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(54) Titre : POLYNUCLEOTIDES ET POLYPEPTIDES ISOLES, ET LEURS PROCEDES D'UTILISATION POUR L'AUGMENTATION DE LA TOLERANCE AU STRESS ABIOTIQUE, DU RENDEMENT, DE LA VITESSE DE CROISSANCE, DE LA VITALITE, DE LA BIOMASSE, DE LA TENEUR EN HUILE, ET/OU DE L'EFFICACITE DE L'UTILISATION D'AZOTE DES PLANTES

(54) Title: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES, AND METHODS OF USING SAME FOR INCREASING ABIOTIC STRESS TOLERANCE, YIELD, GROWTH RATE, VIGOR, BIOMASS, OIL CONTENT, AND/OR NITROGEN USE EFFICIENCY OF PLANTS

(57) Abrégé/Abstract:
Polynucleotides and isolated polypeptides, nucleic acid constructs comprising the isolated polynucleotides, transgenic plants expressing same and methods of using same for increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant are disclosed.

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(57) Abstract: Polynucleotides and isolated polypeptides, nucleic acid constructs comprising the isolated polynucleotides, transgenic plants expressing same and methods of using same for increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant are disclosed.

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THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE THAN ONE VOLUME.

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ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES, AND METHODS OF USING SAME FOR INCREASING ABIOTIC STRESS TOLERANCE, YIELD, GROWTH RATE, VIGOR, BIOMASS, OIL CONTENT, AND/OR NITROGEN USE EFFICIENCY OF PLANTS

FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to isolated polypeptides and polynucleotides, nucleic acid constructs comprising same, transgenic plants expressing same and methods of using same for increasing abiotic stress tolerance (ABST), water use efficiency (WUE), yield (e.g., grain quantity and/or quality), biomass, oil content, growth rate, vigor, nitrogen use efficiency (NUE) and/or fertilizer use efficiency (FUE) of a plant.

The ever-increasing world population and the decreasing availability in arable land for agriculture affect the yield of plants and plant-related products. The global shortage of water supply, desertification, abiotic stress (ABS) conditions (e.g., salinity, drought, flood, suboptimal temperature and toxic chemical pollution), and/or limited nitrogen and fertilizer sources cause substantial damage to agricultural plants such as major alterations in the plant metabolism, cell death, and decreases in plant growth and crop productivity.

Drought is a gradual phenomenon, which involves periods of abnormally dry weather that persists long enough to produce serious hydrologic imbalances such as crop damage, water supply shortage and increased susceptibility to various diseases.

Salinity, high salt levels, affects one in five hectares of irrigated land. None of the top five food crops, *i.e.*, wheat, corn, rice, potatoes, and soybean, can tolerate excessive salt. Detrimental effects of salt on plants result from both water deficit, which leads to osmotic stress (similar to drought stress), and the effect of excess sodium ions on critical biochemical processes. As with freezing and drought, high salt causes water deficit; and the presence of high salt makes it difficult for plant roots to extract water from their environment. Thus, salination of soils that are used for agricultural production is a significant and increasing problem in regions that rely heavily on agriculture, and is worsen by over-utilization, over-fertilization and water shortage, typically caused by climatic change and the demands of increasing population.

Suboptimal temperatures affect plant growth and development through the whole plant life cycle. Thus, low temperatures reduce germination rate and high temperatures result in leaf necrosis. In addition, mature plants that are exposed to excess heat may experience heat shock, which may arise in various organs, including leaves and particularly fruit, when transpiration is insufficient to overcome heat stress. Heat also damages cellular structures, including organelles and cytoskeleton, and impairs membrane function. Heat shock may produce a decrease in overall protein synthesis, accompanied by expression of heat shock proteins, e.g., chaperones, which are involved in refolding proteins denatured by heat. High-temperature damage to pollen almost always occurs in conjunction with drought stress, and rarely occurs under well-watered conditions. Combined stress can alter plant metabolism in novel ways. Excessive chilling conditions, e.g., low, but above freezing, temperatures affect crops of tropical origins, such as soybean, rice, maize, and cotton. Typical chilling damage includes wilting, necrosis, chlorosis or leakage of ions from cell membranes. In addition, chilling may lead to yield losses and lower product quality through the delayed ripening of maize. Excessive light conditions, which occur under clear atmospheric conditions subsequent to cold late summer/autumn night's, can lead to photoinhibition of photosynthesis (disruption of photosynthesis).

Suboptimal nutrient (macro and micro nutrient) affect plant growth and development through the whole plant life cycle. One of the essential macronutrients for the plant is Nitrogen. Nitrogen is responsible for biosynthesis of amino acids and nucleic acids, prosthetic groups, plant hormones, plant chemical defenses, and the like. Nitrogen is often the rate-limiting element in plant growth and all field crops have a fundamental dependence on inorganic nitrogenous fertilizer. Since fertilizer is rapidly depleted from most soil types, it must be supplied to growing crops two or three times during the growing season. Additional important macronutrients are Phosphorous (P) and Potassium (K), which have a direct correlation to yield and general plant tolerance.

Yield is affected by various factors, such as, the number and size of the plant organs, plant architecture (for example, the number of branches), grains set length, number of filled grains, vigor (e.g. seedling), growth rate, root development, utilization of water, nutrients (e.g., nitrogen) and fertilizers, and stress tolerance.

Crops such as, corn, rice, wheat, canola and soybean account for over half of total human caloric intake, whether through direct consumption of the seeds themselves or through consumption of meat products raised on processed seeds or forage. Seeds are also a source of sugars, protein and oils and metabolites used in industrial processes. The ability to increase plant yield, whether through increase dry matter accumulation rate, modifying cellulose or lignin composition, increase stalk strength, enlarge meristem size, change of plant branching pattern, erectness of leaves, increase in fertilization efficiency, enhanced seed dry matter accumulation rate, modification of seed development, enhanced seed filling or by increasing the content of oil, starch or protein in the seeds would have many applications in agricultural and non-agricultural uses such as in the biotechnological production of pharmaceuticals, antibodies or vaccines.

Studies have shown that plant adaptations to adverse environmental conditions are complex genetic traits with polygenic nature. Conventional means for crop and horticultural improvements utilize selective breeding techniques to identify plants having desirable characteristics. However, selective breeding is tedious, time consuming and has an unpredictable outcome. Furthermore, limited germplasm resources for yield improvement and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Advances in genetic engineering have allowed mankind to modify the germplasm of plants by expression of genes-of-interest in plants. Such a technology has the capacity to generate crops or plants with improved economic, agronomic or horticultural traits.

WO publication No. 2009/013750 discloses genes, constructs and methods of increasing abiotic stress tolerance, biomass and/or yield in plants generated thereby.

WO publication No. 2008/122980 discloses genes constructs and methods for increasing oil content, growth rate and biomass of plants.

WO publication No. 2008/075364 discloses polynucleotides involved in plant fiber development and methods of using same.

WO publication No. 2007/049275 discloses isolated polypeptides, polynucleotides encoding same, transgenic plants expressing same and methods of using same for increasing plant abiotic stress tolerance and biomass.

WO publication No. 2004/104162 discloses methods of increasing abiotic stress tolerance and/or biomass in plants and plants generated thereby.

WO publication No. 2005/121364 discloses polynucleotides and polypeptides involved in plant fiber development and methods of using same for improving fiber quality, yield and/or biomass of a fiber producing plant.

WO publication No. 2007/020638 discloses methods of increasing abiotic stress tolerance and/or biomass in plants and plants generated thereby.

WO publication No. 2009/083958 discloses methods of increasing water use efficiency, fertilizer use efficiency, biotic/abiotic stress tolerance, yield and biomass in plant and plants generated thereby.

WO publication No. 2010/020941 discloses methods of increasing nitrogen use efficiency, abiotic stress tolerance, yield and biomass in plants and plants generated thereby.

SUMMARY OF THE INVENTION

According to an aspect of some embodiments of the present invention there is provided a method of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO:1-473, 783-1272, 1277-4139, 4142, 4146-5508 or 5509, thereby increasing the abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-473, 783-1272, 1274, 1275, 1277-4142, and 4146-5509, thereby increasing the abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least 80 % identical to SEQ ID NO:474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, 7548-8735 or 8736, thereby increasing the abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, and 7548-8736, thereby increasing the abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO:1-473, 783-1272, 1277-4139, 4142, 4146-5508 or 5509, wherein the nucleic acid sequence is capable of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-473, 783-1272, 1274, 1275, 1277-4142, and 4146-5509.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises an amino acid sequence at least 80 % homologous to the amino acid sequence set forth in SEQ ID NO:474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, 7548-8735 or 8736, wherein the amino

acid sequence is capable of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises the amino acid sequence selected from the group consisting of SEQ ID NOs:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, and 7548-8736.

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

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 SEQ ID NO:474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, 7548-8735 or 8736, wherein the amino acid sequence is capable of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NOs:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, and 7548-8736.

According to an aspect of some embodiments of the present invention there is provided a plant cell exogenously expressing the polynucleotide of some embodiments of the invention, or the nucleic acid construct of some embodiments of the invention.

According to an aspect of some embodiments of the present invention there is provided a plant cell exogenously expressing the polypeptide of some embodiments of the invention.

According to some embodiments of the invention, the nucleic acid sequence is as set forth in SEQ ID NO:1-473, 783-1272, 1274, 1275, 1277-4142, 4146-5508 or 5509.

According to some embodiments of the invention, the polynucleotide consists of the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-473, 783-1272, 1274, 1275, 1277-4142, and 4146-5509.

According to some embodiments of the invention, the nucleic acid sequence encodes an amino acid sequence at least 80 % homologous to SEQ ID NO:474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, 7548-8735 or 8736.

According to some embodiments of the invention, the nucleic acid sequence encodes the amino acid sequence selected from the group consisting of SEQ ID NOs:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, and 7548-8736.

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

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 abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

According to some embodiments of the invention, the yield comprises seed yield or oil yield.

According to some embodiments of the invention, the promoter is heterologous to the isolated polynucleotide and/or to the host cell.

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, 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.

Implementation of the method and/or system of embodiments of the invention can involve performing or completing selected tasks manually, automatically, or a

combination thereof. Moreover, according to actual instrumentation and equipment of embodiments of the method and/or system of the invention, several selected tasks could be implemented by hardware, by software or by firmware or by a combination thereof using an operating system.

For example, hardware for performing selected tasks according to embodiments of the invention could be implemented as a chip or a circuit. As software, selected tasks according to embodiments of the invention could be implemented as a plurality of software instructions being executed by a computer using any suitable operating system. In an exemplary embodiment of the invention, one or more tasks according to exemplary embodiments of method and/or system as described herein are performed by a data processor, such as a computing platform for executing a plurality of instructions. Optionally, the data processor includes a volatile memory for storing instructions and/or data and/or a non-volatile storage, for example, a magnetic hard-disk and/or removable media, for storing instructions and/or data. Optionally, a network connection is provided as well. A display and/or a user input device such as a keyboard or mouse are optionally provided as well.

BRIEF DESCRIPTION OF THE DRAWINGS

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:

FIG. 1 is a schematic illustration of the modified pGI binary plasmid containing the new At6669 promoter (SEQ ID NO:8741) and the GUSintron (pQYN_6669) used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; MCS – Multiple cloning site; RE – any restriction enzyme; 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 the invention were cloned into the vector while replacing the GUSintron reporter gene.

FIG. 2 is a schematic illustration of the modified pGI binary plasmid containing the new At6669 promoter (SEQ ID NO:8741) (pQFN) used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; MCS – Multiple cloning site; RE – any restriction enzyme; 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 the invention were cloned into the MCS of the vector.

FIGs. 3A-F are images depicting visualization of root development of transgenic plants exogenously expressing the polynucleotide of some embodiments of the invention when grown in transparent agar plates under normal (Figures 3A-B), osmotic stress (15 % PEG; Figures 3C-D) or nitrogen-limiting (Figures 3E-F) conditions. The different transgenes were grown in transparent agar plates for 17 days (7 days nursery and 10 days after transplanting). The plates were photographed every 3-4 days starting at day 1 after transplanting. Figure 3A – An image of a photograph of plants taken following 10 after transplanting days on agar plates when grown under normal (standard) conditions. Figure 3B – An image of root analysis of the plants shown in Figure 3A in which the lengths of the roots measured are represented by arrows. Figure 3C – An image of a photograph of plants taken following 10 days after transplanting on agar plates, grown under high osmotic (PEG 15 %) conditions. Figure 3D – An image of root analysis of the plants shown in Figure 3C in which the lengths of the roots measured are represented by arrows. Figure 3E – An image of a photograph of plants taken following 10 days after transplanting on agar plates, grown under low nitrogen conditions. Figure 3F – An image of root analysis of the plants shown in Figure 3E in which the lengths of the roots measured are represented by arrows.

FIG. 4 is a schematic illustration of the modified pGI binary plasmid containing the Root Promoter (pQNa_RP) used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); The isolated

polynucleotide sequences according to some embodiments of the invention were cloned into the MCS of the vector.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

The present invention, in some embodiments thereof, relates to isolated polypeptides and polynucleotides, nucleic acid constructs comprising the isolated polypeptides, transgenic plants expressing same and methods of using same for increasing abiotic stress tolerance (ABST), water use efficiency (WUE), yield (e.g., grain quantity and/or quality), biomass, oil content, growth rate, vigor, nitrogen use efficiency (NUE) and/or fertilizer use efficiency (FUE) of a plant.

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.

The present inventors have identified novel polypeptides and polynucleotides which can be used to increase abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant.

Thus, as shown in the Examples section which follows, the present inventors have utilized bioinformatics tools to identify polynucleotides which enhance abiotic stress tolerance, yield (e.g., seed yield, oil yield, oil content), biomass, growth rate, vigor, and/or nitrogen use efficiency of a plant. Genes which affect the trait-of-interest were identified based on expression profiles of genes of several Arabidopsis ecotypes and tissues, Tomato, Sorghum, Maize and Barley varieties (Examples 1-8), homology with genes known to affect the trait-of-interest and using digital expression profile in specific tissues and conditions (Tables 1-53, Examples 1-8; polynucleotides SEQ ID NOs:1-274; polypeptides SEQ ID NOs:474-731). Homologous polypeptides and polynucleotides having the same function were also identified (Table 54, Example 10; polynucleotides SEQ ID NOs:783-5509; polypeptides SEQ ID NOs:5510-8736). Transgenic plants over-expressing the identified polynucleotides and polypeptides (Table 55, Example 11) were found to exhibit increased abiotic stress tolerance (e.g., under osmotic stress or salinity stress), nitrogen use efficiency (e.g., root performance), biomass (under stress conditions or normal/standard conditions), growth rate (under

stress conditions or normal/standard conditions), and yield (Tables 56-83); Examples 14-15). Altogether, these results suggest the use of the novel polynucleotides and polypeptides of the invention for increasing abiotic stress tolerance, yield (including oil yield, seed yield and oil content), growth rate, biomass, vigor and/or nitrogen use efficiency of a plant.

Thus, according to an aspect of some embodiments of the invention, there is provided method of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO:1-473, 783-1272, 1277-4139, 4142, 4146-5508 or 5509, thereby increasing the abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of the plant.

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.

Plants are subject to a range of environmental challenges. Several of these, including salt stress, general osmotic stress, drought stress and freezing stress, have the ability to impact whole plant and cellular water availability. Not surprisingly, then, plant responses to this collection of stresses are related. Zhu (2002) Ann. Rev. Plant Biol. 53: 247-273 et al. note that "most studies on water stress signaling have focused on salt stress primarily because plant responses to salt and drought are closely related and the mechanisms overlap". Many examples of similar responses and pathways to this set of stresses have been documented. For example, the CBF transcription factors have been shown to condition resistance to salt, freezing and drought (Kasuga et al. (1999) Nature Biotech. 17: 287-291). The Arabidopsis rd29B gene is induced in response to both salt

and dehydration stress, a process that is mediated largely through an ABA signal transduction process (Uno et al. (2000) Proc. Natl. Acad. Sci. USA 97: 11632-11637), resulting in altered activity of transcription factors that bind to an upstream element within the rd29B promoter. In Mesembryanthemum crystallinum (ice plant), Patharker and Cushman have shown that a calcium-dependent protein kinase (McCDPK1) is induced by exposure to both drought and salt stresses (Patharker and Cushman (2000) Plant J. 24: 679-691). The stress-induced kinase was also shown to phosphorylate a transcription factor, presumably altering its activity, although transcript levels of the target transcription factor are not altered in response to salt or drought stress. Similarly, Saijo et al. demonstrated that a rice salt/drought-induced calmodulin-dependent protein kinase (OsCDPK7) conferred increased salt and drought tolerance to rice when overexpressed (Saijo et al. (2000) Plant J. 23: 319-327).

Exposure to dehydration invokes similar survival strategies in plants as does freezing stress (see, for example, Yelenosky (1989) Plant Physiol 89: 444-451) and drought stress induces freezing tolerance (see, for example, Siminovitch et al. (1982) Plant Physiol 69: 250-255; and Guy et al. (1992) Planta 188: 265-270). In addition to the induction of cold-acclimation proteins, strategies that allow plants to survive in low water conditions may include, for example, reduced surface area, or surface oil or wax production. In another example increased solute content of the plant prevents evaporation and water loss due to heat, drought, salinity, osmoticum, and the like therefore providing a better plant tolerance to the above stresses.

It will be appreciated that some pathways involved in resistance to one stress (as described above), will also be involved in resistance to other stresses, regulated by the same or homologous genes. Of course, the overall resistance pathways are related, not identical, and therefore not all genes controlling resistance to one stress will control resistance to the other stresses. Nonetheless, if a gene conditions resistance to one of these stresses, it would be apparent to one skilled in the art to test for resistance to these related stresses. Methods of assessing stress resistance are further provided in the Examples section which follows.

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 metabolic process(es) which lead to an increase in the plant's yield, biomass, vigor, and growth rate per fertilizer unit applied. The metabolic process can be the uptake, spread, absorbent, accumulation, relocation (within the plant) and use of one or more of the minerals and organic moieties absorbed by the plant, such as nitrogen, phosphates and/or potassium.

As used herein the phrase "fertilizer-limiting conditions" refers to growth conditions which include a level (e.g., concentration) of a fertilizer applied which is below the level needed for normal plant metabolism, growth, reproduction and/or viability.

As used herein the phrase "nitrogen use efficiency (NUE)" refers to the metabolic process(es) which lead to an increase in the plant's yield, biomass, vigor, and growth rate per nitrogen unit applied. The metabolic process can be the uptake, spread, absorbent, accumulation, relocation (within the plant) and use of nitrogen absorbed by the plant.

As used herein the phrase "nitrogen-limiting conditions" refers to growth conditions which include a level (e.g., concentration) of nitrogen (e.g., ammonium or nitrate) applied which is below the level needed for normal plant metabolism, growth, reproduction and/or viability.

Improved plant NUE and FUE is translated in the field into either harvesting similar quantities of yield, while implementing less fertilizers, or increased yields gained by implementing the same levels of fertilizers. Thus, improved NUE or FUE has a direct effect on plant yield in the field. Thus, the polynucleotides and polypeptides of some embodiments of the invention positively affect plant yield, seed yield, and plant biomass. In addition, the benefit of improved plant NUE will certainly improve crop quality and biochemical constituents of the seed such as protein yield and oil yield.

It should be noted that improved ABST will confer plants with improved vigor also under non-stress conditions, resulting in crops having improved biomass and/or yield e.g., elongated fibers for the cotton industry, higher oil content.

As used herein the phrase "plant yield" refers to the amount (e.g., as determined by weight or size) or quantity (numbers) of tissues or organs 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.

It should be noted that a plant yield can be affected by various parameters including, but not limited to, plant biomass; plant vigor; growth rate; seed yield; seed or grain quantity; seed or grain quality; oil yield; content of oil, starch and/or protein in harvested organs (e.g., seeds or vegetative parts of the plant); number of flowers (florets) per panicle (expressed as a ratio of number of filled seeds over number of primary panicles); harvest index; number of plants grown per area; number and size of harvested organs per plant and per area; number of plants per growing area (density); number of harvested organs in field; total leaf area; carbon assimilation and carbon partitioning (the distribution/allocation of carbon within the plant); resistance to shade; number of harvestable organs (e.g. seeds), seeds per pod, weight per seed; and modified architecture [such as increase stalk diameter, thickness or improvement of physical properties (e.g. elasticity)] .

As used herein the phrase "seed yield" refers to the number or weight of the seeds per plant, seeds per pod, or per growing area or to the weight of a single seed, or to the oil extracted per seed. Hence seed yield can be affected by seed dimensions (e.g., length, width, perimeter, area and/or volume), number of (filled) seeds and seed filling rate and by seed oil content. Hence increase seed yield per plant could affect the economic benefit one can obtain from the plant in a certain growing area and/or growing time; and increase seed yield per growing area could be achieved by increasing seed yield per plant, and/or by increasing number of plants grown on the same given area.

The term "seed" (also referred to as "grain" or "kernel") as used herein refers to a small embryonic plant enclosed in a covering called the seed coat (usually with some stored food), the product of the ripened ovule of gymnosperm and angiosperm plants which occurs after fertilization and some growth within the mother plant.

The phrase "oil content" as used herein refers to the amount of lipids in a given plant organ, either the seeds (seed oil content) or the vegetative portion of the plant (vegetative oil content) and is typically expressed as percentage of dry weight (10 % humidity of seeds) or wet weight (for vegetative portion).

It should be noted that oil content is affected by intrinsic oil production of a tissue (e.g., seed, vegetative portion), as well as the mass or size of the oil-producing tissue per plant or per growth period.

In one embodiment, increase in oil content of the plant can be achieved by increasing the size/mass of a plant's tissue(s) which comprise oil per growth period. Thus, increased oil content of a plant can be achieved by increasing the yield, growth rate, biomass and vigor of the plant.

As used herein the phrase "plant biomass" refers to the amount (e.g., 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. An increase in plant biomass can be in the whole plant or in parts thereof such as aboveground (harvestable) parts, vegetative biomass, roots and seeds.

As used herein the phrase "growth rate" refers to the increase in plant organ/tissue size per time (can be measured in cm^2 per day).

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 increased vigor could determine or affect the plant yield or the yield per growing time or growing area. In addition, early vigor (seed and/or seedling) results in improved field stand.

Improving early vigor is an important objective of modern rice breeding programs in both temperate and tropical rice cultivars. Long roots are important for proper soil anchorage in water-seeded rice. Where rice is sown directly into flooded fields, and where plants must emerge rapidly through water, longer shoots are associated with vigor. Where drill-seeding is practiced, longer mesocotyls and coleoptiles are important for good seedling emergence. The ability to engineer early vigor into plants would be of great importance in agriculture. For example, poor early vigor has been a limitation to the introduction of maize (Zea mays L.) hybrids based on Corn Belt germplasm in the European Atlantic.

It should be noted that a plant yield can be determined under stress (e.g., abiotic stress, nitrogen-limiting conditions) and/or non-stress (normal) conditions.

As used herein, the phrase "non-stress conditions" refers to the growth conditions (e.g., water, temperature, light-dark cycles, humidity, salt concentration, fertilizer concentration in soil, nutrient supply such as nitrogen, phosphorous and/or

potassium), that do not significantly go beyond the everyday climatic and other abiotic conditions that plants may encounter, and which allow optimal growth, metabolism, reproduction and/or viability of a plant at any stage in its life cycle (e.g., in a crop plant from seed to a mature plant and back to seed again). Persons skilled in the art are aware of normal soil conditions and climatic conditions for a given plant in a given geographic location. It should be noted that while the non-stress conditions may include some mild variations from the optimal conditions (which vary from one type/species of a plant to another), such variations do not cause the plant to cease growing without the capacity to resume growth.

The term "fiber" is usually inclusive of thick-walled conducting cells such as vessels and tracheids and to fibrillar aggregates of many individual fiber cells. Hence, the term "fiber" refers to (a) thick-walled conducting and non-conducting cells of the xylem; (b) fibers of extraxylary origin, including those from phloem, bark, ground tissue, and epidermis; and (c) fibers from stems, leaves, roots, seeds, and flowers or inflorescences (such as those of Sorghum vulgare used in the manufacture of brushes and brooms).

Example of fiber producing plants, include, but are not limited to, agricultural crops such as cotton, silk cotton tree (Kapok, Ceiba pentandra), desert willow, creosote bush, winterfat, balsa, kenaf, roselle, jute, sisal abaca, flax, corn, sugar cane, hemp, ramie, kapok, coir, bamboo, spanish moss and Agave spp. (e.g. sisal).

As used herein the phrase "fiber quality" refers to at least one fiber parameter which is agriculturally desired, or required in the fiber industry (further described hereinbelow). Examples of such parameters, include but are not limited to, fiber length, fiber strength, fiber fitness, fiber weight per unit length, maturity ratio and uniformity (further described hereinbelow.

Cotton fiber (lint) quality is typically measured according to fiber length, strength and fineness. Accordingly, the lint quality is considered higher when the fiber is longer, stronger and finer.

As used herein the phrase "fiber yield" refers to the amount or quantity of fibers produced from the fiber producing plant.

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 abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant 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).

The phrase "expressing within the plant an exogenous polynucleotide" as used herein refers to upregulating the expression level of an exogenous polynucleotide within the plant by introducing the exogenous polynucleotide into a plant cell or plant and expressing by recombinant means, as further described herein below.

As used herein "expressing" refers to expression at the mRNA and optionally polypeptide level.

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.

The term "endogenous" as used herein refers to any polynucleotide or polypeptide which is present and/or naturally expressed within a plant or a cell thereof.

According to some embodiments of the invention the exogenous polynucleotide comprises a nucleic acid sequence which is 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:1-473, 783-1272, 1277-4139, 4142, and 4146-5509.

According to some embodiments of the invention, the homology is a global homology, *i.e.*, an homology over the entire amino acid or nucleic acid sequences of the invention and not over portions thereof.

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 is 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 polynucleotide selected from the group consisting of SEQ ID NOs:1-473, 783-1272, 1277-4139, 4142, and 4146-5509.

According to some embodiments of the invention the exogenous polynucleotide is set forth by SEQ ID NO:1-473, 783-1272, 1274, 1275, 1277-4142, 4146-5508 or 5509.

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).

The term "isolated" refers to at least partially separated from the natural environment e.g., from a plant cell.

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 exogenous polynucleotide of the invention encodes a polypeptide having an amino acid sequence 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: 474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, and 7548-8736.

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. 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 rational a paralogue (homolog to a gene in the same organism) is found. In case of large sequence families, the ClustalW program may be used, followed by a neighbor-joining tree 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:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, 7548-8735 or 8736.

Nucleic acid sequences encoding the polypeptides of the present invention may be optimized for expression. 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 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 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 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 SDCU = n = 1 N [(Xn - Yn) / Yn] 2 / N, where Xn refers to the frequency of usage of

codon n in highly expressed plant genes, where Yn 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).

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. The Codon Usage Database contains codon usage tables for a number of different species, with each codon usage Table 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 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 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 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 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.

According to some embodiments of the invention, the exogenous polynucleotide is a non-coding RNA.

As used herein the phrase 'non-coding RNA" refers to an RNA molecule which does not encode an amino acid sequence (a polypeptide). Examples of such non-coding RNA molecules include, but are not limited to, an antisense RNA, a pre-miRNA (precursor of a microRNA), or a precursor of a Piwi-interacting RNA (piRNA).

Non-limiting examples of non-coding RNA polynucleotides are provided in SEQ ID NOs:217, 273, 274, and 473.

Thus, the invention encompasses nucleic acid sequences described hereinabove; 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.

The invention provides an isolated polynucleotide comprising a nucleic acid sequence 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 polynucleotide selected from the group consisting of SEQ ID NOs:1-473, 783-1272, 1277-4139, 4142, and 4146-5509.

According to some embodiments of the invention the nucleic acid sequence is capable of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant.

According to some embodiments of the invention the isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-473, 783-1272, 1274, 1275, 1277-4142, and 4146-5509.

According to some embodiments of the invention the isolated polynucleotide is set forth by SEQ ID NO:1-473, 783-1272, 1274, 1275, 1277-4142, 4146-5508 or 5509.

The invention provides an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises an amino acid sequence 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 the amino acid sequence selected from the group consisting of SEQ ID NOs: 474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, and 7548-8736.

According to some embodiments of the invention the amino acid sequence is capable of increasing abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant.

The invention provides an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises the amino acid sequence selected from the group consisting of SEQ ID NOs:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, and 7548-8736.

The invention provides an isolated polypeptide comprising an amino acid sequence 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: 474-562, 564-620, 622-750, 752-782, 5510-5939, 5946-6856, 6858-7540, 7543, 7544, and 7548-8736.

According to some embodiments of the invention, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, and 7548-8736.

According to some embodiments of the invention, the polypeptide is set forth by SEQ ID NO:474-782, 5510-5940, 5942, 5943, 5945-6856, 6858-7544, 7548-8735 or 8736.

According to some embodiments of the 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 of the isolated polynucleotide in a host cell.

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 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, 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 amplectens, Dioclea spp, Dolichos spp., Dorycnium rectum, Echinochloa pyramidalis, Ehraffia spp., Eleusine coracana, Eragrestis spp., Erythrina spp., Eucalypfus spp., Euclea schimperi, Eulalia vi/losa, Pagopyrum spp., Feijoa sellowlana, Fragaria spp., Flemingia spp, Freycinetia banksli, Geranium thunbergii, GinAgo biloba, Glycine javanica, Gliricidia spp, Gossypium hirsutum, Grevillea spp., Guibourtia coleosperma, Hedysarum spp., Hemaffhia altissima, Heteropogon contoffus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hypeffhelia dissolute, Indigo

incamata, Iris spp., Leptarrhena pyrolifolia, Lespediza spp., Lettuca 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 spp., Phoenix canariensis, Phormium cookianum, Photinia spp., Picea glauca, Pinus spp., Pisum sativam, Podocarpus totara, Pogonarthria fleckii, Pogonaffhria squarrosa, Populus spp., Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus communis, Quercus spp., Rhaphiolepsis umbellata, Rhopalostylis sapida, Rhus natalensis, Ribes grossularia, Ribes spp., Robinia pseudoacacia, Rosa spp., Rubus spp., 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, 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 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, millet, leguminosae (bean, pea), flax, lupinus, rapeseed, tobacco, poplar and cotton.

According to some embodiments of the invention, there is provided a plant cell exogenously expressing the polynucleotide of some embodiments of the invention, the nucleic acid construct of some embodiments of the invention and/or the polypeptide of some embodiments of the invention.

According to some embodiments of the invention, expressing the exogenous polynucleotide of the invention within the plant is 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 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 for directing transcription of the exogenous polynucleotide in a host cell (a plant cell). Further details of suitable transformation approaches are provided hereinbelow.

As mentioned, the nucleic acid construct according to some embodiments of the invention comprises a promoter sequence and the isolated polynucleotide of the invention.

According to some embodiments of the invention, the isolated polynucleotide is operably linked to the promoter sequence.

A coding nucleic acid sequence is "operably linked" to a regulatory sequence (e.g., promoter) if the regulatory sequence is capable of exerting a regulatory effect on the coding sequence linked thereto.

As used herein, the term "promoter" refers to a region of DNA which lies 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 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:8739; Odell et al., Nature 313:810-812, 1985); Arabidopsis At6669 promoter (SEQ ID NO:8738; see PCT Publication No. WO04081173A2); Arabidopsis new At6669 promoter (SEQ ID NO:8741); maize Ubi 1 (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 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.

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 90:9586-9590, 1993], seed-preferred promoters [e.g., Napin (originated from Brassica napus which is characterized by a seed specific promoter activity; Stuitje A. R. et.al. Plant Biotechnology Journal 1 (4): 301–309; SEQ ID NO:8740), 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 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 ltrl 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), 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 family (Plant J 12:235-46, 1997), sorgum 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, chalene synthase (chsA) (Van der Meer, et al., Plant Mol. Biol. 15, 95-109, 1990), LAT52 (Twell et al Mol. Gen Genet. 217:240-245; 1989), apetala- 3], and root promoters such as the ROOTP promoter [SEQ ID NO: 8742].

Suitable abiotic stress-inducible promoters include, but not limited to, salt-inducible promoters such as RD29A (Yamaguchi-Shinozalei 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. al., Plant J. 11:1285-1295, 1997) and maize Ivr2 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 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.

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 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.

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 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 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 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 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), Galon et al. (1992), Atreya et al. (1992) and Huet et al. (1994).

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 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-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 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 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. A polypeptide can thus be produced by the protein expression system of the chloroplast and become integrated into the chloroplast's inner membrane.

Since processes which increase abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency of a plant 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 tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency.

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 than 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 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 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 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.

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 abiotic stress tolerance, water use efficiency, fertilizer use efficiency, growth, biomass, yield and/or vigor traits, using conventional plant breeding techniques.

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

Non-limiting examples of abiotic stress conditions include, salinity, drought, water deprivation, excess of water (e.g., flood, waterlogging), etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

Thus, the invention encompasses plants exogenously expressing the polynucleotide(s), the nucleic acid constructs 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 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 Immuno Sorbent Assay (ELISA), radio-immuno-assays (RIA), immunohistochemistry, immunocytochemistry, immunofluorescence and the like.

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.

The sequence information and annotations uncovered by the present teachings can be harnessed in favor of classical breeding. Thus, sub-sequence data of those polynucleotides described above, can be used as markers for marker assisted selection (MAS), in which a marker is used for indirect selection of a genetic determinant or determinants of a trait of interest (e.g., abiotic stress tolerance, yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, and/or nitrogen use efficiency). Nucleic acid data of the present teachings (DNA or RNA sequence) may contain or be linked to polymorphic sites or genetic markers on the genome such as restriction fragment length polymorphism (RFLP), microsatellites and single nucleotide polymorphism (SNP), DNA fingerprinting (DFP), amplified fragment length polymorphism (AFLP), expression level polymorphism, polymorphism of the encoded polypeptide and any other polymorphism at the DNA or RNA sequence.

Examples of marker assisted selections include, but are not limited to, selection for a morphological trait (e.g., a gene that affects form, coloration, male sterility or resistance such as the presence or absence of awn, leaf sheath coloration, height, grain color, aroma of rice); selection for a biochemical trait (e.g., a gene that encodes a protein that can be extracted and observed; for example, isozymes and storage proteins); selection for a biological trait (e.g., pathogen races or insect biotypes based on host pathogen or host parasite interaction can be used as a marker since the genetic constitution of an organism can affect its susceptibility to pathogens or parasites).

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

Plant lines exogenously expressing the polynucleotide or the polypeptide of the invention are screened to identify those that show the greatest increase of the desired plant trait.

The effect of the transgene (the exogenous polynucleotide encoding the polypeptide) on abiotic stress tolerance can be determined using known methods such as detailed below and in the Examples section which follows.

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, growth rate, leaf size, leaf coverage (overall leaf area), 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.

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.

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: RWC = [(FW – DW) / (TW – DW)] x 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 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 conditions.

Nitrogen use efficiency – To analyze whether the transgenic plants (e.g., Arabidopsis plants) are more responsive to nitrogen, plant are grown in 0.75-3 mM (nitrogen deficient conditions) or 6-10 mM (optimal nitrogen concentration). Plants are allowed to grow for additional 25 days or until seed production. The plants are then analyzed for their overall size, time to flowering, yield, protein content of shoot and/or grain/ seed production. The parameters checked can be the overall size of the plant, 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 greenness is highly correlated), amino acid and the total protein content of the seeds or other plant parts such as leaves or shoots and oil content. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher measured parameters levels than wild-type plants, are identified as nitrogen use efficient plants.

Nitrogen Use efficiency assay using plantlets – The assay is done according to Yanagisawa-S. et al. with minor modifications ("Metabolic engineering with Dof1 transcription factor in plants: Improved nitrogen assimilation and growth under low-nitrogen conditions" *Proc. Natl. Acad. Sci. USA* 101, 7833-7838). Briefly, transgenic plants which are grown for 7-10 days in 0.5 x MS [Murashige-Skoog] supplemented with a selection agent are transferred to two nitrogen-limiting conditions: MS media in which the combined nitrogen concentration (NH_4NO_3 and KNO_3) was 0.75 mM (nitrogen deficient conditions) or 6-15 mM (optimal nitrogen concentration). Plants are allowed to grow for additional 30-40 days and then photographed, individually removed from the Agar (the shoot without the roots) and immediately weighed (fresh weight) for later statistical analysis. Constructs for which only T1 seeds are available are sown on selective media and at least 20 seedlings (each one representing an independent transformation event) are carefully transferred to the nitrogen-limiting media. For constructs for which T2 seeds are available, different transformation events are analyzed. Usually, 20 randomly selected plants from each event are transferred to the nitrogen-limiting media allowed to grow for 3-4 additional weeks and individually weighed at the end of that period. Transgenic plants are compared to control plants grown in parallel under the same conditions. Mock- transgenic plants expressing the

uidA reporter gene (GUS) under the same promoter or transgenic plants carrying the same promoter but lacking a reporter gene are used as control.

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^- mediated reduction of NO_3^- to NO_2^- (Vodovotz 1996 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.

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).

The effect of the transgene on plant's vigor, growth rate, biomass, yield and/or oil content can be determined using known methods.

Plant vigor - 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.

Growth rate - 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 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.

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 cm^2 per day of leaf area).

Relative growth area can be calculated using Formula II.

Formula II: Relative growth rate area = Regression coefficient of area along time course.

Seed yield - Evaluation of the seed yield per plant can be done by measuring the amount (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.

For example, the total seeds from 8-16 plants can be collected, weighted using e.g., an analytical balance and the total weight can be divided by the number of plants. Seed yield 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.

In addition, seed yield can be determined via the weight of 1000 seeds. The weight of 1000 seeds can be determined as follows: seeds are scattered on a glass tray and a picture is taken. Each sample is weighted and then using the digital analysis, the number of seeds in each sample is calculated.

The 1000 seeds weight can be calculated using formula III:

Formula III: 1000 Seed Weight = number of seed in sample/ sample weight X 1000.

The Harvest Index can be calculated using Formula IV.

Formula IV: Harvest Index = Average seed yield per plant/ Average dry weight.

Grain protein concentration - Grain protein content (g grain protein m^{-2}) is 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 (g grain protein kg^{-1} grain).

Fiber length - 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.

According to some embodiments of the invention, increased yield of corn may be manifested as one or more of the following: increase in the number of plants per growing area, increase in the number of ears per plant, increase in the number of rows per ear, number of kernels per ear row, kernel weight, thousand kernel weight (1000-weight), ear length/diameter, increase oil content per kernel and increase starch content per kernel.

As mentioned, the increase of plant yield can be determined by various parameters. For example, increased yield of rice may be manifested by an increase in one or more of the following: number of plants per growing area, number of panicles per plant, number of spikelets per panicle, number of flowers per panicle, increase in the seed filling rate, increase in thousand kernel weight (1000-weight), increase oil content per seed, increase starch content per seed, among others. An increase in yield may also result in modified architecture, or may occur because of modified architecture.

Similarly, increased yield of soybean may be manifested by an increase in one or more of the following: number of plants per growing area, number of pods per plant, number of seeds per pod, increase in the seed filling rate, increase in thousand seed weight (1000-weight), reduce pod shattering, increase oil content per seed, increase protein content per seed, among others. An increase in yield may also result in modified architecture, or may occur because of modified architecture.

Increased yield of canola may be manifested by an increase in one or more of the following: number of plants per growing area, number of pods per plant, number of seeds per pod, increase in the seed filling rate, increase in thousand seed weight (1000-weight), reduce pod shattering, increase oil content per seed, among others. An increase in yield may also result in modified architecture, or may occur because of modified architecture.

