverage on day 3	7.04			9.64	0.00	8.13	0.00	8.67	0.02
Plot Coverage on day 5	12.30	15.05	0.05	16.04	0.00			14.98	0.00
Plot Coverage on day 8	31.90	37.48	0.00	40.39	0.00			38.57	0.00
Leaf Number on day 3	5.08	5.81	0.00	5.88	0.00	5.56	0.00	5.50	0.00
Leaf Number on day 8	8.66					9.38	0.02		
RGR of Leaf Number between day 1 and 3	0.12	0.17	0.01						

Table 41: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 42
MAB74 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	7982.1		7983.6		7983.9	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.70			2.06	0.10	1.94	0.00
Rosette Diameter on day 5	2.36					2.62	0.06
Rosette Diameter on day 8	3.77					4.05	0.02
Rosette Area on day 3	0.90			1.14	0.02		
Rosette Area on day 5	1.56			1.83	0.05	1.85	0.10
Rosette Area on day 8	4.06					4.46	0.03
Plot Coverage on day 3	7.04			9.13	0.02		
Plot Coverage on day 5	12.30			14.62	0.03	14.79	0.08
Plot Coverage on day 8	31.90					35.66	0.01
Leaf Number on day 3	5.08			5.75	0.04	5.31	0.07
Leaf Number on day 5	6.86					7.25	0.04
RGR of Rosette Area between day 3 and 5	0.37	0.42	0.07				
1000 Seeds weight [gr]	0.02	0.02	0.02			0.02	0.05
Yield [gr]/Plant	0.04	0.06	0.05				
Harvest Index	0.11	0.20	0.06				

Table 42: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 43
MAB76 - Salt irrigation (40-80 mM NaCl)

Event No.	Control	7633.1		7633.2	
		A	P	A	P

<i>Event No.</i>	<i>Control</i>	<i>7633.1</i>		<i>7633.2</i>	
		A	P	A	P
Leaf Number on day 3	5.08			5.44	0.02
Leaf Number on day 8	8.66	9.13	0.07		

Table 43: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 44
MAB77 - Salt irrigation (40-80 mM NaCl)

<i>Event No.</i>	<i>Control</i>	<i>7931.11</i>		<i>8212.2</i>	
		A	P	A	P
Leaf Number on day 8	8.66			9.75	0.09
RGR of Rosette Area between day 1 and 3	0.45	0.52	0.10		
Harvest Index	0.11			0.15	0.07

Table 44: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 45
MAB79 - Salt irrigation (40-80 mM NaCl)

<i>Event No.</i>	<i>Control</i>	<i>7323.10 ,</i>		<i>7961.1 ,</i>		<i>7962.2 ,</i>		<i>7962.2 ,</i>	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.70			1.84	0.10	1.93	0.05		
Rosette Diameter on day 5	2.36			2.53	0.01				
Rosette Diameter on day 8	3.77			4.32	0.03	4.01	0.04		
Rosette Area on day 3	0.90			1.08	0.09				
Rosette Area on day 8	4.06			5.29	0.03	4.78	0.05		
Plot Coverage on day 3	7.04			8.63	0.08				
Plot Coverage on day 8	31.90			42.32	0.03	38.27	0.05		
Leaf Number on day 3	5.08	5.63	0.00					5.75	0.04
Leaf Number on day 5	6.86							7.44	0.01
RGR of Leaf Number between day 5 and 8	0.09			0.11	0.01				
RGR of Rosette Area between day 5 and 8	0.53							0.59	0.01
1000 Seeds weight [gr]	0.02			0.02	0.00				
Harvest Index	0.11			0.19	0.00				

Table 45: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under salinity irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Tables 46-58 depict analyses of plant parameters (as describe above) overexpressing the polynucleotides of the invention under the regulation of the 6669 promoter under Normal Growth conditions [Normal irrigation included NaCl Electrical conductivity (E.C.) of 1-2].

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Table 46
MAB115 – Normal Growth Conditions

Event No.	Control	8564.1		8565.1		8565.2	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.67	1.80	0.09	1.75	0.04	1.95	0.04
Rosette Diameter on day 8	3.60			4.00	0.09		
Rosette Area on day 5	1.54			1.70	0.09		
Rosette Area on day 8	3.98			4.38	0.06		
Plot Coverage on day 5	12.30			13.61	0.06		
Plot Coverage on day 8	31.82			35.07	0.02		
Leaf Number on day 3	5.25			5.94	0.00		
Leaf Number on day 5	6.52			7.38	0.05		
Leaf Number on day 8	8.92					9.31	0.00
RGR of Leaf Number between day 3 and 5	0.12			0.12	0.04		
RGR of Rosette Area between day 5 and 8	0.53	0.62	0.01				

Table 46: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 47
MAB54 – Normal Growth Conditions

Event No.	Control	8181.2		8182.2		8184.3		8185.4	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 5	2.24	2.70	0.02	2.64	0.00			2.81	0.03
Rosette Diameter on day 8	3.60	4.00	0.08					4.29	0.05
Rosette Area on day 3	0.89			1.19	0.04			1.35	0.01
Rosette Area on day 8	3.98							5.91	0.05
Plot Coverage on day 3	7.10			9.52	0.04	7.49	0.08	10.76	0.01
Plot Coverage on day 8	31.82							47.28	0.06
Leaf Number on day 3	5.25	6.19	0.06					6.25	0.00
Leaf Number on day 5	6.52							7.94	0.03
Leaf Number on day 8	8.92	9.38	0.00					9.50	0.01
RGR of Leaf Number between day 3 and 5	0.12	0.13	0.08						
RGR of Rosette Area between day 1 and 3	0.46	0.52	0.01					0.51	0.05
1000 Seeds weight [gr]	0.02			0.02	0.00	0.02	0.00		

Table 47: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 48
MAB55 – Normal Growth Conditions

Event No.	Control	6802.5		6805.4	
		A	P	A	P
Rosette Area on day 5	1.54	1.70	0.03		
Rosette Area on day 8	3.98			4.63	0.02
Plot Coverage on day 5	12.30	13.60	0.02		
Plot Coverage on day 8	31.82			37.03	0.01

Table 48: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 49
MAB56 – Normal Growth Conditions