Increased yield of cotton may be manifested by an increase in one or more of the following: number of plants per growing area, number of bolls per plant, number of seeds per boll, increase in the seed filling rate, increase in thousand seed weight (1000-

weight), increase oil content per seed, improve fiber length, fiber strength, among others. An increase in yield may also result in modified architecture, or may occur because of modified architecture.

Oil content - The oil content of a plant can be determined by extraction of the oil 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 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 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.

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).

Any of the transgenic plants described hereinabove or parts thereof may be processed to produce a feed, meal, protein or oil preparation, such as for ruminant animals.

The transgenic plants described hereinabove, which exhibit an increased oil content can be used to produce plant oil (by extracting the oil from the plant).

The plant oil (including the seed oil and/or the vegetative portion oil) produced according to the method of the invention may be combined with a variety of other ingredients. The specific ingredients included in a product are determined according to the intended use. Exemplary products include animal feed, raw material for chemical modification, biodegradable plastic, blended food product, edible oil, biofuel, cooking oil, lubricant, biodiesel, snack food, cosmetics, and fermentation process raw material. Exemplary products to be incorporated to the plant oil include animal feeds, human food

products such as extruded snack foods, breads, as a food binding agent, aquaculture feeds, fermentable mixtures, food supplements, sport drinks, nutritional food bars, multi-vitamin supplements, diet drinks, and cereal foods.

According to some embodiments of the invention, the oil comprises a seed oil.

According to some embodiments of the invention, the oil comprises a vegetative portion oil.

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

As used herein the term "about" refers to ± 10 %.

The terms "comprises", "comprising", "includes", "including", "having" and 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.

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.

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.

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.

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.

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 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.

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 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

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. (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. 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). 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

GENERAL EXPERIMENTAL AND BIOINFORMATICS METHODS

RNA extraction – Tissues growing at various growth conditions (as described below) were sampled and RNA was extracted using TRIzol Reagent from Invitrogen. Approximately 30-50 mg of tissue was taken from samples. The weighed tissues were ground using pestle and mortar in liquid nitrogen and resuspended in 500 µl of TRIzol Reagent. To the homogenized lysate, 100 µl of chloroform was

added followed by precipitation using isopropanol and two washes with 75 % ethanol. The RNA was eluted in 30 μl of RNase-free water. RNA samples were cleaned up using Qiagen's RNeasy minikit clean-up protocol as per the manufacturer's protocol (QIAGEN Inc, CA USA). For convenience, each micro-array expression information tissue type has received an expression Set ID.

Correlation analysis – was performed for selected genes according to some embodiments of the invention, in which the characterized parameters (measured parameters according to the correlation IDs) were used as "x axis" for correlation with the tissue transcriptom which was used as the "Y axis". For each gene and measured parameter a correlation coefficient "R" was calculated (using Pearson correlation) along with a p-value for the significance of the correlation. When the correlation coefficient (R) between the levels of a gene's expression in a certain tissue and a phenotypic performance across ecotypes/variety/hybrid is high in absolute value (between 0.5-1), there is an association between the gene (specifically the expression level of this gene) the phenotypic characteristic (e.g., improved nitrogen use efficiency, abiotic stress tolerance, yield, growth rate and the like).

EXAMPLE 1

BIO-INFORMATICS TOOLS FOR IDENTIFICATION OF GENES WHICH INCREASE ABIOTIC STRESS TOLERANCE, YIELD AND AGRONOMICAL IMPORTANT TRAITS IN PLANTS

The present inventors have identified polynucleotides which upregulation of expression thereof can increase abiotic stress tolerance (ABST), water use efficiency (WUE), yield, oil content, growth rate, vigor, biomass, nitrogen use efficiency (NUE), and fertilizer use efficiency (FUE) of a plant.

All nucleotide sequence datasets used here were originated from publicly available databases or from performing sequencing using the Solexa technology (e.g. Barley and Sorghum). Sequence data from 100 different plant species was introduced into a single, comprehensive database. Other information on gene expression, protein annotation, enzymes and pathways were also incorporated. Major databases used include:

- ***Genomes***

- Arabidopsis genome [TAIR genome version 6].
- Rice genome [IRGSP build 4.0].
- Poplar [Populus trichocarpa release 1.1 from JGI (assembly release v1.0)].
- Brachypodium [JGI 4x assembly].
- Soybean [DOE-JGI SCP, version Glyma0].
- Grape [French-Italian Public Consortium for Grapevine Genome Characterization grapevine genome].
- Castobean [TIGR/J Craig Venter Institute 4x assembly].
- Sorghum [DOE-JGI SCP, version Sbi1].
- Partially assembled genome of Maize.

- ***Expressed EST and mRNA sequences were extracted from the following databases:***

- GenBank versions 154, 157, 160, 161, 164, 165, 166 and 168.
- RefSeq
- TAIR

- ***Protein and pathway databases***

- Uniprot
- AraCyc
- ENZYME

- ***Microarray datasets were downloaded from:***

- GEO
- TAIR .
- Proprietary microarray data (WO2008/122980 and Example 2 below).

- ***QTL and SNPs information***

- Gramene
- Panzea

Database assembly - was performed to build a wide, rich, reliable annotated and easy to analyze database comprised of publicly available genomic mRNA, ESTs DNA sequences, data from various crops as well as gene expression, protein annotation and pathway data QTLs, and other relevant information.

Database assembly is comprised of a toolbox of gene refining, structuring, annotation and analysis tools enabling to construct a tailored database for each gene discovery project. Gene refining and structuring tools enable to reliably detect splice variants and antisense transcripts, generating understanding of various potential phenotypic outcomes of a single gene. The capabilities of the "LEADS" platform of Compugen LTD for analyzing human genome have been confirmed and accepted by the scientific community [see e.g., "Widespread Antisense Transcription", Yelin, et al. (2003) Nature Biotechnology 21, 379-85; "Splicing of Alu Sequences", Lev-Maor, et al. (2003) Science 300 (5623), 1288-91; "Computational analysis of alternative splicing using EST tissue information", Xie H et al. Genomics 2002], and have been proven most efficient in plant genomics as well.

EST clustering and gene assembly - For gene clustering and assembly of organisms with available genome sequence data (arabidopsis, rice, castorbean, grape, brachypodium, poplar, soybean, sorghum) the genomic LEADS version (GANG) was employed. This tool allows most accurate clustering of ESTs and mRNA sequences on genome, and predicts gene structure as well as alternative splicing events and anti-sense transcription.

For organisms with no available full genome sequence data, "expressed LEADS" clustering software was applied.

Gene annotation - Predicted genes and proteins were annotated as follows: Blast search against all plant UniProt sequences was performed. Open reading frames of each putative transcript were analyzed and longest ORF with higher number of homologues was selected as predicted protein of the transcript. The predicted proteins were analyzed by InterPro.

Blast against proteins from AraCyc and ENZYME databases was used to map the predicted transcripts to AraCyc pathways.

Predicted proteins from different species were compared using blast algorithm to validate the accuracy of the predicted protein sequence, and for efficient detection of orthologs.

Gene expression profiling - Several data sources were exploited for gene expression profiling, namely microarray data and digital expression profile (see below). According to gene expression profile, a correlation analysis was performed to identify genes which are co-regulated under different development stages and environmental conditions and associated with different phenotypes.

Publicly available microarray datasets were downloaded from TAIR and NCBI GEO sites, renormalized, and integrated into the database. Expression profiling is one of the most important resource data for identifying genes important for ABST, increased yield, growth rate, vigor, biomass, oil content, WUE, NUE and FUE of a plant.

A digital expression profile summary was compiled for each cluster according to all keywords included in the sequence records comprising the cluster. Digital expression, also known as electronic Northern Blot, is a tool that displays virtual expression profile based on the EST sequences forming the gene cluster. The tool provides the expression profile of a cluster in terms of plant anatomy (e.g., the tissue/organ in which the gene is expressed), developmental stage (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). Given a random distribution of ESTs in the different clusters,

the digital expression provides a probability value that describes the probability of a cluster having a total of N ESTs to contain X ESTs from a certain collection of libraries. For the probability calculations, the following is taken into consideration: a) the number of ESTs in the cluster, b) the number of ESTs of the implicated and related libraries, c) the overall number of ESTs available representing the species. Thereby clusters with low probability values are highly enriched with ESTs from the group of libraries of interest indicating a specialized expression.

Recently, the accuracy of this system was demonstrated by Portnoy et al., 2009 (Analysis Of The Melon Fruit Transcriptome Based On 454 Pyrosequencing) in: Plant & Animal Genomes XVII Conference, San Diego, CA. Transcriptomic analysis, based on relative EST abundance in data was performed by 454 pyrosequencing of cDNA representing mRNA of the melon fruit. Fourteen double strand cDNA samples obtained from two genotypes, two fruit tissues (flesh and rind) and four developmental stages were sequenced. GS FLX pyrosequencing (Roche/454 Life Sciences) of non-normalized and purified cDNA samples yielded 1,150,657 expressed sequence tags, that assembled into 67,477 unigenes (32,357 singletons and 35,120 contigs). Analysis of the data obtained against the Cucurbit Genomics Database confirmed the accuracy of the sequencing and assembly. Expression patterns of selected genes fitted well their qRT-PCR data.

EXAMPLE 2

PRODUCTION OF TOMATO TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS USING 44K TOMATO OLIGONUCLEOTIDE MICRO-ARRAY

In order to produce a high throughput correlation analysis, the present inventors utilized a Tomato oligonucleotide micro-array, produced by Agilent Technologies. The array oligonucleotide represents about 44,000 Toamto genes and transcripts. In order to define correlations between the levels of RNA expression with ABST, yield components or vigor related parameters various plant characteristics of 18 different Tomato varieties were analyzed. Among them, 10

varieties encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Correlation of Tomato varieties across ecotype grown under 50 % irrigation conditions

Experimental procedures

Growth procedure - Tomato variety was grown under normal conditions (4-6 Liters/m^2 per day) until flower stage. At this time, irrigation was reduced to 50 % compared to normal conditions.

RNA extraction – Two tissues at different developmental stages [flower and leaf], representing different plant characteristics, were sampled and RNA was extracted as described above. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table 1 below.

Table 1
Tomato transcriptom expression sets

Expression Set	*Set ID*
Leaf grown under Normal Irrigation	A
Leaf grown under 50% Irrigation	B
Flower grown under Normal Irrigation	C
Flower grown under 50% Irrigation	D

Table 1: Provided are the identification (ID) letters of each of the tomato expression sets.

Tomato yield components and vigor related parameters under 50 % water irrigation assessment – 10 Tomato varieties in 3 repetitive blocks (named A, B, and C,), each containing 6 plants per plot were grown at net house. Plants were phenotyped on a daily basis following the standard descriptor of tomato (Table 2, below). Harvest was conducted while 50 % of the fruits were red (mature). Plants were separated to the vegetative part and fruits, of them, 2 nodes were analyzed for additional inflorescent parameters such as size, number of flowers, and inflorescent weight. Fresh weight of all vegetative material was measured. Fruits were separated to colors (red *vs.* green) and in accordance with the fruit size (small, medium and large). Next, analyzed data was

saved to text files and processed using the JMP statistical analysis software (SAS institute).

Data parameters collected are summarized in Table 2, hereinbelow.

Table 2
Tomato correlated parameters (vectors)

Correlated parameter with	*Correlation Id*
50 % Irrigation; Vegetative fresh weight [gr.]	1
50 % Irrigation; Fruit per plant [gr.]	2
50 % Irrigation; Inflorescence weight [gr.]	3
50 % Irrigation; number of flowers	4
50 % Irrigation; relative Water use efficiency	5
50 % Irrigation; Ripe fruit average weight [gr.]	7
50 % Irrigation: SPAD	8
Normal Irrigation; vegetative fresh weight [gr.]	9
Normal Irrigation; Fruit per plant [gr.]	10
Normal Irrigation; Inflorescence weight [gr.]	11
Normal Irrigation; number of flowers	12
Normal Irrigation; relative Water use efficiency	13
Normal Irrigation; number of fruit per plant	14
Normal Irrigation; Ripe fruit average weight [gr.]	15
Normal Irrigation; SPAD	16
50 % Irrigation; Vegetative fresh weight [gr.]/ Normal Irrigation; vegetative fresh weight [gr.]	17
50 % Irrigation; Fruit per plant [gr.]/ Normal Irrigation; Fruit per plant [gr.]	18
50 % Irrigation; Inflorescence weight [gr.]/ Normal Irrigation; Inflorescence weight [gr.]	19
50 % Irrigation; number of flowers/ Normal Irrigation; number of flowers	20
50 % Irrigation; relative Water use efficiency/ Normal Irrigation; Water use efficiency	21
50 % Irrigation; Ripe fruit average weight [gr.]/ Normal Irrigation; Ripe fruit average weight [gr.]	22
50 % Irrigation: SPAD/ Normal Irrigation; SPAD	23

Table 2. Provided are the tomato correlated parameters. "gr." = grams; "SPAD" = chlorophyll levels;

Fruit Weight (grams) - At the end of the experiment [when 50 % of the fruit were ripe (red)] all fruits from plots within blocks A-C were collected. The total fruits were counted and weighted. The average fruits weight was calculated by dividing the total fruit weight by the number of fruits.

Plant vegetative Weight (grams) - At the end of the experiment [when 50 % of the fruit were ripe (red)] all plants from plots within blocks A-C were collected. Fresh weight was measured (grams).

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Inflorescence Weight (grams) - At the end of the experiment [when 50 % of the fruits were ripe (red)] two Inflorescence from plots within blocks A-C were collected. The Inflorescence weight (gr.) and number of flowers per inflorescence were counted.

SPAD - Chlorophyll content was determined using a Minolta SPAD 502 chlorophyll meter and measurement was performed at time of flowering. SPAD meter readings were done on young fully developed leaf. Three measurements per leaf were taken per plot.

Water use efficiency (WUE) – can be determined as the biomass produced per unit transpiration. To analyze WUE, leaf relative water content was measured in control and transgenic plants. Fresh weight (FW) was immediately recorded; then leaves were soaked for 8 hours in distilled water at room temperature in the dark, and the turgid weight (TW) was recorded. Total dry weight (DW) was recorded after drying the leaves at 60 °C to a constant weight. Relative water content (RWC) was calculated according to the following Formula I [(FW - DW)/(TW - DW) x 100] as described above.

Plants that maintain high relative water content (RWC) compared to control lines were considered more tolerant to drought than those exhibiting reduced relative water content

Experimental Results

10 different Tomato varieties were grown and characterized for 27 parameters as described above. The average for each of the measured parameter was calculated using the JMP software and values are summarized in Tables 3, 4 and 5 below. Subsequent correlation analysis between the various transcriptom sets (Table 1) and the average parameters was conducted, and results were integrated to the database.

Table 3
Tomato accessions, measured parameters

Variety	*2*	*10*	*1*	*9*	*7*	*15*	*18*	*17*
612	0.47	0.83	2.62	1.53	0.01	0.05	0.57	1.72
613	0.48	0.34	1.09	3.17	0.19	0.01	1.41	0.34
617	2.04	0.49	2.63	2.24	0.10	0.01	4.20	1.18
618	0.25	0.45	2.71	1.98	0.00	0.05	0.55	1.36
622	0.29	0.21	1.95	3.21	0.01	0.01	1.39	0.61
623	1.02	0.31	1.76	2.75	0.00	0.01	3.28	0.64
626	0.27	0.85	2.21	1.89	0.00	0.03	0.32	1.17
629	0.53	0.33	1.76	1.65	0.14	0.00	1.62	1.06
630	0.55	0.31	0.63	3.01	0.04	0.00	1.76	0.21

Variety	2	10	1	9	7	15	18	17
631	0.41	0.29	1.11	2.29	0.09	0.01	1.42	0.48

Table 3: Provided are the measured yield components and vigor related parameters under 50 % water irrigation for the tomato accessions (Varieties) according to the Correlation ID numbers (described in Table 2 above) as follows: 2 [50 % Irrigation; Fruit per plant (gr.)]; 10 [Normal Irrigation; Fruit per plant (gr.)]; 1 [50 % Irrigation; Vegetative fresh weight (gr.)]; 9 [Normal Irrigation; vegetative fresh weight (gr.)]; 7 [50 % Irrigation; ripe Fruit average weight (gr.)]; 15 [Normal Irrigation; Ripe fruit average weight (gr.)]; 18 [50 % Irrigation; Fruit per plant (gr.)/ Normal Irrigation; Fruit per plant (gr.)]; 17 [50 % Irrigation; Vegetative fresh weight (gr.)/ Normal Irrigation; vegetative fresh weight (gr.)].

Table 4
Tomato accessions, additional measured parameters

Variety	22	8	16	5	13	23
612	0.19	49.30	49.70	72.12	72.83	0.99
613	24.37	67.10	37.20	74.51	76.47	1.80
617	20.26	56.00	48.20	66.13	54.79	1.16
618	0.04	38.90	43.40	68.33	77.61	0.90
622	0.86	50.20	58.50	73.21	64.71	0.86
623	0.74	60.50	51.10	62.50	75.25	1.18
626	0.17	54.70	57.90	62.82	56.77	0.94
629	27.89	47.70	54.50	75.22	100.00	0.88
630	11.79	58.10	41.60	63.68	63.16	1.40
631	9.98	59.40	59.10	62.31	75.13	1.01

Table 4: Provided are the measured yield components and vigor related parameters under 50 % water irrigation for the tomato accessions (Varieties) according to the Correlation (Corr.) ID numbers (described in Table 2 above) as follows: 22 [50 % Irrigation; Ripe fruit average weight (gr.)/Normal Irrigation; Ripe fruit average weight (gr.)]; 8 [50 % Irrigation: SPAD]; 16 [Normal Irrigation; SPAD]; 5 [50 % Irrigation; relative Water use efficiency]; 13 [Normal Irrigation; relative Water use efficiency]; 23 [50 % Irrigation: SPAD/ Normal Irrigation; SPAD].

Table 5
Tomato accessions, additional measured parameters

Variety	21	4	12	3	11	20	19
612	0.99	16.67	5.67	0.37	1.17	2.94	0.32
613	0.97	6.50	19.33	0.41	0.34	0.34	1.19
617	1.21	11.67	9.67	0.55	0.44	1.21	1.25
618	0.88	25.33	8.33	0.31	11.31	3.04	0.03
622	1.13	14.67	10.00	0.30	0.73	1.47	0.42
623	0.83	29.67	7.00	0.31	0.83	4.24	0.38
626	1.11	18.33	5.33	8.36	1.02	3.44	8.20
629	0.75	12.67	9.00	0.44	0.66	1.41	0.67
630	1.01	12.67	10.67	0.27	0.70	1.19	0.38
631	0.83	11.33	9.00	0.43	0.33	1.26	1.31

Table 5: Provided are the measured yield components and vigor related parameters under 50 % water irrigation for the tomato accessions (Varieties) according to the Correlation (Corr.) ID numbers (described in Table 2 above) as follows: 21 [50 % Irrigation; relative Water use efficiency/ Normal Irrigation; Water use efficiency]; 4 [50 % Irrigation; number of flowers]; 12 [Normal Irrigation; number of flowers]; 3 [50 % Irrigation; Inflorescence weight (gr.)]; 11 [Normal Irrigation; Inflorescence weight (gr.)]; 20 [50 % Irrigation; number of flowers/ Normal Irrigation; number of flowers]; 19 [50 % Irrigation; Inflorescence weight (gr.)/ Normal Irrigation; Inflorescence weight (gr.)].

Correlation of early vigor traits across collection of Tomato ecotypes under high salinity concentration – Ten Tomato varieties were grown in 3 repetitive plots, each containing 17 plants, at a net house under semi-hydroponics conditions. Briefly, the growing protocol was as follows: Tomato seeds were sown in trays filled with a mix of vermiculite and peat in a 1:1 ratio. Following germination, the trays were transferred for the high salinity to 100 mM NaCl solution or to the normal growth solution [full Hogland; KNO3 - 0.808 grams/liter, MgSO4 - 0.12 grams/liter, KH2 PO4 - 0.172 grams/liter and 0.01 % (volume/volume) of 'Super coratin' micro elements (Iron-EDDHA [ethylenediamine-N,N'-bis(2-hydroxyphenylacetic acid)]- 40.5 grams/liter; Mn - 20.2 grams/liter; Zn 10.1 grams/liter; Co 1.5 grams/liter; and Mo 1.1 grams/liter), solution's pH should be 6.5 – 6.8].

RNA extraction – All 10 selected Tomato varieties were sample per each treatment. Two tissues [leaves and flowers] growing at 50% irrigation or under Normal conditions were sampled and RNA was extracted as described above.

Table 6
Tomato transcriptom experimental sets

Expression Set	*Set ID*
Leaves at 100 mM NaCl	Q
Leaves at Normal conditions	R
Roots at 100 mM NaCl	S
Roots at Normal conditions	T

Table 6. Provided are the tomato transcriptom experimental sets Q-T.

Tomato vigor related parameters under 100 mM NaCl – following 5 weeks of growing, plant were harvested and analyzed for leaf number, plant height, and plant weight. Next, analyzed data was saved to text files and processed using the JMP statistical analysis software (SAS institute).

Data parameters collected are summarize in Table 7, hereinbelow.

Table 7
Tomato correlated parameters (vectors)

Correlated parameter with	*Correlation Id*
100 mM NaCl: leaf Number	24
100 mM NaCl: Plant height	25
100 mM NaCl: Plant biomass	26
Normal: leaf Number	27
Normal: Plant height	28
100 mM NaCl: leaf Number/Normal: leaf Number	29
100 mM NaCl: Plant height/Normal: Plant height	30

Table 7. Provided are the tomato correlated parameters (ID numbers 1-7).

Experimental Results

10 different Tomato varieties were grown and characterized for 3 parameters as described above. The average for each of the measured parameter was calculated using the JMP software and values are summarized in Tables 8 below. Subsequent correlation analysis between the various transcriptom sets (Table 6) and the average parameters, was conducted. Follow, results were integrated to the database.

Table 8
Tomato accessions, measured parameters

Variety	*24*	*27*	*25*	*28*	*26*	*29*	*30*
1139	3.56	6.56	5.60	45.33	0.36	0.54	0.12
2078	3.94	6.89	6.46	47.78	0.44	0.57	0.14
2958	5.00	7.33	8.47	40.78	0.26	0.68	0.21
5077	4.00	6.22	8.56	55.33	0.71	0.64	0.15
5080	3.56	6.33	8.87	56.22	0.46	0.56	0.16
5084	4.39	6.44	7.56	48.67	0.54	0.68	0.16
5085	3.17	5.89	8.64	55.78	0.66	0.54	0.15
5088	3.72	5.56	5.57	37.44	0.40	0.67	0.15
5089	4.00	6.11	5.82	49.56	0.52	0.65	0.12
5092	4.28	5.67	9.36	46.33	0.45	0.75	0.20

Table 8. Provided are the measured vigor related parameters under 100 mM NaCl for the tomato accessions (Varieties) according to the Correlation (Corr.) ID numbers (described in Table 7 above) as follows: 24 [100 mM NaCl: leaf Number]; 27 [Normal: leaf Number]; 25 [100 mM NaCl: Plant height]; 28 [Normal: Plant height]; 26 [100 mM NaCl: Plant biomass]; 29 [100 mM NaCl: leaf Number/Normal: leaf Number]; 30 [100 mM NaCl: Plant height/Normal: Plant height].

Table 9

Correlation analysis between the expression level of selected Genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or drought conditions

Gene Name	*R*	*P value*	*Exp. set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. set*	*Corr. Set ID*

Table 9. "Corr. Set ID " – correlation set ID according to the correlated parameters Tables 2 and 7 above.

Table 10

Correlation analysis between the expression level of selected Orthologs genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or drought conditions

Gene Name	*R*	*P value*	*Exp. set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. set*	*Corr. Set ID*

Table 10. "Corr. Set ID " – correlation set ID according to the correlated parameters Tables 2 and 7 above.

EXAMPLE 3

PRODUCTION OF SORGHUM TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS USING 44 K SORGUHM OLIGONUCLEOTIDE MICRO-ARRAYS

In order to produce a high throughput correlation analysis, the present inventors utilized a Sorghum oligonucleotide micro-array, produced by Agilent Technologies. The array oligonucleotide represents about 44,000 Sorghum genes and transcripts. In order to define correlations between the levels of RNA expression with ABST and yield components or vigor related parameters, various plant characteristics of 17 different sorghum varieties were analyzed. Among them, 10 varieties encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Correlation of Sorghum varieties across ecotype grown under severe drought conditions

Experimental procedures

17 Sorghum varieties were grown in 3 repetitive plots, in field. Briefly, the growing protocol was as follows: sorghum seeds were sown in soil and grown under normal condition until around 35 days from sowing, around V8 (Last leaf visible, but still rolled up, ear beginning to swell). At this point, irrigation was stopped, and severe drought stress was developed. In order to define correlations between the levels of RNA expression with drought, yield components or vigor related parameters, the 17 different sorghum varieties were analyzed. Among them, 10 varieties encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

RNA extraction – All 10 selected Sorghum varieties were sample per each treatment. Plant tissues [Flag leaf and Flower meristem] growing under severe drought stress and plants grown under Normal conditions were sampled and RNA was extracted as described above. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table 11 below. Data parameters collected are summarize in Table 12, hereinbelow.

Table 11
Sorghum transcriptom experimental sets

Expression Set	*Set ID*
Drought Stress: Flag leaf	U
Drought Stress: Flower meristem	V
Drought Stress: inflorescence	W
Normal conditions: Flag leaf	X
Normal conditions: Flower meristem	Y
Normal conditions: inflorescence	Z

Table 11: Provided are the sorghum transcriptom experimental set U-Z.

Data parameters collected are summarize in Table 12, hereinbelow.

Table 12
Sorghum correlated parameters (vectors)

Correlated parameter with	*Correlation Id*
DW Drought [gr.]	1
DW (5I) Drought [gr.]	2
FW Inflorescence (5I) Drought [gr.]	3
DW Inflorescence (5I) Drought [gr.]	4
Grain per Inflorescence Drought [gr.]	5
Grain per Inflorescence(5I) Drought [gr.]	6
SPAD Drought	7
Harvest Index Drought	8
Leaf TP1 Drought	9
Leaf TP2 Drought	10
Leaf TP3 Drought	11
Leaf TP4 Drought	12
Leaf TP5 Drought	13
Leaf TP6 Drought	14
Plant Height TP2 Drought [cm]	15
Plant Height TP3 Drought [cm]	16
Plant Height TP4 Drought [cm]	17
Plant Height TP5 Drought [cm]	18
Plant Height TP6 Drought [cm]	19
DW Normal [gr.]	20
DW (5I) Normal [gr.]	21
FW Inflorescence(5I) Normal [gr.]	22
DW Inflorescence(5I) Normal [gr.]	23
Grain per Plant Normal [gr.]	24
Grain per Plant (5I) Normal [gr.]	25
SPAD Normal	26
Harvest Index Normal	27
Leaf TP1 Normal	28
Leaf TP2 Normal	29
Leaf TP3 Normal	30
Leaf TP4 Normal	31
Leaf TP5 Normal	32
Leaf TP6 Normal	33
Plant Height TP2 Normal [cm]	34
Plant Height TP3 Normal [cm]	35
Plant Height TP4 Normal [cm]	36
Plant Height TP5 Normal [cm]	37
Plant Height TP6 Normal [cm]	38
DW Drought/Normal [gr.]	39
Grain per Plant drought/Normal [gr.]	40
SPAD Drought/Normal	41
Harvest Index drought/Normal	42
FW(5I) Drought/Normal [gr.]	43
DW(5I) Drought/Normal [gr.]	44
Grain per Plant (5I) Drought/Normal [gr.]	45
Plant HightTP5 Drought/Normal [cm]	46

Correlated parameter with	*Correlation Id*
LeafTP5 Drought/Normal	47

Table 12. Provided are the Sorghum correlated parameters (vectors). "DW" = Dry Weight; (5I)" = Average of five Inflorescences; "FW" = Fresh Weight; "gr." = grams; "cm" = centimeter; "SPAD" = chlorophyll levels; "TP1" = X days after sowing; "TP2" = X days after sowing; "TP3" = X days after sowing; "TP4" = X days after sowing; "TP5" = X days after sowing; "TP6" = X days after sowing.

Grain per Plant (gr.) - At the end of the experiment (Inflorescence were dry) all spikes from plots within blocks A-C were collected. 5 Inflorescence were separately threshed and grains were weighted, all addition Inflorescence were threshed together and weighted as well. The average weight per Inflorescence was calculated by dividing the total grain weight by number of total Inflorescence per plot, or in case of 5 inflorescence, by weight by the total grain number by 5.

Plant height – Plant were characterize for height during groin period in 6 time Points. In each measure, plants were measured for its height using measuring tape. Height was measured from ground level to top of the longest leaf.

Inflorescence Weight (gr.) - At the end of the experiment (when Inflorescence were dry) five Inflorescence from plots within blocks A-C were collected. The Inflorescence were weighted (gr.).

SPAD - Chlorophyll content was determined using a Minolta SPAD 502 chlorophyll meter and measurement was performed at time of flowering. SPAD meter readings were done on young fully developed leaf. Three measurements per leaf were taken per plot.

Vegetative dry weight and Inflorescence - At the end of the experiment (when Inflorescence were dry) all Inflorescence and vegetative material from plots within blocks A-C were collected. The biomass and Inflorescence weight of each plot was separated, measured and divided by the number of Inflorescence.

Dry weight = total weight of the vegetative portion above ground (excluding roots) after drying at 70 °C in oven for 48 hours;

Harvest Index (for sorghum) - The harvest index is calculated using Formula V.

Formula V: Harvest Index = Average grain dry weight per Inflorescence / (Average vegetative dry weight per Inflorescence + Average Inflorescence dry weight)

Experimental Results

16 different sorghum varieties were grown and characterized for 49 parameters as described above. The average for each of the measured parameter was calculated using the JMP software and values are summarized in Tables 13-18 below. Subsequent correlation analysis between the various transcriptom sets (Table 11) and the average parameters, was conducted. Follow, results were integrated to the database.

Table 13
Sorghum accessions, measured parameters

Seed ID	*1*	*2*	*3*	*4*	*5*	*6*	*7*	*8*
20	0.20	0.47	0.39	0.01	0.03	0.05	38.33	0.13
21	0.20	0.49	0.43	0.01	0.03	0.05	38.98	0.15
22	0.34	0.73	0.30	0.01	0.02	0.04	42.33	0.06
25	0.54	0.54	0.21	0.02	0.03	0.04	43.15	0.05
26	0.36	0.61	0.30	0.01	0.02	0.04	39.85	0.06
27	0.15	0.48	0.44	0.01	0.05	0.07	42.68	0.34
28	0.13	0.44	0.38	0.01	0.03	0.04	43.31	0.21
29	0.18	0.51	0.47	0.01	0.05	0.08		0.29
30	0.12	0.45	0.40	0.01	0.04	0.05	42.71	0.30
31	0.10	0.44	0.38	0.00	0.03	0.04	40.08	0.29
32	0.13	0.43	0.38	0.01	0.03	0.04	43.98	0.20
33	0.12	0.48	0.43	0.01	0.03	0.07	45.44	0.25
34	0.18	0.54	0.43	0.01	0.05	0.10	44.75	0.29
35	0.14	0.46	0.41	0.01	0.04	0.05	42.58	0.25
36	0.13	0.42	0.38	0.01	0.04	0.04	43.81	0.32
37	0.18	0.50	0.43	0.01	0.04	0.05	46.73	0.23

Table 13: Provided are the measured parameters under 50 % irrigation conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 12 above) as follows: 1 [DW Drought (gr.)]; 2 [W(5I) Drought (gr.)]; 3 [FW Inflorescence(5I) Drought (gr.)]; 4 [DW Inflorescence (5I) Drought (gr.)]; 5 [Grain per Inflorescence Drought (gr.)]; 6 [Grain per Inflorescence(5I) Drought (gr.)]; 7 [SPAD Drought]; 8 [Harvest Index Drought.

Table 14
Sorghum accessions, addition measured parameters

Seed ID	*9*	*10*	*11*	*12*	*13*	*14*	*15*	*16*
20	3.00	5.33	4.50	7.75	7.08	7.75	10.75	22.25
21	4.25	5.50	5.75	7.92	8.58	7.92	8.00	18.50
22	5.00	5.83	5.75	8.67	9.08	8.67	16.00	30.33
25	4.25	5.25	5.50	8.17	9.58	8.17	13.83	27.92
26	5.50	6.25	6.00	9.38	9.75	9.38	16.33	32.67
27	5.00	6.50	6.17	9.13	9.08	9.13	15.17	32.25
28	4.75	5.75	5.83	8.58	7.75	8.58	13.50	28.92
29	5.25	6.50	5.17	9.50	8.50	8.25	16.42	26.83
30	5.50	6.25	5.92	7.83	7.08	7.83	17.58	34.17

Seed ID	9	10	11	12	13	14	15	16
31	5.00	6.75	6.08	7.25	6.75	13.08	15.83	30.50
32	5.50	6.25	5.92	9.00	8.25	9.00	17.00	30.58
33	5.00	6.42	6.08	7.50	7.92	7.50	13.92	27.17
34	5.00	6.33	6.08	10.00	9.83	10.00	14.83	27.58
35	5.00	5.50	5.42	8.38	8.50	8.38	12.50	28.00
36	4.75	6.33	5.33	8.67	9.17	8.67	17.58	29.33
37	5.25	5.58	5.50	10.00	10.58	9.50	15.92	30.42

Table 14: Provided are the measured parameters under 50 % irrigation conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 12 above) as follows: 9 [Leaf TP1 Drought]; 10 [Leaf TP2 Drought]; 11 [Leaf TP3 Drought]; 12 [Leaf TP4 Drought]; 13 [Leaf TP5 Drought]; 14 [Leaf TP6 Drought]; 15 [Plant Height TP2 Drought (cm)]; 16 [Plant Height TP3 Drought (cm)].

Table 15
Sorghum accessions, addition measured parameters

Seed ID	17	18	19	20	21	22	23	24
20	38.00	50.25	38.00	0.16	0.46	0.41	0.008	0.031
21	30.83	45.25	30.83	0.25	0.69	0.49	0.012	0.026
22	110.83	92.08	60.83	0.33	0.44	0.15	0.007	0.019
25	49.58	73.92	49.58	0.46	0.56	0.09	0.015	0.027
26	49.75	100.50	49.75	0.36	0.55	0.13	0.010	0.046
27	46.88	58.67	46.88	0.15	0.47	0.42	0.009	0.048
28	41.92	70.75	41.92	0.14	0.45	0.39	0.007	0.031
29	46.13	67.67	46.13	0.17	0.48	0.41	0.010	0.040
30	50.17	68.50	50.17	0.13	0.46	0.33	0.008	0.038
31	43.58	65.67	43.58	0.10	0.42	0.39	0.005	0.032
32	50.83	79.25	50.92	0.10	0.42	0.41	0.008	0.033
33	42.42	57.67	42.42	0.11	0.50	0.43	0.010	0.033
34	45.50	78.58	45.50	0.16	0.49	0.44	0.010	0.052
35	50.38	60.75	50.38	0.13	0.45	0.42	0.008	0.036
36	48.83	71.17	53.83	0.14	0.47	0.43	0.008	0.038
37	49.83	73.92	51.42	0.21	0.52	0.43	0.013	0.042

Table 15: Provided are the measured parameters under 50 % irrigation conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 12 above) as follows: 17 [Plant Height TP4 Drought (cm)]; 18 [Plant Height TP5 Drought (cm)]; 19 [Plant Height TP6 Drought (cm)]; 20 [DW Normal (gr.)]; 21 [DW (5I) Normal (gr.)]; 22 [FW Inflorescence(5I) Normal (gr.)]; 23 [DW Inflorescence(5I) Normal (gr.)]; 24 [Grain per Plant Normal (gr.)].

Table 16
Sorghum accessions, addition measured parameters

Seed ID	25	26	27	28	29	30	31	32
20	0.05	43.01	0.20	4.33	5.31	5.44	6.73	6.75
21	0.05	40.70	0.11	4.00	6.08	6.38	.	8.38
22	0.03	43.26	0.05	4.67	6.00	6.56	8.44	9.81
25	0.03	45.76	0.05	4.33	5.38	5.13	7.88	8.69

Seed ID	25	26	27	28	29	30	31	32
26	0.07	41.61	0.12	5.17	6.31	6.31	8.13	9.50
27	0.06	45.21	0.33	4.83	6.13	6.19	9.13	9.19
28	0.04	45.14	0.23	4.33	6.06	6.06	7.50	6.69
29	0.06	43.03	0.24	4.67	6.13	5.63	8.25	9.00
30	0.06	45.59	0.30	4.17	6.44	5.94	7.00	6.75
31	0.05	44.83	0.34	5.00	7.00	6.00	6.75	6.38
32	0.06	45.33	0.35	4.83	6.31	6.38	8.06	7.81
33	0.07	46.54	0.29	4.67	6.25	6.31	6.94	7.88
34	0.07	43.99	0.41	4.67	6.25	5.94	7.94	9.94
35	0.05	45.09	0.29	4.33	5.63	5.94	8.06	8.69
36	0.06	45.14	0.28	4.67	6.38	5.75	7.56	8.56
37	0.05	43.13	0.20	4.17	5.88	6.56	7.94	10.31

Table 16: Provided are the measured parameters under 50 % irrigation conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 12 above) as follows: 25 [Grain per Plant (5I) Normal (gr.)]; 26 [SPAD Normal]; 27 [Harvest Index Normal]; 28 [Leaf TP1 Normal]; 29 [Leaf TP2 Normal]; 30 [Leaf TP3 Normal]; 31 [Leaf TP4 Normal]; 32 [Leaf TP5 Normal].

Table 17
Sorghum accessions, addition measured parameters

Seed ID	33	34	35	36	37	38	39	40
20	6.73	10.63	24.50	37.31	47.13	37.31	1.26	0.83
21	.	8.00	19.88	.	40.06	.	0.81	1.19
22	8.44	16.00	31.13	47.75	82.94	47.75	1.02	1.03
25	7.88	14.19	27.25	45.94	74.13	45.94	1.16	0.94
26	8.13	15.31	27.25	41.44	79.69	41.44	1.01	0.48
27	9.13	15.69	31.19	44.88	58.00	44.88	0.99	1.05
28	7.50	15.88	30.25	42.13	58.81	42.13	0.94	0.89
29	8.25	14.63	26.19	41.00	64.31	41.00	1.06	1.28
30	7.00	18.38	31.88	42.50	58.69	42.06	0.96	0.96
31	6.75	18.13	32.19	41.88	59.25	41.88	1.04	0.92
32	8.06	17.25	29.75	43.38	66.88	43.38	1.33	0.82
33	6.94	14.88	28.13	39.81	60.63	39.81	1.05	0.90
34	7.94	13.50	27.00	40.63	73.38	40.63	1.12	0.99
35	8.06	14.63	29.19	44.38	59.63	44.38	1.10	1.04
36	7.56	16.38	27.75	43.25	64.69	43.25	0.94	1.04
37	7.94	17.31	31.63	41.00	73.81	41.00	0.86	0.98

Table 17: Provided are the measured parameters under 50 % irrigation conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 12 above) as follows: 33 [Leaf TP6 Normal]; 34 [Plant Height TP2 Normal (cm)]; 35 [Plant Height TP3 Normal (cm)]; 36 [Plant Height TP4 Normal (cm)]; 37 [Plant Height TP5 Normal (cm)]; 38 [Plant Height TP6 Normal (cm)]; 39 [DW Drought/Normal (gr.)]; 40 [Grain per Plant drought/Normal (gr.)].

Table 18
Sorghum accessions, addition measured parameters

Seed ID	*41*	*42*	*43*	*44*	*45*	*46*	*47*
20	0.89	0.66	0.95	1.03	1.06	1.07	1.05
21	0.96	1.38	0.88	0.71	1.13	1.13	1.02
22	0.98	1.09	2.01	1.67	1.27	1.11	0.93
25	0.94	0.86	2.26	0.96	1.18	1.00	1.10
26	0.96	0.52	2.37	1.10	0.55	1.26	1.03
27	0.94	1.04	1.03	1.02	1.13	1.01	0.99
28	0.96	0.93	0.97	0.97	0.79	1.20	1.16
29	0.91	1.19	1.16	1.06	1.35	1.05	0.94
30	0.94	0.97	1.23	0.98	0.88	1.17	1.05
31	0.89	0.86	0.98	1.04	0.94	1.11	1.06
32	0.97	0.58	0.91	1.03	0.66	1.19	1.06
33	0.98	0.84	0.99	0.97	0.97	0.95	1.01
34	1.02	0.70	0.98	1.12	1.37	1.07	0.99
35	0.94	0.89	0.98	1.02	0.91	1.02	0.98
36	0.97	1.12	0.88	0.88	0.73	1.10	1.07
37	1.08	1.14	1.01	0.96	0.99	1.00	1.03

Table 18: Provided are the measured parameters under 50 % irrigation conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 12 above) as follows: 41 [SPAD Drought/Normal]; 42 [Harvest Index drought/Normal]; 43 [FW(5I) Drought/Normal (gr.)]; 44 [DW(5I) Drought/Normal (gr.)]; 45 [Grain per Plant (5I) Drought/Normal (gr.)]; 46 [Plant HightTP5 Drought/Normal (cm)]; 47 [LcafTP5 Drought/Normal].

Sorghum vigor related parameters under 100 mM NaCl and low temperature (8-10 ºC) – Ten Sorghum varieties were grown in 3 repetitive plots, each containing 17 plants, at a net house under semi-hydroponics conditions. Briefly, the growing protocol was as follows: Sorghum seeds were sown in trays filled with a mix of vermiculite and peat in a 1:1 ratio. Following germination, the trays were transferred to the high salinity solution (100 mM NaCl) solution, low temperature (8-10 ºC) or at Normal growth solution [full Hogland; KNO3 - 0.808 grams/liter, MgSO4 - 0.12 grams/liter, KH2 PO4 - 0.172 grams/liter and 0.01 % (volume/volume) of 'Super coratin' micro elements (Iron-EDDHA [ethylenediamine-N,N'-bis(2-hydroxyphenylacetic acid)]- 40.5 grams/liter; Mn - 20.2 grams/liter; Zn 10.1 grams/liter; Co 1.5 grams/liter; and Mo 1.1 grams/liter), solution's pH should be 6.5 – 6.8].

RNA extraction – All 10 selected Sorghum varieties were sample per each treatment. Two tissues [leaves and roots] growing at 100 mM NaCl, low temperature (8-10 ºC) or under Normal conditions were sampled and RNA was extracted as described above.

Table 19
Sorghum correlated parameters (vectors)

Correlated parameter with	*Correlation Id*
100 mM NaCl: leaf Number	48
100 mM NaCl: Plant height	49
100 mM NaCl: Shoot DW	50
100 mM NaCl: Root DW	51
100 mM NaCl: SPAD	52
low temperature: leaf Number	53
low temperature: Plant height	54
low temperature: Shoot DW	55
low temperature: Root DW	56
low temperature: SPAD	57
Normal: leaf Number	58
Normal: Plant height	59
Normal: Shoot DW	60
Normal: Root DW	61
Normal: SPAD	62
leaf Number 100 mM NaCl/Normal	63
Plant height 100 mM NaCl/Normal	64
Shoot DW 100 mM NaCl/Normal	65
Root DW 100 mM NaCl/Normal	66
SPAD 100 mM NaCl/Normal	67
leaf Number low temperature /Normal	68
Plant height low temperature /Normal	69
Shoot DW low temperature /Normal	70
Root DW low temperature /Normal	71
SPAD low temperature /Normal	72

Table 19: provided are the Sorghum correlated parameters (vectors).

Experimental Results

10 different Sorghum varieties were grown and characterized for 25 parameters as described above (Table 19). The average for each of the measured parameter was calculated using the JMP software and values are summarized in Tables 20-22 below. Subsequent correlation analysis between the various transcriptom sets (Table 11) and the average parameters (Tables 20-22), was conducted (Tables 23 and 24). Follow, results were integrated to the database.

Table 20
Sorghum accessions, measured parameters

Seed ID	*48*	*51*	*50*	*52*	*49*	*53*	*56*
20	3.67	0.35	0.66	32.73	14.63	3.88	0.83
22	3.88	1.45	2.43	35.14	16.31	4.16	0.95
26	4.28	1.49	2.40	27.97	20.56	4.52	1.47

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Seed ID	48	51	50	52	49	53	56
27	4.03	0.81	1.61	30.93	14.70	4.28	1.06
28	3.97	1.03	1.77	34.53	16.43	4.33	0.71
29	3.98	0.95	1.66	29.99	16.12	4.17	1.38
30	3.90	2.00	2.23	32.09	15.61	3.94	2.04
31	4.18	1.39	2.76	31.86	18.71	4.26	1.03
34	3.70	1.29	1.29	32.51	13.65	4.20	1.01
37	3.82	1.76	1.55	34.32	15.72	4.04	1.01

Table 20: Provided are the measured parameters under 100 mM NaCl and low temperature (8-10 °C) conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 19 above) as follows: 48 [100 mM NaCl: leaf Number]; 51 [100 mM NaCl: Root DW]; 50 [100 mM NaCl: Shoot DW]; 52 [100 mM NaCl: SPAD]; 49 [100 mM NaCl: Plant height]; 53 [low temperature: leaf Number]; 56 [low temperature: Root DW].

Table 21
Sorghum accessions, addition measured parameters

Seed ID	55	57	54	58	59	61	60
20	1.03	28.62	8.83	4.17	11.22	0.42	0.81
22	1.34	30.31	12.32	4.48	13.77	1.07	1.89
26	1.71	27.04	14.42	4.93	17.48	1.38	2.51
27	1.28	32.28	9.50	4.53	13.08	0.83	1.26
28	1.12	28.28	12.53	4.52	13.50	0.86	1.55
29	1.69	29.89	11.82	4.64	13.53	0.96	1.50
30	2.24	32.47	11.28	4.49	16.75	1.11	1.93
31	1.26	28.63	13.22	4.79	16.15	0.99	1.95
34	1.08	31.71	9.97	4.37	13.95	0.80	1.48
37	1.02	29.61	10.02	4.54	15.28	0.88	1.85

Table 21: Provided are the measured parameters under 100 mM NaCl and low temperature (8-10 °C) conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 19 above) as follows: 55 [low temperature: Shoot DW]; 57 [low temperature: SPAD]; 54 [low temperature: Plant height]; 58 [Normal: leaf Number]; 59 [Normal: Plant height]; 61 [Normal: Root DW]; 60 [Normal: Shoot DW].

Table 22
Sorghum accessions, addition measured parameters

Seed ID	66	71	70	67	72
20	0.83	1.97	1.28	1.23	1.07
22	1.35	0.88	0.71	1.20	1.03
26	1.08	1.07	0.68	0.94	0.91
27	0.98	1.29	1.02	1.06	1.11
28	1.20	0.83	0.72	1.38	1.13
29	0.99	1.45	1.12	1.22	1.21
30	1.80	1.83	1.16	1.04	1.05
31	1.40	1.03	0.65	1.25	1.12

Seed ID	66	71	70	67	72
34	1.63	1.27	0.73	0.99	0.96
37	2.00	1.14	0.55	1.02	0.88

Table 22: Provided are the measured parameters under 100 mM NaCl and low temperature (8-10 ºC) conditions of Sorghum accessions (Seed ID) according to the Correlation ID numbers (described in Table 19 above) as follows: 66 [Root DW 100 mM NaCl/Normal]; 71 [Root DW low temperature /Normal]; 70 [Shoot DW low temperature /Normal]; 67 [SPAD 100 mM NaCl/Normal]; 72 [SPAD low temperature /Normal].

Tables 23 and 24 hereinbelow, provide correlation analysis between the characterized parameters (as described above in Examples 2 and 3) and the tissue transcriptom.

Table 23

Correlation analysis between the expression level of selected Genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or drought conditions

Gene Name	R	P value	Exp. set	Corr. Set ID	Gene Name	R	P value	Exp. set	Corr. Set ID
LAB276	0.7	0.03523	X	24	LAB174	0.8	0.004143	V	5
LAB174	0.81	0.006827	Y	24	LAB290	0.9	0.000239	U	1
LAB290	0.83	0.00258	Y	24	LAB290	0.8	0.004123	W	1
LAB347	0.78	0.00722	V	4	LAB295	0.8	0.002967	V	3
LAB295	0.83	0.00311	V	5	LAB295	0.8	0.010068	Y	24
LAB304	0.80	0.01113	Z	21	LAB304	0.7	0.023194	W	6

Table 23. "Corr. Set ID " – correlation set ID according to the correlated parameters Table

Table 24

Correlation analysis between the expression level of selected Orthologs genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or drought conditions

Gene Name	R	P value	Exp. set	Corr. Set ID	Gene Name	R	P value	Exp. set	Corr. Set ID

Table 24. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

EXAMPLE 4

PRODUCTION OF MAIZE TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS WITH YIELD AND NUE RELATED PARAMETERS USING 44K MAIZE OLIGONUCLEOTIDE MICRO-ARRAYS

In order to produce a high throughput correlation analysis between plant phenotype and gene expression level, the present inventors utilized a maize

oligonucleotide micro-array, produced by Agilent Technologies. The array oligonucleotide represents about 44,000 maize genes and transcripts. In order to define correlations between the levels of RNA expression with yield and NUE components or vigor related parameters, various plant characteristics of 12 different maize hybrids were analyzed. Among them, 10 hybrids encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Correlation of Maize hybrids across ecotypes grown under regular growth conditions

Experimental procedures

12 Maize hybrids were grown in 3 repetitive plots, in field. Maize seeds were planted and plants were grown in the field using commercial fertilization and irrigation protocols. In order to define correlations between the levels of RNA expression with NUE and yield components or vigor related parameters, the 12 different maize hybrids were analyzed. Among them, 10 hybrids encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Analyzed Sorghum tissues – All 10 selected maize hybrids were sample per each treatment. Plant tissues [Flag leaf, Flower meristem, Grain, Cobs, Internodes] growing under Normal conditions were sampled and RNA was extracted as described above. Each micro-array expression information tissue type has received a Set ID as summarized in Table 25 below.

Table 25
Maize transcriptom expression sets

Expression Set	Set ID
Maize field/Normal/flower meristem	A
Maize field/Normal/Ear	B
Maize field/Normal/ Grain Distal	C
Maize field/Normal/Grain Basal	D

Maize field/Normal/Internode	E
Maize field/Normal/Leaf	F

Table 25: Provided are the maize transcriptom expression sets. Leaf = the leaf below the main ear; Flower meristem = Apical meristem following male flower initiation; Ear = the female flower at the anthesis day. Grain Distal= maize developing grains from the cob extreme area, Grain Basal= maize developing grains from the cob basal area; Internodes = internodes located above and below the main ear in the plant.

The following parameters were collected using digital imaging system:

Grain Area (cm^2) - At the end of the growing period the grains were separated from the ear. A sample of ~200 grains were weight, photographed and images were processed using the below described image processing system. The grain area was measured from those images and was divided by the number of grains.

Grain Length and Grain width (cm) - At the end of the growing period the grains were separated from the ear. A sample of ~200 grains were weight, photographed and images were processed using the below described image processing system. The sum of grain lengths /or width (longest axis) was measured from those images and was divided by the number of grains.

Ear Area (cm^2)- At the end of the growing period 5 ears were, photographed and images were processed using the below described image processing system. The Ear area was measured from those images and was divided by the number of Ears.

Ear Length and Ear Width (cm) At the end of the growing period 5 ears were, photographed and images were processed using the below described image processing system. The Ear length and width (longest axis) was measured from those images and was divided by the number of ears.

The image processing system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.37, Java based image processing software, which was developed at the U.S. National Institutes of Health and is freely available on the internet. Images were captured in resolution of 10 Mega Pixels (3888x2592 pixels) and stored in a low compression JPEG (Joint Photographic Experts Group standard) format. Next, image processing output data for seed area and seed length was saved to text files and analyzed using the JMP statistical analysis software (SAS institute).

Additional parameters were collected either by sampling 6 plants per plot or by measuring the parameter across all the plants within the plot.

Normalized Grain Weight per plant (gr.) - At the end of the experiment all ears from plots within blocks A-C were collected. 6 ears were separately threshed and grains were weighted, all additional ears were threshed together and weighted as well. The average grain weight per ear was calculated by dividing the total grain weight by number of total ears per plot (based on plot). In case of 6 ears, the total grains weight of 6 ears was divided by 6.

Ear FW (gr.) - At the end of the experiment (when ears were harvested) total and 6 selected ears per plots within blocks A-C were collected separately. The plants with (total and 6) were weighted (gr.) separately and the average ear per plant was calculated for total (Ear FW per plot) and for 6 (Ear FW per plant).

Plant height and Ear height - Plants were characterized for height at harvesting. In each measure, 6 plants were measured for their height using a measuring tape. Height was measured from ground level to top of the plant below the tassel. Ear height was measured from the ground level to the place were the main ear is located

Leaf number per plant - Plants were characterized for leaf number during growing period at 5 time points. In each measure, plants were measured for their leaf number by counting all the leaves of 3 selected plants per plot.

Relative Growth Rate was calculated using Formula II (described above).

SPAD - Chlorophyll content was determined using a Minolta SPAD 502 chlorophyll meter and measurement was performed 64 days post sowing. SPAD meter readings were done on young fully developed leaf. Three measurements per leaf were taken per plot. Data were taken after 46 and 54 days after sowing (DPS)

Dry weight per plant - At the end of the experiment (when Inflorescence were dry) all vegetative material from plots within blocks A-C were collected.

Dry weight = total weight of the vegetative portion above ground (excluding roots) after drying at 70 °C in oven for 48 hours;

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

Formula VI: ***Harvest Index*** = Average grain dry weight per Ear / (Average vegetative dry weight per Ear + Average Ear dry weight)

Percent Filled Ear [%] - it was calculated as the percentage of the Ear area with grains out of the total ear.

Cob diameter [cm]- The diameter of the cob without grains was measured using a ruler.

Kernel Row Number per Ear- The number of rows in each ear was counted.

Experimental Results

12 different maize hybrids were grown and characterized for different parameters: The average for each of the measured parameter was calculated using the JMP software (Tables 27-88) and a subsequent correlation analysis was performed (Tables 29-30). Results were then integrated to the database.

Table 26
Maize correlated parameters (vectors)

Correlations	*Correlation ID*
SPAD 54DPS [SPAD units]	1
SPAD 46DPS [SPAD units]	2
Growth Rate Leaf Num	3
Plant Height per Plot [cm]	4
Ear Height [cm]	5
Leaf Number per Plant [number]	6
Ear Length [cm]	7
Percent Filled Ear [%]	8
Cob Diameter [mm]	9
Kernel Row Number per Ear [number]	10
DW per Plant [gr]	11
Ear FW per Plant gr]	12
Normalized Grain Weight per plant [gr]	13
Ears FW per plot [gr]	14
Normalized Grain Weight per plot [gr]	15
Ear Area [cm2]	16
Ear Width [cm]	17
Grain Area [cm2]	18
Grain Length [cm]	19
Grain Width [cm]	20

Table 26. SPAD 46DPS and SPAD 54DPS: Chlorophyl level after 46 and 54 days after sowing (DPS).

Table 27
Measured parameters in Maize accessions under normal conditions

Seed ID	*1*	*2*	*3*	*4*	*5*	*6*	*7*	*8*	*9*	*10*	*11*
Line 1	54.8	55.3	0.306	287	135	11.9	20.9	80.4	28.7	16.2	656
Line 2	54.3	51.7	0.283	278	135	12	19.7	80.6	29	16.2	658
Line 3	57.2	56.4	0.221	270	116	8.4	19.1	94.3	23.8	15	472
Line 4	56	53.5	0.281	275	132	11.7	20.5	82.1	28.1	16.2	641

Seed ID	1	2	3	4	5	6	7	8	9	10	11
Line 5	59.7	55.2	0.269	238	114	11.8	21.3	92.7	25.7	15.9	581
Line 6	59.1	59.4	0.244	225	94.3	12.3	18.2	82.8	25.8	15.2	569
Line 7	58	58.5	0.244	264	121	12.4	19	73.2	26.4	16	511
Line 8	60.4	55.9	0.266	252	108	12.2	18.6	81.1	25.2	14.8	544
Line 9	54.8	53									
Line 10	53.3	50									
Line 11	61.1	59.7	0.301	278	112	12.6	21.7	91.6	26.7	15.4	522
Line 12	51.4	53.9	0.194	164	60.4	9.28	16.7	81.1	14.3	574	141

Table 27. Provided are the values of each of the parameters (as described above) measured in maize accessions (Seed ID) under regular growth conditions. Growth conditions are specified in the experimental procedure section.

Table 28

Additional measured parameters in Maize accessions under regular growth conditions

Seed ID	12	13	14	15	16	17	18	19	20
Line 1	272	157	280	140	91.6	5.73	0.806	1.23	0.824
Line 2	246	141	278	154	85.1	5.58	0.753	1.17	0.81
Line 3	190	129	190	121	77.9	5.1	0.674	1.07	0.794
Line 4	262	154	288	152	90.5	5.67	0.755	1.18	0.803
Line 5	264	177	248	159	96	5.53	0.766	1.2	0.803
Line 6	178	120	176	117	72.4	5.23	0.713	1.12	0.803
Line 7	189	120	192	123	74	5.22	0.714	1.14	0.791
Line 8	197	134	205	131	76.5	5.33	0.753	1.13	0.837
Line 9									
Line 10									
Line 11	261	173	264	171	95.4	5.58	0.762	1.18	0.812
Line 12	54.3	143	40.8	55.2	4.12	0.796	0.921	0.675	

Table 28. Provided are the values of each of the parameters (as described above) measured in maize accessions (Seed ID) under regular growth conditions. Growth conditions are specified in the experimental procedure section.

Table 29

Correlation between the expression level of selected Genes of some embodiments of the invention in various tissues and the phenotypic performance under normal across maize accessions

Gene Name	R	P value	Exp. set	Corr. Set ID	Gene Name	R	P value	Exp. set	Corr. Set ID

Table 29. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

Table 30

Correlation between the expression level of selected ABST homologous genes of some embodiments of the invention in various tissues and the phenotypic performance under normal across maize accessions

Gene Name	*R*	*P value*	*Exp. Set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. Set*	*Corr. Set ID*

Table 30. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

EXAMPLE 5

PRODUCTION OF BARLEY TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS USING 44K BARLEY OLIGONUCLEOTIDE MICRO-ARRAY

In order to produce a high throughput correlation analysis comparing between plant phenotype and gene expression level, the present inventors utilized a Barley oligonucleotide micro-array, produced by Agilent Technologies. The array oligonucleotide represents about 47,500 Barley genes and transcripts. In order to define correlations between the levels of RNA expression and yield or vigor related parameters, various plant characteristics of 25 different Barley accessions were analyzed. Among them, 13 accessions encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Experimental procedures

Analyzed Barley tissues – Five tissues at different developmental stages [meristem, flower, booting spike, stem, flag leaf], representing different plant characteristics, were sampled and RNA was extracted as described above. Each micro-array expression information tissue type has received a Set ID as summarized in Table 31 below.

Table 31
Barley transcriptom expression sets

Expression Set	*Set ID*
Meristem	A
Flower	B
Booting spike	C
Stem	D
Flag leaf	E

Table 31.

Barley yield components and vigor related parameters assessment – 25 Barley accessions in 4 repetitive blocks (named A, B, C, and D), each containing 4 plants per plot were grown at net house. Plants were phenotyped on a daily basis following the standard descriptor of barley (Table 32, below). Harvest was conducted while 50 % of the spikes were dry to avoid spontaneous release of the seeds. Plants were separated to the vegetative part and spikes, of them, 5 spikes were threshed (grains were separated from the glumes) for additional grain analysis such as size measurement, grain count per spike and grain yield per spike. All material was oven dried and the seeds were threshed manually from the spikes prior to measurement of the seed characteristics (weight and size) using scanning and image analysis. The image analysis system included a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.37 (Java based image processing program, which was developed at the U.S. National Institutes of Health and freely available on the internet. Next, analyzed data was saved to text files and processed using the JMP statistical analysis software (SAS institute).

Table 32
Barley standard descriptors

Trait	*Parameter*	*Range*	*Description*
Growth habit	Scoring	1-9	Prostrate (1) or Erect (9)
Hairiness of basal leaves	Scoring	P (Presence)/A (Absence)	Absence (1) or Presence (2)
Stem pigmentation	Scoring	1-5	Green (1), Basal only or Half or more (5)
Days to Flowering	Days		Days from sowing to emergence of awns
Plant height	Centimeter (cm)		Height from ground level to top of the longest spike excluding awns
Spikes per plant	Number		Terminal Counting

Trait	*Parameter*	*Range*	*Description*
Spike length	Centimeter (cm)		Terminal Counting 5 spikes per plant
Grains per spike	Number		Terminal Counting 5 spikes per plant
Vegetative dry weight	Gram		Oven-dried for 48 hours at 70°C
Spikes dry weight	Gram		Oven-dried for 48 hours at 30°C

Table 32.

Grains per spike - At the end of the experiment (50 % of the spikes were dry) all spikes from plots within blocks A-D are collected. The total number of grains from 5 spikes that were manually threshed was counted. The average grain per spike is calculated by dividing the total grain number by the number of spikes.

Grain average size (cm) - At the end of the experiment (50 % of the spikes were dry) all spikes from plots within blocks A-D are collected. The total grains from 5 spikes that were manually threshed were scanned and images were analyzed using the digital imaging system. Grain scanning was done using Brother scanner (model DCP-135), at the 200 dpi resolution and analyzed with Image J software. The average grain size was calculated by dividing the total grain size by the total grain number.

Grain average weight (mgr) - At the end of the experiment (50 % of the spikes were dry) all spikes from plots within blocks A-D are collected. The total grains from 5 spikes that were manually threshed were counted and weight. The average weight was calculated by dividing the total weight by the total grain number.

Grain yield per spike (gr) - At the end of the experiment (50 % of the spikes were dry) all spikes from plots within blocks A-D are collected. The total grains from 5 spikes that were manually threshed were weight. The grain yield was calculated by dividing the total weight by the spike number.

Spike length analysis - At the end of the experiment (50 % of the spikes were dry) all spikes from plots within blocks A-D are collected. The five chosen spikes per plant were measured using measuring tape excluding the awns.

Spike number analysis - At the end of the experiment (50 % of the spikes were dry) all spikes from plots within blocks A-D are collected. The spikes per plant were counted.

Growth habit scoring – At the growth stage 10 (booting), each of the plants was scored for its growth habit nature. The scale that was used was 1 for prostate nature till 9 for erect.

Hairiness of basal leaves - At the growth stage 5 (leaf sheath strongly erect; end of tillering), each of the plants was scored for its hairiness nature of the leaf before the last. The scale that was used was 1 for prostate nature till 9 for erect.

Plant height – At the harvest stage (50 % of spikes were dry) each of the plants was measured for its height using measuring tape. Height was measured from ground level to top of the longest spike excluding awns.

Days to flowering – Each of the plants was monitored for flowering date. Days of flowering was calculated from sowing date till flowering date.

Stem pigmentation - At the growth stage 10 (booting), each of the plants was scored for its stem color. The scale that was used was 1 for green till 5 for full purple.

Vegetative dry weight and spike yield - At the end of the experiment (50 % of the spikes were dry) all spikes and vegetative material from plots within blocks A-D are collected. The biomass and spikes weight of each plot was separated, measured and divided by the number of plants.

Dry weight = total weight of the vegetative portion above ground (excluding roots) after drying at 70 °C in oven for 48 hours;

Spike yield per plant = total spike weight per plant (gr) after drying at 30 °C in oven for 48 hours.

Harvest Index (for barley) - The harvest index is calculated using Formula XVI.

Formula XVI: ***Harvest Index*** = Average spike dry weight per plant/ (Average vegetative dry weight per plant + Average spike dry weight per plant)

Table 33
Barley correlated parameters (vectors)

Correlated parameter with (units)	*Correlation Id*
Grains per spike (numbers)	1
Grains size (mm^2)	2
Grain weight (miligrams)	3
Grain Yield per spike (gr/spike)	4
Spike length (cm)	5
Spikes per plant (numbers)	6
Growth habit (scores 1-9)	7

Correlated parameter with (units)	*Correlation Id*
Hairiness of basal leaves (scoring 1-2)	8
Plant height (cm)	9
Days to flowering (days)	10
Stem pigmentation (scoring 1-5)	11
Vegetative dry weight (gram)	12
Harvest Index (ratio)	13

Table 33.

Experimental Results

13 different Barley accessions were grown and characterized for 13 parameters as described above. The average for each of the measured parameter was calculated using the JMP software and values are summarized in Tables 34 and 35 below. Subsequent correlation analysis between the various transcriptom sets (Table 31) and the average parameters, was conducted (Tables 36 and 37). Follow, results were integrated to the database.

Table 34
Measured parameters of correlation Ids in Barley accessions

Accession /Parameter	*6*	*10*	*3*	*5*	*2*	*1*	*7*
Amatzya	48.85	62.40	35.05	12.04	0.27	20.23	2.60
Ashqelon	48.27	64.08	28.06	10.93	0.23	17.98	2.00
Canada park	37.42	65.15	28.76	11.83	0.24	17.27	1.92
Havarim stream	61.92	58.92	17.87	9.90	0.17	17.73	3.17
Jordan est	33.27	63.00	41.22	11.68	0.29	14.47	4.33
Klil	41.69	70.54	29.73	11.53	0.28	16.78	2.69
Maale Efraim	ND	52.80	25.22	8.86	0.22	13.47	3.60
Mt Arbel	40.63	60.88	34.99	11.22	0.28	14.07	3.50
Mt Harif	62.00	58.10	20.58	11.11	0.19	21.54	3.00
Neomi	49.33	53.00	27.50	8.58	0.22	12.10	3.67
Neot Kdumim	50.60	60.40	37.13	10.18	0.27	14.36	2.47
Oren canyon	43.09	64.58	29.56	10.51	0.27	15.28	3.50
Yeruham	51.40	56.00	19.58	9.80	0.18	17.07	3.00

Table 34. Provided are the values of each of the parameters measured in Barley accessions according to the following correlation identifications (Correlation Ids): 6 = Spikes per plant; 10 = Days to flowering; 3 = Grain weight; 5 = Spike length; 2 = Grains Size; 1 = Grains per spike; 7 = Growth habit.

Table 35
Barley accessions, additional measured parameters

Accession /Parameter	*8*	*9*	*4*	*11*	*12*	*13*
Amatzya	1.53	134.27	3.56	1.13	78.87	0.45

Ashqelon	1.33	130.50	2.54	2.50	66.14	0.42
Canada park	1.69	138.77	2.58	1.69	68.49	0.40
Havarim stream	1.08	114.58	1.57	1.75	53.39	0.44
Jordan est	1.42	127.75	3.03	2.33	68.30	0.43
Klil	1.69	129.38	2.52	2.31	74.17	0.40
Maale Efraim	1.30	103.89	1.55	1.70	35.35	0.52
Mt Arbel	1.19	121.63	2.62	2.19	58.33	0.48
Mt Harif	1.00	126.80	2.30	2.30	62.23	0.44
Neomi	1.17	99.83	1.68	1.83	38.32	0.49
Neot Kdumim	1.60	121.40	2.68	3.07	68.31	0.45
Oren canyon	1.08	118.42	2.35	1.58	56.15	ND
Yeruham	1.17	117.17	1.67	2.17	42.68	ND

Table 35. Provided are the values of each of the parameters measured in Barley accessions according to the following correlation identifications (Correlation Ids): 8 = Hairiness of basal leaves; 9 = Plant height; 4 = Grain yield per spike; 11 = Stem pigmentation; 12 = Vegetative dry weight; 13 = Harvest Index.

Table 36

Correlation between the expression level of selected Genes of some embodiments of the invention in various tissues and the phenotypic performance under normal conditions across barley accessions

Gene Name	*R*	*P value*	*Exp. Set ID*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. Set ID*	*Corr. Set ID*
LAB195	0.80	0.193838	D	5	LAB195	0.73	0.2649	D	12

Table 36. "Corr. Set ID " – correlation set ID according to the correlated parameters Table

Table 37

Correlation between the expression level of selected Orthologs genes of some embodiments of the invention in various tissues and the phenotypic performance under normal conditions across barley accessions

Gene Name	*R*	*P value*	*Exp. Set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. Set*	*Corr. Set ID*
LAB352_H0	0.71	0.0470	C	6					

Table 37. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

EXAMPLE 6

PRODUCTION OF ARABIDOPSIS TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS USING 44K ARABIDOPSIS OLIGONUCLEOTIDE MICRO-ARRAY

In order to produce a high throughput correlation analysis comparing between plant phenotype and gene expression level, the present inventors utilized a Arabidopsis oligonucleotide micro-array, produced by Agilent Technologies.

The array oligonucleotide represents about 44,000 Arabidopsis genes and transcripts. To define correlations between the levels of RNA expression with NUE, yield components or vigor related parameters various plant characteristics of 14 different Arabidopsis ecotypes were analyzed. Among them, ten ecotypes encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Experimental Procedures

Analyzed Arabidopsis tissues – Two tissues of plants [leaves and stems] growing at two different nitrogen fertilization levels (1.5 mM Nitrogen or 6 mM Nitrogen) were sampled and RNA was extracted as described above. Each micro-array expression information tissue type has received a Set ID as summarized Table 38 below.

Table 38
Arabidopsis transcriptom experimental sets

Expression Set	*Set ID*
Leaves at 1.5 mM Nitrogen fertilization	A
Leaves at 6 mM Nitrogen fertilization	B
Stems at 1.5 mM Nitrogen fertilization	C
Stem at 6 mM Nitrogen fertilization	D

Table 38.

Arabidopsis yield components and vigor related parameters under different nitrogen fertilization levels assessment – 10 Arabidopsis accessions in 2 repetitive plots each containing 8 plants per plot were grown at greenhouse. The growing protocol used was as follows: surface sterilized seeds were sown in Eppendorf tubes containing 0.5 x Murashige-Skoog basal salt medium and grown at 23 °C under 12-hour light and 12-hour dark daily cycles for 10 days. Then, seedlings of similar size were carefully transferred to pots filled with a mix of perlite and peat in a 1:1 ratio. Constant nitrogen limiting conditions were achieved by irrigating the plants with a solution containing 1.5 mM inorganic nitrogen in the form of KNO_3, supplemented with 2 mM $CaCl_2$, 1.25 mM KH_2PO_4, 1.50 mM $MgSO_4$, 5 mM KCl, 0.01 mM H_3BO_3 and microelements, while

normal irrigation conditions was achieved by applying a solution of 6 mM inorganic nitrogen also in the form of KNO_3, supplemented with 2 mM $CaCl_2$, 1.25 mM KH_2PO_4, 1.50 mM $MgSO_4$, 0.01 mM H_3BO_3 and microelements. To follow plant growth, trays were photographed the day nitrogen limiting conditions were initiated and subsequently every 3 days for about 15 additional days. Rosette plant area was then determined from the digital pictures. ImageJ software was used for quantifying the plant size from the digital pictures utilizing proprietary scripts designed to analyze the size of rosette area from individual plants as a function of time. The image analysis system included a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.37 (Java based image processing program, which was developed at the U.S. National Institutes of Health and freely available on the internet. Next, analyzed data was saved to text files and processed using the JMP statistical analysis software (SAS institute).

Data parameters collected are summarized in Table 39, hereinbelow.

Table 39
Arabidopsis correlated parameters (vectors)

Correlated parameter with	*Correlation Id*
N 1.5 mM; Rosette Area at day 8 [cm^2]	1
N 1.5 mM; Rosette Area at day 10 [cm^2]	2
N 1.5 mM; Plot Coverage at day 8 [%]	3
N 1.5 mM; Plot Coverage at day 10 [%]	4
N 1.5 mM; Leaf Number at day 10	5
N 1.5 mM; Leaf Blade Area at day 10 [cm^2]	6
N 1.5 mM; RGR of Rosette Area at day 3 [cm^2/day]	7
N 1.5 mM; t50 Flowering [day]	8
N 1.5 mM; Dry Weight [gr/plant]	9
N 1.5 mM; Seed Yield [gr/plant]	10
N 1.5 mM; Harvest Index	11
N 1.5 mM; 1000 Seeds weight [gr]	12
N 1.5 mM; seed yield/ rosette area at day 10 [gr/cm^2]	13
N 1.5 mM; seed yield/leaf blade [gr/cm^2]	14
N 1.5 mM; % Seed yield reduction compared to N 6 mM	15
N 1.5 mM; % Biomass reduction compared to N 6 mM	16
N 1.5 mM; N level /DW [SPAD unit/gr]	17
N 1.5 mM; DW/ N level [gr/ SPAD unit]	18
N 1.5 mM; seed yield/ N level [gr/ SPAD unit]	19
N 6 mM; Rosette Area at day 8 [cm^2]	20
N 6 mM; Rosette Area at day 10 [cm^2]	21
N 6 mM; Plot Coverage at day 8 [%]	22

Correlated parameter with	*Correlation Id*
N 6 mM; Plot Coverage at day 10 [%]	23
N 6 mM; Leaf Number at day 10	24
N 6 mM; Leaf Blade Area at day 10	25
N 6 mM; RGR of Rosette Area at day 3 [cm^2/gr]	26
N 6 mM; t50 Flowering [day]	27
N 6 mM; Dry Weight [gr/plant]	28
N 6 mM; Seed Yield [gr/plant]	29
N 6 mM; Harvest Index	30
N 6 mM; 1000 Seeds weight [gr]	31
N 6 mM; seed yield/ rosette area day at day 10 [gr/cm^2]	32
N 6 mM; seed yield/leaf blade [gr/cm^2]	33
N 6 mM; N level / FW	34
N 6 mM; DW/ N level [gr/ SPAD unit]	35
N 6 mM; N level /DW (SPAD unit/gr plant)	36
N 6 mM; Seed yield/N unit [gr/ SPAD unit]	37

Table 39. "N" = Nitrogen at the noted concentrations; "gr." = grams; "SPAD" = chlorophyll levels; "t50" = time where 50% of plants flowered; "gr/ SPAD unit" = plant biomass expressed in grams per unit of nitrogen in plant measured by SPAD. "DW" = plant dry weight; "N level /DW" = plant Nitrogen level measured in SPAD unit per plant biomass [gr]; "DW/ N level" = plant biomass per plant [gr]/SPAD unit;

Assessment of NUE, yield components and vigor-related parameters - Ten Arabidopsis ecotypes were grown in trays, each containing 8 plants per plot, in a greenhouse with controlled temperature conditions for about 12 weeks. Plants were irrigated with different nitrogen concentration as described above depending on the treatment applied. During this time, data was collected documented and analyzed. Most of chosen parameters were analyzed by digital imaging.

Digital imaging – Greenhouse assay

An image acquisition system, which consists of a digital reflex camera (Canon EOS 400D) attached with a 55 mm focal length lens (Canon EF-S series) placed in a custom made Aluminum mount, was used for capturing images of plants planted in containers within an environmental controlled greenhouse. The image capturing process is repeated every 2-3 days starting at day 9-12 till day 16-19 (respectively) from transplanting.

An image processing system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.37, Java based image processing software, which was developed at the U.S. National Institutes of Health and is freely available on the internet at. Images were captured in resolution of 10 Mega

Pixels (3888x2592 pixels) and stored in a low compression JPEG (Joint Photographic Experts Group standard) format. Next, image processing output data was saved to text files and analyzed using the JMP statistical analysis software (SAS institute).

Leaf analysis - Using the digital analysis leaves data was calculated, including leaf number, leaf blade area, Rosette diameter and area.

Vegetative growth rate: the relative growth rate (RGR) of leaf blade area (Formula VIII), leaf number (Formula IX), rosette area (Formula X), rosette diameter (Formula XI), plot coverage (Formula XII) and Petiole Relative Area (XIII) are calculated as follows:

Formula VIII: Relative growth rate of leaf blade area = Regression coefficient of leaf area along time course.

Formula IX: Relative growth rate of plant leaf number = Regression coefficient of plant leaf number along time course.

Formula X: Relative growth rate of rosette area = Regression coefficient of rosette area along time course.

Formula XI: Relative growth rate of rosette diameter = Regression coefficient of rosette diameter along time course.

Formula XII: Relative growth rate of plot coverage = Regression coefficient of plot.

Formula XIII: Petiole Relative Area= [(Leaf blade*Leaf number)/Rosette.

Seed yield and 1000 seeds weight - At the end of the experiment all seeds from all plots were collected and weighed in order to measure seed yield per plant in terms of total seed weight per plant (gr). For the calculation of 1000 seed weight, an average weight of 0.02 grams was measured from each sample, 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.

Dry weight and seed yield - At the end of the experiment, plant were harvested and left to dry at 30 °C in a drying chamber. The biomass was separated from the seeds, weighed and divided by the number of plants. Dry weight = total weight of the vegetative portion above ground (excluding roots) after drying at 30 °C in a drying chamber.

Harvest Index - The harvest index was calculated using Formula IV as described above.

T_{50} days to flowering – Each of the repeats was monitored for flowering date. Days of flowering was calculated from sowing date till 50 % of the plots flowered.

Plant nitrogen level - The chlorophyll content of leaves is a good indicator of the nitrogen plant status since the degree of leaf greenness is highly correlated to this parameter. Chlorophyll content was determined using a Minolta SPAD 502 chlorophyll meter and measurement was performed at time of flowering. SPAD meter readings were done on young fully developed leaf. Three measurements per leaf were taken per plot. Based on this measurement, parameters such as the ratio between seed yield per nitrogen unit [seed yield/N level = seed yield per plant [gr]/SPAD unit], plant DW per nitrogen unit [DW/ N level= plant biomass per plant [g]/SPAD unit], and nitrogen level per gram of biomass [N level/DW= SPAD unit/ plant biomass per plant (gr)] were calculated.

Percent of seed yield reduction- measures the amount of seeds obtained in plants when grown under nitrogen-limiting conditions compared to seed yield produced at normal nitrogen levels expressed in %.

Experimental Results

10 different Arabidopsis accessions (ecotypes) were grown and characterized for 37 parameters as described above. The average for each of the measured parameters was calculated using the JMP software and values are summarized in Table 40 below. Subsequent correlation analysis between the various transcriptom sets (Table 38) and the measured parameters was conducted (Tables 41 and 42 below). Following are the results integrated to the database.