Event No.	Control	6691.2		6691.3		6693.2		6695.7	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.67			1.89	0.05	1.97	0.07		
Rosette Diameter on day 5	2.24			2.55	0.09	2.58	0.01		
Rosette Area on day 3	0.89	1.06	0.00	1.15	0.02	1.23	0.08		
Rosette Area on day 5	1.54			1.94	0.02	1.94	0.03		
Plot Coverage on day 3	7.10	8.45	0.00	9.21	0.01	9.82	0.07		
Plot Coverage on day 5	12.30			15.49	0.01	15.53	0.02		
Plot Coverage on day 8	31.82					34.82	0.05		
Leaf Number on day 3	5.25	5.50	0.00	5.81	0.00	6.00	0.02		
Leaf Number on day 5	6.52			7.38	0.01	7.50	0.02		
RGR of Leaf Number between day 3 and 5	0.12					0.13	0.06		
RGR of Leaf Number between day 5 and 8	0.12							0.14	0.01
RGR of Rosette Area between day 5 and 8	0.53							0.62	0.02
1000 Seeds weight [gr]	0.02	0.02	0.08						

Table 49: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 50
MAB57 – Normal Growth Conditions

Event No.	Control	6912.1		6912.6		6912.9	
		A	P	A	P	A	P
Rosette Area on day 8	3.98			4.48	0.02		
Plot Coverage on day 8	31.82			35.81	0.01		
Leaf Number on day 3	5.25					5.69	0.00
Leaf Number on day 5	6.52	8.13	0.06	8.13	0.06		
Leaf Number on day 8	8.92					9.56	0.06
RGR of Rosette Area between day 5 and 8	0.53					0.58	0.10
1000 Seeds weight [gr]	0.02					0.02	0.00

Table 50: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 51
MAB58 – Normal Growth Conditions

Event No.	Control	6783.2		7522.10		7522.3		7523.6	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.67					2.11	0.00		
Rosette Diameter on day 5	2.24	2.57	0.00						
Rosette Diameter on day 8	3.60			4.06	0.07	4.54	0.00		
Rosette Area on day 3	0.89					1.36	0.00		
Rosette Area on day 5	1.54					2.29	0.00		
Rosette Area on day 8	3.98					5.98	0.00		
Plot Coverage on day 3	7.10					10.90	0.00		
Plot Coverage on day 5	12.30					18.32	0.00		
Plot Coverage on day 8	31.82					47.88	0.00		
Leaf Number on day 3	5.25					6.06	0.00	6.44	0.05

Event No.	Control	6783.2		7522.10		7522.3		7523.6	
		A	P	A	P	A	P	A	P
Leaf Number on day 5	6.52							8.38	0.00
Leaf Number on day 8	8.92	9.25	0.04			9.81	0.04		
RGR of Leaf Number between day 5 and 8	0.12	0.12	0.03						
1000 Seeds weight [gr]	0.02	0.02	0.08						

Table 51: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 52
MAB59 – Normal Growth Conditions

Event No.	Control	6793.4		6794.4		6794.5	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.67			2.38	0.05		
Rosette Diameter on day 5	2.24	2.73	0.06				
Rosette Area on day 3	0.89	1.27	0.06	1.65	0.03		
Plot Coverage on day 3	7.10	10.15	0.06	13.19	0.03		
Leaf Number on day 3	5.25	6.00	0.02	6.75	0.01		
Leaf Number on day 5	6.52	7.69	0.05	8.00	0.07		
Leaf Number on day 8	8.92			9.38	0.02		
RGR of Rosette Area between day 1 and 3	0.46					0.49	0.02
1000 Seeds weight [gr]	0.02					0.02	0.00

Table 52: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 53
MAB69 – Normal Growth Conditions

Event No.	Control	6651.11		6651.12		8341.1		8342.1	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.67	1.92	0.01						
Rosette Area on day 3	0.89	1.09	0.00						
Rosette Area on day 8	3.98	5.05	0.04						
Plot Coverage on day 3	7.10	8.74	0.00						
Plot Coverage on day 8	31.82	40.41	0.04						
Leaf Number on day 3	5.25	5.69	0.00					5.94	0.09
Leaf Number on day 8	8.92					8.94	0.08	9.31	0.00
RGR of Rosette Area between day 1 and 3	0.46	0.51	0.04						
1000 Seeds weight [gr]	0.02			0.02	0.01				

Table 53: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 54
MAB70 – Normal Growth Conditions

Event No.	Control	7971.3		7972.1		7974.3	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.67			1.94	0.00	2.27	0.00
Rosette Diameter on day 5	2.24			2.62	0.04	3.03	0.00
Rosette Diameter on day 8	3.60	4.40	0.00			5.01	0.05

Rosette Area on day 3	0.89	1.20	0.07	1.12	0.01	1.52	0.04
Rosette Area on day 5	1.54	2.06	0.05	1.87	0.00	2.49	0.10
Rosette Area on day 8	3.98	5.86	0.06			7.03	0.05
Plot Coverage on day 3	7.10	9.61	0.06	9.00	0.01	12.12	0.04
Plot Coverage on day 5	12.30	16.46	0.04	14.93	0.00	19.90	0.09
Plot Coverage on day 8	31.82	46.87	0.06			56.23	0.05
Leaf Number on day 3	5.25					6.44	0.05
Leaf Number on day 5	6.52					8.13	0.00
Leaf Number on day 8	8.92			9.75	0.09	10.38	0.05
RGR of Rosette Area between day 5 and 8	0.53	0.62	0.01			0.61	0.03

Table 54: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 55
MAB71 – Normal Growth Conditions

Event No.	Control	7331.4		7332.2		7333.5		7334.5	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 5	2.24			2.52	0.02				
Rosette Diameter on day 8	3.60	4.33	0.01						
Rosette Area on day 5	1.54							1.88	0.07
Rosette Area on day 8	3.98							4.68	0.00
Plot Coverage on day 5	12.30			14.25	0.08			15.05	0.05
Plot Coverage on day 8	31.82							37.48	0.00
Leaf Number on day 3	5.25			5.47	0.06			5.81	0.00
Leaf Number on day 5	6.52	7.56	0.00						
RGR of Leaf Number between day 1 and 3	0.16							0.17	0.01
RGR of Leaf Number between day 3 and 5	0.12					0.12	0.10		
RGR of Leaf Number between day 5 and 8	0.12					0.12	0.01		
RGR of Rosette Area between day 5 and 8	0.53					0.61	0.04		