Table 40
Measured parameters in Arabidopsis accessions

Ecotype \Treatment	*Line -1*	*Line -2*	*Line -3*	*Line -4*	*Line -5*	*Line -6*	*Line -7*	*Line -8*	*Line -9*	*Line-10*
N 1.5 mM; Rosette Area at day 8	0.760	0.709	1.061	1.157	0.996	1.000	0.910	0.942	1.118	0.638
N 1.5 mM; Rosette Area at day 10	1.430	1.325	1.766	1.971	1.754	1.832	1.818	1.636	1.996	1.150
N 1.5 mM; Plot Coverage% at day 8	3.221	3.003	4.497	4.902	4.220	4.238	3.858	3.990	4.738	2.705

Ecotype \Treatment	*Line -1*	*Line -2*	*Line -3*	*Line -4*	*Line -5*	*Line -6*	*Line -7*	*Line -8*	*Line -9*	*Line-10*
N 1.5 mM; Plot Coverage% at day 10	6.058	5.614	7.484	8.351	7.432	7.764	7.702	6.933	8.458	4.871
N 1.5 mM; Leaf Number at day 10	6.875	7.313	7.313	7.875	7.938	7.750	7.625	7.188	8.625	5.929
N 1.5 mM; Leaf Blade Area at day 10	0.335	0.266	0.374	0.387	0.373	0.370	0.386	0.350	0.379	0.307
N 1.5 mM; RGR of Rosette Area at day 3	0.631	0.793	0.502	0.491	0.605	0.720	0.825	0.646	0.668	0.636
N 1.5 mM; t50 Flowering [day]	15.967	20.968	14.836	24.708	23.566	23.698	18.059	19.488	23.568	21.888
N 1.5 mM; Dry Weight [gr/plant]	0.164	0.124	0.082	0.113	0.184	0.124	0.134	0.106	0.148	0.171
N 1.5 mM; Seed Yield [gr/plant]	0.032	0.025	0.023	0.010	0.006	0.009	0.032	0.019	0.012	0.014
N 1.5 mM; Harvest Index	0.192	0.203	0.295	0.085	0.031	0.071	0.241	0.179	0.081	0.079
N 1.5 mM; 1000 Seeds weight[gr]	0.016	0.016	0.018	0.014	0.018	0.022	0.015	0.014	0.022	0.019
N 1.5 mM; seed yield/ rosette area day at day 10	0.022	0.019	0.014	0.005	0.003	0.005	0.018	0.013	0.007	0.012
N 1.5 mM; seed yield/leaf blade	0.095	0.095	0.063	0.026	0.015	0.024	0.084	0.059	0.034	0.044
N 1.5 mM; % Seed yield reduction compared to 6 mM	72.559	84.701	78.784	87.996	91.820	92.622	76.710	81.938	91.301	85.757
N 1.5 mM; %Biomass reduction compared to 6 mM	60.746	76.706	78.560	78.140	62.972	78.641	73.192	83.068	77.190	70.120
N 1.5 mM; Spad / FW	45.590			42.108	28.151		53.111			67.000
N 1.5 mM; SPAD/DW	167.300			241.061	157.823		194.977			169.343
N 1.5 mM; DW/SPAD	0.006			0.004	0.006		0.005			0.006
N 1.5 mM; seed yield/spad	0.001			0.000	0.000		0.001			0.000
N 6 mM; Rosette Area at day 8	0.759	0.857	1.477	1.278	1.224	1.095	1.236	1.094	1.410	0.891
N 6 mM; Rosette Area at day 10	1.406	1.570	2.673	2.418	2.207	2.142	2.474	1.965	2.721	1.642
N 6 mM; Plot Coverage% at day 8	3.216	3.631	6.259	5.413	5.187	4.641	5.236	4.634	5.974	3.774
N 6 mM; Plot Coverage% at day 10	5.957	6.654	11.324	10.244	9.352	9.076	10.485	8.327	11.528	6.958
N 6 mM; Leaf Number at day 10	6.250	7.313	8.063	8.750	8.063	8.750	8.375	7.125	9.438	6.313
N 6 mM; Leaf Blade Area at day 10	0.342	0.315	0.523	0.449	0.430	0.430	0.497	0.428	0.509	0.405

Ecotype \Treatment	*Line -1*	*Line -2*	*Line -3*	*Line -4*	*Line -5*	*Line -6*	*Line -7*	*Line -8*	*Line -9*	*Line-10*
N 6 mM; RGR of Rosette Area at day 3	0.689	1.024	0.614	0.601	0.477	0.651	0.676	0.584	0.613	0.515
N 6 mM; t50 Flowering [day]	16.371	20.500	14.635	24.000	23.378	23.595	15.033	19.750	22.887	18.804
N 6 mM; Dry Weight [gr/plant]	0.419	0.531	0.382	0.518	0.496	0.579	0.501	0.628	0.649	0.573
N 6 mM; Seed Yield [gr/plant]	0.116	0.165	0.108	0.082	0.068	0.119	0.139	0.107	0.138	0.095
N 6 mM; Harvest Index	0.280	0.309	0.284	0.158	0.136	0.206	0.276	0.171	0.212	0.166
N 6 mM; 1000 Seeds weight[gr]	0.015	0.017	0.018	0.012	0.016	0.016	0.015	0.014	0.017	0.016
N 6 mM; seed yield/ rosette area day at day 10	0.082	0.106	0.041	0.034	0.031	0.056	0.057	0.055	0.051	0.058
N 6 mM; seed yield/leaf blade	0.339	0.526	0.207	0.183	0.158	0.277	0.281	0.252	0.271	0.235
N 6 mM; Spad / FW	22.489			28.268	17.641		33.323			39.003
N 6 mM; DW/SPAD (biomass/ N unit)	0.019			0.018	0.028		0.015			0.015
N 6 mM; spad/DW (gN/g plant)	53.705			54.625	35.548		66.479			68.054
N 6 mM; Seed yield/N unit	0.004			0.003	0.002		0.005			0.003

Table 40. Provided are the measured parameters under various treatments in various ecotypes (Arabidopsis accessions).

Table 41

Correlation between the expression level of selected Genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or low nitrogen fertilization conditions across Arabidopsis accessions

Gene Name	*R*	*P value*	*Exp. set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. set*	*Corr. Set ID*
LAB190	0.88	0.0495	D	37	LAB190	0.84	0.0021	A	19

Table 41. "Corr. Set ID " – correlation set ID according to the correlated parameters Table

Table 42

Correlation between the expression level of selected Orthologs genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or low nitrogen fertilization conditions across Arabidopsis accessions

Gene Name	*R*	*P value*	*Exp. Set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. Set*	*Corr. Set ID*

Table 42. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

EXAMPLE 7

PRODUCTION OF ARABIDOPSIS TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS OF YIELD, BIOMASS AND/OR VIGOR RELATED PARAMETERS USING 44K ARABIDOPSIS FULL GENOME OLIGONUCLEOTIDE MICRO-ARRAY

To produce a high throughput correlation analysis comparing between plant phenotype and gene expression level, the present inventors utilized an Arabidopsis thaliana oligonucleotide micro-array, produced by Agilent Technologies. The array oligonucleotide represents about 40,000 *A. thaliana* genes and transcripts designed based on data from the TIGR ATH1 v.5 database and Arabidopsis MPSS (University of Delaware) databases. To define correlations between the levels of RNA expression and yield, biomass components or vigor related parameters, various plant characteristics of 15 different Arabidopsis ecotypes were analyzed. Among them, nine ecotypes encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Experimental procedures

Analyzed Arabidopsis tissues –Five tissues at different developmental stages including root, leaf, flower at anthesis, seed at 5 days after flowering (DAF) and seed at 12 DAF, representing different plant characteristics, were sampled and RNA was extracted as described above. Each micro-array expression information tissue type has received a Set ID as summarized in Table 43 below.

Table 43
Tissues used for Arabidopsis transcriptom expression sets

Expression Set	*Set ID*
Root	A
Leaf	B
Flower	C
Seed 5 DAF	D
Seed 12 DAF	E

Table 43: Provided are the identification (ID) letters of each of the *Arabidopsis* expression sets (A-E). DAF = days after flowering.

Yield components and vigor related parameters assessment - Eight out of the nine Arabidopsis ecotypes were used in each of 5 repetitive blocks (named A, B, C, D and E), each containing 20 plants per plot. The plants were grown in a greenhouse at controlled conditions in 22 °C, and the N:P:K fertilizer (20:20:20; weight ratios) [nitrogen (N), phosphorus (P) and potassium (K)] was added. During this time data was collected, documented and analyzed. Additional data was collected through the seedling stage of plants grown in a tissue culture in vertical grown transparent agar plates. Most of chosen parameters were analyzed by digital imaging.

Digital imaging in Tissue culture - A laboratory image acquisition system was used for capturing images of plantlets sawn in square agar plates. The image acquisition system consists of a digital reflex camera (Canon EOS 300D) attached to 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.

Digital imaging in Greenhouse - The image capturing process was repeated every 3-4 days starting at day 7 till day 30. The same camera attached to a 24 mm focal length lens (Canon EF series), 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 white tubs were square shape with measurements of 36 x 26.2 cm and 7.5 cm deep. During the capture process, the tubs were placed beneath the iron mount, while avoiding direct sun light and casting of shadows. This process was repeated every 3-4 days for up to 30 days.

An image analysis system was used, which consists of a personal desktop computer(Intel P43.0 GHz processor) and a public domain program - ImageJ 1.37, Java based image processing program, which was developed at the U.S National Institutes of Health and is freely available on the internet at. Images were captured in resolution of 6 Mega Pixels (3072 x 2048 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. On day 30, 3-4 representative plants were chosen from each plot of blocks A, B and C. The plants were dissected, each leaf was separated and was introduced between two glass trays, a photo of each plant was taken and the various parameters (such as leaf total area, laminar length etc.) were calculated from the images. The blade circularity was calculated as laminar width divided by laminar length.

Root analysis - During 17 days, the different ecotypes were grown in transparent agar plates. The plates were photographed every 3 days starting at day 7 in the photography room and the roots development was documented (see examples in Figures 3A-F). The growth rate of roots was calculated according to **Formula XIV:** Relative growth rate of root coverage = Regression coefficient of root coverage along time course.

Vegetative growth rate analysis - was calculated according to Formulas VIII-XIII above. The analysis was ended with the appearance of overlapping plants.

For comparison between ecotypes the calculated rate was normalized using plant developmental stage as represented by the number of true leaves. In cases where plants with 8 leaves had been sampled twice (for example at day 10 and day 13), only the largest sample was chosen and added to the Anova comparison.

Seeds in siliques analysis - On day 70, 15-17 siliques were collected from each plot in blocks D and E. The chosen siliques were light brown color but still intact. The siliques were opened in the photography room and the seeds were scatter on a glass tray, a high resolution digital picture was taken for each plot. Using the images the number of seeds per silique was determined.

Seeds average weight - At the end of the experiment all seeds from plots of blocks A-C were collected. An average weight of 0.02 grams was measured from each sample, 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.

Oil percentage in seeds - At the end of the experiment all seeds from plots of blocks A-C were collected. Columbia seeds from 3 plots were mixed grounded and then mounted onto the extraction chamber. 210 ml of n-Hexane (Cat No. 080951 Biolab Ltd.) were used as the solvent. The extraction was performed for 30 hours at medium

heat 50 °C. Once the extraction has ended the n-Hexane was evaporated using the evaporator at 35 °C and vacuum conditions. The process was repeated twice. The information gained from the Soxhlet extractor (Soxhlet, F. Die gewichtsanalytische Bestimmung des Milchfettes, Polytechnisches J. (Dingler's) 1879, 232, 461) was used to create a calibration curve for the Low Resonance NMR. The content of oil of all seed samples was determined using the Low Resonance NMR (MARAN Ultra– Oxford Instrument) and its MultiQuant sowftware package.

Silique length analysis - On day 50 from sowing, 30 siliques from different plants in each plot were sampled in block A. The chosen siliques were green-yellow in color and were collected from the bottom parts of a grown plant's stem. A digital photograph was taken to determine silique's length.

Dry weight and seed yield - On day 80 from sowing, the plants from blocks A-C were harvested and left to dry at 30 °C in a drying chamber. The biomass and seed weight of each plot was separated, measured and divided by the number of plants. 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).

Oil yield - The oil yield was calculated using Formula XV.

Formula XV: Seed Oil yield = Seed yield per plant (gr) * Oil % in seed.

Harvest Index (seed) - The harvest index was calculated using Formula IV (described above).

Experimental Results

Nine different *Arabidopsis* ecotypes were grown and characterized for 18 parameters (named as vectors).

Table 44
Arabidopsis correlated parameters (vectors)

Correlated parameter with	*Correlation ID*
Root length day 13 (cm)	1
Root length day 7 (cm)	2
Relative root growth (cm /day) day 13	3
Fresh weight per plant (gr) at bolting stage	4
Dry matter per plant (gr)	5
Vegetative growth rate (cm^2 / day) till 8 true leaves	6
Blade circularity	7
Lamina width (cm)	8

Correlated parameter with	*Correlation ID*
Lamina length (cm)	9
Total leaf area per plant (cm)	10
1000 Seed weight (gr)	11
Oil % per seed	12
Seeds per silique	13
Silique length (cm)	14
Seed yield per plant (gr)	15
Oil yield per plant (mg)	16
Harvest Index	17
Leaf width/length	18

Table 44. Provided are the Arabidopsis correlated parameters (correlation ID Nos. 1-18). Abbreviations: Cm = centimeter(s); gr = gram(s); mg = milligram(s).

The characterized values are summarized in Tables 45 and 46 below.

Table 45
Measured parameters in Arabidopsis ecotypes

Ecotype	*15*	*16*	*12*	*11*	*5*	*17*	*10*	*13*	*14*
An-1	0.34	118.63	34.42	0.0203	0.64	0.53	46.86	45.44	1.06
Col-0	0.44	138.73	31.19	0.0230	1.27	0.35	109.89	53.47	1.26
Ct-1	0.59	224.06	38.05	0.0252	1.05	0.56	58.36	58.47	1.31
Cvi (N8580)	0.42	116.26	27.76	0.0344	1.28	0.33	56.80	35.27	1.47
Gr-6	0.61	218.27	35.49	0.0202	1.69	0.37	114.66	48.56	1.24
Kondara	0.43	142.11	32.91	0.0263	1.34	0.32	110.82	37.00	1.09
Ler-1	0.36	114.15	31.56	0.0205	0.81	0.45	88.49	39.38	1.18
Mt-0	0.62	190.06	30.79	0.0226	1.21	0.51	121.79	40.53	1.18
Shakdara	0.55	187.62	34.02	0.0235	1.35	0.41	93.04	25.53	1.00

Table 45. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: 15 = Seed yield per plant (gram); 16 = oil yield per plant (mg); 12 = oil % per seed; 11 = 1000 seed weight (gr); 5 = dry matter per plant (gr); 17 = harvest index; 10 = total leaf area per plant (cm); 13 = seeds per silique; 14 = Silique length (cm).

Table 46
Additional measured parameters in Arabidopsis ecotypes

Ecotype	*6*	*3*	*2*	*1*	*4*	*9*	*8*	*18*	*7*
An-1	0.313	0.631	0.937	4.419	1.510	2.767	1.385	0.353	0.509
Col-0	0.378	0.664	1.759	8.530	3.607	3.544	1.697	0.288	0.481
Ct-1	0.484	1.176	0.701	5.621	1.935	3.274	1.460	0.316	0.450
Cvi (N8580)	0.474	1.089	0.728	4.834	2.082	3.785	1.374	0.258	0.370
Gr-6	0.425	0.907	0.991	5.957	3.556	3.690	1.828	0.356	0.501
Kondara	0.645	0.774	1.163	6.372	4.338	4.597	1.650	0.273	0.376
Ler-1	0.430	0.606	1.284	5.649	3.467	3.877	1.510	0.305	0.394
Mt-0	0.384	0.701	1.414	7.060	3.479	3.717	1.817	0.335	0.491
Shakdara	0.471	0.782	1.251	7.041	3.710	4.149	1.668	0.307	0.409

Table 46. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: 6 = Vegetative growth rate (cm^2/day) until 8 true leaves; 3 = relative root growth (cm/day) (day 13); 2 = Root length day 7 (cm); 1 = Root length day 13 (cm); 4 = fresh weight per plant (gr) at bolting stage; 9. = Lamima length (cm); 8 = Lamina width (cm); 18 = Leaf width/length; 7 = Blade circularity.

Tables 47 and 48 provide the correlation analyses.

Table 47

Correlation between the expression level of selected Genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or low nitrogen fertilization conditions across Arabidopsis accessions

Gene Name	*R*	*P value*	*Exp. set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. set*	*Corr. Set ID*

Table 47. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

Table 48

Correlation between the expression level of selected Orthologs genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or low nitrogen fertilization conditions across Arabidopsis accessions

Gene Name	*R*	*P value*	*Exp. Set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. Set*	*Corr. Set ID*

Table 48. "Corr. Set ID " – correlation set ID according to the correlated parameters Table above.

EXAMPLE 8

PLANT FIBER DEVELOPMENT IN COTTON

PRODUCTION OF COTTON TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS USING COTTON OLIGONUCLEOTIDE MICROARRAY

In order to conduct high throughput gene expression correlation analysis, the present inventors used cotton oligonucleotide microarray, designed and produced by "Comparative Evolutionary Genomics of Cotton". This Cotton Oligonucleotide Microarray is composed of 12,006 Integrated DNA Technologies (IDT) oligonucleotides derived from an assembly of more than 180,000 Gossypium ESTs sequenced from 30 cDNA libraries. For additional details see PCT/IL2005/000627 and PCT/IL2007/001590.

Table 49
Cotton transcriptom experimental sets

Expression Set	*Set ID*
cotton fiber 5d	A
cotton fiber 10d	B

Table 49.

In order to define correlations between the levels of RNA expression and fiber length, fibers from 8 different cotton lines were analyzed. These fibers were selected showing very good fiber quality and high lint index (Pima types, originating from other cotton species, namely G. barbadense), different levels of quality and lint indexes from various G. hirsutum lines: good quality and high lint index (Acala type), and poor quality and short lint index (Tamcot type, and old varieties). A summary of the fiber length of the different lines is provided in Table 50.

Experimental procedures

RNA extraction - Fiber development stages, representing different fiber characteristics, at 5, 10 and 15 DPA were sampled and RNA was extracted as described above.

Fiber length assessment - Fiber length of the selected cotton lines was 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.

Experimental Results

Eight different cotton lines were grown, and their fiber length was measured. The fibers UHM values are summarized in Table 50 hereinbelow. The R square was calculated for each of the genes.

Table 50
Summary of the fiber length of the 8 different cotton lines

Cotton variety	*Length (UHM)*	
	Mean	*STD*
SA 217 SD	0.89	0.04
SA 68 SD	1.01	0.03

Cotton variety	*Length (UHM)*	
	Mean	*STD*
Tamcot	1.06	0.01
DP 90	1.1	0.08
ZG 236	1.15	0.00
Coker 310	1.21	0.02
S7	1.26	0.02
Pima	1.36	0.00

Table 50: Presented are the means and standard deviations (STD) of 8 different cotton lines.

Table 51

Correlation between the expression level of selected genes of some embodiments of the invention in various tissues and the phenotypic performance under normal conditions in cotton

Gene Name	*R*	*P value*	*Exp. set*	*Corr. Set ID*	*Gene Name*	*R*	*P value*	*Exp. set*	*Corr. Set ID*

Table 51. "Corr. Set ID " – correlation set refer to fiber length

Table 52

Correlation between the expression level of selected orthologs genes of some embodiments of the invention in various tissues and the phenotypic performance under normal conditions in cotton

Gene Name	*R*	*P value*	*Exp. Set*	*Corrl. Set ID*	*Gene Name*	*R*	*P value*	*Exp. Set*	*Corr. Set ID*

Table 52. "Corr. Set ID " – correlation set refer to fiber length

EXAMPLE 9

IDENTIFICATION OF GENES WHICH INCREASE ABST, GROWTH RATE, VIGOR, YIELD, BIOMASS, OIL CONTENT, WUE, NUE AND/OR FUE IN PLANTS

Based on the above described bioinformatics and experimental tools, the present inventors have identified 217 which exhibit a major impact on abiotic stress tolerance, plant yield, oil content, growth rate, vigor, biomass, growth rate, nitrogen use efficiency, water use efficiency and fertilizer use efficiency when expression thereof is increased in plants. The identified genes, their curated polynucleotide and polypeptide sequences, as well as their updated sequences according to GenBank database are summarized in Table 53, hereinbelow.

Table 53

Identified genes for increasing abiotic stress tolerance, water use efficiency, yield, growth rate, vigor, biomass, growth rate, oil content, nitrogen use efficiency and fertilizer use efficiency of a plant

Gene Name	*Cluster Name*	*Organism*	*Polynucl. SEQ ID NO:*	*Polypep. SEQ ID NO:*
LAB53	barley|gb157SOLEXA|AF000939	barley	1	474
LAB54	barley|gb157SOLEXA|AF026538	barley	2	475
LAB55	barley|gb157SOLEXA|AJ477127	barley	3	476
LAB56	barley|gb157SOLEXA|AL504663	barley	4	477
LAB58	barley|gb157SOLEXA|BE420577	barley	5	478
LAB64	barley|gb157SOLEXA|BF624328	barley	6	479
LAB65	barley|gb157SOLEXA|BQ662625	barley	7	480
LAB67	brachypodium|gb169|BE414847	brachypodium	8	481
LAB68	brachypodium|gb169|BE415661	brachypodium	9	482
LAB69	brachypodium|gb169|BE418188	brachypodium	10	483
LAB70	canola|gb161|CD814191	canola	11	484
LAB71	cotton|gb164|BE052211	cotton	12	485
LAB72	cotton|gb164|CO132512	cotton	13	486
LAB73	grape|gb160|BM436750	grape	14	487
LAB74	grape|gb160|CB004439	grape	15	488
LAB76	grape|gb160|CB974118	grape	16	489
LAB80	rice|gb170|OS01G09620	rice	17	490
LAB81	rice|gb170|OS02G54780	rice	18	491
LAB82	rice|gb170|OS02G54890	rice	19	492
LAB83	rice|gb170|OS03G21640	rice	20	493
LAB84	rice|gb170|OS04G58810	rice	21	494
LAB86	rice|gb170|OS08G37660	rice	22	495
LAB88	rice|gb170|OS09G27820	rice	23	496
LAB89	rice|gb170|OS10G37760	rice	24	497
LAB92	sorghum|gb161.crp|AI724271	sorghum	25	498
LAB93	sorghum|gb161.crp|AI783065	sorghum	26	499
LAB94	sorghum|gb161.crp|AW282995	sorghum	27	500
LAB97	sorghum|gb161.crp|AW283405	sorghum	28	501
LAB98	sorghum|gb161.crp|AW285328	sorghum	29	502
LAB101	sorghum|gb161.crp|AW677797	sorghum	30	503
LAB102	sorghum|gb161.crp|AW679677	sorghum	31	504
LAB106	sorghum|gb161.crp|BE363251	sorghum	32	505
LAB107	sorghum|gb161.crp|BE366167	sorghum	33	506
LAB108	sorghum|gb161.crp|BE366746	sorghum	34	507
LAB109	sorghum|gb161.crp|BG047558	sorghum	35	508
LAB110	sorghum|gb161.crp|BM322761	sorghum	36	509
LAB113	tomato|gb164|AA824960	tomato	37	510
LAB115	tomato|gb164|AI488164	tomato	38	511
LAB116	tomato|gb164|AI637375	tomato	39	512
LAB117	tomato|gb164|AI772185	tomato	40	513
LAB119	tomato|gb164|AI772981	tomato	41	514
LAB120	tomato|gb164|AW218593	tomato	42	515

Gene Name	*Cluster Name*	*Organism*	*Polynucl. SEQ ID NO:*	*Polypep. SEQ ID NO:*
LAB121	tomato|gb164|AW223810	tomato	43	516
LAB122	tomato|gb164|AW442266	tomato	44	517
LAB123	tomato|gb164|AW442830	tomato	45	518
LAB124	tomato|gb164|BG123767	tomato	46	519
LAB125	tomato|gb164|BG124210	tomato	47	520
LAB126	tomato|gb164|BG126148	tomato	48	521
LAB127	tomato|gb164|BG127842	tomato	49	522
LAB128	tomato|gb164|BG128502	tomato	50	523
LAB129	tomato|gb164|BG129905	tomato	51	524
LAB130	tomato|gb164|BG133230	tomato	52	525
LAB131	tomato|gb164|BG626085	tomato	53	526
LAB133	tomato|gb164|BG629133	tomato	54	527
LAB137	wheat|gb164|BE416704	wheat	55	528
LAB138	wheat|gb164|BE426494	wheat	56	529
LAB141	wheat|gb164|BE591380	wheat	57	530
LAB145	rice|gb170|OS12G25090	rice	58	531
LAB147	rice|gb170|OS05G49940	rice	59	532
LAB152	sorghum|gb161.crp|AW746652	sorghum	60	533
LAB153	sorghum|gb161.crp|AW923691	sorghum	61	534
LAB154	sorghum|gb161.crp|AW923843	sorghum	62	535
LAB156	sorghum|gb161.crp|BG357440	sorghum	63	536
LAB157	sorghum|gb161.crp|BI075600	sorghum	64	537
LAB158	sorghum|gb161.crp|BI098554	sorghum	65	538
LAB159	sorghum|gb161.crp|BM317501	sorghum	66	539
LAB160	sorghum|gb161.crp|BM329994	sorghum	67	540
LAB161	sorghum|gb161.crp|BQ704124	sorghum	68	541
LAB162	sorghum|gb161.crp|CD949495	sorghum	69	542
LAB163	sorghum|gb161.crp|CF074481	sorghum	70	543
LAB164	sorghum|gb161.crp|CF430071	sorghum	71	544
LAB165	sorghum|gb161.crp|SBGWP119861	sorghum	72	545
LAB166	sorghum|gb161.crp|BG239954	sorghum	73	546
LAB167	sorghum|gb161.crp|AI724270	sorghum	74	547
LAB169	sorghum|gb161.crp|AW053133	sorghum	75	548
LAB170	sorghum|gb161.crp|AW065993	sorghum	76	549
LAB171	sorghum|gb161.crp|AW155674	sorghum	77	550
LAB172	sorghum|gb161.crp|AW453175	sorghum	78	551
LAB174	sorghum|gb161.crp|AW679828	sorghum	79	552
LAB175	sorghum|gb161.crp|AW745804	sorghum	80	553
LAB176	sorghum|gb161.crp|CD205409	sorghum	81	554
LAB177	sorghum|gb161.crp|CF431793	sorghum	82	555
LAB178	tomato|gb164|AI490504	tomato	83	556
LAB179	wheat|gb164|CV763774	wheat	84	557
LAB181	arabidopsis|gb165|AT1G30500	arabidopsis	85	558
LAB182	arabidopsis|gb165|AT1G54160	arabidopsis	86	559
LAB183	arabidopsis|gb165|AT2G17500	arabidopsis	87	560
LAB185	arabidopsis|gb165|AT2G28400	arabidopsis	88	561
LAB186	arabidopsis|gb165|AT2G42520	arabidopsis	89	562
LAB187	arabidopsis|gb165|AT3G11410	arabidopsis	90	563

Gene Name	*Cluster Name*	*Organism*	*Polynucl. SEQ ID NO:*	*Polypep. SEQ ID NO:*
LAB188	arabidopsis|gb165|AT3G44860	arabidopsis	91	564
LAB189	arabidopsis|gb165|AT3G58570	arabidopsis	92	565
LAB190	arabidopsis|gb165|AT5G39050	arabidopsis	93	566
LAB191	arabidopsis|gb165|AT5G47640	arabidopsis	94	567
LAB193	barley|gb157SOLEXA|AL500288	barley	95	568
LAB195	barley|gb157SOLEXA|AL502556	barley	96	569
LAB197	barley|gb157SOLEXA|AV832785	barley	97	570
LAB204	barley|gb157SOLEXA|BE411310	barley	98	571
LAB206	barley|gb157SOLEXA|BE420904	barley	99	572
LAB207	barley|gb157SOLEXA|BE421932	barley	100	573
LAB210	barley|gb157SOLEXA|BG365882	barley	101	574
LAB211	barley|gb157SOLEXA|BG368375	barley	102	575
LAB212	barley|gb157SOLEXA|BG418029	barley	103	576
LAB213	barley|gb157SOLEXA|BI949346	barley	104	577
LAB217	cotton|gb164|AI731250	cotton	105	578
LAB218	cotton|gb164|BG443778	cotton	106	579
LAB220	maize|gb170|AI615250	maize	107	580
LAB221	maize|gb170|AI622102	maize	108	581
LAB222	maize|gb170|CA400624	maize	109	582
LAB224	rice|gb170|OS01G14440	rice	110	583
LAB225	rice|gb170|OS01G52110	rice	111	584
LAB228	rice|gb170|OS01G68320	rice	112	585
LAB229	rice|gb170|OS01G68370	rice	113	586
LAB230	rice|gb170|OS01G68730	rice	114	587
LAB231	rice|gb170|OS01G68750	rice	115	588
LAB232	rice|gb170|OS01G68760	rice	116	589
LAB233	rice|gb170|OS01G68810	rice	117	590
LAB234	rice|gb170|OS01G68820	rice	118	591
LAB235	rice|gb170|OS01G68860	rice	119	592
LAB236	rice|gb170|OS02G08440	rice	120	593
LAB237	rice|gb170|OS02G32520	rice	121	594
LAB238	rice|gb170|OS02G51750	rice	122	595
LAB240	rice|gb170|OS03G04770	rice	123	596
LAB241	rice|gb170|OS03G05310	rice	124	597
LAB242	rice|gb170|OS03G15890	rice	125	598
LAB243	rice|gb170|OS03G49440	rice	126	599
LAB247	rice|gb170|OS05G27780	rice	127	600
LAB249	rice|gb170|OS05G46480	rice	128	601
LAB250	rice|gb170|OS05G51510	rice	129	602
LAB252	rice|gb170|OS08G35620	rice	130	603
LAB253	rice|gb170|OS09G15670	rice	131	604
LAB254	rice|gb170|OS09G31031	rice	132	605
LAB255	rice|gb170|OS09G31090T2	rice	133	606
LAB258	rice|gb170|OS09G31478	rice	134	607
LAB259	rice|gb170|OS09G31482	rice	135	608
LAB260	rice|gb170|OS10G11580	rice	136	609
LAB261	rice|gb170|OS10G28200	rice	137	610
LAB262	rice|gb170|OS10G35460	rice	138	611

Gene Name	*Cluster Name*	*Organism*	*Polynucl. SEQ ID NO:*	*Polypep. SEQ ID NO:*
LAB263	rice|gb170|OS10G36550	rice	139	612
LAB264	rice|gb170|OS10G37340	rice	140	613
LAB265	rice|gb170|OS12G41880	rice	141	614
LAB267	sorghum|gb161.crp|AF083327	sorghum	142	615
LAB268	sorghum|gb161.crp|AI391767	sorghum	143	616
LAB269	sorghum|gb161.crp|AI714721	sorghum	144	617
LAB270	sorghum|gb161.crp|AI834359	sorghum	145	618
LAB271	sorghum|gb161.crp|AI855376	sorghum	146	619
LAB272	sorghum|gb161.crp|AW067349	sorghum	147	620
LAB274	sorghum|gb161.crp|AW283715	sorghum	148	621
LAB275	sorghum|gb161.crp|AW287164	sorghum	149	622
LAB276	sorghum|gb161.crp|AW676813	sorghum	150	623
LAB277	sorghum|gb161.crp|AW677021	sorghum	151	624
LAB278	sorghum|gb161.crp|AW678652	sorghum	152	625
LAB279	sorghum|gb161.crp|AW745740	sorghum	153	626
LAB280	sorghum|gb161.crp|AW924546	sorghum	154	627
LAB281	sorghum|gb161.crp|AW924680	sorghum	155	628
LAB282	sorghum|gb161.crp|BE126094	sorghum	156	629
LAB283	sorghum|gb161.crp|BE363639	sorghum	157	630
LAB284	sorghum|gb161.crp|BE366498	sorghum	158	631
LAB286	sorghum|gb161.crp|BE599941	sorghum	159	632
LAB289	sorghum|gb161.crp|BG050539	sorghum	160	633
LAB290	sorghum|gb161.crp|BG050987	sorghum	161	634
LAB292	sorghum|gb161.crp|BG051832	sorghum	162	635
LAB293	sorghum|gb161.crp|BG104129	sorghum	163	636
LAB294	sorghum|gb161.crp|BG158316	sorghum	164	637
LAB295	sorghum|gb161.crp|BG558012	sorghum	165	638
LAB296	sorghum|gb161.crp|BM259168	sorghum	166	639
LAB297	sorghum|gb161.crp|BM417007	sorghum	167	640
LAB298	sorghum|gb161.crp|BM737392	sorghum	168	641
LAB299	sorghum|gb161.crp|CB924966	sorghum	169	642
LAB300	sorghum|gb161.crp|CD220284	sorghum	170	643
LAB302	sorghum|gb161.crp|CD233103	sorghum	171	644
LAB303	sorghum|gb161.crp|CD233331	sorghum	172	645
LAB304	sorghum|gb161.crp|EB406896	sorghum	173	646
LAB306	soybean|gb168|AW684299	soybean	174	647
LAB307	soybean|gb168|BE822951	soybean	175	648
LAB308	soybean|gb168|BF633506	soybean	176	649
LAB309	soybean|gb168|BF637946	soybean	177	650
LAB310	soybean|gb168|BM521769	soybean	178	651
LAB311	sunflower|gb162|DY950975	sunflower	179	652
LAB312	tomato|gb164|AF079231	tomato	180	653
LAB314	tomato|gb164|AI485630	tomato	181	654
LAB315	tomato|gb164|AI487529	tomato	182	655
LAB316	tomato|gb164|AI773156	tomato	183	656
LAB317	tomato|gb164|AI773737	tomato	184	657
LAB318	tomato|gb164|AI899075	tomato	185	658
LAB319	tomato|gb164|AW032666	tomato	186	659

Gene Name	*Cluster Name*	*Organism*	*Polynucl. SEQ ID NO:*	*Polypep. SEQ ID NO:*
LAB320	tomato|gb164|AW979674	tomato	187	660
LAB323	tomato|gb164|BG132099	tomato	188	661
LAB324	tomato|gb164|BG628155	tomato	189	662
LAB325	tomato|gb164|BG630481	tomato	190	663
LAB326	tomato|gb164|BG642701	tomato	191	664
LAB327	tomato|gb164|BP889760	tomato	192	665
LAB329	tomato|gb164|X51904	tomato	193	666
LAB335	wheat|gb164|BE488670	wheat	194	667
LAB336	wheat|gb164|BE490582	wheat	195	668
LAB337	wheat|gb164|BE498413	wheat	196	669
LAB339	wheat|gb164|BE604530	wheat	197	670
LAB340	wheat|gb164|BF478640	wheat	198	671
LAB342	brachypodium|gb169|BE404202	brachypodium	199	672
LAB343	canola|gb161|CX187805	canola	200	673
LAB344	maize|gb170|AI665177	maize	201	674
LAB345	rice|gb170|OS02G48730	rice	202	675
LAB346	rice|gb170|OS06G18000	rice	203	676
LAB347	sorghum|gb161.crp|BG239839	sorghum	204	677
LAB348	sorghum|gb161.crp|EB407478	sorghum	205	678
LAB349	soybean|gb168|BE820344	soybean	206	679
LAB351	switchgrass|gb167|DN148583	switchgrass	207	680
LAB352	wheat|gb164|BE604638	wheat	208	681
LAB353	wheat|gb164|BF428610	wheat	209	682
LAB355	brachypodium|gb169|BF473402	brachypodium	210	683
LAB367	canola|gb161|CN726397	canola	211	684
LAB381	poplar|gb170|CV256220	poplar	212	685
LAB383	soybean|gb168|CA850722	soybean	213	686
LAB276_H0	maize|gb170|BG321080	maize	214	687
LAB290_H0	maize|gb170|AI665410	maize	215	688
LAB347_H0	maize|gb170|BM381583	maize	216	689
LAB291	sorghum|gb161.crp|BG051306	sorghum	217	-
LAB109	sorghum|gb161.crp|BG047558	sorghum	35	699
LAB55	barley|gb157SOLEXA|AJ477127	barley	218	690
LAB64	barley|gb157SOLEXA|BF624328	barley	219	691
LAB64	barley|gb157SOLEXA|BF624328	barley	220	692
LAB65	barley|gb157SOLEXA|BQ662625	barley	221	693
LAB67	brachypodium|gb169|BE414847	brachypodium	222	481
LAB68	brachypodium|gb169|BE415661	brachypodium	223	482
LAB69	brachypodium|gb169|BE418188	brachypodium	224	483
LAB72	cotton|gb164|CO132512	cotton	225	694
LAB83	rice|gb170|OS03G21640	rice	226	493
LAB89	rice|gb170|OS10G37760	rice	227	695
LAB92	sorghum|gb161.crp|AI724271	sorghum	228	498
LAB97	sorghum|gb161.crp|AW283405	sorghum	229	696
LAB97	sorghum|gb161.crp|AW283405	sorghum	230	697
LAB106	sorghum|gb161.crp|BE363251	sorghum	231	698
LAB110	sorghum|gb161.crp|BM322761	sorghum	232	509
LAB120	tomato|gb164|AW218593	tomato	233	700

Gene Name	*Cluster Name*	*Organism*	*Polynucl. SEQ ID NO:*	*Polypep. SEQ ID NO:*
LAB125	tomato|gb164|BG124210	tomato	234	701
LAB133	tomato|gb164|BG629133	tomato	235	702
LAB158	sorghum|gb161.crp|BI098554	sorghum	236	703
LAB160	sorghum|gb161.crp|BM329994	sorghum	237	704
LAB161	sorghum|gb161.crp|BQ704124	sorghum	238	705
LAB162	sorghum|gb161.crp|CD949495	sorghum	239	542
LAB165	sorghum|gb161.crp|SBGWP119861	sorghum	240	706
LAB177	sorghum|gb161.crp|CF431793	sorghum	241	707
LAB178	tomato|gb164|AI490504	tomato	242	556
LAB179	wheat|gb164|CV763774	wheat	243	708
LAB193	barley|gb157SOLEXA|AL500288	barley	244	709
LAB193	barley|gb157SOLEXA|AL500288	barley	245	568
LAB207	barley|gb157SOLEXA|BE421932	barley	246	573
LAB218	cotton|gb164|BG443778	cotton	247	710
LAB221	maize|gb170|AI622102	maize	248	711
LAB222	maize|gb170|CA400624	maize	249	712
LAB224	rice|gb170|OS01G14440	rice	250	583
LAB274	sorghum|gb161.crp|AW283715	sorghum	251	713
LAB280	sorghum|gb161.crp|AW924546	sorghum	252	714
LAB293	sorghum|gb161.crp|BG104129	sorghum	253	715
LAB293	sorghum|gb161.crp|BG104129	sorghum	254	716
LAB295	sorghum|gb161.crp|BG558012	sorghum	255	717
LAB297	sorghum|gb161.crp|BM417007	sorghum	256	718
LAB298	sorghum|gb161.crp|BM737392	sorghum	257	641
LAB300	sorghum|gb161.crp|CD220284	sorghum	258	719
LAB303	sorghum|gb161.crp|CD233331	sorghum	259	720
LAB311	sunflower|gb162|DY950975	sunflower	260	721
LAB314	tomato|gb164|AI485630	tomato	261	722
LAB316	tomato|gb164|AI773156	tomato	262	723
LAB320	tomato|gb164|AW979674	tomato	263	724
LAB323	tomato|gb164|BG132099	tomato	264	725
LAB326	tomato|gb164|BG642701	tomato	265	726
LAB327	tomato|gb164|BP889760	tomato	266	727
LAB348	sorghum|gb161.crp|EB407478	sorghum	267	728
LAB349	soybean|gb168|BE820344	soybean	268	729
LAB381	poplar|gb170|CV256220	poplar	269	730
LAB276_H0	maize|gb170|BG321080	maize	270	687
LAB290_H0	maize|gb170|AI665410	maize	271	688
LAB347_H0	maize|gb170|BM381583	maize	272	731
LAB176	sorghum|gb161.crp|CD205409	sorghum	273	-
LAB291	sorghum|gb161.crp|BG051306	sorghum	274	-

Table 53. Provided are the identified genes which expression thereof in plants increases abiotic stress tolerance, water use efficiency, yield, growth rate, vigor, biomass, growth rate, oil content, nitrogen use efficiency and fertilizer use efficiency of a plant. "Polynucl." - polynucleotide; "Polypep." – polypeptide.

EXAMPLE 10

IDENTIFICATION OF HOMOLOGUES WHICH AFFECT ABST, WUE, YIELD, GROWTH RATE, VIGOR, BIOMASS, OIL CONTENT, NUE AND/OR FUE OF A PLANT

The concepts of orthology and paralogy have recently been applied to functional characterizations and classifications on the scale of whole-genome comparisons. Orthologs and paralogs constitute two major types of homologs: The first evolved from a common ancestor by specialization, and the latter are related by duplication events. It is assumed that paralogs arising from ancient duplication events are likely to have diverged in function while true orthologs are more likely to retain identical function over evolutionary time.

To further investigate and identify putative ortholog genes of the genes affecting ABST, WUE, yield (e.g., seed yield, oil yield, biomass, grain quantity and/or quality), oil content, growth rate, vigor, NUE and FUE (presented in Table 53, Example 9 above), all sequences were aligned using the BLAST (/Basic Local Alignment Search Tool/). Sequences sufficiently similar were tentatively grouped. These putative orthologs were further organized under a Phylogram - a branching diagram (tree) assumed to be a representation of the evolutionary relationships among the biological taxa. Putative ortholog groups were analyzed as to their agreement with the phylogram and in cases of disagreements these ortholog groups were broken accordingly

Expression data was analyzed and the EST libraries were classified using a fixed vocabulary of custom terms such as developmental stages (e.g., genes showing similar expression profile through development with up regulation at specific stage, such as at the seed filling stage) and/or plant organ (e.g., genes showing similar expression profile across their organs with up regulation at specific organs such as seed). The annotations from all the ESTs clustered to a gene were analyzed statistically by comparing their frequency in the cluster versus their abundance in the database, allowing to construct a numeric and graphic expression profile of that gene, which is termed "digital expression". The rationale of using these two complementary methods with methods of phenotypic association studies of QTLs, SNPs and phenotype expression correlation is based on the assumption that true orthologs are likely to retain identical function over evolutionary time. These methods provide different sets of indications on function

similarities between two homologous genes, similarities in the sequence level - identical amino acids in the protein domains and similarity in expression profiles.

Methods for searching and identifying homologues of yield and improved agronomic traits such as ABS tolerance and FUE related polypeptides or polynucleotides are well within the realm of the skilled artisan. The search and identification of homologous genes involves the screening of sequence information available, for example, in public databases, which include but are not limited to the DNA Database of Japan (DDBJ), Genbank, and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) or versions thereof or the MIPS database. A number of different search algorithms have been developed, including but not limited to the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequence queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, Trends in Biotechnology: 76-80, 1994; Birren et al., Genome Analysis, I: 543, 1997). Such methods involve alignment and comparison of sequences. The BLAST algorithm calculates percent sequence identity and performs a statistical analysis of the similarity between the two sequences. The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information. Other such software or algorithms are GAP, BESTFIT, FASTA and TFASTA. GAP uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48: 443-453, 1970) to find the alignment of two complete sequences that maximizes the number of matches and minimizes the number of gaps.

The homologous genes may belong to the same gene family. The analysis of a gene family may be carried out using sequence similarity analysis. To perform this analysis one may use standard programs for multiple alignments e.g. Clustal W. A neighbour-joining tree of the proteins homologous to the genes in this invention may be used to provide an overview of structural and ancestral relationships. Sequence identity may be calculated using an alignment program as described above. It is expected that other plants will carry a similar functional gene (orthologue) or a family of similar genes and those genes will provide the same preferred phenotype as the genes presented here. Advantageously, these family members may be useful in the methods of the invention. Example of other plants are included here but not limited to, barley

(Hordeum vulgare), Arabidopsis (Arabidopsis thaliana), maize (Zea mays), cotton (Gossypium), Oilseed rape (Brassica napus), Rice (Oryza sativa), Sugar cane (Saccharum officinarum), Sorghum (Sorghum bicolor), Soybean (Glycine max), Sunflower (Helianthus annuus), Tomato (Lycopersicon esculentum), Wheat (Triticum aestivum)

The above-mentioned analyses for sequence homology is preferably carried out on a full-length sequence, but may also be based on a comparison of certain regions such as conserved domains. The identification of such domains would also be well within the realm of the person skilled in the art and would involve, for example, a computer readable format of the nucleic acids of the present invention, the use of alignment software programs and the use of publicly available information on protein domains, conserved motifs and boxes. This information is available in the PRODOM, PIR or Pfam database. Sequence analysis programs designed for motif searching may be used for identification of fragments, regions and conserved domains as mentioned above. Preferred computer programs include, but are not limited to, MEME, SIGNALSCAN, and GENESCAN.

A person skilled in the art may use the homologous sequences provided herein to find similar sequences in other species and other organisms. Homologues of a protein encompass, peptides, oligopeptides, polypeptides, proteins and enzymes having amino acid substitutions, deletions and/or insertions relative to the unmodified protein in question and having similar biological and functional activity as the unmodified protein from which they are derived. To produce such homologues, amino acids of the protein may be replaced by other amino acids having similar properties (conservative changes, such as similar hydrophobicity, hydrophilicity, antigenicity, propensity to form or break a-helical structures or 3-sheet structures). Conservative substitution tables are well known in the art (see for example Creighton (1984) Proteins. W.H. Freeman and Company). Homologues of a nucleic acid encompass nucleic acids having nucleotide substitutions, deletions and/or insertions relative to the unmodified nucleic acid in

question and having similar biological and functional activity as the unmodified nucleic acid from which they are derived.

Polynucleotides and polypeptides with significant homology to the identified genes and polypeptides described in Table 53 above have been identified from the databases using BLAST software using the Blastp and tBlastn algorithms. The query nucleotide and polypeptide sequences are described in Table 53 above (polynucleotide SEQ ID NOs: 1-217, and 218-274; polypeptide SEQ ID NOs:474-689, and 690-731) and the identified homologues are provided in Table 54, below.

Table 54

Homologues of the identified genes/polypeptides for increasing abiotic stress tolerance, water use efficiency, yield, growth rate, vigor, oil content, biomass, growth rate, nitrogen use efficiency and fertilizer use efficiency of a plant

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Homm. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
783	LAB53	brachypodium|09v1|TMPLAF000939T1	5510	474	95	globlastp
784	LAB53	leymus|gb166|EG375693	5511	474	95	globlastp
785	LAB53	wheat|gb164|BE517987	5512	474	94.2	globlastp
786	LAB53	wheat|gb164|BE415276	5513	474	93.3	globlastp
787	LAB53	pseudoroegneria|gb167|FF342766	5514	474	91.3	globlastp
788	LAB53	oat|10v1|GO594607	5515	474	82.1	globlastp
789	LAB54	pseudoroegneria|gb167|FF342146	5516	475	82	globlastp
790	LAB54	wheat|gb164|BE428598	5517	475	81.1	globlastp
791	LAB54	wheat|gb164|BE428634	5518	475	80.1	globlastp
792	LAB55	wheat|gb164|BE499218	5519	476	94.3	globlastp
793	LAB55	wheat|gb164|BE415921	5520	476	93.9	globlastp
794	LAB55	brachypodium|09v1|DV476207	5521	476	89	globlastp
795	LAB55	brachypodium|gb169|BE500339	5521	476	89	globlastp
796	LAB55	cenchrus|gb166|EB653436	5522	476	84.2	globlastp
797	LAB55	switchgrass|gb167|FE647153	5523	476	82.9	globlastp
798	LAB55	rice|gb170|OS10G33250	5524	476	82.6	globlastp
799	LAB55	sorghum|gb161.crp|BG051887	5525	476	82.6	globlastp
800	LAB55	maize|gb170|AW313258	5526	476	81.9	globlastp
801	LAB55	switchgrass|gb167|DN151704	5527	476	81.1	globlastp
802	LAB55	brachypodium|gb169|BF485087	5528	476	81	globlastp
803	LAB56	wheat|gb164|AF022915	5529	477	97.7	globlastp
804	LAB56	brachypodium|09v1|DV471918	5530	477	94.1	globlastp
805	LAB56	brachypodium|gb169|AF022915	5530	477	94.1	globlastp
806	LAB56	sorghum|09v1|SB09G023310	5531	477	91.6	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
807	LAB56	sorghum|gb161.crp|AW037050	5531	477	91.6	globlastp
808	LAB56	ricc|gb170|OS05G39770	5532	477	91	globlastp
809	LAB56	maize|gb170|AI711957	5533	477	90.8	globlastp
810	LAB56	switchgrass|gb167|DN141956	5534	477	89.6	globlastp
811	LAB56	maize|gb170|AI795602	5535	477	88.3	globlastp
812	LAB58	wheat|gb164|BE411978	5536	478	99.2	globlastp
813	LAB58	wheat|gb164|BE419135	5537	478	98.5	globlastp
814	LAB58	pseudoroegneria|gb167|FF342690	5538	478	97.7	globlastp
815	LAB58	leymus|gb166|EG386152	5539	478	97.3	globlastp
816	LAB58	leymus|gb166|EG393155	5540	478	95.5	globlastp
817	LAB58	rice|gb170|OS04G58280	5541	478	85.2	globlastp
818	LAB58	switchgrass|gb167|DN150075	5542	478	83.5	globlastp
819	LAB58	switchgrass|gb167|DN150641	5543	478	83	globlastp
820	LAB58	sugarcane|gb157.3|CA067894	5544	478	81.1	globlastp
821	LAB58	sugarcane|gb157.3|CA131680	5545	478	80.7	globlastp
822	LAB58	sugarcane|gb157.3|CA067846	5546	478	80.2	globlastp
823	LAB67	oat|10v1|GR325144	5547	481	82.3	globlastp
824	LAB69	lolium|10v1|AU246926	5548	483	92.3	globlastp
825	LAB69	oat|10v1|GR318171	5549	483	91.2	globlastp
826	LAB69	oat|10v1|GR313573	5550	483	90.6	globlastp
827	LAB69	barley|10v1|BE437673	5551	483	89	globlastp
828	LAB69	barley|gb157SOLEXA|BE437673	5551	483	89	globlastp
829	LAB69	wheat|gb164|CA684829	5552	483	89	globlastp
830	LAB69	leymus|gb166|EG380193	5553	483	88.5	globlastp
831	LAB69	wheat|gb164|BE418188	5554	483	87.9	globlastp
832	LAB69	wheat|gb164|BF478406	5555	483	87.9	globlastp
833	LAB69	rice|gb170|OS01G60830	5556	483	80.2	globlastp
834	LAB70	b_rapa|gb162|CV544933	484	484	100	globlastp
835	LAB70	b_oleracea|gb161|AM386651	5557	484	97.3	globlastp
836	LAB70	canola|gb161|CD826649	5557	484	97.3	globlastp
837	LAB70	arabidopsis|gb165|AT2G32150	5558	484	89.7	globlastp
838	LAB70	arabidopsis_lyrata|09v1|JGIAL014318	5559	484	89	globlastp
839	LAB70	radish|gb164|EV550109	5560	484	88.51	glotblastn
840	LAB76	cassava|09v1|DV447303	5561	489	81.57	glotblastn
840	LAB72	cassava|09v1|DV447303	5561	694	81.25	glotblastn
841	LAB80	switchgrass|gb167|FE606158	5562	490	81.7	globlastp
841	LAB92	switchgrass|gb167|FE606158	5562	498	85.5	globlastp
842	LAB80	barley|gb157SOLEXA|BE438039	5563	490	81.3	globlastp
843	LAB80	barley|10v1|BE438039	5563	490	81.3	globlastp
844	LAB81	brachypodium|09v1|DV488004	5564	491	86.7	globlastp
845	LAB81	brachypodium|gb169|BE421729	5564	491	86.7	globlastp
846	LAB81	sorghum|09v1|SB04G035550	5565	491	86.3	globlastp
847	LAB81	sorghum|gb161.crp|BG411926	5565	491	86.3	globlastp
848	LAB81	maize|gb170|BM266787	5566	491	85.6	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
849	LAB81	oat|10v1|GR336389	5567	491	84.7	globlastp
850	LAB82	switchgrass|gb167|DN145536	5568	492	96.34	glotblastn
851	LAB82	sorghum|09v1|SB04G035630	5569	492	95.9	globlastp
852	LAB82	sorghum|gb161.crp|AW360697	5569	492	95.9	globlastp
853	LAB82	maize|gb170|AI619207	5570	492	95.7	globlastp
854	LAB82	maize|gb170|BM380723	5571	492	95.2	globlastp
855	LAB82	brachypodium|09v1|GT811044	5572	492	94.8	globlastp
856	LAB82	brachypodium|gb169|BE425568	5572	492	94.8	globlastp
857	LAB82	oat|10v1|GR316374	5573	492	94.52	glotblastn
858	LAB82	wheat|gb164|BE425568	5574	492	93.2	globlastp
859	LAB82	barley|10v1|BQ757459	5575	492	90.8	globlastp
860	LAB82	barley|gb157SOLEXA|AV834539	5576	492	90.4	globlastp
861	LAB82	brachypodium|09v1|BRADI1G47000	5577	492	89.3	globlastp
862	LAB82	maize|gb170|BQ528947	5578	492	88.4	globlastp
863	LAB82	sorghum|gb161.crp|BQ528947	5579	492	87.7	globlastp
864	LAB82	sorghum|09v1|SB10G005920	5580	492	87.5	globlastp
865	LAB82	brachypodium|gb169|CRPBD005242	5581	492	85.2	globlastp
866	LAB82	sorghum|09v1|TMPLBM380723T1	5582	492	84.7	globlastp
867	LAB82	apple|gb171|CN495624	5583	492	84.1	globlastp
868	LAB82	castorbean|09v1|EE256668	5584	492	84.1	globlastp
869	LAB82	castorbean|gb160|EE256668	5585	492	83.8	globlastp
870	LAB82	chestnut|gb170|SRR006295S0005865	5586	492	83.3	globlastp
871	LAB82	melon|gb165|AM716067	5587	492	83.1	globlastp
872	LAB82	cucumber|09v1|AM716067	5588	492	82.9	globlastp
873	LAB82	bean|gb167|CV532271	5589	492	82.6	globlastp
874	LAB82	oak|gb170|DB996638	5590	492	82.6	globlastp
875	LAB82	cassava|09v1|CK649453	5591	492	82.2	globlastp
876	LAB82	citrus|gb166|BQ624759	5592	492	82	globlastp
877	LAB82	lotus|09v1|BI417308	5593	492	82	globlastp
878	LAB82	lotus|gb157.2|BI417308	5593	492	82	globlastp
879	LAB82	maize|gb170|AW498313	5594	492	82	globlastp
880	LAB82	poplar|10v1|BI125519	5595	492	82	globlastp
881	LAB82	poplar|gb170|BI125519	5595	492	82	globlastp
882	LAB82	soybean|gb168|AW351046	5596	492	82	globlastp
883	LAB82	soybean|gb168|BE821006	5597	492	81.5	globlastp
884	LAB82	cassava|gb164|CK649453	5598	492	81.3	globlastp
885	LAB82	cotton|gb164|AI726355	5599	492	81.3	globlastp
886	LAB82	poplar|10v1|BI139040	5600	492	81.3	globlastp
887	LAB82	poplar|gb170|BI139040	5600	492	81.3	globlastp
888	LAB82	chickpea|09v2|FE668469	5601	492	81.28	glotblastn
889	LAB82	arabidopsis_lyrata|09v1|JGIAL025004	5602	492	81.1	globlastp
890	LAB82	arabidopsis|gb165|AT4G30440	5602	492	81.1	globlastp
891	LAB82	aquilegia|10v1|DR925021	5603	492	81	globlastp
892	LAB82	rice|gb170|OS06G08810	5604	492	81	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
893	LAB82	strawberry|gb164|CO817269	5605	492	81	globlastp
894	LAB82	solanum_phurcja|09v1|SPHBG137061	5606	492	80.4	globlastp
895	LAB82	spurge|gb161|DV120331	5607	492	80.4	globlastp
896	LAB82	nasturtium|10v1|SRR032558S0298847	5608	492	80.32	glotblastn
897	LAB82	potato|10v1|BG597853	5609	492	80.32	glotblastn
898	LAB82	potato|gb157.2|BI176457	5609	492	80.32	glotblastn
899	LAB82	canola|10v1|EE419654	5610	492	80.2	globlastp
900	LAB82	canola|10v1|DY023561	5611	492	80	globlastp
901	LAB82	canola|gb161|DY023561	5611	492	80	globlastp
902	LAB82	canola|gb161|EE419654	5612	492	80	globlastp
903	LAB88	rice|gb170|OS09G27750	5613	496	93.2	globlastp
904	LAB88	sugarcane|10v1|BQ533005	5614	496	86.7	globlastp
905	LAB88	maize|gb170|BE639051	5615	496	86.2	globlastp
906	LAB88	sugarcane|gb157.3|BQ533005	5616	496	86.1	globlastp
907	LAB88	cenchrus|gb166|EB653325	5617	496	86	globlastp
908	LAB88	switchgrass|gb167|FE647922	5618	496	85.8	globlastp
909	LAB88	switchgrass|gb167|FL702178	5619	496	85.54	glotblastn
910	LAB88	barley|10v1|BG300899	5620	496	84.3	globlastp
911	LAB88	barley|gb157SOLEXA|BG300899	5620	496	84.3	globlastp
912	LAB88	brachypodium|09v1|DV475195	5621	496	83.6	globlastp
913	LAB88	wheat|gb164|BE516906	5622	496	83.2	globlastp
914	LAB88	leymus|gb166|EG374982	5623	496	83	globlastp
915	LAB88	switchgrass|gb167|FL692984	5624	496	82.93	glotblastn
916	LAB88	wheat|gb164|AL823095	5625	496	82.9	globlastp
917	LAB88	wheat|gb164|BE498656	5626	496	82.9	globlastp
918	LAB88	brachypodium|gb169|BE425783	5627	496	82.72	glotblastn
919	LAB88	sorghum|09v1|SB02G026280	5628	496	81.7	globlastp
920	LAB88	sorghum|gb161.crp|AW677026	5628	496	81.7	globlastp
921	LAB89	sorghum|09v1|SB01G031210	5629	497	84.1	globlastp
922	LAB89	maize|gb170|AI745764	5630	497	82.8	globlastp
923	LAB89	switchgrass|gb167|DW177254	5631	497	80.7	globlastp
924	LAB92	maize|gb170|BE056189	5632	498	86.9	globlastp
925	LAB92	maize|gb170|AW054623	5633	498	84.21	glotblastn
926	LAB92	cenchrus|gb166|BM084651	5634	498	82.2	globlastp
927	LAB93	sugarcane|10v1|CA088623	5635	499	96	globlastp
928	LAB93	sugarcane|gb157.3|BQ536470	5636	499	95.7	globlastp
929	LAB93	switchgrass|gb167|FE618012	5637	499	87.7	globlastp
930	LAB93	maize|gb170|AI783065	5638	499	85.9	globlastp
931	LAB93	rice|gb170|OS03G02530	5639	499	82	globlastp
932	LAB93	brachypodium|09v1|DV469218	5640	499	80.2	globlastp
933	LAB94	sugarcane|10v1|CA078203	5641	500	98.9	globlastp
934	LAB94	sugarcane|gb157.3|CA078203	5642	500	98.9	globlastp
935	LAB94	maize|gb170|AW216139	5643	500	97.2	globlastp
936	LAB94	switchgrass|gb167|DN143081	5644	500	97.2	globlastp

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937	LAB94	maize|gb170|BG842835	5645	500	96.1	globlastp
938	LAB94	switchgrass|gb167|FE624707	5646	500	95.73	glotblastn
939	LAB94	cenchrus|gb166|EB655101	5647	500	94.7	globlastp
940	LAB94	rice|gb170|OS03G16670	5648	500	88.7	globlastp
941	LAB94	brachypodium|09v1|DV472385	5649	500	87.9	globlastp
942	LAB94	brachypodium|gb169|BE421885	5649	500	87.9	globlastp
943	LAB94	barley|10v1|BE193799	5650	500	87.6	globlastp
944	LAB94	barley|gb157SOLEXA|BE421885	5650	500	87.6	globlastp
945	LAB94	oat|10v1|GO586906	5651	500	87.3	globlastp
946	LAB94	wheat|gb164|BE426589	5652	500	87.3	globlastp
947	LAB94	wheat|gb164|BE443811	5653	500	87.3	globlastp
948	LAB94	leymus|gb166|EG392526	5654	500	87.2	globlastp
949	LAB94	wheat|gb164|AL826955	5655	500	86.9	globlastp
950	LAB94	pseudoroegneria|gb167|FF345077	5656	500	86.6	globlastp
951	LAB97	maize|gb170|AI964653	5657	501	93.5	globlastp
952	LAB97	switchgrass|gb167|FE603346	5658	501	93.5	globlastp
953	LAB97	millet|09v1|EVO454PM004428	5659	501	89.5	globlastp
954	LAB97	sugarcane|10v1|CA070094	5660	501	89.5	globlastp
955	LAB97	switchgrass|gb167|FE622833	5661	501	86.2	globlastp
956	LAB97	switchgrass|gb167|FE634485	5662	501	83.1	globlastp
957	LAB97	oat|10v1|GO589167	5663	501	81.45	glotblastn
958	LAB97	switchgrass|gb167|FE632663	5664	501	80.9	globlastp
959	LAB98	sugarcane|gb157.3|CA094179	5665	502	90.9	globlastp
960	LAB98	sugarcane|gb157.3|BQ534494	5666	502	86.7	globlastp
961	LAB98	sugarcane|10v1|CA075265	5667	502	86.7	globlastp
962	LAB98	sugarcane|gb157.3|CA095912	5668	502	84.85	glotblastn
963	LAB98	maize|gb170|AA979797	5669	502	84.1	globlastp
964	LAB98	sugarcane|gb157.3|CA213458	5670	502	83	globlastp
965	LAB98	maize|gb170|DN218642	5671	502	81.71	glotblastn
966	LAB101	sugarcane|gb157.3|CA092106	5672	503	92.15	glotblastn
967	LAB101	maize|gb170|AW506976	5673	503	89.3	globlastp
968	LAB101	switchgrass|gb167|FE623004	5674	503	85.2	globlastp
969	LAB101	sugarcane|10v1|CA092106	5675	503	83.14	glotblastn
970	LAB101	sorghum|09v1|SB05G020410	5676	503	82.3	globlastp
971	LAB102	sugarcane|gb157.3|CA085176	5677	504	94.1	globlastp
972	LAB102	sugarcane|10v1|CA085176	5678	504	93.41	glotblastn
973	LAB102	sugarcane|gb157.3|CA133383	5679	504	92.7	globlastp
974	LAB102	switchgrass|gb167|FL786617	5680	504	90.2	globlastp
975	LAB102	maize|gb170|AW330714	5681	504	80.6	globlastp
976	LAB106	maize|gb170|CD960060	5682	505	85.6	globlastp
977	LAB106	maize|gb170|AI372243	5683	505	84.5	globlastp
978	LAB106	switchgrass|gb167|FE605362	5684	505	84	globlastp
979	LAB107	maize|gb170|CA399032	5685	506	96.1	globlastp
980	LAB107	sugarcane|gb157.3|CA065542	5686	506	93.92	glotblastn

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981	LAB107	switchgrass|gb167|DN142686	5687	506	84.6	globlastp
982	LAB107	sugarcane|10v1|CA065611	5688	506	84.5	globlastp
983	LAB107	rice|gb170|OS10G32680	5689	506	82.97	glotblastn
984	LAB109	maize|gb170|CD948529	5690	508	86	globlastp
985	LAB113	potato|10v1|BQ119431	5691	510	93.8	globlastp
986	LAB113	potato|gb157.2|BQ119431	5691	510	93.8	globlastp
987	LAB113	eggplant|10v1|FS017035	5692	510	90	globlastp
988	LAB115	solanum_phureja|09v1|SPHAI488164	5693	511	97.7	globlastp
989	LAB115	potato|gb157.2|BG590998	5694	511	96.5	glotblastn
990	LAB115	eggplant|10v1|FS001103	5695	511	93.8	globlastp
991	LAB115	pepper|gb171|BM062112	5696	511	92.6	globlastp
992	LAB115	petunia|gb171|EB174978	5697	511	86.7	globlastp
993	LAB115	tobacco|gb162|EB426842	5698	511	83.8	globlastp
994	LAB116	solanum_phureja|09v1|SPHAI637375	5699	512	94.8	globlastp
995	LAB116	potato|10v1|BG596647	5699	512	94.8	globlastp
996	LAB116	potato|gb157.2|BE923899	5699	512	94.8	globlastp
997	LAB117	solanum_phureja|09v1|SPHAI772185	5700	513	93	globlastp
998	LAB117	tobacco|gb162|AB073628	5701	513	82.2	globlastp
999	LAB119	potato|10v1|BE919943	5702	514	91.2	globlastp
1000	LAB119	solanum_phureja|09v1|SPHAI772981	5703	514	90.7	globlastp
1001	LAB119	potato|gb157.2|BE919943	5704	514	90.7	globlastp
1002	LAB119	pepper|gb171|CA523161	5705	514	84.5	globlastp
1003	LAB120	solanum_phureja|09v1|SPHAW218593	5706	515	96.7	globlastp
1004	LAB121	solanum_phureja|09v1|SPHAW223810	5707	516	98.7	globlastp
1005	LAB121	potato|gb157.2|CN463702	5708	516	98.1	globlastp
1006	LAB121	potato|10v1|BI919647	5708	516	98.1	globlastp
1007	LAB121	potato|10v1|BG888636	5709	516	96.8	globlastp
1008	LAB121	potato|gb157.2|BG888636	5709	516	96.8	globlastp
1009	LAB121	potato|gb157.2|CK863276	5710	516	96.1	globlastp
1010	LAB121	tomato|gb164|AW216800	5711	516	94.2	globlastp
1011	LAB121	eggplant|10v1|FS012746	5712	516	93.51	glotblastn
1012	LAB121	potato|10v1|CV476486	5713	516	93.5	globlastp
1013	LAB121	solanum_phureja|09v1|SPHAW216800	5714	516	93.5	globlastp
1014	LAB121	solanum_phureja|09v1|SPHCRPSP004689	5715	516	93.5	globlastp
1015	LAB121	potato|gb157.2|BG887542	5716	516	92.9	globlastp
1016	LAB121	tobacco|gb162|AY329069	5717	516	92.9	globlastp
1017	LAB121	tomato|gb164|AI774877	5718	516	92.9	globlastp
1018	LAB121	solanum_phureja|09v1|SPHAF123255	5719	516	92.2	globlastp
1019	LAB121	potato|gb157.2|BG592733	5719	516	92.2	globlastp
1020	LAB121	tobacco|gb162|AY329067	5720	516	92.2	globlastp
1021	LAB121	potato|10v1|BF053349	5719	516	92.2	globlastp
1022	LAB121	solanum_phureja|09v1|SPHCV477365	5721	516	91.6	globlastp
1023	LAB121	tomato|gb164|AF123255	5722	516	91.6	globlastp

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1024	LAB121	pcppcr|gb171|BM060336	5723	516	91.6	globlastp
1025	LAB121	pcppcr|gb171|CA522343	5724	516	91.6	globlastp
1026	LAB121	tomato|09v1|AF123255	5722	516	91.6	globlastp
1027	LAB121	eggplant|10v1|FS033633	5725	516	90.9	globlastp
1028	LAB121	potato|gb157.2|CV477365	5726	516	90.9	globlastp
1029	LAB121	solanum_phureja|09v1|SPHCRPSP039416	5727	516	90.26	glotblastn
1030	LAB121	potato|10v1|CN464789	5728	516	89.6	globlastp
1031	LAB121	potato|10v1|DN590196	5729	516	89.6	globlastp
1032	LAB121	pepper|gb171|CA522586	5730	516	89.6	globlastp
1033	LAB121	solanum_phureja|09v1|SPHCN464789	5731	516	88.3	globlastp
1034	LAB121	soybean|gb168|AW980952	5732	516	83.8	globlastp
1035	LAB121	medicago|gb157.2|BG647589	5733	516	83.1	globlastp
1036	LAB121	soybean|gb168|AW567705	5734	516	83.1	globlastp
1037	LAB121	papaya|gb165|EX251993	5735	516	82.6	globlastp
1038	LAB121	peanut|gb171|EG373080	5736	516	82.6	globlastp
1039	LAB121	medicago|09v1|AW683787	5737	516	82.5	globlastp
1040	LAB121	medicago|gb157.2|AW683787	5737	516	82.5	globlastp
1041	LAB121	medicago|09v1|AW684008	5738	516	82.5	globlastp
1042	LAB121	tobacco|gb162|AY329073	5739	516	82.5	globlastp
1043	LAB121	cotton|gb164|BE051984	5740	516	82.4	globlastp
1044	LAB121	cacao|gb167|CA796637	5741	516	82.2	globlastp
1045	LAB121	cotton|gb164|BE054707	5742	516	81.9	globlastp
1046	LAB121	cotton|gb164|BF272955	5743	516	81.9	globlastp
1047	LAB121	papaya|gb165|EX252008	5744	516	81.9	globlastp
1048	LAB121	peanut|gb171|EE123664	5745	516	81.9	globlastp
1049	LAB121	soybean|gb168|BG646416	5746	516	81.9	globlastp
1050	LAB121	jatropha|09v1|FM890538	5747	516	81.6	globlastp
1051	LAB121	papaya|gb165|AY387588	5748	516	81.3	globlastp
1052	LAB121	peanut|gb171|EC365300	5749	516	81.3	globlastp
1053	LAB121	peanut|gb171|EE126279	5750	516	81.3	globlastp
1054	LAB121	soybean|gb168|CA798992	5751	516	81.3	globlastp
1055	LAB121	tomato|09v1|DV103969	5752	516	81.2	globlastp
1056	LAB121	soybean|gb168|BU548154	5753	516	81.2	globlastp
1057	LAB121	spurge|gb161|DV112249	5754	516	81.2	globlastp
1058	LAB121	spurge|gb161|DV116657	5755	516	81.2	globlastp
1059	LAB121	medicago|09v1|LLBG452648	5756	516	81.1	globlastp
1060	LAB121	medicago|gb157.2|BG452648	5756	516	81.1	globlastp
1061	LAB121	cassava|09v1|DR084888	5757	516	81	globlastp
1062	LAB121	cotton|gb164|BF269213	5758	516	80.9	globlastp
1063	LAB121	cotton|gb164|CA993196	5759	516	80.9	globlastp
1064	LAB121	cichorium|gb171|EH690049	5760	516	80.8	globlastp
1065	LAB121	potato|gb157.2|CV476486	5761	516	80.65	glotblastn
1066	LAB121	cotton|gb164|BQ403095	5762	516	80.6	globlastp

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1067	LAB121	papaya|gb165|EX252058	5763	516	80.6	globlastp
1068	LAB121	peanut|gb171|EE127248	5764	516	80.6	globlastp
1069	LAB121	soybean|gb168|BM886953	5765	516	80.5	globlastp
1070	LAB121	cassava|09v1|DR086686	5766	516	80.4	globlastp
1071	LAB121	cassava|gb164|DR084888	5767	516	80.4	globlastp
1072	LAB121	cassava|gb164|DR086686	5766	516	80.4	globlastp
1073	LAB121	poplar|10v1|BU813549	5768	516	80.3	globlastp
1074	LAB121	cacao|gb167|CU476839	5769	516	80.3	globlastp
1075	LAB121	cotton|gb164|BQ409689	5770	516	80.3	globlastp
1076	LAB121	lettuce|10v1|DW075714	5771	516	80.3	globlastp
1077	LAB121	lettuce|gb157.2|DW075714	5771	516	80.3	globlastp
1078	LAB121	poplar|10v1|DT507125	5768	516	80.3	globlastp
1079	LAB121	poplar|gb170|BU813549	5768	516	80.3	globlastp
1080	LAB121	dandelion|gb161|DY824523	5772	516	80.1	globlastp
1081	LAB121	soybean|gb168|BQ630709	5773	516	80	globlastp
1082	LAB121	cotton|gb164|CA993586	5774	516	80	globlastp
1083	LAB122	solanum_phureja|09v1|SPHAW442266	5775	517	98.3	globlastp
1084	LAB122	potato|gb157.2|BG889978	5775	517	98.3	globlastp
1085	LAB122	potato|10v1|BG888028	5775	517	98.3	globlastp
1086	LAB122	potato|gb157.2|BG888028	5776	517	96.9	globlastp
1087	LAB122	eggplant|10v1|FS078554	5777	517	92.3	globlastp
1088	LAB122	tobacco|gb162|EB430956	5778	517	89.2	globlastp
1089	LAB123	solanum_phureja|09v1|SPHAW442830	5779	518	87.4	globlastp
1090	LAB123	potato|10v1|BF460376	5780	518	87	globlastp
1091	LAB123	potato|gb157.2|BF460376	5781	518	87	globlastp
1092	LAB124	potato|10v1|BF154317	5782	519	91.9	globlastp
1093	LAB124	potato|gb157.2|BF154317	5782	519	91.9	globlastp
1094	LAB124	solanum_phureja|09v1|SPHBG123767	5783	519	89	globlastp
1095	LAB127	solanum_phureja|09v1|SPHBG127842	5784	522	96.9	globlastp
1096	LAB127	potato|10v1|CK269532	5784	522	96.9	globlastp
1097	LAB127	potato|gb157.2|CK269532	5785	522	96.5	globlastp
1098	LAB127	eggplant|10v1|FS089521	5786	522	93.4	globlastp
1099	LAB128	potato|gb157.2|BE922546	5787	523	92.6	globlastp
1100	LAB128	potato|10v1|BE922546	5787	523	92.6	globlastp
1101	LAB128	potato|10v1|BQ111829	5788	523	92.3	globlastp
1102	LAB128	potato|gb157.2|BG598290	5789	523	92.28	glotblastn
1103	LAB128	solanum_phureja|09v1|SPHBG128502	5790	523	92	globlastp
1104	LAB128	eggplant|10v1|FS007523	5791	523	87.5	globlastp
1105	LAB128	petunia|gb171|CV295560	5792	523	85.5	globlastp
1106	LAB128	tobacco|gb162|EH618301	5793	523	84.2	globlastp
1107	LAB129	solanum_phureja|09v1|SPHBG129905	5794	524	91.2	globlastp
1108	LAB129	pepper|gb171|GD052614	5795	524	80	glotblastn
1109	LAB130	solanum_phureja|09v1|SPHBG133230	5796	525	89.23	glotblastn
1110	LAB131	potato|10v1|BG890172	5797	526	97.3	globlastp