Table 55: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 54
MAB72 – Normal Growth Conditions

Event No.	Control	8552.4		8553.2		8553.3	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.67	1.90	0.05			1.83	0.00
Rosette Diameter on day 5	2.24	2.67	0.00			2.55	0.01
Rosette Diameter on day 8	3.60	4.06	0.08	4.15	0.10		
Rosette Area on day 3	0.89	1.20	0.00	1.02	0.00	1.08	0.02
Rosette Area on day 5	1.54	2.00	0.00			1.87	0.00
Rosette Area on day 8	3.98	5.05	0.00			4.82	0.00
Plot Coverage on day 3	7.10	9.64	0.00	8.13	0.00	8.67	0.02
Plot Coverage on day 5	12.30	16.04	0.00			14.98	0.00
Plot Coverage on day 8	31.82	40.39	0.00			38.57	0.00
Leaf Number on day 3	5.25	5.88	0.00	5.56	0.00	5.50	0.00
Leaf Number on day 8	8.92			9.38	0.02		

Table 54: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 55
MAB74 – Normal Growth Conditions

Event No.	Control	7981.1		7982.4		7983.6		7983.9	
		A	P	A	P	A	P	A	P
Rosette Diameter on day 3	1.67			2.06	0.10	1.94	0.00		
Rosette Diameter on day 5	2.24					2.62	0.06		
Rosette Diameter on day 8	3.60					4.05	0.02		
Rosette Area on day 3	0.89			1.14	0.02				
Rosette Area on day 5	1.54			1.83	0.05	1.85	0.10		
Rosette Area on day 8	3.98					4.46	0.03		
Plot Coverage on day 3	7.10			9.13	0.02				
Plot Coverage on day 5	12.30			14.62	0.03	14.79	0.08		
Plot Coverage on day 8	31.82					35.66	0.01		
Leaf Number on day 3	5.25			5.75	0.04	5.31	0.07		
Leaf Number on day 5	6.52	6.26	0.02			7.25	0.04		
Leaf Number on day 8	8.92							9.13	0.07
RGR of Leaf Number between day 3 and 5	0.12			0.13	0.08			0.12	0.03
RGR of Rosette Area between day 1 and 3	0.46							0.33	0.00
RGR of Rosette Area between day 3 and 5	0.36	0.42	0.07						
Biomass DW [gr]	3.07								
1000 Seeds weight [gr]	0.02	0.02	0.02			0.02	0.05		

Table 55: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 56
MAB76 – Normal Growth Conditions

Event No.	Control	7633.1		7635.16	
		A	P	A	P
Rosette Diameter on day 3	1.67			1.93	0.04
Leaf Number on day 3	5.25	5.44	0.02		
Leaf Number on day 5	6.52			7.25	0.04

Table 56: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 57
MAB77 – Normal Growth Conditions

Event No.	Control	8212.1		8212.2	
		A	P	A	P
Leaf Number on day 3	5.25			5.63	0.00
Leaf Number on day 8	8.92	9.75	0.09		

Table 57: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 58
MAB79 – Normal Growth Conditions

Event No.	Control	7324.1		7961.1		7962.2	
		A	P	A	P	A	P
Rosette Diameter on day 3	1.67	1.84	0.10	1.93	0.05		
Rosette Diameter on day 5	2.24	2.53	0.01				
Rosette Diameter on day 8	3.60	4.32	0.03	4.01	0.04		
Rosette Area on day 3	0.89	1.08	0.09				
Rosette Area on day 8	3.98	5.29	0.03	4.78	0.05		
Plot Coverage on day 3	7.10	8.63	0.08				
Plot Coverage on day 8	31.82	42.32	0.03	38.27	0.05		
Leaf Number on day 3	5.25					5.75	0.04
Leaf Number on day 5	6.52					7.44	0.01
RGR of Rosette Area between day 5 and 8	0.53					0.59	0.01
1000 Seeds weight [gr]	0.02	0.02	0.00				

Table 58: Provided are the growth, biomass and yield parameters of transgenic or control plants as measured in Green House under normal irrigation. A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

EXAMPLE 7

IMPROVED FERTILIZER USE EFFICIENCY IN ARABIDOPSIS TISSUE CULTURE ASSAY

Plants transgenic to the following MAB genes were assayed for fertilizer use efficiency in a tissue culture assay: MAB115, MAB54, MAB55, MAB56, MAB57, MAB58, MAB59, MAB69, MAB70, MAB71, MAB72, MAB74, MAB76, MAB77, MAB79, MAB116, and MAB117 (the sequence identifiers of the cloned polynucleotides and their expressed polypeptides are provided in Table 7 above).

Assay 1: plant growth at nitrogen deficiency under tissue culture conditions

The present inventors have found the nitrogen use efficiency (NUE) assay to be relevant for the evaluation of the ABST candidate genes, since NUE deficiency encourages root elongation, increase of root coverage and allows detecting the potential of the plant to generate a better root system under drought conditions. In addition, there are indications in the literature that biological mechanisms of NUE and drought tolerance are linked (Wesley et al., 2002 Journal of Experiment Botany Vol 53, No.366, pp. 13-25).

Surface sterilized seeds were sown in basal media [50 % Murashige-Skoog medium (MS) supplemented with 0.8 % plant agar as solidifying agent] in the presence of Kanamycin (for selecting only transgenic plants). After sowing, plates were transferred for 2-3 days for stratification at 4 °C and then grown at 25 °C under 12-hour

light 12-hour dark daily cycles for 7 to 10 days. At this time point, seedlings randomly chosen were carefully transferred to plates with nitrogen-limiting conditions: 0.5 MS media in which the combined nitrogen concentration (NH_4NO_3 and KNO_3) is 0.75 mM (nitrogen deficient conditions) or 3 mM [Normal (optimal) nitrogen concentration].

- 5 Each plate contains 5 seedlings of same event, and 3-4 different plates (replicates) for each event. For each polynucleotide of the invention at least four independent transformation events were analyzed from each construct. Plants expressing the polynucleotides of the invention were compared to the average measurement of the control plants (empty vector or GUS reporter under the same promoter) used in the same experiment.

Digital imaging and statistical analysis - Parameters were measured and analyzed as previously described in Example 5, Assay 1 above.