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1111	LAB131	solanum_phurcja|09v1|SPHBG127715	5798	526	96.7	globlastp
1112	LAB131	tobacco|gb162|EB424672	5799	526	90.9	globlastp
1113	LAB131	potato|gb157.2|BF460303	5800	526	89.4	globlastp
1114	LAB131	solanum_phureja|09v1|SPHAF204790	5801	526	89.1	globlastp
1115	LAB131	pepper|gb171|AF082722	5802	526	88.8	globlastp
1116	LAB131	potato|gb157.2|BF054105	5803	526	88.8	globlastp
1117	LAB131	potato|10v1|BF460303	5803	526	88.8	globlastp
1118	LAB131	tomato|gb164|AF204790	5804	526	88.4	globlastp
1119	LAB131	tomato|09v1|AF204790	5805	526	88.1	globlastp
1120	LAB131	eggplant|10v1|FS008074	5806	526	87.2	globlastp
1121	LAB131	tomato|gb164|BG127715	5807	526	83.6	globlastp
1122	LAB131	potato|gb157.2|BG890172	5808	526	82.4	globlastp
1123	LAB131	citrus|gb166|BQ623443	5809	526	81.3	globlastp
1124	LAB131	ipomoea_nil|10v1|BJ558237	5810	526	81.2	globlastp
1125	LAB131	arabidopsis_lyrata|09v1|JGIAL032554	5811	526	80.9	globlastp
1126	LAB131	monkeyflower|10v1|GO946694	5812	526	80.9	globlastp
1127	LAB131	ipomoea|gb157.2|BJ558237	5813	526	80.9	globlastp
1128	LAB131	canola|10v1|CN828978	5814	526	80.5	globlastp
1129	LAB131	canola|gb161|CN828978	5814	526	80.5	globlastp
1130	LAB131	coffea|10v1|DV675045	5815	526	80.2	globlastp
1131	LAB131	radish|gb164|EX764030	5816	526	80.2	globlastp
1132	LAB133	solanum_phureja|09v1|SPHBG629133	5817	527	87	globlastp
1133	LAB137	brachypodium|gb169|BE416704	5818	528	85.97	glotblastn
1134	LAB137	brachypodium|09v1|DV479869	5819	528	85.2	globlastp
1135	LAB141	barley|gb157SOLEXA|BI953426	5820	530	97.34	glotblastn
1136	LAB141	barley|10v1|BI953426	5821	530	97.09	glotblastn
1137	LAB141	brachypodium|09v1|DV478705	5822	530	92.01	glotblastn
1138	LAB141	brachypodium|gb169|BE591380	5823	530	92.01	glotblastn
1139	LAB141	rice|gb170|OS09G27050	5824	530	84.99	glotblastn
1140	LAB141	sorghum|09v1|SB02G025930	5825	530	84.75	glotblastn
1141	LAB141	sorghum|gb161.crp|AW283712	5825	530	84.75	glotblastn
1142	LAB141	maize|gb170|LLCD940999	5826	530	82.25	glotblastn
1143	LAB141	sorghum|09v1|SB07G022430	5827	530	81.64	glotblastn
1143	LAB252	sorghum|09v1|SB07G022430	5827	603	87.6	globlastp
1144	LAB141	sorghum|gb161.crp|AW287657	5828	530	81.64	glotblastn
1144	LAB252	sorghum|gb161.crp|AW287657	5828	603	87.3	globlastp
1145	LAB141	switchgrass|gb167|FL754019	5829	530	80.63	glotblastn
1146	LAB141	maize|gb170|BQ441996	5830	530	80.39	glotblastn
1146	LAB252	maize|gb170|BQ441996	5830	603	87.2	globlastp
1147	LAB145	sugarcane|10v1|CA288211	5831	531	84.62	glotblastn
1147	LAB167	sugarcane|10v1|CA288211	5831	547	80.3	globlastp
1148	LAB145	sugarcane|gb157.3|CA288211	5831	531	84.62	glotblastn
1148	LAB167	sugarcane|gb157.3|CA288211	5831	547	80.3	globlastp
1149	LAB145	sugarcane|10v1|CF571685	5832	531	80	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1149	LAB167	sugarcane|10v1|CF571685	5832	547	86.8	globlastp
1150	LAB145	sugarcane|gb157.3|CF571685	5832	531	80	glotblastn
1150	LAB167	sugarcane|gb157.3|CF571685	5832	547	86.8	globlastp
1151	LAB152	maize|gb170|AI901645	5833	533	92.6	globlastp
1152	LAB152	sugarcane|gb157.3|CA150670	5834	533	92.57	glotblastn
1153	LAB152	switchgrass|gb167|FL692374	5835	533	82.7	globlastp
1154	LAB152	switchgrass|gb167|FL713549	5836	533	81	globlastp
1155	LAB153	sugarcane|10v1|CA123230	5837	534	97.6	globlastp
1156	LAB153	sugarcane|gb157.3|CA123230	5837	534	97.6	globlastp
1157	LAB153	maize|gb170|T18415	5838	534	92.5	globlastp
1158	LAB153	switchgrass|gb167|FE637514	5839	534	90.6	globlastp
1159	LAB153	switchgrass|gb167|FL789468	5840	534	89.4	globlastp
1160	LAB153	cenchrus|gb166|EB655013	5841	534	85.4	globlastp
1161	LAB153	brachypodium|09v1|DV480172	5842	534	83.1	globlastp
1162	LAB153	brachypodium|gb169|BE421446	5842	534	83.1	globlastp
1163	LAB153	rice|gb170|OS02G54060	5843	534	82.7	globlastp
1164	LAB154	maize|gb170|AW066925	5844	535	94.1	globlastp
1165	LAB154	barley|10v1|AV833850	5845	535	90.2	globlastp
1166	LAB154	barley|10v1|BI958438	5846	535	90.2	globlastp
1167	LAB154	brachypodium|09v1|DV469301	5847	535	89.9	globlastp
1168	LAB154	brachypodium|gb169|BE637762	5847	535	89.9	globlastp
1169	LAB154	wheat|gb164|BE515523	5848	535	89.9	globlastp
1170	LAB154	wheat|gb164|BF483856	5849	535	89.6	globlastp
1171	LAB154	wheat|gb164|CA660347	5850	535	89.3	globlastp
1172	LAB154	oat|10v1|GR356133	5851	535	88.7	globlastp
1173	LAB154	rice|gb170|OS04G55710	5852	535	88.7	globlastp
1174	LAB154	oat|10v1|GR358853	5853	535	87.8	globlastp
1175	LAB154	barley|gb157SOLEXA|AL499742	5854	535	81.6	globlastp
1176	LAB159	sugarcane|10v1|DN195185	5855	539	96.6	globlastp
1177	LAB159	maize|gb170|BM340195	5856	539	94.8	globlastp
1178	LAB159	switchgrass|gb167|DN148099	5857	539	92.4	globlastp
1179	LAB159	rice|gb170|OS07G04990	5858	539	88.5	globlastp
1180	LAB159	wheat|gb164|BE605214	5859	539	85.4	globlastp
1181	LAB159	leymus|gb166|EG386154	5860	539	85.2	globlastp
1182	LAB159	barley|10v1|BI951567	5861	539	84.9	globlastp
1183	LAB159	barley|gb157SOLEXA|BI951567	5861	539	84.9	globlastp
1184	LAB159	wheat|gb164|BE604066	5862	539	84.9	globlastp
1185	LAB159	oat|10v1|CN817195	5863	539	83.3	globlastp
1186	LAB159	fescue|gb161|DT679429	5864	539	83.3	globlastp
1187	LAB159	brachypodium|09v1|DV479518	5865	539	82.9	globlastp
1188	LAB159	brachypodium|gb169|BE704541	5865	539	82.9	globlastp
1189	LAB161	maize|gb170|AI622212	5866	541	95.5	globlastp
1190	LAB161	switchgrass|gb167|DT948963	5867	541	92.42	glotblastn
1191	LAB161	rice|gb170|OS09G18320	5868	541	81.6	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1192	LAB162	maize|gb170|AI586902	5869	542	93.7	globlastp
1193	LAB162	switchgrass|gb167|FE658082	5870	542	91.9	globlastp
1194	LAB162	rice|gb170|OS06G04610	5871	542	86.2	globlastp
1195	LAB162	oat|10v1|CN819671	5872	542	84.3	globlastp
1196	LAB162	leymus|gb166|EG384069	5873	542	83.6	globlastp
1197	LAB162	wheat|gb164|BF201230	5874	542	83.18	glotblastn
1198	LAB162	brachypodium|09v1|GT776617	5875	542	82.5	globlastp
1199	LAB162	wheat|gb164|BG606378	5876	542	82.16	glotblastn
1200	LAB164	brachypodium|gb169|BE445505	5877	544	82.2	globlastp
1201	LAB165	sorghum|09v1|SB04G027460	5878	545	97.53	glotblastn
1202	LAB165	maize|gb170|CD936465	5879	545	91.36	glotblastn
1203	LAB165	rice|gb170|OS02G51910	5880	545	84.9	globlastp
1204	LAB166	maize|gb170|AI444676	5881	546	91.9	globlastp
1205	LAB166	rice|gb170|OS10G36390	5882	546	82.2	globlastp
1206	LAB167	sugarcane|gb157.3|CA070500	5883	547	87.84	glotblastn
1207	LAB167	sorghum|09v1|SB09G001020	5884	547	87.8	globlastp
1208	LAB167	sorghum|gb161.crp|AI723995	5884	547	87.8	globlastp
1209	LAB167	wheat|gb164|CA484885	5885	547	86.5	globlastp
1210	LAB167	switchgrass|gb167|FL825143	5886	547	83.8	globlastp
1211	LAB167	sugarcane|10v1|BQ534981	5887	547	83.6	globlastp
1212	LAB167	sugarcane|gb157.3|BQ534981	5887	547	83.6	globlastp
1213	LAB167	sugarcane|10v1|CO373473	5888	547	82.43	glotblastn
1214	LAB167	sugarcane|gb157.3|CO373473	5888	547	82.43	glotblastn
1215	LAB167	sugarcane|10v1|BQ534583	5889	547	82.4	globlastp
1216	LAB167	sugarcane|gb157.3|BQ534583	5889	547	82.4	globlastp
1217	LAB167	maize|gb170|LLAW202534	5890	547	82.2	globlastp
1218	LAB167	maize|gb170|T23379	5890	547	82.2	globlastp
1219	LAB167	sugarcane|10v1|CA277083	5891	547	80.8	globlastp
1220	LAB167	sugarcane|10v1|CA297188	5892	547	80	globlastp
1221	LAB169	maize|gb170|AW053133	5893	548	97.5	globlastp
1222	LAB169	switchgrass|gb167|FE613776	5894	548	95.9	globlastp
1223	LAB169	rice|gb170|OS04G44890	5895	548	91.6	globlastp
1224	LAB169	brachypodium|09v1|DV487916	5896	548	89.1	globlastp
1225	LAB169	brachypodium|gb169|BF202199	5896	548	89.1	globlastp
1226	LAB169	barley|10v1|BI955502	5897	548	85.9	globlastp
1227	LAB169	wheat|gb164|BF202199	5898	548	85	globlastp
1228	LAB169	castorbean|09v1|XM002528859	5899	548	82.81	glotblastn
1229	LAB169	coffea|10v1|DV691567	5900	548	80.94	glotblastn
1230	LAB169	tomato|09v1|BG135211	5901	548	80.62	glotblastn
1231	LAB169	cassava|09v1|JGICASSAVA19698M1	5902	548	80.31	glotblastn
1232	LAB169	solanum_phureja|09v1|SPHBG135211	5903	548	80	glotblastn
1233	LAB169	potato|gb157.2|BI405380	5904	548	80	glotblastn
1234	LAB170	sugarcane|10v1|BU103703	5905	549	97.1	globlastp
1235	LAB170	sugarcane|gb157.3|BU103703	5906	549	97	globlastp

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1236	LAB170	maize|gb170|AW066983	5907	549	94.1	globlastp
1237	LAB170	switchgrass|gb167|FL704262	5908	549	94.1	globlastp
1238	LAB170	barley|10v1|AV833506	5909	549	88.8	globlastp
1239	LAB170	barley|gb157SOLEXA|AV833506	5909	549	88.8	globlastp
1240	LAB170	rice|gb170|OS01G62900	5910	549	88.3	globlastp
1241	LAB170	brachypodium|09v1|DV484814	5911	549	87.7	globlastp
1242	LAB170	brachypodium|gb169|AF022914	5911	549	87.7	globlastp
1243	LAB170	wheat|gb164|BE403675	5912	549	84.5	globlastp
1244	LAB170	millet|09v1|EVO454PM003201	5913	549	82.2	globlastp
1245	LAB171	maize|gb170|AI941956	5914	550	95.6	globlastp
1246	LAB171	switchgrass|gb167|FL777596	5915	550	89.9	globlastp
1246	LAB179	switchgrass|gb167|FL777596	5915	557	81.1	globlastp
1247	LAB171	millet|09v1|EVO454PM014599	5916	550	86.3	globlastp
1248	LAB171	switchgrass|gb167|FL724893	5917	550	86.29	glotblastn
1249	LAB171	brachypodium|09v1|GT862474	5918	550	83.1	globlastp
1249	LAB179	brachypodium|09v1|GT862474	5918	557	86.7	globlastp
1250	LAB171	oat|10v1|GO596792	5919	550	81	globlastp
1250	LAB179	oat|10v1|GO596792	5919	557	87.6	globlastp
1251	LAB172	sugarcane|gb157.3|CA081142	5920	551	97.3	globlastp
1252	LAB172	sugarcane|10v1|CA081142	5921	551	97	globlastp
1253	LAB172	maize|gb170|AW360590	5922	551	94.4	globlastp
1254	LAB172	brachypodium|09v1|DV470791	5923	551	80.7	globlastp
1255	LAB172	brachypodium|gb169|BQ801920	5923	551	80.7	globlastp
1256	LAB172	barley|gb157SOLEXA|AL508671	5924	551	80.5	globlastp
1257	LAB172	pseudoroegneria|gb167|FF357868	5925	551	80.5	globlastp
1258	LAB172	wheat|gb164|BE428307	5926	551	80.4	glotblastn
1259	LAB172	rice|gb170|OS10G37830	5927	551	80.1	globlastp
1260	LAB178	solanum_phureja|09v1|SPHAI490504	5928	556	91	globlastp
1261	LAB178	solanum_phureja|09v1|SPHAI899607	5929	556	90.3	globlastp
1262	LAB178	solanum_phureja|09v1|SPHAW030648	5930	556	86.3	globlastp
1263	LAB178	solanum_phureja|09v1|SPHFS190963	5931	556	82.95	glotblastn
1264	LAB181	arabidopsis_lyrata|09v1|JGIAL003163	5932	558	90.7	globlastp
1265	LAB182	arabidopsis_lyrata|09v1|JGIAL004937	5933	559	91.9	globlastp
1266	LAB183	arabidopsis_lyrata|09v1|JGIAL012211	5934	560	97.2	globlastp
1267	LAB185	arabidopsis_lyrata|09v1|JGIAL013760	5935	561	92.1	globlastp
1268	LAB185	canola|10v1|DW999895	5936	561	81.4	globlastp
1269	LAB186	arabidopsis_lyrata|09v1|JGIAL015590	5937	562	97.5	globlastp
1270	LAB186	arabidopsis_lyrata|09v1|JGIAL019152	5938	562	83.3	globlastp
1271	LAB186	arabidopsis|gb165|AT3G58510	5939	562	83.3	globlastp
1272	LAB187	arabidopsis_lyrata|09v1|JGIAL009567	5940	563	94.1	globlastp
1273	LAB187	canola|gb161|H74489	5941	563	81.2	globlastp
1274	LAB187	canola|10v1|CD824785	5942	563	81.2	globlastp
1275	LAB187	canola|gb161|CD824785	5943	563	80.7	globlastp
1276	LAB187	b_rapa|gb162|BG543902	5944	563	80.3	globlastp

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1277	LAB187	canola|10v1|CD832364	5945	563	80.2	globlastp
1278	LAB187	canola|gb161|CD832364	5945	563	80.2	globlastp
1279	LAB188	arabidopsis_lyrata|09v1|JGIAL017529	5946	564	96.3	globlastp
1280	LAB188	canola|10v1|CN829728	5947	564	93.1	globlastp
1281	LAB188	canola|10v1|DQ388372	5948	564	92.8	globlastp
1282	LAB188	canola|gb161|DQ388372	5949	564	91.4	globlastp
1283	LAB188	b_rapa|gb162|DN965719	5950	564	87.6	globlastp
1284	LAB189	arabidopsis_lyrata|09v1|JGIAL019157	5951	565	97.7	globlastp
1285	LAB191	arabidopsis_lyrata|09v1|JGIAL028028	5952	567	97.9	globlastp
1286	LAB191	arabidopsis_lyrata|09v1|JGIAL028027	5953	567	91.05	glotblastn
1287	LAB191	canola|10v1|H07767	5954	567	90.62	glotblastn
1288	LAB191	canola|gb161|EV061394	5955	567	90.1	globlastp
1289	LAB191	canola|gb161|EV215362	5956	567	90.1	globlastp
1290	LAB191	radish|gb164|EV526745	5957	567	89.6	globlastp
1291	LAB191	b_rapa|gb162|EX068278	5958	567	89.5	globlastp
1292	LAB191	radish|gb164|EX746054	5959	567	88	globlastp
1293	LAB191	radish|gb164|EV543483	5960	567	84.21	glotblastn
1294	LAB195	brachypodium|09v1|GT845006	5961	569	90.81	glotblastn
1295	LAB195	oat|10v1|GO588363	5962	569	88.24	glotblastn
1296	LAB195	maize|gb170|AI670624	5963	569	84.56	glotblastn
1297	LAB195	rice|gb170|OS09G34910	5964	569	83.82	glotblastn
1298	LAB195	sorghum|09v1|SB02G030210	5965	569	83.82	glotblastn
1299	LAB195	sorghum|gb161.crp|AW282915	5965	569	83.82	glotblastn
1300	LAB195	maize|gb170|AW052938	5966	569	83.46	glotblastn
1301	LAB195	sugarcane|10v1|CA081151	5967	569	83.46	glotblastn
1302	LAB195	sugarcane|gb157.3|CA081151	5967	569	83.46	glotblastn
1303	LAB195	switchgrass|gb167|FE630684	5968	569	83.46	glotblastn
1304	LAB197	wheat|gb164|BE402477	5969	570	96.31	glotblastn
1305	LAB197	pseudoroegneria|gb167|FF344208	5970	570	95.1	globlastp
1306	LAB197	oat|10v1|GR346117	5971	570	86.8	globlastp
1307	LAB197	wheat|gb164|AL818272	5972	570	84.2	globlastp
1308	LAB197	brachypodium|09v1|DV469420	5973	570	82.7	globlastp
1309	LAB197	wheat|gb164|BE427619	5974	570	80.3	globlastp
1310	LAB204	brachypodium|09v1|DV475244	571	571	100	globlastp
1311	LAB204	brachypodium|gb169|BE415626	571	571	100	globlastp
1312	LAB204	wheat|gb164|AL829402	571	571	100	globlastp
1313	LAB204	wheat|gb164|BE415626	571	571	100	globlastp
1314	LAB204	wheat|gb164|BE415779	5975	571	100	glotblastn
1315	LAB204	wheat|gb164|BE493037	5976	571	100	glotblastn
1316	LAB204	wheat|gb164|CA610936	5977	571	100	glotblastn
1317	LAB204	leymus|gb166|AB161676	5978	571	96.4	globlastp
1318	LAB204	rice|gb170|OS05G04700	5979	571	96.4	globlastp
1319	LAB204	wheat|gb164|CA502718	5979	571	96.4	globlastp
1320	LAB204	pseudoroegneria|gb167|FF340236	5980	571	94.5	globlastp

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1321	LAB204	nasturtium|10v1|GH164512	5981	571	92.7	globlastp
1322	LAB204	barley|gb157SOLEXA|DN182019	5982	571	90.9	globlastp
1323	LAB204	leymus|gb166|AB161677	5983	571	90.9	globlastp
1324	LAB204	banana|gb167|DN238253	5984	571	89.5	globlastp
1325	LAB204	banana|gb167|FL657642	5984	571	89.5	globlastp
1326	LAB204	orobanche|10v1|SRR023189S0012323	5985	571	89.3	globlastp
1327	LAB204	flax|09v1|CV478078	5986	571	89.1	globlastp
1328	LAB204	millet|09v1|EVO454PM008364	5987	571	89.1	globlastp
1329	LAB204	oat|10v1|GR359931	5988	571	89.1	globlastp
1330	LAB204	flax|gb157.3|CV478078	5986	571	89.1	globlastp
1331	LAB204	switchgrass|gb167|DN145053	5989	571	89.1	globlastp
1332	LAB204	ginger|gb164|DY355348	5990	571	87.7	globlastp
1333	LAB204	poplar|10v1|BI069568	5991	571	87.7	globlastp
1334	LAB204	poplar|gb170|BI069568	5992	571	87.7	globlastp
1335	LAB204	sugarcane|gb157.3|BQ535255	5993	571	87.7	globlastp
1336	LAB204	lovegrass|gb167|DN481436	5994	571	87.5	globlastp
1337	LAB204	sugarcane|gb157.3|BQ534432	5995	571	87.5	globlastp
1338	LAB204	sugarcane|gb157.3|BQ534680	5995	571	87.5	globlastp
1339	LAB204	sugarcane|10v1|BQ535088	5995	571	87.5	globlastp
1340	LAB204	sugarcane|gb157.3|BQ535088	5995	571	87.5	globlastp
1341	LAB204	sugarcane|gb157.3|CA096029	5995	571	87.5	globlastp
1342	LAB204	sugarcane|gb157.3|CA286362	5995	571	87.5	globlastp
1343	LAB204	sugarcane|gb157.3|CF576753	5996	571	87.5	globlastp
1344	LAB204	switchgrass|gb167|DN150647	5997	571	87.5	globlastp
1345	LAB204	switchgrass|gb167|FL772644	5998	571	87.5	globlastp
1346	LAB204	sugarcane|10v1|BQ534432	5995	571	87.5	globlastp
1347	LAB204	sugarcane|10v1|BQ534516	5995	571	87.5	globlastp
1348	LAB204	triphysaria|10v1|SRR023500S0003316	5999	571	87.3	globlastp
1349	LAB204	triphysaria|10v1|SRR023500S0037696	5999	571	87.3	globlastp
1350	LAB204	rye|gb164|BF145228	6000	571	87.3	globlastp
1351	LAB204	spurge|gb161|DV123416	6001	571	87.3	globlastp
1352	LAB204	canola|gb161|ES902627	6002	571	87.27	glotblastn
1353	LAB204	cryptomeria|gb166|BJ937299	6003	571	87.27	glotblastn
1354	LAB204	spurge|gb161|DV112180	6004	571	87.27	glotblastn
1355	LAB204	banana|gb167|DN239184	6005	571	86	globlastp
1356	LAB204	eucalyptus|gb166|CD668637	6006	571	85.5	globlastp
1357	LAB204	liriodendron|gb166|CK747388	6007	571	85.5	globlastp
1358	LAB204	lotus|09v1|CB828766	6008	571	85.5	globlastp
1359	LAB204	lotus|gb157.2|CB828766	6008	571	85.5	globlastp
1360	LAB204	medicago|09v1|BE323170	6009	571	85.5	globlastp
1361	LAB204	medicago|gb157.2|BE323170	6009	571	85.5	globlastp
1362	LAB204	spruce|gb162|CO215808	6010	571	85.5	globlastp
1363	LAB204	cryptomeria|gb166|BB940612	6011	571	85.45	glotblastn
1364	LAB204	cryptomeria|gb166|BP173716	6012	571	85.45	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1365	LAB204	spruce|gb162|CO241929	6013	571	85.45	glotblastn
1366	LAB204	spruce|gb162|EX402169	6014	571	85.45	glotblastn
1367	LAB204	citrus|gb166|CB610761	6015	571	84.5	globlastp
1368	LAB204	citrus|gb166|CX635312	6015	571	84.5	globlastp
1369	LAB204	maize|gb170|LLT23394	6016	571	84.5	globlastp
1370	LAB204	maize|gb170|T14760	6016	571	84.5	globlastp
1371	LAB204	banana|gb167|FF560276	6017	571	84.2	globlastp
1372	LAB204	liquorice|gb171|FS240532	6018	571	84.2	globlastp
1373	LAB204	salvia|10v1|CV163287	6019	571	83.9	globlastp
1374	LAB204	maize|gb170|AI396387	6020	571	83.9	globlastp
1375	LAB204	millet|09v1|AY823549	6021	571	83.9	globlastp
1376	LAB204	millet|gb161|AY823549	6021	571	83.9	globlastp
1377	LAB204	wheat|gb164|CA486803	6022	571	83.9	globlastp
1378	LAB204	monkeyflower|10v1|SRR037228S0018011	6023	571	83.64	glotblastn
1379	LAB204	nasturtium|10v1|SRR032558S0000444	6024	571	83.64	glotblastn
1380	LAB204	lettuce|gb157.2|DW048006	6025	571	83.64	glotblastn
1381	LAB204	peanut|gb171|CX128241	6026	571	83.64	glotblastn
1382	LAB204	spruce|gb162|CO222473	6027	571	83.64	glotblastn
1383	LAB204	spruce|gb162|DR510117	6028	571	83.64	glotblastn
1384	LAB204	wheat|gb164|CA484233	6029	571	83.64	glotblastn
1385	LAB204	cichorium|gb171|EL369595	-	571	83.64	glotblastn
1386	LAB204	chickpea|09v2|FE672441	6030	571	83.6	globlastp
1387	LAB204	banana|gb167|FF558319	6031	571	83.6	globlastp
1388	LAB204	poplar|10v1|BI122249	6032	571	83.6	globlastp
1389	LAB204	poplar|gb170|BI122249	6032	571	83.6	globlastp
1390	LAB204	poplar|10v1|BU811582	6033	571	83.6	globlastp
1391	LAB204	poplar|gb170|BU811582	6033	571	83.6	globlastp
1392	LAB204	lettuce|10v1|DW048006	6034	571	83.6	globlastp
1393	LAB204	cucumber|09v1|EB715890	6035	571	82.5	globlastp
1394	LAB204	barley|gb157SOLEXA|BE413132	6036	571	82.5	globlastp
1395	LAB204	barley|10v1|BE413132	6036	571	82.5	globlastp
1396	LAB204	barley|gb157SOLEXA|BF257032	6036	571	82.5	globlastp
1397	LAB204	bean|gb167|CV540757	6037	571	82.5	globlastp
1398	LAB204	beech|gb170|SRR006293S0011201	6038	571	82.5	globlastp
1399	LAB204	chestnut|gb170|SRR006295S0007559	6039	571	82.5	globlastp
1400	LAB204	chestnut|gb170|SRR006295S0017671	6039	571	82.5	globlastp
1401	LAB204	eucalyptus|gb166|CD668872	6040	571	82.5	globlastp
1402	LAB204	kiwi|gb166|FG437405	6041	571	82.5	globlastp
1403	LAB204	oak|gb170|CU639520	6039	571	82.5	globlastp
1404	LAB204	sorghum|09v1|SB09G003060	6042	571	82.5	globlastp
1405	LAB204	sorghum|gb161.crp|CD231944	6042	571	82.5	globlastp
1406	LAB204	soybean|gb168|BE323170	6043	571	82.5	globlastp
1407	LAB204	sugarcane|gb157.3|BQ536812	6044	571	82.5	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1408	LAB204	walnuts|gb166|EL894694	6045	571	82.5	globlastp
1409	LAB204	wheat|gb164|BE418414	6036	571	82.5	globlastp
1410	LAB204	wheat|gb164|BE637945	6046	571	82.46	glotblastn
1411	LAB204	wheat|gb164|BE425311	6047	571	82.46	glotblastn
1412	LAB204	flax|09v1|EU830057	6048	571	82.1	globlastp
1413	LAB204	rhizophora|10v1|SRR005792S0007548	6049	571	82.1	globlastp
1414	LAB204	salvia|10v1|SRR014553S0009878	6050	571	82.1	globlastp
1415	LAB204	bruguiera|gb166|BP940238	6051	571	82.1	globlastp
1416	LAB204	catharanthus|gb166|EG560916	6052	571	82.1	globlastp
1417	LAB204	cenchrus|gb166|BM084728	6053	571	82.1	globlastp
1418	LAB204	millet|09v1|CD724750	6054	571	82.1	globlastp
1419	LAB204	millet|gb161|CD726612	6054	571	82.1	globlastp
1420	LAB204	rice|gb170|OS07G44180	6055	571	82.1	globlastp
1421	LAB204	sugarcane|10v1|BQ537279	6056	571	82.1	globlastp
1422	LAB204	sugarcane|gb157.3|BQ537279	6056	571	82.1	globlastp
1423	LAB204	sugarcane|10v1|CA155635	6056	571	82.1	globlastp
1424	LAB204	sugarcane|gb157.3|CA155635	6056	571	82.1	globlastp
1425	LAB204	switchgrass|gb167|DN143186	6057	571	82.1	globlastp
1426	LAB204	switchgrass|gb167|DN151023	6057	571	82.1	globlastp
1427	LAB204	switchgrass|gb167|FE629432	6057	571	82.1	globlastp
1428	LAB204	switchgrass|gb167|FL986616	6058	571	82.1	globlastp
1429	LAB204	artemisia|10v1|ES582125	6059	571	81.82	glotblastn
1430	LAB204	sugarcane|10v1|DV731065	6060	571	81.82	glotblastn
1431	LAB204	artemisia|gb164|ES582125	6061	571	81.82	glotblastn
1432	LAB204	fescue|gb161|DT678660	6062	571	81.82	glotblastn
1433	LAB204	maize|gb170|AI855258	6063	571	81.82	glotblastn
1434	LAB204	maize|gb170|CD990565	6060	571	81.82	glotblastn
1435	LAB204	pine|10v1|BG319022	6064	571	81.82	glotblastn
1436	LAB204	pine|gb157.2|BG319022	6064	571	81.82	glotblastn
1437	LAB204	rice|gb170|CB678398	6065	571	81.82	glotblastn
1438	LAB204	sorghum|09v1|SB03G011700	6060	571	81.82	glotblastn
1439	LAB204	sorghum|gb161.crp|AW564566	6060	571	81.82	glotblastn
1440	LAB204	strawberry|gb164|CO378683	6066	571	81.82	glotblastn
1441	LAB204	wheat|gb164|CA618246	6067	571	81.82	glotblastn
1442	LAB204	artemisia|10v1|GW331462	6068	571	81.8	globlastp
1443	LAB204	ginseng|10v1|GR873554	6069	571	81.8	globlastp
1444	LAB204	sorghum|09v1|SB09G003050	6070	571	81.8	globlastp
1445	LAB204	clover|gb162|BB909236	6071	571	81.8	globlastp
1446	LAB204	fescue|gb161|DT679002	6072	571	81.8	globlastp
1447	LAB204	lettuce|10v1|DW078717	6073	571	81.8	globlastp
1448	LAB204	lettuce|gb157.2|DW078717	6073	571	81.8	globlastp
1449	LAB204	sugarcane|gb157.3|BQ534516	6070	571	81.8	globlastp
1450	LAB204	sugarcane|10v1|BQ535033	6070	571	81.8	globlastp
1451	LAB204	sugarcane|gb157.3|BQ534594	6070	571	81.8	globlastp

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1452	LAB204	walnuts|gb166|CB303483	6074	571	81.4	globlastp
1453	LAB204	walnuts|gb166|EL895529	6074	571	81.4	globlastp
1454	LAB204	heritiera|10v1|SRR005794S0002184	6075	571	80.7	globlastp
1455	LAB204	jatropha|09v1|GO246525	6076	571	80.7	globlastp
1456	LAB204	oat|10v1|CN821388	6077	571	80.7	globlastp
1457	LAB204	barley|gb157SOLEXA|BF253394	6078	571	80.7	globlastp
1458	LAB204	brachypodium|09v1|DV482704	6077	571	80.7	globlastp
1459	LAB204	brachypodium|gb169|BE413132	6077	571	80.7	globlastp
1460	LAB204	cassava|09v1|DR086796	6079	571	80.7	globlastp
1461	LAB204	cassava|gb164|DR086796	6079	571	80.7	globlastp
1462	LAB204	citrus|gb166|CB290651	6080	571	80.7	glotblastn
1463	LAB204	cotton|gb164|BE055465	6081	571	80.7	glotblastn
1464	LAB204	cowpea|gb166|FF390328	6082	571	80.7	globlastp
1465	LAB204	cowpea|gb166|FG844338	6083	571	80.7	globlastp
1466	LAB204	melon|gb165|EB715890	6084	571	80.7	globlastp
1467	LAB204	oat|10v1|CN816104	6077	571	80.7	globlastp
1468	LAB204	oat|gb164|CN816104	6085	571	80.7	glotblastn
1469	LAB204	rye|gb164|BE587105	6086	571	80.7	glotblastn
1470	LAB204	gerbera|09v1|AJ750828	6087	571	80.4	globlastp
1471	LAB204	ginseng|10v1|GR874639	6088	571	80.4	globlastp
1472	LAB204	tragopogon|10v1|SRR020205S0037758	6089	571	80.4	globlastp
1473	LAB204	castorbean|09v1|EE258813	6090	571	80.4	globlastp
1474	LAB204	castorbean|gb160|EE258813	6090	571	80.4	globlastp
1475	LAB204	nuphar|gb166|CD475184	6091	571	80.4	globlastp
1476	LAB204	peanut|gb171|CD037685	6092	571	80.4	globlastp
1477	LAB204	switchgrass|gb167|FL876572	6093	571	80.4	globlastp
1478	LAB204	medicago|09v1|LLCO512569	6094	571	80	globlastp
1479	LAB204	pine|10v1|BF778634	6095	571	80	glotblastn
1480	LAB204	b_oleracea|gb161|AM059255	6096	571	80	globlastp
1481	LAB204	centaurea|gb166|EH738262	6097	571	80	globlastp
1482	LAB204	chestnut|gb170|SRR006296S0016630	6098	571	80	glotblastn
1483	LAB204	lettuce|gb157.2|DW121013	6099	571	80	globlastp
1484	LAB204	lettuce|10v1|DW146833	6097	571	80	globlastp
1485	LAB204	lettuce|gb157.2|DW146833	6097	571	80	globlastp
1486	LAB204	lovegrass|gb167|DN481408	6100	571	80	glotblastn
1487	LAB204	lovegrass|gb167|EH186434	6101	571	80	glotblastn
1488	LAB204	maize|gb170|LLCD940855	6102	571	80	glotblastn
1489	LAB204	pine|gb157.2|BF778634	6103	571	80	glotblastn
1490	LAB204	pine|10v1|CR393204	6104	571	80	glotblastn
1491	LAB204	pine|gb157.2|CR393204	6104	571	80	glotblastn
1492	LAB204	prunus|gb167|BU040273	6105	571	80	glotblastn
1493	LAB204	prunus|gb167|CB819364	6106	571	80	glotblastn
1494	LAB204	safflower|gb162|EL402061	6107	571	80	glotblastn
1495	LAB204	spruce|gb162|CO490368	6108	571	80	globlastp

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1496	LAB204	sunflower|gb162|CD853978	6109	571	80	glotblastn
1497	LAB204	sunflower|gb162|DY954887	6109	571	80	glotblastn
1498	LAB204	sunflower|gb162|EE655129	6110	571	80	glotblastn
1499	LAB204	switchgrass|gb167|FE644351	6111	571	80	glotblastn
1500	LAB210	barley|10v1|BE412504	6112	574	84.1	globlastp
1501	LAB210	wheat|gb164|BQ788771	6113	574	82.2	globlastp
1502	LAB210	oat|10v1|GO587376	6114	574	80.7	globlastp
1503	LAB211	pseudoroegneria|gb167|FF348619	6115	575	95.6	globlastp
1504	LAB211	wheat|gb164|BE413647	6116	575	95.1	globlastp
1505	LAB211	brachypodium|09v1|GT809811	6117	575	86.6	globlastp
1506	LAB211	brachypodium|gb169|BE413647	6118	575	86.1	glotblastn
1507	LAB211	switchgrass|gb167|FE632800	6119	575	84.8	globlastp
1508	LAB211	cenchrus|gb166|EB654815	6120	575	84.7	globlastp
1509	LAB211	sorghum|09v1|SB09G022810	6121	575	84.7	globlastp
1510	LAB211	maize|gb170|BM332575	6122	575	84.2	globlastp
1511	LAB211	sorghum|gb161.crp|BE356560	6123	575	84.2	globlastp
1512	LAB211	maize|gb170|T15302	6124	575	83.7	globlastp
1513	LAB211	rice|gb170|OS05G38820	6125	575	81.58	glotblastn
1514	LAB212	leymus|gb166|EG375667	6126	576	94.2	globlastp
1515	LAB212	wheat|gb164|BE515978	6127	576	94	globlastp
1516	LAB212	pseudoroegneria|gb167|FF352847	6128	576	93.5	globlastp
1517	LAB212	wheat|gb164|BE429733	6129	576	92.7	globlastp
1518	LAB212	wheat|gb164|BE427710	6130	576	88.9	globlastp
1519	LAB212	brachypodium|09v1|DV478766	6131	576	88.3	globlastp
1520	LAB212	brachypodium|gb169|BG418029	6132	576	88	globlastp
1521	LAB212	switchgrass|gb167|FE619498	6133	576	85.2	globlastp
1522	LAB212	switchgrass|gb167|DN142544	6134	576	84.6	globlastp
1523	LAB212	maize|gb170|AW066846	6135	576	82.9	globlastp
1524	LAB212	sorghum|gb161.crp|AW679903	6136	576	82.7	globlastp
1525	LAB212	sorghum|09v1|SB10G027540	6136	576	82.7	globlastp
1526	LAB212	sugarcane|10v1|CA110713	6137	576	81.9	globlastp
1527	LAB212	sugarcane|gb157.3|CA110713	6137	576	81.9	globlastp
1528	LAB217	cotton|gb164|AI725612	6138	578	82.6	globlastp
1529	LAB217	clover|gb162|BB907588	6139	578	82.58	glotblastn
1530	LAB217	papaya|gb165|EX275064	6140	578	82.58	glotblastn
1531	LAB217	bean|gb167|CA902400	6141	578	82.1	globlastp
1532	LAB217	medicago|09v1|AW775623	6142	578	82.02	glotblastn
1533	LAB217	chestnut|gb170|SRR006295S0010554	6143	578	81.46	glotblastn
1534	LAB217	melon|gb165|AM714820	6144	578	81.46	glotblastn
1535	LAB217	poplar|gb170|CV243355	6145	578	81.11	glotblastn
1536	LAB217	cucumber|09v1|CO995825	6146	578	80.9	glotblastn
1537	LAB217	prunus|gb167|AJ823322	6147	578	80.9	glotblastn
1538	LAB217	poplar|10v1|CV243355	6148	578	80.7	globlastp
1539	LAB217	spurge|gb161|DV112896	6149	578	80.56	glotblastn

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1540	LAB217	lotus|09v1|AV420653	6150	578	80.45	glotblastn
1541	LAB217	medicago|gb157.2|AW775623	6151	578	80.4	globlastp
1542	LAB217	soybean|gb168|BI970816	6152	578	80.4	globlastp
1543	LAB217	soybean|gb168|CA902400	6153	578	80.4	globlastp
1544	LAB217	tobacco|gb162|EB444355	6154	578	80.22	glotblastn
1545	LAB220	switchgrass|gb167|DN147462	6155	580	80.6	globlastp
1546	LAB225	sugarcane|10v1|BQ535168	6156	584	86.4	globlastp
1547	LAB225	sorghum|09v1|SB03G033040	6157	584	86.1	globlastp
1548	LAB225	sorghum|gb161.crp|AW331066	6157	584	86.1	globlastp
1549	LAB225	millet|09v1|EVO454PM001578	6158	584	85.8	globlastp
1550	LAB225	switchgrass|gb167|DN144268	6159	584	85.4	globlastp
1551	LAB225	switchgrass|gb167|FE640178	6160	584	85.4	globlastp
1552	LAB225	maize|gb170|T15331	6161	584	85.1	globlastp
1553	LAB225	brachypodium|09v1|DV469255	6162	584	82.5	globlastp
1554	LAB225	wheat|gb164|BE406587	6163	584	82.1	globlastp
1555	LAB225	brachypodium|gb169|BE406587	6164	584	81.46	glotblastn
1556	LAB225	wheat|gb164|BE497128	6165	584	80.8	globlastp
1557	LAB225	barley|10v1|BI950307	6166	584	80.5	globlastp
1558	LAB225	barley|gb157SOLEXA|AL505025	6166	584	80.5	globlastp
1559	LAB228	brachypodium|09v1|DV470077	6167	585	87.9	globlastp
1560	LAB228	sorghum|gb161.crp|BM325428	6168	585	87.8	globlastp
1561	LAB228	maize|gb170|AW267639	6169	585	87.6	globlastp
1562	LAB228	switchgrass|gb167|FE615121	6170	585	87.02	glotblastn
1563	LAB228	barley|gb157SOLEXA|BE412583	6171	585	85.6	globlastp
1564	LAB228	oat|10v1|CN818930	6172	585	85.2	globlastp
1565	LAB231	sorghum|09v1|SB03G043730	6173	588	90.1	globlastp
1566	LAB231	sorghum|gb161.crp|AW677963	6173	588	90.1	globlastp
1567	LAB231	brachypodium|09v1|GT814580	6174	588	88.4	globlastp
1568	LAB231	maize|gb170|BE638867	6175	588	88.3	globlastp
1569	LAB231	barley|10v1|AV834675	6176	588	87.6	globlastp
1570	LAB231	brachypodium|gb169|BE591738	6177	588	87.33	glotblastn
1571	LAB231	maize|gb170|AW171971	6178	588	86.3	globlastp
1572	LAB233	brachypodium|09v1|TMPLOS01G68810T1	6179	590	99.4	globlastp
1573	LAB233	brachypodium|09v1|GT772015	6180	590	82.3	globlastp
1574	LAB233	brachypodium|09v1|DV478709	6181	590	82.01	glotblastn
1575	LAB233	sorghum|09v1|SB03G043780	6182	590	80	globlastp
1576	LAB235	oat|10v1|BE439122	6183	592	83.8	globlastp
1577	LAB235	wheat|gb164|BE419355	6184	592	83.7	globlastp
1578	LAB235	barley|10v1|BI946772	6185	592	83.5	globlastp
1579	LAB235	barley|gb157SOLEXA|BI946772	6185	592	83.5	globlastp
1580	LAB235	switchgrass|gb167|DN146646	6186	592	82.8	globlastp
1581	LAB235	brachypodium|09v1|DV486036	6187	592	82.7	globlastp
1582	LAB235	sorghum|09v1|SB03G043810	6188	592	81.9	globlastp