- Tables 59-68 depict analyses of seedling parameters (as describe above) overexpressing the polynucleotides of the invention under the regulation of At6669 promoter under Nitrogene Deficiency conditions.

Table 59
MAB70 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	7971.3		7972.1		7974.1		7974.3	
		A	P	A	P	A	P	A	P
Dry Weight [gr]	0.01							0.01	0.00
Fresh Wight [gr]	0.10							0.18	0.04
Leaf Area on day 10	0.36					0.47	0.04	0.55	0.00
Leaf Area on day 5	0.14							0.24	0.04
Roots Coverage on day 10	5.58	7.93	0.01	7.45	0.06				
Roots Coverage on day 5	1.75	2.41	0.00					2.58	0.06
Roots Length on day 10	5.19	6.16	0.00						
Roots Length on day 5	2.86	3.16	0.05						
RGR of Roots Coverage between day 5 and 10	0.45					0.67	0.05		
RGR of Roots Coverage between day 1 and 5	0.81	2.35	0.02	2.01	0.06	2.10	0.05	2.23	0.02
RGR of Roots Length between day 1 and 5	0.16					0.24	0.04		
RGR of Roots Length between day 5 and 10	0.20	0.50	0.00	0.48	0.00	0.56	0.00	0.58	0.00

- 20 **Table 59:** Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 60
MAB71 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	7331.5		7332.2		7333.5		7334.4	
		A	P	A	P	A	P	A	P
Dry Weight [gr]	0.01	0.01	0.00	0.01	0.01	0.01	0.01	0.01	0.01
Fresh Wight [gr]	0.10	0.22	0.00	0.18	0.02	0.13	0.09		
Leaf Area on day 10	0.36	0.55	0.00					0.52	0.00
Leaf Area on day 5	0.14	0.28	0.00					0.21	0.00
Roots Coverage on day 10	5.58					8.19	0.05	9.47	0.03
Roots Coverage on day 5	1.75	2.33	0.10					2.99	0.02
Roots Length on day 10	5.19							6.69	0.03
Roots Length on day 5	2.86							3.84	0.01
RGR of Roots Length between day 1 and 5	0.16			0.20	0.07				
RGR of Roots Length between day 5 and 10	0.20	0.66	0.05			0.26	0.08		

Table 60: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 61
MAB74 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	7982.4		7983.9	
		A	P	A	P
Roots Coverage on day 10	5.58			9.76	0.06
Roots Length on day 10	5.19			6.70	0.00
RGR Leaf Area between day 5 and 10	0.30			0.44	0.09
RGR of Roots Coverage between day 5 and 10	0.45	0.63	0.08		

Table 61: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 62
MAB76 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	7635.4	
		A	P
RGR of Roots Coverage between day 5 and 10	0.45	0.70	0.07
RGR of Roots Length between day 1 and 5	0.16	0.26	0.07

Table 62: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

Table 63
MAB77 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	7931.11		8211.8		8212.2	
		A	P	A	P	A	P
Dry Weight [gr]	0.01					0.01	0.00
Fresh Wight [gr]	0.10			0.13	0.03	0.14	0.01
Roots Coverage on day 5	1.75	2.26	0.03				
RGR of Roots Coverage between day 5 and 10	0.45			0.71	0.01	0.75	0.05
RGR of Roots Length between day 1 and 5	0.16			0.24	0.03		
RGR of Roots Length between day 5 and 10	0.20	0.31	0.05	0.99	0.04	0.86	0.08

Table 63: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 64
MAB79 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	7323.3		7324.1		7961.1	
		A	P	A	P	A	P
Dry Weight [gr]	0.01	0.01	0.00	0.01	0.03	0.01	0.01
Fresh Wight [gr]	0.10	0.16	0.00			0.11	0.10
RGR of Roots Coverage between day 5 and 10	0.45	0.71	0.09				
RGR of Roots Coverage between day 1 and 5	0.81	3.11	0.00				
RGR of Roots Length between day 5 and 10	0.20	0.67	0.00	0.49	0.09		

Table 64: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 65
MAB115 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	8561.2		8564.2		8565.1	
		A	P	A	P	A	P
Dry Weight [gr]	0.005	0.006	0.00	0.010	0.00	0.009	0.00
Leaf Area on day 10	0.24					0.27	0.00
Leaf Area on day 5	0.35					0.38	0.01
Roots Coverage on day 10	1.67					2.13	0.02
Roots Coverage on day 5	3.38					4.80	0.03
Roots Length on day 10	2.39					2.74	0.00
Roots Length on day 5	3.46					4.22	0.02
RGR Leaf Area between day 5 and 10	0.37	0.43	0.00			0.48	0.00
RGR Leaf Area between day 1 and 5	0.16	0.19	0.00				
RGR of Roots Coverage between day 5 and 10	1.89	3.21	0.00	2.23	0.02	3.47	0.01
RGR of Roots Coverage between day 1 and 5	0.33	0.35	0.00	0.43	0.00	0.44	0.00
RGR of Roots Length between day 1 and 5	0.37	0.56	0.02	0.53	0.06	0.68	0.00
RGR of Roots Length between day 5 and 10	0.15			0.17	0.00	0.18	0.00

Table 65: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 66
MAB54 – Nitrogene Deficiency (0.75 mM Nitrogen)

Event No.	Control	8181.2		8182.2		8185.3	
		A	P	A	P	A	P
Dry Weight [gr]	0.005	0.009	0.00	0.008	0.00	0.007	0.00
Roots Coverage on day 10	1.67	1.80	0.04				
Roots Coverage on day 5	3.38	4.27	0.02	3.40	0.00		
Roots Length on day 10	2.39	2.52	0.01				
Roots Length on day 5	3.46	4.11	0.02	3.50	0.00		
RGR Leaf Area between day 5 and 10	0.37	0.45	0.00				
RGR Leaf Area between day 1 and 5	0.16	0.17	0.04			0.19	0.00
RGR of Roots Coverage between day 5 and 10	1.89	3.59	0.00	3.60	0.01	2.20	0.01
RGR of Roots Coverage between day 1 and 5	0.33	0.52	0.00	0.55	0.00	0.36	0.00