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1583	LAB235	sorghum|gb161.crp|AW745048	6188	592	81.9	globlastp
1584	LAB235	sugarcane|10v1|CA081661	6189	592	81.2	globlastp
1585	LAB235	sugarcane|gb157.3|CA081661	6190	592	81.2	globlastp
1586	LAB235	maize|gb170|AI372227	6191	592	80	glotblastn
1587	LAB237	brachypodium|09v1|DV474202	6192	594	86.8	globlastp
1588	LAB237	sorghum|09v1|SB04G021410	6193	594	85.3	globlastp
1589	LAB237	maize|gb170|AW787360	6194	594	82.2	globlastp
1590	LAB237	sorghum|gb161.crp|BE345738	6195	594	82.1	globlastp
1591	LAB237	oat|10v1|CN816886	6196	594	81.2	globlastp
1592	LAB238	brachypodium|09v1|GT767992	6197	595	91.7	globlastp
1593	LAB238	brachypodium|gb169|BE406876	6197	595	91.7	globlastp
1594	LAB238	fescue|gb161|DT675438	6198	595	90.5	globlastp
1595	LAB238	leymus|gb166|EG393183	6199	595	90.2	globlastp
1596	LAB238	maize|gb170|AI438615	6200	595	89.8	globlastp
1597	LAB238	sugarcane|10v1|CA087915	6201	595	89.8	globlastp
1598	LAB238	sorghum|09v1|SB04G027590	6202	595	89.5	globlastp
1599	LAB238	sorghum|gb161.crp|AI920758	6202	595	89.5	globlastp
1600	LAB238	sugarcane|gb157.3|CA141903	6203	595	89.5	globlastp
1601	LAB238	pseudoroegneria|gb167|FF346705	6204	595	88.6	globlastp
1602	LAB238	barley|gb157SOLEXA|BE412737	6205	595	87.9	globlastp
1603	LAB238	oat|10v1|CN820263	6206	595	87.6	globlastp
1604	LAB238	wheat|gb164|BE415762	6207	595	87.3	globlastp
1605	LAB238	wheat|gb164|BE406876	6208	595	86.7	globlastp
1606	LAB238	barley|10v1|BE412737	6209	595	85.99	glotblastn
1607	LAB238	brachypodium|09v1|GT792040	6210	595	84.1	globlastp
1608	LAB238	brachypodium|gb169|BE445674	6210	595	84.1	globlastp
1609	LAB238	sugarcane|gb157.3|BQ536599	6211	595	84.1	globlastp
1610	LAB238	sorghum|gb161.crp|AW091473	6212	595	84.1	globlastp
1611	LAB238	rice|gb170|OS06G11800	6213	595	83.9	globlastp
1612	LAB238	sorghum|09v1|SB10G007760	6214	595	83.8	globlastp
1613	LAB238	maize|gb170|AW091473	6215	595	83.4	globlastp
1614	LAB238	switchgrass|gb167|DN144426	6216	595	83.1	globlastp
1615	LAB238	oat|10v1|GR344417	6217	595	81.2	globlastp
1616	LAB238	barley|10v1|BI947155	6218	595	81.2	globlastp
1617	LAB238	barley|gb157SOLEXA|AL450690	6218	595	81.2	globlastp
1618	LAB238	pseudoroegneria|gb167|FF341263	6219	595	81.2	globlastp
1619	LAB238	leymus|gb166|EG374932	6220	595	80.3	globlastp
1620	LAB240	switchgrass|gb167|DN142418	6221	596	85.5	globlastp
1621	LAB240	sorghum|09v1|SB01G047500	6222	596	84.5	globlastp
1622	LAB240	sorghum|gb161.crp|AW621098	6222	596	84.5	globlastp
1623	LAB240	maize|gb170|AW061639	6223	596	84	globlastp
1624	LAB240	wheat|gb164|BE498578	6224	596	80.2	globlastp
1625	LAB252	brachypodium|09v1|DV469506	6225	603	89.6	globlastp
1626	LAB252	brachypodium|gb169|DT715392	6226	603	85	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1627	LAB254	brachypodium|gb169|CA679165	6227	605	84.3	globlastp
1628	LAB254	ricc|gb170|OS09G27930	6228	605	83	globlastp
1629	LAB254	barley|gb157SOLEXA|BI948415	6229	605	82.14	glotblastn
1630	LAB254	wheat|gb164|CJ655025	6230	605	82.1	globlastp
1631	LAB254	barley|gb157SOLEXA|BI952431	6231	605	81.43	glotblastn
1632	LAB254	barley|10v1|BI948415	6232	605	81	globlastp
1633	LAB254	brachypodium|09v1|GT778632	6233	605	80.85	glotblastn
1634	LAB254	sorghum|09v1|SB02G032360	6234	605	80.4	globlastp
1635	LAB254	wheat|gb164|AL830764	6235	605	80.14	glotblastn
1636	LAB254	rice|gb170|OS07G30640	6236	605	80	globlastp
1637	LAB259	switchgrass|gb167|FE633179	6237	608	84.2	globlastp
1638	LAB259	maize|gb170|AI491620	6238	608	83.7	globlastp
1639	LAB259	switchgrass|gb167|FE658096	6239	608	83.6	globlastp
1640	LAB259	brachypodium|09v1|SRR031795S0049444	6240	608	83.3	globlastp
1641	LAB259	brachypodium|gb169|BE488380	6241	608	82.7	globlastp
1642	LAB259	cenchrus|gb166|EB653342	6242	608	82.7	globlastp
1643	LAB259	pseudoroegneria|gb167|FF343851	6243	608	82.6	globlastp
1644	LAB259	sorghum|gb161.crp|BE594723	6244	608	82.6	globlastp
1645	LAB259	wheat|gb164|BE400850	6245	608	82.49	glotblastn
1646	LAB259	sugarcane|gb157.3|CA099266	6246	608	82.27	glotblastn
1647	LAB259	wheat|gb164|BE497098	6247	608	82.21	glotblastn
1648	LAB259	oat|10v1|GO582575	6248	608	82.2	globlastp
1649	LAB259	barley|10v1|BF622384	6249	608	81.14	glotblastn
1650	LAB261	sorghum|09v1|SB01G021890	6250	610	96.8	globlastp
1651	LAB261	sorghum|gb161.crp|AA979985	6250	610	96.8	globlastp
1652	LAB261	maize|gb170|AA979985	6251	610	96.6	globlastp
1653	LAB261	sugarcane|10v1|CA089729	6252	610	96.6	globlastp
1654	LAB261	sugarcane|gb157.3|CA089729	6253	610	96.3	globlastp
1655	LAB261	switchgrass|gb167|FE613678	6254	610	96.3	globlastp
1656	LAB261	switchgrass|gb167|FE612491	6255	610	96.1	globlastp
1657	LAB261	millet|09v1|EVO454PM012321	6256	610	95.3	globlastp
1658	LAB261	brachypodium|09v1|DV475368	6257	610	94.7	globlastp
1659	LAB261	brachypodium|gb169|BE403608	6257	610	94.7	globlastp
1660	LAB261	oak|gb170|CU639846	6258	610	94.2	globlastp
1661	LAB261	cenchrus|gb166|EB657433	6259	610	94	globlastp
1662	LAB261	chestnut|gb170|SRR006295S0002108	6260	610	93.9	globlastp
1663	LAB261	castorbean|09v1|EG657682	6261	610	93.7	globlastp
1664	LAB261	castorbean|gb160|EG657682	6261	610	93.7	globlastp
1665	LAB261	citrus|gb166|CB292297	6262	610	93.7	globlastp
1666	LAB261	barley|10v1|BI951489	6263	610	93.4	globlastp
1667	LAB261	barley|gb157SOLEXA|BI951489	6263	610	93.4	globlastp
1668	LAB261	cacao|gb167|CF974396	6264	610	93.4	globlastp
1669	LAB261	eschscholzia|10v1|CD476664	6265	610	93.1	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1670	LAB261	petunia|gb171|DY395574	6266	610	93.1	globlastp
1671	LAB261	cleome_gynandra|10v1|SRR015532S0007556	6267	610	92.9	globlastp
1672	LAB261	cotton|gb164|BF276437	6268	610	92.9	globlastp
1673	LAB261	grape|gb160|BM436812	6269	610	92.9	globlastp
1674	LAB261	papaya|gb165|EX245895	6270	610	92.9	globlastp
1675	LAB261	wheat|gb164|AL828650	6271	610	92.9	globlastp
1676	LAB261	wheat|gb164|BE403608	6271	610	92.9	globlastp
1677	LAB261	wheat|gb164|BE471112	6271	610	92.9	globlastp
1678	LAB261	grape|gb160|BQ798967	6272	610	92.6	globlastp
1679	LAB261	cassava|09v1|CK644886	6273	610	92.3	globlastp
1680	LAB261	cycas|gb166|CB088840	6274	610	92.3	globlastp
1681	LAB261	kiwi|gb166|FG404410	6275	610	92.3	globlastp
1682	LAB261	cucumber|09v1|DV633870	6276	610	92.1	globlastp
1683	LAB261	cassava|09v1|CK645201	6277	610	92.1	globlastp
1684	LAB261	cassava|gb164|CK645201	6277	610	92.1	globlastp
1685	LAB261	bean|gb167|CA900293	6278	610	91.8	globlastp
1686	LAB261	peanut|gb171|CD037806	6279	610	91.8	globlastp
1687	LAB261	poplar|10v1|BI138784	6280	610	91.8	globlastp
1688	LAB261	prunus|gb167|BU039320	6281	610	91.8	globlastp
1689	LAB261	tobacco|gb162|CV016319	6282	610	91.8	globlastp
1690	LAB261	cotton|gb164|BM359655	6283	610	91.5	globlastp
1691	LAB261	cowpea|gb166|FF382735	6284	610	91.5	globlastp
1692	LAB261	pepper|gb171|BM063583	6285	610	91.5	globlastp
1693	LAB261	pine|10v1|AA739737	6286	610	91.5	globlastp
1694	LAB261	pine|gb157.2|AA739737	6286	610	91.5	globlastp
1695	LAB261	poplar|gb170|BI138784	6287	610	91.5	globlastp
1696	LAB261	strawberry|gb164|CO816775	6288	610	91.5	globlastp
1697	LAB261	tobacco|gb162|DW002414	6289	610	91.5	globlastp
1698	LAB261	tobacco|gb162|EB444412	6290	610	91.5	globlastp
1699	LAB261	ipomoea|gb157.2|BJ553883	6291	610	91.3	globlastp
1700	LAB261	soybean|gb168|AW720478	6292	610	91.3	globlastp
1701	LAB261	tomato|09v1|BG124641	6293	610	91.3	globlastp
1702	LAB261	tomato|gb164|BG124641	6293	610	91.3	globlastp
1703	LAB261	triphysaria|gb164|EY179701	6294	610	91.3	globlastp
1704	LAB261	millet|09v1|EVO454PM004697	6295	610	91	globlastp
1705	LAB261	nasturtium|10v1|SRR032558S0011340	6296	610	91	globlastp
1706	LAB261	solanum_phureja|09v1|SPHBG124641	6297	610	91	globlastp
1707	LAB261	pine|10v1|AA739586	6298	610	91	globlastp
1708	LAB261	pine|gb157.2|AA739586	6298	610	91	globlastp
1709	LAB261	poplar|10v1|BI121493	6299	610	91	globlastp
1710	LAB261	poplar|gb170|BI121493	6299	610	91	globlastp
1711	LAB261	potato|10v1|BF153891	6297	610	91	globlastp
1712	LAB261	potato|gb157.2|BF153891	6297	610	91	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1713	LAB261	ricc|gb170|OS11G37890	6300	610	91	globlastp
1714	LAB261	sprucc|gb162|CO227086	6301	610	91	globlastp
1715	LAB261	switchgrass|gb167|DN140657	6295	610	91	globlastp
1716	LAB261	triphysaria|10v1|EY179701	6302	610	91	globlastp
1717	LAB261	aquilegia|10v1|DR926102	6303	610	90.8	globlastp
1718	LAB261	aquilegia|gb157.3|DR926102	6303	610	90.8	globlastp
1719	LAB261	sugarcane|10v1|CA070225	6304	610	90.8	globlastp
1720	LAB261	sugarcane|gb157.3|CA070225	6304	610	90.8	globlastp
1721	LAB261	eggplant|10v1|FS012567	6305	610	90.7	globlastp
1722	LAB261	monkeyflower|10v1|DV207215	6306	610	90.7	globlastp
1723	LAB261	monkeyflower|10v1|GO993454	6307	610	90.7	globlastp
1724	LAB261	bean|gb167|CA900782	6308	610	90.7	globlastp
1725	LAB261	petunia|gb171|FN001638	6309	610	90.7	globlastp
1726	LAB261	soybean|gb168|BE943442	6310	610	90.7	globlastp
1727	LAB261	spruce|gb162|CO230551	6311	610	90.7	globlastp
1728	LAB261	nasturtium|10v1|SRR032558S0012367	6312	610	90.5	globlastp
1729	LAB261	salvia|10v1|SRR014553S0011018	6313	610	90.5	globlastp
1730	LAB261	sorghum|09v1|SB05G022890	6314	610	90.5	globlastp
1731	LAB261	apple|gb171|CN489582	6315	610	90.5	globlastp
1732	LAB261	cowpea|gb166|FF548366	6316	610	90.5	globlastp
1733	LAB261	lotus|09v1|LLAF000387	6317	610	90.5	globlastp
1734	LAB261	lotus|gb157.2|AF000387	6317	610	90.5	globlastp
1735	LAB261	medicago|09v1|AW684320	6318	610	90.5	globlastp
1736	LAB261	medicago|gb157.2|AW684320	6318	610	90.5	globlastp
1737	LAB261	pepper|gb171|CA847567	6319	610	90.5	globlastp
1738	LAB261	soybean|gb168|AW720589	6320	610	90.5	glotblastn
1739	LAB261	sorghum|gb161.crp|AI621789	6314	610	90.5	globlastp
1740	LAB261	medicago|09v1|LLAW287978	6321	610	90.3	globlastp
1741	LAB261	medicago|gb157.2|AW287978	6321	610	90.3	globlastp
1742	LAB261	apple|gb171|CN491348	6322	610	90.2	globlastp
1743	LAB261	arabidopsis|gb165|AT5G28840	6323	610	90.2	globlastp
1744	LAB261	artemisia|10v1|EY051556	6324	610	90.2	globlastp
1745	LAB261	potato|10v1|BG096609	6325	610	90.2	globlastp
1746	LAB261	potato|gb157.2|BG096609	6325	610	90.2	globlastp
1747	LAB261	sunflower|gb162|CD851148	6326	610	90.2	globlastp
1748	LAB261	tomato|09v1|BG124848	6327	610	90.2	globlastp
1749	LAB261	tomato|gb164|BG124848	6327	610	90.2	globlastp
1750	LAB261	lettuce|10v1|DW145532	6328	610	89.9	globlastp
1751	LAB261	solanum_phureja|09v1|SPHBG124848	6329	610	89.9	globlastp
1752	LAB261	artemisia|gb164|EY051556	6330	610	89.9	globlastp
1753	LAB261	lettuce|gb157.2|DW104433	6328	610	89.9	globlastp
1754	LAB261	lettuce|gb157.2|DW145532	6328	610	89.9	globlastp
1755	LAB261	sunflower|gb162|DY905774	6331	610	89.9	globlastp
1756	LAB261	lettuce|10v1|DW057783	6328	610	89.9	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1757	LAB261	arabidopsis_lyrata|09v1|JGIAL022633	6332	610	89.7	globlastp
1758	LAB261	lettuce|gb157.2|DW044085	6333	610	89.7	globlastp
1759	LAB261	radish|gb164|EV537961	6334	610	89.7	globlastp
1760	LAB261	b_rapa|gb162|CO750452	6335	610	89.4	globlastp
1761	LAB261	canola|gb161|BQ704449	6335	610	89.4	globlastp
1762	LAB261	canola|10v1|BQ704449	6335	610	89.4	globlastp
1763	LAB261	canola|gb161|CD830432	6335	610	89.4	globlastp
1764	LAB261	centaurea|gb166|EH738056	6336	610	89.2	globlastp
1765	LAB261	cichorium|gb171|EH675975	6337	610	89.2	globlastp
1766	LAB261	safflower|gb162|EL377966	6338	610	89.2	globlastp
1767	LAB261	tragopogon|10v1|SRR020205S0000342	6339	610	89.15	glotblastn
1768	LAB261	brachypodium|09v1|DV472085	6340	610	88.9	globlastp
1769	LAB261	brachypodium|gb169|BE412805	6340	610	88.9	globlastp
1770	LAB261	barley|10v1|BE412761	6341	610	88.7	globlastp
1771	LAB261	barley|gb157SOLEXA|BE412805	6341	610	88.7	globlastp
1772	LAB261	maize|gb170|AI621789	6342	610	88.7	globlastp
1773	LAB261	radish|gb164|EY935796	6343	610	88.7	globlastp
1774	LAB261	b_oleracea|gb161|AM395321	6344	610	88.65	glotblastn
1775	LAB261	soybean|gb168|AW719861	6345	610	88.17	glotblastn
1776	LAB261	wheat|gb164|BE470986	6346	610	88.13	glotblastn
1777	LAB261	wheat|gb164|BE415328	6347	610	87.57	glotblastn
1778	LAB261	lolium|10v1|AU246974	6348	610	87.3	globlastp
1779	LAB261	oat|10v1|CN815416	6349	610	87.3	globlastp
1780	LAB261	cassava|09v1|JGICASSAVA38534M1	6350	610	87	globlastp
1781	LAB261	spikemoss|gb165|DN838866	6351	610	86.3	globlastp
1782	LAB261	spikemoss|gb165|FE443875	6352	610	86.3	globlastp
1783	LAB261	banana|gb167|DN240198	6353	610	85.8	globlastp
1784	LAB261	physcomitrella|10v1|AW145217	6354	610	85.3	globlastp
1785	LAB261	physcomitrella|gb157|AW145217	6354	610	85.3	globlastp
1786	LAB261	physcomitrella|10v1|BJ176425	6355	610	84.2	globlastp
1787	LAB261	gerbera|09v1|AJ753310	6356	610	84.13	glotblastn
1788	LAB261	coffea|10v1|DV685976	6357	610	84.1	globlastp
1789	LAB261	physcomitrella|10v1|BJ172060	6358	610	84	globlastp
1790	LAB261	fescue|gb161|DT680485	6359	610	83.7	globlastp
1791	LAB261	marchantia|gb166|BJ840495	6360	610	83.4	globlastp
1792	LAB261	spikemoss|gb165|FE449379	6361	610	82.6	globlastp
1793	LAB261	avocado|10v1|CK754925	6362	610	81	globlastp
1794	LAB261	avocado|gb164|CK754925	6362	610	81	globlastp
1795	LAB263	millet|09v1|EVO454PM004666	6363	612	95.1	globlastp
1796	LAB263	switchgrass|gb167|DN144095	6364	612	94.4	globlastp
1797	LAB263	switchgrass|gb167|FL896428	6364	612	94.4	globlastp
1798	LAB263	sugarcane|10v1|CA073725	6365	612	93.7	globlastp
1799	LAB263	cenchrus|gb166|EB657377	6366	612	93.7	globlastp
1800	LAB263	sorghum|09v1|SB01G017460	6365	612	93.7	globlastp