RGR of Roots Length between day 1 and 5	0.37	0.70	0.00	0.73	0.00	0.51	0.02
RGR of Roots Length between day 5 and 10	0.15	0.21	0.01	0.22	0.01	0.17	0.00

Table 66: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 67**MAB57 – Nitrogene Deficiency (0.75 mM Nitrogen)**

Event No.	6912.14			6912.20		6912.60	
	Control	A	P	A	P	A	P
Roots Coverage on day 7	5.55			6.71	0.10		
Roots Coverage on day 14	15.02	17.33	0.05				
Roots Length on day 7	4.93	5.54	0.10	6.12	0.02	6.34	0.02
Roots Length on day 14	7.83	8.76	0.02				
Fresh Weight	0.19	0.24	0.09				

Table 67: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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Table 68**MAB72 – Nitrogene Deficiency (0.75 mM Nitrogen)**

Event No.	Control	8552.1		8552.4		8553.2	
		A	P	A	P	A	P
Dry Weight [gr]	0.005	0.01	0.00	0.01	0.00	0.01	0.00
Leaf Area on day 10	0.24	0.24	0.01				
Roots Coverage on day 10	1.67	1.84	0.01	1.93	0.02	1.89	0.03
Roots Coverage on day 5	3.38	3.60	0.04	3.90	0.06	4.50	0.00
Roots Length on day 10	2.39	2.48	0.01				
Roots Length on day 5	3.46	3.70	0.04	3.65	0.04	3.84	0.00
RGR Leaf Area between day 5 and 10	0.37	0.47	0.00	0.39	0.00		
RGR Leaf Area between day 1 and 5	0.16			0.20	0.09		
RGR of Roots Coverage between day 5 and 10	1.89	1.93	0.03	2.29	0.06	3.04	0.01
RGR of Roots Coverage between day 1 and 5	0.33			0.35	0.00	0.52	0.00
RGR of Roots Length between day 1 and 5	0.37					0.55	0.01
RGR of Roots Length between day 5 and 10	0.15	0.16	0.00	0.18	0.00	0.22	0.01

Table 68: Provided are the growth and biomass parameters of transgenic or control plants as measured in Tissue Culture growth under Nitrogene Deficiency (0.75 mM N). A = average; P = p value; RGR = Relative Growth Rate. The indicated days refer to days from planting.

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EXAMPLE 8

**TRANSGENIC TOMATO AND ARABIDOPSIS PLANTS SHOW IMPROVED
TOLERANCE TO SALT AND WATER-DEFICIENCY STRESSES UNDER FIELD
CONDITIONS**

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To test the impact of AQP TIP2 genes on plant's stress tolerance, the present inventors have previously cloned and overexpressed a polynucleotide which comprises the nucleic acid sequence set forth by SEQ ID NO:2827 (also known as ABST36 set forth by SEQ ID NO:13 in WO2004/104162; or SITIP2;2) and which encodes the TIP2

polypeptide set forth by SEQ ID NO:2828 (which comprises the consensus sequence TLXFXFAGVGS; SEQ ID NO:2826). The nucleic acid constructs which comprises the ABST36 polynucleotide under the regulation of the constitutive Arabidopsis At6669 promoter (SEQ ID NO: 2823) (further referred to as the At6669::ABST36 construct) was further transformed into tomato (*Solanum lycopersicum*) as a model crop plant (Tom-ABST36), as well as into *Arabidopsis thaliana*. Four independent, T₂ transgenic tomato genotypes, overexpressing ABST36 in heterozygous form, were evaluated for their tolerance to salt and water deficiency in two different salt-stress field trials and one water-deficiency-stress field trial consisting of two water-deficiency regimes. Transgenic genotypes in each field trial were compared to their null-segregant counterparts as controls.

Materials and Experimental Methods

Tomato Salt-stress field trial - All field trials were performed in a light soil, in an open field (net-house) near Rehovot, Israel. The F1 hybrids of four independent events of the cross between ABST36-transgenic MicroTom plants and M82 tomato plants were grown for the first 3 weeks in a nursery under normal irrigation conditions. The seedlings were then transplanted into rows and grown in a commercial greenhouse. The salt-stress trial was divided into four blocks. In each block, two different irrigation systems were established: a normal water regime for tomato cultivation and a continuous irrigation with saline water (addition of 180 to 200 mM NaCl). Each block consisted of a total of 60 plants divided as follows: six plants per event and six seedling null segregants were planted in the control row and a similar number of plants were planted in the salt-stressed row. At the stage of about 80 % red fruits *in planta*, fruit yield, plant fresh weight, and harvest index were calculated. Harvest index was calculated as yield/plant biomass.

Tomato Water-deficiency-stress field trial - All field trials were performed in a light soil, in an open field (net-house) near Rehovot, Israel. The F1 hybrids of the four independent events were initially grown as described above. Three-week-old seedlings were transplanted to a net-greenhouse. The experiment was structured in four blocks containing three rows irrigated with different water levels and intervals (WLI-0, WLI-1, WLI-2). In each block, six transgenic plants per event analyzed and six non transgenic plants were transplanted in each row. Seedlings were transplanted after 4 weeks into

wet soil. The amount of water used to uniformly irrigate before transplanting reached maximum water capacity [20 % weight per weight (w/w)] at 60 cm depth, but without the creation of water overload. Each plant was transplanted near a dripper, with a 30-cm distance between plants, giving a total density of 2,600 plants per 1,000 m², according to a commercial growth protocol. Soil water capacity was measured using the standard procedures by sampling soil from the following three depths: 0 to 20 cm, 20 to 40 cm, and 40 to 60 cm. The water content in these soil layers was measured routinely every week. The soil contained 5 % hygroscopic water while the maximum water capacity of the soil was 20 %. All fertilizers were applied in the soil prior to plant transplantation.

The amount of both phosphorus and potassium was calculated to be sufficient for all seasons. Nitrogen was applied as recommended, equally to all treatments, through the irrigation system. Each row contained three dripping irrigation lines creating a coverage of nine drippers per 1 m². The water control was performed separately for each treatment. The soil was dried completely before the beginning of the experiment. The different water regimes were begun only 4 weeks after transplanting when plants initiated the flowering stage. The amount of water supplied every week during the assay was calculated at the beginning of every week following the recommendations of standard growth protocols. WLI-0 treatment (control) received the recommended total weekly irrigation volume divided into three irrigations. WLI-1 was irrigated three times a week, but the amount of water supplied was half that supplied to WLI-0. At the end of every week, WLI-1 plants received the amount of water required to reach maximum soil water capacity. WLI-2 plants were irrigated only once a week, at the beginning of the week. The water-stress experiment lasted throughout the flowering period (23 days), corresponding to four cycles of the above-described stresses. Afterwards, all treatments received the recommended amount of water. The calculated water amount was equal to the difference between the water contents in dry soil and in soil with maximum water capacity. At the end of each stress cycle, the water amounts were compared between treatments according to actual water content in the soil (S3). During the stress period, treatments WLI-1 and WLI-2 received a total of 75 % less water than the controls (WLI-0).

Experimental Results

Transgenic plants exhibit increased tolerance to salt stress - To induce salt stress, transgenic and control tomato plants were continuously irrigated in field trials with 180 to 200 mM NaCl. As shown in Figures 3a-c, 3g-j and Table 69 below, Tom-ABST36 plants appeared to be more vigorous in all of the experiments than the control plants, which were smaller and showed severe symptoms of leaf and shoot necrosis (see for example, Figure 3j). This was also associated with higher fruit yield in Tom-ABST36 plants relative to controls (Figure 3a).

Table 69
Salt-stress field trial

	Control			180 mM NaCl			
	Plant FW (tn/acre)	Fruit yield (tn/acre)	Harvest index	Plant FW (tn/acre)	Fruit yield (tn/acre)	%*	Harvest index
S/TIP2;2	ND	24.0	ND	2.8 ^a	8.0 ^a	110%	2.8
WT	ND	24.0	ND	1.4 ^b	3.8 ^b	0%	2.7

Table 69: Total yield (ton fruit/acre), plant fresh weight (FW), and harvest index were calculated for TOM ABST36 vs. control plants growing in the field under salt-stress conditions (180 mM NaCl). Results are the average of four independent events. a, b- Values in a column followed by different superscript letters are significantly different.

Transgenic plants exhibit increased tolerance to water-deficiency stress -

Transgenic plants subjected to water-deficiency stress exhibited a significantly higher (26 %, $p \leq 0.05$) plant biomass compared to control plants (Figure 3e). Moreover the Tom-ABST36 plants showed a significant (up to 21 %, $p \leq 0.05$) increment of fruit yield under water-deficient regimes (water level intervals WLI-1), while under normal irrigation, the yield improvement was even higher (27 %, $p \leq 0.05$; Figure 3d). The harvest index of the Tom-ABST36 plants was also higher when plants grew under regular and WLI-1 conditions while it remained similar to control when the water-deficient regime consisted of once-a-week irrigation (WLI-2) (Figure 3f).

The results from the three field trials provided strong evidence that the tomato Tom-ABST36 plants show improved tolerance to salt and water-deficiency stress relative to the control plants, which is translated into significant increments in plant biomass and more importantly, fruit yield.

Arabidopsis Salt-stress green house trial - A complementary experiment with transgenic Arabidopsis plants expressing the ABST36 construct showed increased

tolerance to a salt stress of 150 mM NaCl compared to control plants, as reflected in 42 % higher fresh biomass and 60 % higher dry biomass (Table 70 below).

In-vitro salt-stress assay - Seeds of transgenic *Arabidopsis* plants harboring the At6669::ABST36 construct or 35S::GUS construct (which was used as control) were sown in 1/2 MS media containing 40 mg/l kanamycin for selection. Selected seedlings were sub-cultured to 1/2 MS media with 0 or 150 mM NaCl. Plants were grown for a period of 3 weeks. Results are the average of four independent events that were analyzed in four repeats. For the determination of shoot dry weight, shoot plants were collected and dried for 24 hours at 60 °C and then weighed.

Table 70
Arabidopsis salt-stress assay

	0 mM NaCl		150 mM NaCl	
	Plant FW (mg)	Plant DW (mg)	Plant FW (mg)	Plant DW (mg)
Lines				
S/TIP2;2	408.28 ^a	23.52 ^a	68.55 ^a	4.4 ^a
WT	394.36 ^a	22.63 ^a	48.12 ^b	2.7 ^b

Table 70. *Arabidopsis* seedlings were grown in 0 and 150 mM NaCl under tissue-culture conditions. Shown are the fresh weight (FW) and total dry weight (DW) (both measured in milligrams) of ABST36 (SEQ ID NO: 2827) transgenic or wild type controls under normal conditions (0 mM NaCl) or salinity stress (150 mM NaCl). a, b-Values in a column followed by different superscript letters are significantly different at $P < 0.05$

Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims.

All publications, patents and patent applications mentioned in this specification are herein incorporated in their entirety by reference into the specification, to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference. In addition, citation or identification of any reference in this application shall not be construed as an admission that such reference is available as prior art to the present invention. To the extent that section headings are used, they should not be construed as necessarily limiting.

CD-ROM Content

The following lists the file content of the CD-ROM which is enclosed herewith and filed with the application. File information is provided as: File name/byte size/date of creation/operating system/machine format.

CD-ROM1 (1 file of SEQUENCE LISTING):

1. 44910_ST25.txt"/ 6,002,873 bytes/23 December 2008/ Microsoft Windows XP Professional/ PC

WHAT IS CLAIMED IS:

1. A method of increasing abiotic stress tolerance of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs: 33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259, thereby increasing the abiotic stress tolerance of the plant.

2. A method of increasing water use efficiency (WUE), fertilizer use efficiency (FUE), biomass, vigor and/or yield of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs: 33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259, thereby increasing the water use efficiency (WUE), the fertilizer use efficiency (FUE), the biomass, the vigor and/or the yield of the plant.

3. An isolated polynucleotide comprising a nucleic acid sequence at least 80 % identical to the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857 and 2859-3051.

4. A nucleic acid construct, comprising the isolated polynucleotide of claim 3 and a promoter for directing transcription of said nucleic acid sequence.

5. An isolated polypeptide, comprising an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ

ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

6. A plant cell comprising an exogenous polypeptide having an amino acid sequence at least 80 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

7. A plant cell comprising an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % homologous to the nucleic acid sequence selected from the group consisting of SEQ ID NOs:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857 and 2859-3051.

8. The method of claim 1 or 2, the isolated polynucleotide of claim 3, the nucleic acid construct of claim 4 or the plant cell of claim 7, wherein said polynucleotide is selected from the group consisting of SEQ ID NOs:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857 and 2859-3051.

9. The method of claim 1 or 2, the isolated polypeptide of claim 5 or the plant cell of claim 6, wherein said amino acid sequence is selected from the group consisting of SEQ ID NOs:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

10. The method of claim 1 or 2, the isolated polypeptide of claim 5 or the plant cell of claim 6, wherein said polypeptide is selected from the group consisting of

SEQ ID NOs: 33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065 and 3067-3259.

11. A method of increasing abiotic stress tolerance of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising the amino acid sequence set forth by SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259, thereby increasing the abiotic stress tolerance of the plant.

12. A method of increasing water use efficiency (WUE), fertilizer use efficiency (FUE), biomass, vigor and/or yield of a plant, comprising expressing within the plant an exogenous polynucleotide encoding a polypeptide comprising the amino acid sequence set forth by SEQ ID NO:33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259, thereby increasing the water use efficiency (WUE), the fertilizer use efficiency (FUE), the biomass, the vigor and/or the yield of the plant.

13. An isolated polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO:7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857, 2859-3050 or 3051.

14. A nucleic acid construct, comprising the isolated polynucleotide of claim 13 and a promoter for directing transcription of said nucleic acid sequence.

15. An isolated polypeptide, comprising the amino acid sequence set forth by SEQ ID NO: 33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494,

1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

16. A plant cell comprising an exogenous polypeptide having the amino acid sequence set forth by SEQ ID NO: 33, 34, 30, 27-29, 31, 32, 35-52, 1401-1403, 1405-1435, 1437-1494, 1496-1542, 1544-1553, 1555-1559, 1561-1827, 1829-1866, 1868-2450, 2453-2458, 2460-2463, 2465-2481, 2483, 2485-2746, 2765-2769, 3052-3065, 3067-3258 or 3259.

17. A plant cell comprising an exogenous polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO: 7, 8, 4, 1-3, 5, 6, 9-26, 53-55, 57-87, 89-147, 149-195, 197-206, 208-212, 214-480, 482-519, 521-1103, 1106-1111, 1113-1116, 1118-1134, 1136, 1138-1400, 2748-2764, 2843-2857, 2859-3050 or 3051.

18. The method of claim 1 or 11, wherein the abiotic stress is selected from the group consisting of salinity, water deprivation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

19. The method of claim 1 or 11, further comprising growing the plant expressing said exogenous polynucleotide under the abiotic stress.

20. The nucleic acid construct of claim 4 or 14, wherein said promoter is a constitutive promoter.

21. The plant cell of claim 6, 7, 16 or 17, wherein said plant cell forms a part of a plant.

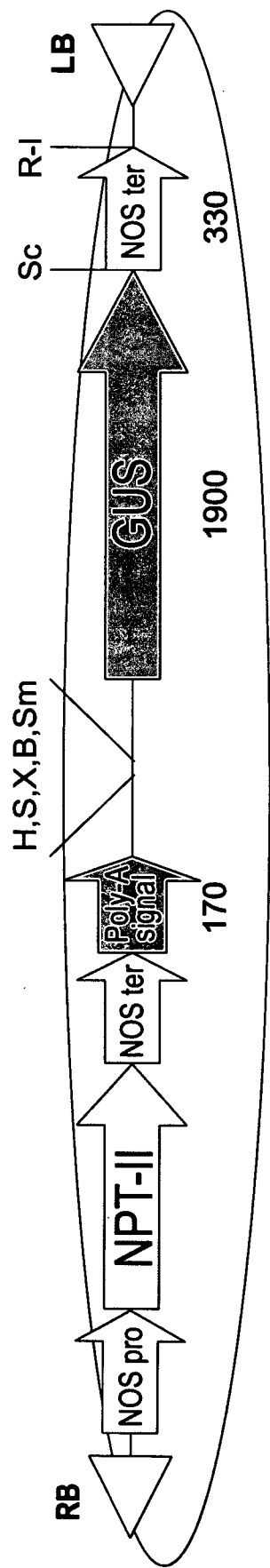


FIG. 1

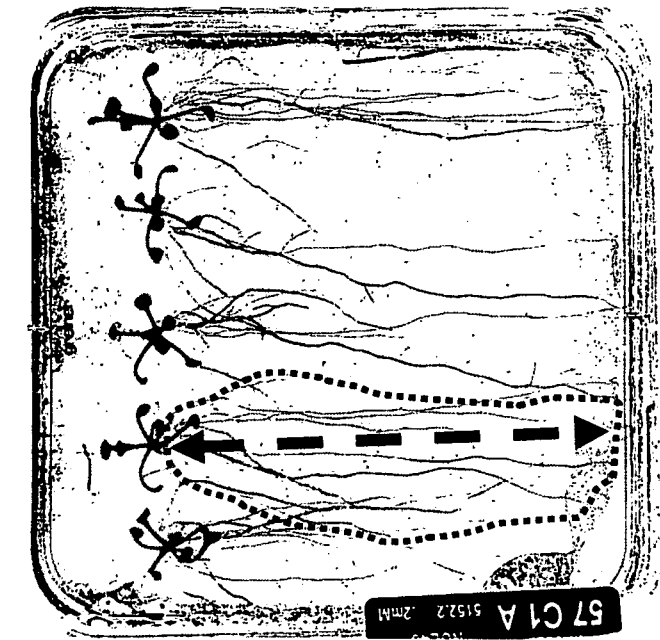


FIG. 2B

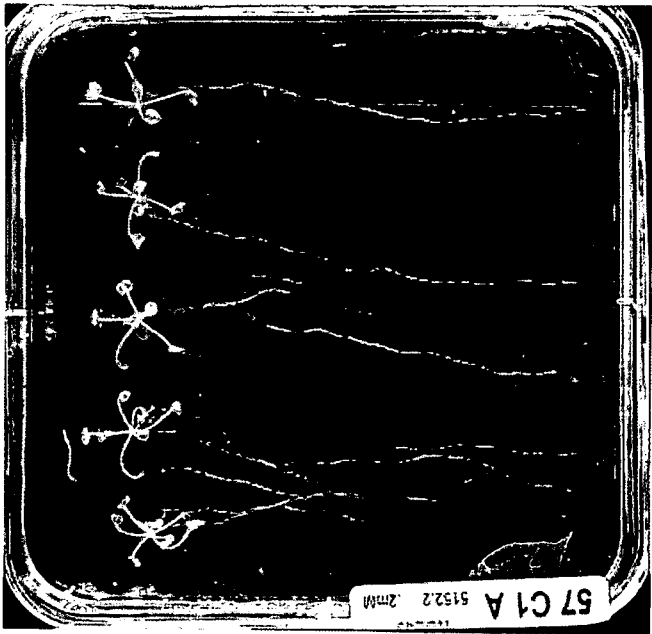
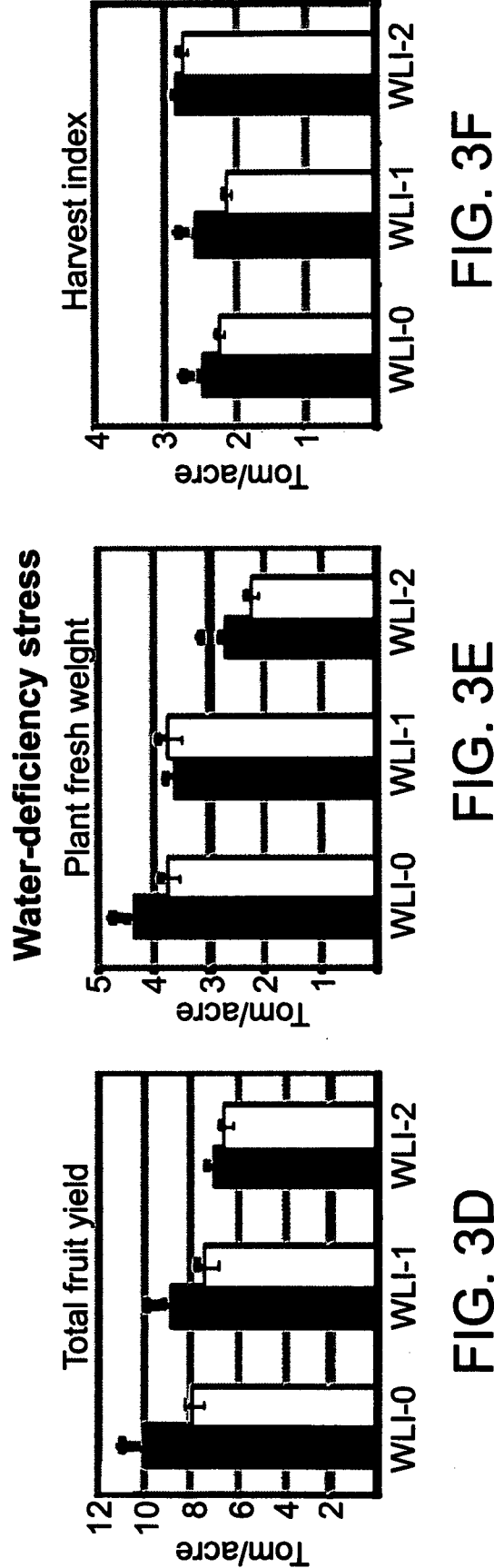
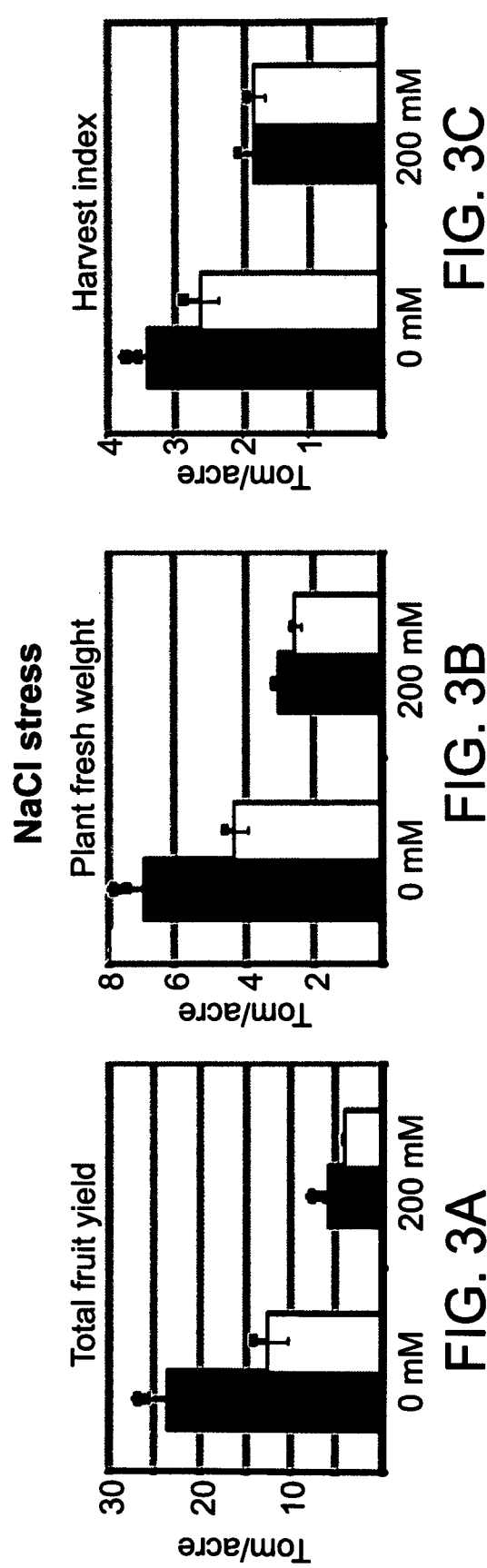


FIG. 2A





200 mM NaCl irrigation

FIG. 3J



FIG. 3I

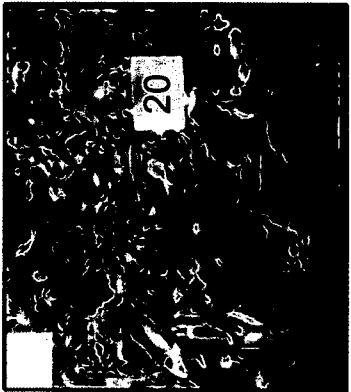


FIG. 3H



Standard irrigation

FIG. 3G