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1801	LAB263	sorghum|gb161.crp|BE345577	6365	612	93.7	globlastp
1802	LAB263	sugarcane|gb157.3|CA069290	6365	612	93.7	globlastp
1803	LAB263	wheat|gb164|AL821110	6367	612	90.9	globlastp
1804	LAB263	wheat|gb164|BG262576	6368	612	90.9	globlastp
1805	LAB263	barley|10v1|BF254790	6369	612	90.2	globlastp
1806	LAB263	barley|gb157SOLEXA|AL505544	6369	612	90.2	globlastp
1807	LAB263	brachypodium|09v1|DV478084	6370	612	89.6	globlastp
1808	LAB263	brachypodium|gb169|BF293509	6370	612	89.6	globlastp
1809	LAB263	lovegrass|gb167|EH189807	6371	612	89.51	glotblastn
1810	LAB263	oat|10v1|GO591788	6372	612	89.5	globlastp
1811	LAB263	fescue|gb161|DT680080	6373	612	89.5	globlastp
1812	LAB263	wheat|gb164|BF293509	6374	612	88.9	globlastp
1813	LAB263	banana|gb167|FF561386	6375	612	83.2	globlastp
1814	LAB264	barley|10v1|BF621209	6376	613	86.7	globlastp
1815	LAB264	wheat|gb164|BF293634	6377	613	86.42	glotblastn
1816	LAB264	barley|gb157SOLEXA|AL506359	6378	613	86.3	globlastp
1817	LAB264	leymus|gb166|EG377220	6379	613	86.2	globlastp
1818	LAB264	maize|gb170|AI664956	6380	613	86.1	globlastp
1819	LAB264	switchgrass|gb167|DN142147	6381	613	86.1	globlastp
1820	LAB264	sorghum|09v1|SB01G017060	6382	613	84.4	globlastp
1821	LAB264	sorghum|gb161.crp|BE355313	6382	613	84.4	globlastp
1822	LAB264	brachypodium|09v1|DV472183	6383	613	83.8	globlastp
1823	LAB264	brachypodium|gb169|BE490826	6384	613	83.5	globlastp
1824	LAB264	maize|gb170|CRPZM2N054279	6385	613	83.3	globlastp
1825	LAB264	sugarcane|gb157.3|CA065380	6386	613	81.16	glotblastn
1826	LAB265	switchgrass|gb167|FL765838	6387	614	80.2	globlastp
1827	LAB267	maize|gb170|AF083327	6388	615	97.5	globlastp
1828	LAB267	rice|gb170|OS05G44340	6389	615	96.5	globlastp
1829	LAB267	brachypodium|gb169|AF083344	6390	615	95.1	globlastp
1830	LAB267	brachypodium|09v1|SRR031797S0356808	6391	615	95	globlastp
1831	LAB267	barley|10v1|BG367325	6392	615	94.1	globlastp
1832	LAB267	wheat|gb164|AF083344	6393	615	93.8	globlastp
1833	LAB267	wheat|gb164|BE515416	6394	615	91.6	globlastp
1834	LAB267	brachypodium|09v1|GT777326	6395	615	91.1	globlastp
1835	LAB267	sorghum|09v1|SB03G034390	6396	615	88.2	globlastp
1836	LAB267	sorghum|gb161.crp|CD204325	6396	615	88.2	globlastp
1837	LAB267	cucumber|09v1|CV003331	6397	615	86.3	globlastp
1838	LAB267	grape|gb160|BM437943	6398	615	85.7	globlastp
1839	LAB267	chestnut|gb170|SRR006296S0007369	6399	615	85.2	globlastp
1840	LAB267	brachypodium|gb169|AV934943	6400	615	84.7	globlastp
1841	LAB267	soybean|gb168|SOYSB100HS	6401	615	84.6	globlastp
1842	LAB267	lotus|09v1|BW598183	6402	615	84.5	globlastp
1843	LAB267	arabidopsis|gb165|AT1G74310	6403	615	84.2	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1844	LAB267	poplar|10v1|AI162541	6404	615	84.1	globlastp
1845	LAB267	arabidopsis_lyrata|09v1|JGIAL007701	6405	615	84	globlastp
1846	LAB267	poplar|gb170|AI162541	6406	615	84	globlastp
1847	LAB267	cassava|09v1|DV445651	6407	615	83.7	globlastp
1848	LAB267	castorbean|09v1|EG656629	6408	615	83.6	globlastp
1849	LAB267	castorbean|gb160|EG656629	6408	615	83.6	globlastp
1850	LAB267	pine|10v1|AA566965	6409	615	82.8	globlastp
1851	LAB267	tobacco|gb162|AF083343	6410	615	82.5	globlastp
1852	LAB267	monkeyflower|10v1|SRR037227S0004657	6411	615	82.3	globlastp
1853	LAB267	tomato|09v1|BG126435	6412	615	82.2	globlastp
1854	LAB267	solanum_phureja|09v1|SPHBG126435	6413	615	81.9	globlastp
1855	LAB268	arabidopsis_lyrata|09v1|CRPALE000200	616	616	100	globlastp
1856	LAB268	arabidopsis_lyrata|09v1|JGIAL000723	616	616	100	globlastp
1857	LAB268	arabidopsis_lyrata|09v1|JGIAL000743	616	616	100	globlastp
1858	LAB268	arabidopsis_lyrata|09v1|JGIAL017658	616	616	100	globlastp
1859	LAB268	arabidopsis_lyrata|09v1|JGIAL017717	616	616	100	globlastp
1860	LAB268	arabidopsis_lyrata|09v1|JGIAL018619	616	616	100	globlastp
1861	LAB268	arabidopsis_lyrata|09v1|JGIAL030589	616	616	100	globlastp
1862	LAB268	arabidopsis_lyrata|09v1|JGIAL030619	616	616	100	globlastp
1863	LAB268	arabidopsis_lyrata|09v1|JGIAL032285	616	616	100	globlastp
1864	LAB268	artemisia|10v1|EF549583	616	616	100	globlastp
1865	LAB268	artemisia|10v1|EY034318	616	616	100	globlastp
1866	LAB268	artemisia|10v1|EY039119	616	616	100	globlastp
1867	LAB268	artemisia|10v1|EY042941	616	616	100	globlastp
1868	LAB268	artemisia|10v1|EY043355	616	616	100	globlastp
1869	LAB268	artemisia|10v1|EY053904	616	616	100	globlastp
1870	LAB268	artemisia|10v1|EY053905	616	616	100	globlastp
1871	LAB268	artemisia|10v1|EY054470	616	616	100	globlastp
1872	LAB268	artemisia|10v1|EY055002	616	616	100	globlastp
1873	LAB268	artemisia|10v1|EY058090	616	616	100	globlastp
1874	LAB268	artemisia|10v1|EY059748	616	616	100	globlastp
1875	LAB268	artemisia|10v1|EY094034	616	616	100	globlastp
1876	LAB268	artemisia|10v1|EY112179	616	616	100	globlastp
1877	LAB268	artemisia|10v1|GW328652	616	616	100	globlastp
1878	LAB268	artemisia|10v1|GW328923	616	616	100	globlastp
1879	LAB268	artemisia|10v1|GW328962	616	616	100	globlastp
1880	LAB268	artemisia|10v1|GW329063	616	616	100	globlastp
1881	LAB268	artemisia|10v1|GW329182	616	616	100	globlastp
1882	LAB268	artemisia|10v1|GW329192	616	616	100	globlastp
1883	LAB268	artemisia|10v1|GW329412	616	616	100	globlastp
1884	LAB268	artemisia|10v1|GW330388	616	616	100	globlastp
1885	LAB268	artemisia|10v1|GW331835	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1886	LAB268	artemisia|10v1|SRR019254S0000375	616	616	100	globlastp
1887	LAB268	artemisia|10v1|SRR019254S0000380	616	616	100	globlastp
1888	LAB268	artemisia|10v1|SRR019254S0000431	616	616	100	globlastp
1889	LAB268	artemisia|10v1|SRR019254S0000460	616	616	100	globlastp
1890	LAB268	artemisia|10v1|SRR019254S0000626	616	616	100	globlastp
1891	LAB268	artemisia|10v1|SRR019254S0001178	616	616	100	globlastp
1892	LAB268	artemisia|10v1|SRR019254S0001487	616	616	100	globlastp
1893	LAB268	artemisia|10v1|SRR019254S0001518	616	616	100	globlastp
1894	LAB268	artemisia|10v1|SRR019254S0003786	616	616	100	globlastp
1895	LAB268	artemisia|10v1|SRR019254S0004038	616	616	100	globlastp
1896	LAB268	artemisia|10v1|SRR019254S0004262	616	616	100	globlastp
1897	LAB268	artemisia|10v1|SRR019254S0005211	616	616	100	globlastp
1898	LAB268	artemisia|10v1|SRR019254S0005860	616	616	100	globlastp
1899	LAB268	artemisia|10v1|SRR019254S0005963	616	616	100	globlastp
1900	LAB268	artemisia|10v1|SRR019254S0006055	616	616	100	globlastp
1901	LAB268	artemisia|10v1|SRR019254S0008243	616	616	100	globlastp
1902	LAB268	artemisia|10v1|SRR019254S0008256	616	616	100	globlastp
1903	LAB268	artemisia|10v1|SRR019254S0009721	616	616	100	globlastp
1904	LAB268	artemisia|10v1|SRR019254S0011742	616	616	100	globlastp
1905	LAB268	artemisia|10v1|SRR019254S0012498	616	616	100	globlastp
1906	LAB268	artemisia|10v1|SRR019254S0013446	616	616	100	globlastp
1907	LAB268	artemisia|10v1|SRR019254S0013783	616	616	100	globlastp
1908	LAB268	artemisia|10v1|SRR019254S0015995	616	616	100	globlastp
1909	LAB268	artemisia|10v1|SRR019254S0017378	616	616	100	globlastp
1910	LAB268	artemisia|10v1|SRR019254S0019913	616	616	100	globlastp
1911	LAB268	artemisia|10v1|SRR019254S0020607	616	616	100	globlastp
1912	LAB268	artemisia|10v1|SRR019254S0022185	616	616	100	globlastp
1913	LAB268	artemisia|10v1|SRR019254S0022238	616	616	100	globlastp
1914	LAB268	artemisia|10v1|SRR019254S0024032	616	616	100	globlastp
1915	LAB268	artemisia|10v1|SRR019254S0024180	616	616	100	globlastp
1916	LAB268	artemisia|10v1|SRR019254S0025912	616	616	100	globlastp
1917	LAB268	artemisia|10v1|SRR019254S0026259	616	616	100	globlastp
1918	LAB268	artemisia|10v1|SRR019254S0029317	616	616	100	globlastp
1919	LAB268	artemisia|10v1|SRR019254S0029360	616	616	100	globlastp
1920	LAB268	artemisia|10v1|SRR019254S0030218	616	616	100	globlastp
1921	LAB268	artemisia|10v1|SRR019254S0030358	616	616	100	globlastp
1922	LAB268	artemisia|10v1|SRR019254S0032259	616	616	100	globlastp
1923	LAB268	artemisia|10v1|SRR019254S0051179	616	616	100	globlastp
1924	LAB268	artemisia|10v1|SRR019254S0052017	616	616	100	globlastp
1925	LAB268	artemisia|10v1|SRR019254S0061794	616	616	100	globlastp
1926	LAB268	artemisia|10v1|SRR019254S0069114	616	616	100	globlastp
1927	LAB268	artemisia|10v1|SRR019254S0074817	616	616	100	globlastp
1928	LAB268	artemisia|10v1|SRR019254S0076339	616	616	100	globlastp
1929	LAB268	artemisia|10v1|SRR019254S0079662	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1930	LAB268	artemisia|10v1|SRR019254S0105221	616	616	100	globlastp
1931	LAB268	artemisia|10v1|SRR019254S0114141	616	616	100	globlastp
1932	LAB268	artemisia|10v1|SRR019254S0120013	616	616	100	globlastp
1933	LAB268	artemisia|10v1|SRR019254S0127473	616	616	100	globlastp
1934	LAB268	artemisia|10v1|SRR019254S0130786	616	616	100	globlastp
1935	LAB268	artemisia|10v1|SRR019254S0140955	616	616	100	globlastp
1936	LAB268	artemisia|10v1|SRR019254S0143768	616	616	100	globlastp
1937	LAB268	artemisia|10v1|SRR019254S0147045	616	616	100	globlastp
1938	LAB268	artemisia|10v1|SRR019254S0266839	616	616	100	globlastp
1939	LAB268	artemisia|10v1|SRR019254S0270614	616	616	100	globlastp
1940	LAB268	artemisia|10v1|SRR019254S0279002	616	616	100	globlastp
1941	LAB268	artemisia|10v1|SRR019254S0387282	616	616	100	globlastp
1942	LAB268	artemisia|10v1|SRR019254S0579805	616	616	100	globlastp
1943	LAB268	artemisia|10v1|SRR019546S0035668	616	616	100	globlastp
1944	LAB268	artemisia|10v1|SRR019546S0183437	616	616	100	globlastp
1945	LAB268	artemisia|10v1|SRR019550S0048076	616	616	100	globlastp
1946	LAB268	artemisia|10v1|SRR019550S0262313	616	616	100	globlastp
1947	LAB268	artemisia|10v1|SRR019550S0292384	616	616	100	globlastp
1948	LAB268	barley|10v1|BE412942	616	616	100	globlastp
1949	LAB268	barley|10v1|BF622067	616	616	100	globlastp
1950	LAB268	barley|10v1|BF626567	616	616	100	globlastp
1951	LAB268	barley|10v1|BI949272	616	616	100	globlastp
1952	LAB268	brachypodium|09v1|GT779131	616	616	100	globlastp
1953	LAB268	canola|10v1|CD812149	616	616	100	globlastp
1954	LAB268	canola|10v1|CD822786	616	616	100	globlastp
1955	LAB268	canola|10v1|CN736543	616	616	100	globlastp
1956	LAB268	canola|10v1|CX187745	616	616	100	globlastp
1957	LAB268	cassava|09v1|BI325167	616	616	100	globlastp
1958	LAB268	cassava|09v1|JGICASSAVA41199M1	616	616	100	globlastp
1959	LAB268	cassava|09v1|JGICASSAVA46265M1	616	616	100	globlastp
1960	LAB268	chickpea|09v2|GR392086	616	616	100	globlastp
1961	LAB268	chickpea|09v2|GR398679	616	616	100	globlastp
1962	LAB268	cleome_gynandra|10v1|SRR015532S0007899	616	616	100	globlastp
1963	LAB268	cleome_gynandra|10v1|SRR015532S0022381	616	616	100	globlastp
1964	LAB268	cleome_gynandra|10v1|SRR015532S0062423	616	616	100	globlastp
1965	LAB268	cleome_gynandra|10v1|SRR015532S0098412	616	616	100	globlastp
1966	LAB268	cleome_gynandra|10v1|SRR015532S0197501	616	616	100	globlastp
1967	LAB268	cleome_spinosa|10v1|GR931018	616	616	100	globlastp
1968	LAB268	cleome_spinosa|10v1|GR932515	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
1969	LAB268	clcomc_spinosa|10v1|SRR015531S0001363	616	616	100	globlastp
1970	LAB268	cucumber|09v1|AM732498	616	616	100	globlastp
1971	LAB268	cucumber|09v1|BGI454H0122642	616	616	100	globlastp
1972	LAB268	cucumber|09v1|BI740176	616	616	100	globlastp
1973	LAB268	cucumber|09v1|CK085478	616	616	100	globlastp
1974	LAB268	cucumber|09v1|CK085975	616	616	100	globlastp
1975	LAB268	cucumber|09v1|CK755431	616	616	100	globlastp
1976	LAB268	cucumber|09v1|DV633267	616	616	100	globlastp
1977	LAB268	eggplant|10v1|AB018245	616	616	100	globlastp
1978	LAB268	eggplant|10v1|FS000621	616	616	100	globlastp
1979	LAB268	eggplant|10v1|FS001270	616	616	100	globlastp
1980	LAB268	eggplant|10v1|FS001671	616	616	100	globlastp
1981	LAB268	eggplant|10v1|FS002906	616	616	100	globlastp
1982	LAB268	eggplant|10v1|FS003423	616	616	100	globlastp
1983	LAB268	eggplant|10v1|FS013921	616	616	100	globlastp
1984	LAB268	eschscholzia|10v1|CD481738	616	616	100	globlastp
1985	LAB268	eschscholzia|10v1|SRR014116S0018648	6414	616	100	glotblastn
1986	LAB268	flax|09v1|EH791223	616	616	100	globlastp
1987	LAB268	gerbera|09v1|AJ750671	616	616	100	globlastp
1988	LAB268	gerbera|09v1|AJ751622	616	616	100	globlastp
1989	LAB268	gerbera|09v1|AJ752458	616	616	100	globlastp
1990	LAB268	gerbera|09v1|AJ752576	616	616	100	globlastp
1991	LAB268	gerbera|09v1|AJ752839	616	616	100	globlastp
1992	LAB268	gerbera|09v1|AJ752885	616	616	100	globlastp
1993	LAB268	gerbera|09v1|AJ752992	616	616	100	globlastp
1994	LAB268	ginseng|10v1|GR871062	616	616	100	globlastp
1995	LAB268	heritiera|10v1|SRR005795S0006089	616	616	100	globlastp
1996	LAB268	ipomoea_batatas|10v1|CB330659	616	616	100	globlastp
1997	LAB268	ipomoea_batatas|10v1|CB330711	616	616	100	globlastp
1997	LAB268	ipomoea|gb157.2|CB330711	616	616	100	globlastp
1998	LAB268	ipomoea_batatas|10v1|CB330950	616	616	100	globlastp
1999	LAB268	ipomoea_batatas|10v1|DV034788	616	616	100	globlastp
2000	LAB268	ipomoea_nil|10v1|BJ553415	616	616	100	globlastp
2001	LAB268	ipomoea_nil|10v1|BJ553690	616	616	100	globlastp
2002	LAB268	ipomoea_nil|10v1|BJ555300	616	616	100	globlastp
2003	LAB268	ipomoea_nil|10v1|BJ556362	616	616	100	globlastp
2004	LAB268	ipomoea_nil|10v1|BJ556445	616	616	100	globlastp
2005	LAB268	ipomoea_nil|10v1|BJ558611	616	616	100	globlastp
2006	LAB268	ipomoea_nil|10v1|BJ560747	616	616	100	globlastp
2007	LAB268	ipomoea_nil|10v1|CJ738107	616	616	100	globlastp
2008	LAB268	jatropha|09v1|FM887562	616	616	100	globlastp
2009	LAB268	jatropha|09v1|GT228453	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2010	LAB268	lcttucc|10v1|DW047742	616	616	100	globlastp
2011	LAB268	lcttucc|10v1|DW073761	616	616	100	globlastp
2012	LAB268	lettuce|10v1|DW075639	616	616	100	globlastp
2013	LAB268	lettuce|10v1|DW104254	616	616	100	globlastp
2014	LAB268	lettuce|10v1|DW121060	616	616	100	globlastp
2015	LAB268	lettuce|10v1|DW163248	616	616	100	globlastp
2016	LAB268	lolium|10v1|AU247171	616	616	100	globlastp
2017	LAB268	lolium|10v1|X79715	616	616	100	globlastp
2018	LAB268	lotus|09v1|BE122552	616	616	100	globlastp
2019	LAB268	lotus|09v1|CB828743	616	616	100	globlastp
2020	LAB268	lotus|09v1|CRPLJ031736	616	616	100	globlastp
2021	LAB268	lotus|09v1|CRPLJ032446	616	616	100	globlastp
2022	LAB268	medicago|09v1|AL366317	616	616	100	globlastp
2023	LAB268	medicago|09v1|LLCO514535	616	616	100	globlastp
2024	LAB268	monkeyflower|10v1|DV206763	616	616	100	globlastp
2025	LAB268	monkeyflower|10v1|DV207134	616	616	100	globlastp
2026	LAB268	monkeyflower|10v1|DV207153	616	616	100	globlastp
2027	LAB268	monkeyflower|10v1|DV207802	616	616	100	globlastp
2028	LAB268	monkeyflower|10v1|DV209939	6415	616	100	glotblastn
2029	LAB268	monkeyflower|10v1|GO967795	616	616	100	globlastp
2030	LAB268	monkeyflower|10v1|GR008873	616	616	100	globlastp
2031	LAB268	nasturtium|10v1|GH167522	616	616	100	globlastp
2032	LAB268	nasturtium|10v1|SRR032558S0008057	616	616	100	globlastp
2033	LAB268	nasturtium|10v1|SRR032558S0034910	616	616	100	globlastp
2034	LAB268	nasturtium|10v1|SRR032558S0046943	616	616	100	globlastp
2035	LAB268	nasturtium|10v1|SRR032558S0089537	616	616	100	globlastp
2036	LAB268	nasturtium|10v1|SRR032558S0209453	616	616	100	globlastp
2037	LAB268	nasturtium|10v1|SRR032558S0317266	616	616	100	globlastp
2038	LAB268	nasturtium|10v1|SRR032562S0059705	616	616	100	globlastp
2039	LAB268	orobanche|10v1|SRR023189S0000081	616	616	100	globlastp
2040	LAB268	orobanche|10v1|SRR023189S0000767	616	616	100	globlastp
2041	LAB268	orobanche|10v1|SRR023189S0001936	616	616	100	globlastp
2042	LAB268	orobanche|10v1|SRR023189S0004131	616	616	100	globlastp
2043	LAB268	orobanche|10v1|SRR023189S0004660	616	616	100	globlastp
2044	LAB268	orobanche|10v1|SRR023189S0006888	616	616	100	globlastp
2045	LAB268	orobanche|10v1|SRR023189S0009928	616	616	100	globlastp
2046	LAB268	orobanche|10v1|SRR023189S0011568	616	616	100	globlastp
2047	LAB268	orobanche|10v1|SRR023189S0013200	616	616	100	globlastp
2048	LAB268	orobanche|10v1|SRR023189S0014259	616	616	100	globlastp
2049	LAB268	orobanche|10v1|SRR023189S0014732	616	616	100	globlastp
2050	LAB268	orobanche|10v1|SRR023189S0015759	616	616	100	globlastp
2051	LAB268	orobanche|10v1|SRR023189S0016379	616	616	100	globlastp
2052	LAB268	orobanche|10v1|SRR023189S0022127	616	616	100	globlastp
2053	LAB268	orobanche|10v1|SRR023189S0032223	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2054	LAB268	orobanche|10v1|SRR023189S0032511	616	616	100	globlastp
2055	LAB268	orobanche|10v1|SRR023189S0046559	616	616	100	globlastp
2056	LAB268	orobanche|10v1|SRR023189S0052369	616	616	100	globlastp
2057	LAB268	orobanche|10v1|SRR023189S0105273	616	616	100	globlastp
2058	LAB268	pea|09v1|EX568819	616	616	100	globlastp
2059	LAB268	pea|09v1|EX568820	616	616	100	globlastp
2060	LAB268	pea|09v1|EX568868	616	616	100	globlastp
2061	LAB268	pea|09v1|EX569051	616	616	100	globlastp
2062	LAB268	pea|09v1|EX570280	616	616	100	globlastp
2063	LAB268	pea|09v1|EX570347	616	616	100	globlastp
2064	LAB268	pea|09v1|EX571335	616	616	100	globlastp
2065	LAB268	pea|09v1|EX571343	616	616	100	globlastp
2066	LAB268	pea|09v1|FG533048	616	616	100	globlastp
2067	LAB268	pea|09v1|PSU10042	616	616	100	globlastp
2068	LAB268	physcomitrella|10v1|DC934350	616	616	100	globlastp
2069	LAB268	physcomitrella|10v1|FC374737	616	616	100	globlastp
2070	LAB268	physcomitrella|10v1|FC381484	616	616	100	globlastp
2071	LAB268	physcomitrella|10v1|FC411388	616	616	100	globlastp
2072	LAB268	physcomitrella|10v1|XM001751677	616	616	100	globlastp
2073	LAB268	physcomitrella|10v1|XM001766297	616	616	100	globlastp
2074	LAB268	physcomitrella|10v1|XM001768151	616	616	100	globlastp
2075	LAB268	physcomitrella|10v1|XM001769639	616	616	100	globlastp
2076	LAB268	physcomitrella|10v1|XM001779929	616	616	100	globlastp
2077	LAB268	physcomitrella|10v1|XM001783766	616	616	100	globlastp
2078	LAB268	pigeonpea|gb171|GR471003	616	616	100	globlastp
2079	LAB268	pinc|10v1|AL750508	616	616	100	globlastp
2080	LAB268	pine|10v1|AW697623	616	616	100	globlastp
2081	LAB268	poplar|10v1|BI119654	616	616	100	globlastp
2082	LAB268	poplar|10v1|BI119694	616	616	100	globlastp
2083	LAB268	poplar|10v1|CA823688	616	616	100	globlastp
2084	LAB268	rhizophora|10v1|SRR005793S0007192	616	616	100	globlastp
2085	LAB268	rose|10v1|EC586164	616	616	100	globlastp
2086	LAB268	salvia|10v1|SRR014553S0011349	616	616	100	globlastp
2087	LAB268	solanum_phureja|09v1|SPHBG124775	616	616	100	globlastp
2088	LAB268	sugarcane|10v1|CA073794	616	616	100	globlastp
2089	LAB268	sugarcane|10v1|CA078899	616	616	100	globlastp
2090	LAB268	tragopogon|10v1|SRR020205S0059721	616	616	100	globlastp
2091	LAB268	tragopogon|10v1|SRR020205S0133874	616	616	100	globlastp
2092	LAB268	triphysaria|10v1|CB815020	616	616	100	globlastp
2093	LAB268	triphysaria|10v1|DR171915	616	616	100	globlastp
2094	LAB268	triphysaria|10v1|EX999454	616	616	100	globlastp
2095	LAB268	triphysaria|10v1|EY151225	616	616	100	globlastp
2096	LAB268	triphysaria|10v1|SRR023500S0026363	616	616	100	globlastp
2097	LAB268	triphysaria|10v1|SRR023500S0047657	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2098	LAB268	amborclla|gb166|CK766783	6416	616	100	glotblastn
2099	LAB268	amborclla|gb166|FD441330	616	616	100	globlastp
2100	LAB268	antirrhinum|gb166|AJ558339	616	616	100	globlastp
2101	LAB268	antirrhinum|gb166|AJ558802	616	616	100	globlastp
2102	LAB268	antirrhinum|gb166|AJ559512	616	616	100	globlastp
2103	LAB268	antirrhinum|gb166|AJ787885	616	616	100	globlastp
2104	LAB268	antirrhinum|gb166|AJ790005	616	616	100	globlastp
2105	LAB268	antirrhinum|gb166|AJ791274	616	616	100	globlastp
2106	LAB268	antirrhinum|gb166|AJ799867	616	616	100	globlastp
2107	LAB268	apple|gb171|CO418311	616	616	100	globlastp
2108	LAB268	arabidopsis|gb165|AT1G07660	616	616	100	globlastp
2109	LAB268	arabidopsis|gb165|AT1G07820	616	616	100	globlastp
2110	LAB268	arabidopsis|gb165|AT3G45930	616	616	100	globlastp
2111	LAB268	arabidopsis|gb165|AT3G46320	616	616	100	globlastp
2112	LAB268	arabidopsis|gb165|AT3G53730	616	616	100	globlastp
2113	LAB268	arabidopsis|gb165|AT5G59690	616	616	100	globlastp
2114	LAB268	arabidopsis|gb165|BP850938	616	616	100	globlastp
2115	LAB268	artemisia|10v1|SRR019254S0004605	616	616	100	globlastp
2116	LAB268	artemisia|gb164|EF549583	616	616	100	globlastp
2117	LAB268	artemisia|gb164|EY032843	616	616	100	globlastp
2118	LAB268	artemisia|10v1|EY064628	616	616	100	globlastp
2119	LAB268	artemisia|10v1|EY035013	616	616	100	globlastp
2120	LAB268	artemisia|10v1|EY037977	616	616	100	globlastp
2121	LAB268	artemisia|10v1|SRR019254S0006003	616	616	100	globlastp
2122	LAB268	artemisia|gb164|EY043355	616	616	100	globlastp
2123	LAB268	artemisia|10v1|SRR019254S0020909	616	616	100	globlastp
2124	LAB268	artemisia|10v1|EY050092	616	616	100	globlastp
2125	LAB268	artemisia|gb164|EY050092	616	616	100	globlastp
2126	LAB268	artemisia|10v1|SRR019254S0044441	616	616	100	globlastp
2127	LAB268	avocado|10v1|CV459682	616	616	100	globlastp
2128	LAB268	avocado|gb164|CV459682	616	616	100	globlastp
2129	LAB268	b_juncea|gb164|EVGN0022802143299 7	6417	616	100	glotblastn
2130	LAB268	b_juncea|gb164|EVGN0027010722024 5	616	616	100	globlastp
2131	LAB268	b_juncea|gb164|EVGN0043521816073 2	616	616	100	globlastp
2132	LAB268	b_juncea|gb164|EVGN0114791398090 7	616	616	100	globlastp
2133	LAB268	b_juncea|gb164|EVGN0121062594108 8	616	616	100	globlastp
2134	LAB268	b_juncea|gb164|EVGN0130411948048 7	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2135	LAB268	b_juncea|gb164|EVGN01378815060926	616	616	100	globlastp
2136	LAB268	b_juncea|gb164|EVGN05791522303266	616	616	100	globlastp
2137	LAB268	b_juncea|gb164|EVGN06271024963259	616	616	100	globlastp
2138	LAB268	b_juncea|gb164|EVGN07020809011906	6418	616	100	glotblastn
2139	LAB268	b_oleracea|gb161|AM057682	616	616	100	globlastp
2140	LAB268	b_oleracea|gb161|AM058666	616	616	100	globlastp
2141	LAB268	b_oleracea|gb161|DY026989	616	616	100	globlastp
2142	LAB268	b_oleracea|gb161|DY027228	616	616	100	globlastp
2143	LAB268	b_oleracea|gb161|DY029054	616	616	100	globlastp
2144	LAB268	b_oleracea|gb161|DY029685	616	616	100	globlastp
2145	LAB268	b_olcracca|gb161|EE530587	616	616	100	globlastp
2146	LAB268	b_oleracea|gb161|EE534424	6419	616	100	glotblastn
2147	LAB268	b_rapa|gb162|CV432481	616	616	100	globlastp
2148	LAB268	b_rapa|gb162|CV433459	616	616	100	globlastp
2149	LAB268	b_rapa|gb162|CV544582	6420	616	100	glotblastn
2150	LAB268	b_rapa|gb162|CX269758	616	616	100	globlastp
2151	LAB268	b_rapa|gb162|CX270371	616	616	100	globlastp
2152	LAB268	b_rapa|gb162|CX270560	616	616	100	globlastp
2153	LAB268	b_rapa|gb162|DN191676	616	616	100	globlastp
2154	LAB268	b_rapa|gb162|DY009323	616	616	100	globlastp
2155	LAB268	b_rapa|gb162|EE519316	616	616	100	globlastp
2156	LAB268	banana|gb167|ES433914	616	616	100	globlastp
2157	LAB268	banana|gb167|FL651053	616	616	100	globlastp
2158	LAB268	banana|gb167|FL658965	616	616	100	globlastp
2159	LAB268	banana|gb167|FL659545	616	616	100	globlastp
2160	LAB268	barley|gb157SOLEXA|AJ434102	616	616	100	globlastp
2161	LAB268	barley|gb157SOLEXA|AJ434845	616	616	100	globlastp
2162	LAB268	barley|10v1|BE421722	616	616	100	globlastp
2163	LAB268	barley|gb157SOLEXA|AJ474132	616	616	100	globlastp
2164	LAB268	barley|gb157SOLEXA|AL503078	616	616	100	globlastp
2165	LAB268	barley|gb157SOLEXA|AL503135	616	616	100	globlastp
2166	LAB268	barley|gb157SOLEXA|AL506117	616	616	100	globlastp
2167	LAB268	barley|gb157SOLEXA|AL507050	616	616	100	globlastp
2168	LAB268	barley|gb157SOLEXA|AL508394	616	616	100	globlastp
2169	LAB268	barley|10v1|AJ434816	616	616	100	globlastp
2170	LAB268	barley|gb157SOLEXA|AL508696	616	616	100	globlastp
2171	LAB268	barley|gb157SOLEXA|AL511720	616	616	100	globlastp
2172	LAB268	barley|gb157SOLEXA|AV914119	616	616	100	globlastp
2173	LAB268	barley|gb157SOLEXA|AV916515	616	616	100	globlastp
2174	LAB268	barley|gb157SOLEXA|AW983193	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2175	LAB268	barley|gb157SOLEXA|AW983479	616	616	100	globlastp
2176	LAB268	barley|gb157SOLEXA|BE060192	616	616	100	globlastp
2177	LAB268	barley|10v1|BE060318	616	616	100	globlastp
2178	LAB268	barley|gb157SOLEXA|BE060318	616	616	100	globlastp
2179	LAB268	barley|gb157SOLEXA|BE060796	616	616	100	globlastp
2180	LAB268	barley|gb157SOLEXA|BE060939	616	616	100	globlastp
2181	LAB268	barley|10v1|AW982907	616	616	100	globlastp
2182	LAB268	barley|gb157SOLEXA|BE194743	616	616	100	globlastp
2183	LAB268	barley|gb157SOLEXA|BE196153	616	616	100	globlastp
2184	LAB268	barley|gb157SOLEXA|BE231189	616	616	100	globlastp
2185	LAB268	barley|gb157SOLEXA|BE412620	616	616	100	globlastp
2186	LAB268	barley|gb157SOLEXA|BE412942	616	616	100	globlastp
2187	LAB268	barley|gb157SOLEXA|BE413182	616	616	100	globlastp
2188	LAB268	barley|10v1|BE413201	616	616	100	globlastp
2189	LAB268	barley|gb157SOLEXA|BE413201	616	616	100	globlastp
2190	LAB268	barley|gb157SOLEXA|BE421722	616	616	100	globlastp
2191	LAB268	barley|gb157SOLEXA|BE421883	616	616	100	globlastp
2192	LAB268	barley|gb157SOLEXA|BE601752	616	616	100	globlastp
2193	LAB268	barley|10v1|BF624980	616	616	100	globlastp
2194	LAB268	barley|gb157SOLEXA|BF254330	616	616	100	globlastp
2195	LAB268	barley|10v1|BF624368	616	616	100	globlastp
2196	LAB268	barley|gb157SOLEXA|BF624368	616	616	100	globlastp
2197	LAB268	barley|gb157SOLEXA|BF624674	6421	616	100	glotblastn
2198	LAB268	barley|10v1|BG299458	616	616	100	globlastp
2199	LAB268	barley|gb157SOLEXA|BG299458	616	616	100	globlastp
2200	LAB268	barley|gb157SOLEXA|BG299823	616	616	100	globlastp
2201	LAB268	barley|gb157SOLEXA|BG342998	616	616	100	globlastp
2202	LAB268	barley|gb157SOLEXA|BG415908	616	616	100	globlastp
2203	LAB268	barley|gb157SOLEXA|BI778954	616	616	100	globlastp
2204	LAB268	barley|gb157SOLEXA|BI950815	616	616	100	globlastp
2205	LAB268	barley|gb157SOLEXA|BI958139	616	616	100	globlastp
2206	LAB268	barley|gb157SOLEXA|BM099991	616	616	100	globlastp
2207	LAB268	barley|gb157SOLEXA|BM374416	616	616	100	globlastp
2208	LAB268	barley|gb157SOLEXA|BQ459166	616	616	100	globlastp
2209	LAB268	barley|gb157SOLEXA|BQ460747	616	616	100	globlastp
2210	LAB268	barley|gb157SOLEXA|BQ470488	616	616	100	globlastp
2211	LAB268	barley|gb157SOLEXA|BQ658061	616	616	100	globlastp
2212	LAB268	barley|gb157SOLEXA|CV054877	616	616	100	globlastp
2213	LAB268	basilicum|10v1|DY329949	616	616	100	globlastp
2214	LAB268	basilicum|gb157.3|DY329949	616	616	100	globlastp
2215	LAB268	bean|gb167|CA898697	616	616	100	globlastp
2216	LAB268	bean|gb167|CA898701	616	616	100	globlastp
2217	LAB268	bean|gb167|CA898715	616	616	100	globlastp
2218	LAB268	bean|gb167|CA898716	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2219	LAB268	bean|gb167|CA898718	616	616	100	globlastp
2220	LAB268	bean|gb167|CA898722	616	616	100	globlastp
2221	LAB268	bean|gb167|CA908438	616	616	100	globlastp
2222	LAB268	bean|gb167|CA908452	616	616	100	globlastp
2223	LAB268	bean|gb167|CA908482	616	616	100	globlastp
2224	LAB268	bean|gb167|CV532208	616	616	100	globlastp
2225	LAB268	bean|gb167|CV539314	616	616	100	globlastp
2226	LAB268	bean|gb167|CV539770	616	616	100	globlastp
2227	LAB268	bean|gb167|FD785198	616	616	100	globlastp
2228	LAB268	brachypodium|09v1|DV488531	616	616	100	globlastp
2229	LAB268	brachypodium|gb169|AL829713	616	616	100	globlastp
2230	LAB268	brachypodium|09v1|SRR031796S0015969	616	616	100	globlastp
2231	LAB268	brachypodium|gb169|BE398313	616	616	100	globlastp
2232	LAB268	brachypodium|09v1|GT777837	616	616	100	globlastp
2233	LAB268	brachypodium|gb169|BE399369	616	616	100	globlastp
2234	LAB268	brachypodium|09v1|DV469193	616	616	100	globlastp
2235	LAB268	brachypodium|gb169|BE399555	616	616	100	globlastp
2236	LAB268	brachypodium|09v1|DV470129	616	616	100	globlastp
2237	LAB268	brachypodium|gb169|BE399592	616	616	100	globlastp
2238	LAB268	brachypodium|09v1|DV477960	616	616	100	globlastp
2239	LAB268	brachypodium|gb169|BE400757	616	616	100	globlastp
2240	LAB268	brachypodium|09v1|GT763632	616	616	100	globlastp
2241	LAB268	brachypodium|gb169|BE403687	616	616	100	globlastp
2242	LAB268	brachypodium|09v1|DV471468	616	616	100	globlastp
2243	LAB268	brachypodium|gb169|BE413182	616	616	100	globlastp
2244	LAB268	brachypodium|09v1|GT767460	616	616	100	globlastp
2245	LAB268	brachypodium|gb169|BE415858	616	616	100	globlastp
2246	LAB268	brachypodium|09v1|BRADI4G30960	616	616	100	globlastp
2247	LAB268	brachypodium|gb169|BE417523	616	616	100	globlastp
2248	LAB268	brachypodium|09v1|SRR031795S0025245	616	616	100	globlastp
2249	LAB268	brachypodium|gb169|BM377866	616	616	100	globlastp
2250	LAB268	brachypodium|09v1|GT814284	616	616	100	globlastp
2251	LAB268	brachypodium|gb169|CA032073	616	616	100	globlastp
2252	LAB268	bruguiera|gb166|BP945440	616	616	100	globlastp
2253	LAB268	cacao|gb167|CA794917	616	616	100	globlastp
2254	LAB268	cacao|gb167|CA796173	616	616	100	globlastp
2255	LAB268	cacao|gb167|CU471543	616	616	100	globlastp
2256	LAB268	cacao|gb167|CU471645	616	616	100	globlastp
2257	LAB268	cacao|gb167|CU471805	616	616	100	globlastp
2258	LAB268	cacao|gb167|CU472042	616	616	100	globlastp
2259	LAB268	cacao|gb167|CU475022	616	616	100	globlastp
2260	LAB268	canola|10v1|CD811780	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2261	LAB268	canola|gb161|CD811780	616	616	100	globlastp
2262	LAB268	canola|10v1|CD844108	616	616	100	globlastp
2263	LAB268	canola|gb161|CD812149	616	616	100	globlastp
2264	LAB268	canola|10v1|CD812235	616	616	100	globlastp
2265	LAB268	canola|10v1|CD812364	616	616	100	globlastp
2266	LAB268	canola|10v1|CD817281	616	616	100	globlastp
2267	LAB268	canola|gb161|CD817281	616	616	100	globlastp
2268	LAB268	canola|gb161|CD818240	616	616	100	globlastp
2269	LAB268	canola|gb161|CD819612	616	616	100	globlastp
2270	LAB268	canola|10v1|CD820828	616	616	100	globlastp
2271	LAB268	canola|gb161|CD820828	616	616	100	globlastp
2272	LAB268	canola|10v1|CD822433	616	616	100	globlastp
2273	LAB268	canola|gb161|CD822433	616	616	100	globlastp
2274	LAB268	canola|gb161|CD822786	6422	616	100	glotblastn
2275	LAB268	canola|10v1|CD824033	616	616	100	globlastp
2276	LAB268	canola|gb161|CD824033	616	616	100	globlastp
2277	LAB268	canola|10v1|CD837998	616	616	100	globlastp
2278	LAB268	canola|gb161|CD837998	616	616	100	globlastp
2279	LAB268	canola|10v1|CD839108	616	616	100	globlastp
2280	LAB268	canola|gb161|CD839108	616	616	100	globlastp
2281	LAB268	canola|10v1|CD842271	616	616	100	globlastp
2282	LAB268	canola|gb161|CD842271	6423	616	100	glotblastn
2283	LAB268	canola|10v1|CN730085	616	616	100	globlastp
2284	LAB268	canola|gb161|CN730085	616	616	100	globlastp
2285	LAB268	canola|10v1|CN730459	616	616	100	globlastp
2286	LAB268	canola|10v1|CN730487	616	616	100	globlastp
2287	LAB268	canola|gb161|CN735734	616	616	100	globlastp
2288	LAB268	canola|gb161|CN736543	616	616	100	globlastp
2289	LAB268	canola|gb161|CN737593	616	616	100	globlastp
2290	LAB268	canola|gb161|CX187745	616	616	100	globlastp
2291	LAB268	canola|10v1|CX195068	616	616	100	globlastp
2292	LAB268	canola|gb161|CX195068	616	616	100	globlastp
2293	LAB268	canola|gb161|EE474117	6424	616	100	glotblastn
2294	LAB268	canola|10v1|EE477324	616	616	100	globlastp
2295	LAB268	canola|gb161|EE477324	616	616	100	globlastp
2296	LAB268	canola|10v1|CD819612	616	616	100	globlastp
2297	LAB268	canola|10v1|CN735734	616	616	100	globlastp
2298	LAB268	canola|gb161|EL592798	616	616	100	globlastp
2299	LAB268	canola|gb161|EV162827	616	616	100	globlastp
2300	LAB268	cassava|09v1|BM259658	616	616	100	globlastp
2301	LAB268	cassava|gb164|BM259658	616	616	100	globlastp
2302	LAB268	cassava|09v1|BM259754	616	616	100	globlastp
2303	LAB268	cassava|09v1|BM260241	616	616	100	globlastp
2304	LAB268	cassava|09v1|BM260294	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2305	LAB268	cassava|gb164|BM260294	616	616	100	globlastp
2306	LAB268	cassava|09v1|CK645687	616	616	100	globlastp
2307	LAB268	cassava|gb164|CK645687	616	616	100	globlastp
2308	LAB268	cassava|09v1|CK650665	616	616	100	globlastp
2309	LAB268	cassava|gb164|CK650665	6425	616	100	glotblastn
2310	LAB268	cassava|09v1|BM260125	616	616	100	globlastp
2311	LAB268	castorbean|09v1|EE257352	616	616	100	globlastp
2312	LAB268	castorbean|gb160|EE257352	616	616	100	globlastp
2313	LAB268	castorbean|09v1|XM002531608	616	616	100	globlastp
2314	LAB268	castorbean|gb160|MDL29582M000246	616	616	100	globlastp
2315	LAB268	castorbean|09v1|XM002531610	616	616	100	globlastp
2316	LAB268	castorbean|gb160|MDL29582M000248	616	616	100	globlastp
2317	LAB268	castorbean|09v1|XM002532762	616	616	100	globlastp
2318	LAB268	castorbean|gb160|MDL30039M000231	616	616	100	globlastp
2319	LAB268	castorbean|09v1|XM002518894	616	616	100	globlastp
2320	LAB268	castorbean|gb160|MDL30068M002607	616	616	100	globlastp
2321	LAB268	castorbean|09v1|T15087	616	616	100	globlastp
2322	LAB268	castorbean|gb160|T15087	616	616	100	globlastp
2323	LAB268	catharanthus|gb166|EG556351	616	616	100	globlastp
2324	LAB268	catharanthus|gb166|FD415203	616	616	100	globlastp
2325	LAB268	cenchrus|gb166|BM084286	616	616	100	globlastp
2326	LAB268	cenchrus|gb166|EB652615	616	616	100	globlastp
2327	LAB268	cenchrus|gb166|EB653521	616	616	100	globlastp
2328	LAB268	cenchrus|gb166|EB654271	616	616	100	globlastp
2329	LAB268	centaurea|gb166|EH741190	616	616	100	globlastp
2330	LAB268	centaurea|gb166|EH760516	616	616	100	globlastp
2331	LAB268	chestnut|gb170|SRR006295S0000023	616	616	100	globlastp
2332	LAB268	chestnut|gb170|SRR006295S0014296	616	616	100	globlastp
2333	LAB268	chestnut|gb170|SRR006295S0026768	616	616	100	globlastp
2334	LAB268	chestnut|gb170|SRR006295S0027790	616	616	100	globlastp
2335	LAB268	chestnut|gb170|SRR006295S0092156	616	616	100	globlastp
2336	LAB268	cichorium|gb171|EH700759	616	616	100	globlastp
2337	LAB268	cichorium|gb171|EH701323	616	616	100	globlastp
2338	LAB268	cichorium|gb171|EH702007	616	616	100	globlastp
2339	LAB268	cichorium|gb171|EH705029	616	616	100	globlastp
2340	LAB268	cichorium|gb171|EL365514	616	616	100	globlastp
2341	LAB268	citrus|gb166|BQ623154	616	616	100	globlastp
2342	LAB268	citrus|gb166|BQ623438	616	616	100	globlastp
2343	LAB268	citrus|gb166|CB611039	616	616	100	globlastp
2344	LAB268	citrus|gb166|CF417550	616	616	100	globlastp
2345	LAB268	clover|gb162|BB915510	616	616	100	globlastp
2346	LAB268	coffea|10v1|DV673331	616	616	100	globlastp
2347	LAB268	coffea|gb157.2|BQ448811	616	616	100	globlastp
2348	LAB268	coffea|10v1|DV664293	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2349	LAB268	coffca|gb157.2|DV664293	616	616	100	globlastp
2350	LAB268	coffca|10v1|DV675511	616	616	100	globlastp
2351	LAB268	coffea|gb157.2|DV675511	616	616	100	globlastp
2352	LAB268	coffea|10v1|EE193937	616	616	100	globlastp
2353	LAB268	coffea|gb157.2|EE193937	616	616	100	globlastp
2354	LAB268	cotton|gb164|AW187455	616	616	100	globlastp
2355	LAB268	cotton|gb164|BE052251	6426	616	100	glotblastn
2356	LAB268	cotton|gb164|BE052729	616	616	100	globlastp
2357	LAB268	cotton|gb164|BE054464	616	616	100	globlastp
2358	LAB268	cotton|gb164|BF271762	616	616	100	globlastp
2359	LAB268	cotton|gb164|BF272645	616	616	100	globlastp
2360	LAB268	cotton|gb164|BG441560	616	616	100	globlastp
2361	LAB268	cotton|gb164|BG444562	616	616	100	globlastp
2362	LAB268	cotton|gb164|DR462256	616	616	100	globlastp
2363	LAB268	cowpea|gb166|FC456858	616	616	100	globlastp
2364	LAB268	cowpea|gb166|FC457669	616	616	100	globlastp
2365	LAB268	cowpea|gb166|FC459715	6427	616	100	glotblastn
2366	LAB268	cowpea|gb166|FC461880	616	616	100	globlastp
2367	LAB268	cowpea|gb166|FF382232	616	616	100	globlastp
2368	LAB268	cowpea|gb166|FF383299	616	616	100	globlastp
2369	LAB268	cowpea|gb166|FF385079	616	616	100	globlastp
2370	LAB268	cowpea|gb166|FG810633	616	616	100	globlastp
2371	LAB268	cryptomeria|gb166|BP175287	616	616	100	globlastp
2372	LAB268	cryptomeria|gb166|BW994999	616	616	100	globlastp
2373	LAB268	cryptomeria|gb166|BW995093	616	616	100	globlastp
2374	LAB268	cycas|gb166|CB089451	616	616	100	globlastp
2375	LAB268	cycas|gb166|CB090291	616	616	100	globlastp
2376	LAB268	cycas|gb166|CB090429	616	616	100	globlastp
2377	LAB268	cycas|gb166|CB090486	616	616	100	globlastp
2378	LAB268	cycas|gb166|CB090617	616	616	100	globlastp
2379	LAB268	cynara|gb167|GE590379	616	616	100	globlastp
2380	LAB268	cynara|gb167|GE592628	616	616	100	globlastp
2381	LAB268	cynara|gb167|GE600719	616	616	100	globlastp
2382	LAB268	dandelion|gb161|DY811410	616	616	100	globlastp
2383	LAB268	dandelion|gb161|DY834572	616	616	100	globlastp
2384	LAB268	dandelion|gb161|DY834792	616	616	100	globlastp
2385	LAB268	dandelion|gb161|DY835769	616	616	100	globlastp
2386	LAB268	dandelion|gb161|DY837571	616	616	100	globlastp
2387	LAB268	dandelion|gb161|DY838255	616	616	100	globlastp
2388	LAB268	dandelion|gb161|DY839212	616	616	100	globlastp
2389	LAB268	eucalyptus|gb166|AJ627789	616	616	100	globlastp
2390	LAB268	eucalyptus|gb166|AY263810	616	616	100	globlastp
2391	LAB268	eucalyptus|gb166|CD668212	616	616	100	globlastp
2392	LAB268	fern|gb171|DK946600	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2393	LAB268	fern|gb171|DK953182	616	616	100	globlastp
2394	LAB268	fescue|gb161|DT687120	616	616	100	globlastp
2395	LAB268	ginger|gb164|DY353177	6428	616	100	glotblastn
2396	LAB268	ginger|gb164|DY356818	616	616	100	globlastp
2397	LAB268	ginger|gb164|DY358348	616	616	100	globlastp
2398	LAB268	grape|gb160|BQ792545	616	616	100	globlastp
2399	LAB268	grape|gb160|CB915320	616	616	100	globlastp
2400	LAB268	grape|gb160|CB918446	616	616	100	globlastp
2401	LAB268	grape|gb160|CB972888	616	616	100	globlastp
2402	LAB268	grape|gb160|CF215612	616	616	100	globlastp
2403	LAB268	iceplant|gb164|BE034500	616	616	100	globlastp
2404	LAB268	iceplant|gb164|BE035965	616	616	100	globlastp
2405	LAB268	ipomoea|gb157.2|BJ553415	6429	616	100	glotblastn
2406	LAB268	ipomoea|gb157.2|BJ553690	616	616	100	globlastp
2407	LAB268	ipomoea|gb157.2|BJ555300	616	616	100	globlastp
2408	LAB268	ipomoea|gb157.2|BJ556362	616	616	100	globlastp
2409	LAB268	ipomoea|gb157.2|BJ556445	616	616	100	globlastp
2410	LAB268	ipomoea|gb157.2|BJ558611	616	616	100	globlastp
2411	LAB268	ipomoea|gb157.2|BJ560747	616	616	100	globlastp
2412	LAB268	ipomoea|gb157.2|EE875704	6430	616	100	glotblastn
2413	LAB268	kiwi|gb166|FG404766	616	616	100	globlastp
2414	LAB268	kiwi|gb166|FG410628	616	616	100	globlastp
2415	LAB268	kiwi|gb166|FG411099	616	616	100	globlastp
2416	LAB268	kiwi|gb166|FG434602	616	616	100	globlastp
2417	LAB268	kiwi|gb166|FG467826	6431	616	100	glotblastn
2418	LAB268	kiwi|gb166|FG487075	616	616	100	globlastp
2419	LAB268	kiwi|gb166|FG487173	616	616	100	globlastp
2420	LAB268	kiwi|gb166|FG487653	616	616	100	globlastp
2421	LAB268	kiwi|gb166|FG490714	616	616	100	globlastp
2422	LAB268	lettuce|10v1|DW044689	616	616	100	globlastp
2423	LAB268	lettuce|gb157.2|DW044689	616	616	100	globlastp
2424	LAB268	lettuce|gb157.2|DW046019	616	616	100	globlastp
2425	LAB268	lettuce|gb157.2|DW046403	616	616	100	globlastp
2426	LAB268	lettuce|10v1|DW047728	616	616	100	globlastp
2427	LAB268	lettuce|gb157.2|DW047742	616	616	100	globlastp
2428	LAB268	lettuce|10v1|DW048625	616	616	100	globlastp
2428	LAB268	lettuce|gb157.2|DW048625	7030	616	83.7	globlastp
2429	LAB268	lettuce|10v1|DW049814	616	616	100	globlastp
2430	LAB268	lettuce|gb157.2|DW052505	616	616	100	globlastp
2431	LAB268	lettuce|gb157.2|DW054176	616	616	100	globlastp
2432	LAB268	lettuce|10v1|DW054329	616	616	100	globlastp
2433	LAB268	lettuce|gb157.2|DW057506	616	616	100	globlastp
2434	LAB268	lettuce|gb157.2|DW058399	616	616	100	globlastp
2435	LAB268	lettuce|10v1|DW059381	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2436	LAB268	lcttucc|10v1|DW060992	616	616	100	globlastp
2437	LAB268	lcttucc|gb157.2|DW060992	616	616	100	globlastp
2438	LAB268	lettuce|gb157.2|DW073761	616	616	100	globlastp
2439	LAB268	lettuce|10v1|DW075486	616	616	100	globlastp
2440	LAB268	lettuce|gb157.2|DW075886	616	616	100	globlastp
2441	LAB268	lettuce|gb157.2|DW076059	616	616	100	globlastp
2442	LAB268	lettuce|10v1|DW080660	616	616	100	globlastp
2443	LAB268	lettuce|gb157.2|DW080660	616	616	100	globlastp
2444	LAB268	lettuce|10v1|DW082101	616	616	100	globlastp
2445	LAB268	lettuce|gb157.2|DW082101	616	616	100	globlastp
2446	LAB268	lettuce|10v1|DW083055	616	616	100	globlastp
2447	LAB268	lettuce|gb157.2|DW083055	616	616	100	globlastp
2448	LAB268	lettuce|gb157.2|DW104254	616	616	100	globlastp
2449	LAB268	lettuce|10v1|DW104257	616	616	100	globlastp
2450	LAB268	lettuce|gb157.2|DW105285	616	616	100	globlastp
2451	LAB268	lettuce|10v1|DW105457	616	616	100	globlastp
2452	LAB268	lettuce|10v1|DW054334	616	616	100	globlastp
2453	LAB268	lettuce|gb157.2|DW107742	616	616	100	globlastp
2454	LAB268	lettuce|gb157.2|DW111256	616	616	100	globlastp
2455	LAB268	lettuce|gb157.2|DW122037	616	616	100	globlastp
2456	LAB268	lettuce|10v1|DW122298	616	616	100	globlastp
2457	LAB268	lettuce|gb157.2|DW122298	616	616	100	globlastp
2458	LAB268	lettuce|gb157.2|DW122562	616	616	100	globlastp
2459	LAB268	lettuce|gb157.2|DW122564	616	616	100	globlastp
2460	LAB268	lettuce|10v1|DW123180	616	616	100	globlastp
2461	LAB268	lettuce|gb157.2|DW146313	616	616	100	globlastp
2462	LAB268	lettuce|10v1|DW147673	616	616	100	globlastp
2463	LAB268	lettuce|gb157.2|DW149190	616	616	100	globlastp
2464	LAB268	lettuce|10v1|DW159071	616	616	100	globlastp
2465	LAB268	lettuce|gb157.2|DW159071	616	616	100	globlastp
2466	LAB268	leymus|gb166|EG386168	616	616	100	globlastp
2467	LAB268	liquorice|gb171|FS238682	616	616	100	globlastp
2468	LAB268	liquorice|gb171|FS240232	616	616	100	globlastp
2469	LAB268	liquorice|gb171|FS248125	616	616	100	globlastp
2470	LAB268	liquorice|gb171|FS252094	616	616	100	globlastp
2471	LAB268	liriodendron|gb166|CK753794	616	616	100	globlastp
2472	LAB268	liriodendron|gb166|FD489954	616	616	100	globlastp
2473	LAB268	lotus|09v1|AW163944	616	616	100	globlastp
2474	LAB268	lotus|09v1|AW719271	616	616	100	globlastp
2475	LAB268	lotus|gb157.2|AW719271	616	616	100	globlastp
2476	LAB268	lotus|09v1|BW597052	616	616	100	globlastp
2477	LAB268	lotus|09v1|CB828182	616	616	100	globlastp
2478	LAB268	lovegrass|gb167|EH188910	616	616	100	globlastp
2479	LAB268	lovegrass|gb167|EH191855	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2480	LAB268	lovegrass|gb167|EH194037	616	616	100	globlastp
2481	LAB268	maize|gb170|AA054815	616	616	100	globlastp
2482	LAB268	maize|gb170|AI372169	616	616	100	globlastp
2483	LAB268	maize|gb170|AI391767	616	616	100	globlastp
2484	LAB268	maize|gb170|AI391810	616	616	100	globlastp
2485	LAB268	maize|gb170|AI395923	616	616	100	globlastp
2486	LAB268	maize|gb170|AI395924	616	616	100	globlastp
2487	LAB268	maize|gb170|AI586817	616	616	100	globlastp
2488	LAB268	maize|gb170|AI586897	616	616	100	globlastp
2489	LAB268	maize|gb170|AI600290	616	616	100	globlastp
2490	LAB268	maize|gb170|AI600370	616	616	100	globlastp
2491	LAB268	maize|gb170|AI665063	616	616	100	globlastp
2492	LAB268	maize|gb170|AI737770	616	616	100	globlastp
2493	LAB268	maize|gb170|AW055622	616	616	100	globlastp
2494	LAB268	maize|gb170|CO452276	616	616	100	globlastp
2495	LAB268	maize|gb170|LLAI987314	616	616	100	globlastp
2496	LAB268	maize|gb170|LLBE639905	616	616	100	globlastp
2497	LAB268	maize|gb170|LLDQ244862	616	616	100	globlastp
2498	LAB268	maize|gb170|LLDQ245092	616	616	100	globlastp
2499	LAB268	maize|gb170|LLDQ245956	616	616	100	globlastp
2500	LAB268	maize|gb170|LLFL026515	616	616	100	globlastp
2501	LAB268	maize|gb170|LLFL123174	616	616	100	globlastp
2502	LAB268	maize|gb170|T70634	616	616	100	globlastp
2503	LAB268	maize|gb170|W59839	616	616	100	globlastp
2504	LAB268	medicago|09v1|AA660565	616	616	100	globlastp
2505	LAB268	medicago|gb157.2|AA660565	616	616	100	globlastp
2506	LAB268	medicago|09v1|AJ389014	616	616	100	globlastp
2507	LAB268	medicago|gb157.2|AJ389014	6432	616	100	glotblastn
2508	LAB268	medicago|09v1|LLAJ498325	616	616	100	globlastp
2509	LAB268	medicago|09v1|LLAL366664	616	616	100	globlastp
2510	LAB268	medicago|09v1|AL371855	616	616	100	globlastp
2511	LAB268	medicago|gb157.2|AL371855	616	616	100	globlastp
2512	LAB268	medicago|gb157.2|AL374021	616	616	100	globlastp
2513	LAB268	medicago|09v1|AL378431	616	616	100	globlastp
2514	LAB268	medicago|09v1|AL379622	616	616	100	globlastp
2515	LAB268	medicago|09v1|AL374021	616	616	100	globlastp
2516	LAB268	medicago|gb157.2|AL380165	6433	616	100	glotblastn
2517	LAB268	medicago|09v1|AW208199	616	616	100	globlastp
2518	LAB268	medicago|gb157.2|AW208199	616	616	100	globlastp
2519	LAB268	melon|gb165|DV633267	616	616	100	globlastp
2520	LAB268	melon|gb165|EB715433	6434	616	100	glotblastn
2521	LAB268	nicotiana_benthamiana|gb162|CN743227	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2522	LAB268	nicotiana_benthamiana|gb162|CN743475	616	616	100	globlastp
2523	LAB268	nicotiana_benthamiana|gb162|ES887469	616	616	100	globlastp
2524	LAB268	nuphar|gb166|CD473517	616	616	100	globlastp
2525	LAB268	nuphar|gb166|CD474514	616	616	100	globlastp
2526	LAB268	nuphar|gb166|CD475677	616	616	100	globlastp
2527	LAB268	nuphar|gb166|CK745661	616	616	100	globlastp
2528	LAB268	nuphar|gb166|CK767296	616	616	100	globlastp
2529	LAB268	oak|gb170|CR627506	616	616	100	globlastp
2530	LAB268	oak|gb170|DB997093	616	616	100	globlastp
2531	LAB268	oak|gb170|SRR006307S0007341	616	616	100	globlastp
2532	LAB268	oak|gb170|SRR006307S0010902	616	616	100	globlastp
2533	LAB268	oil_palm|gb166|DQ400915	616	616	100	globlastp
2534	LAB268	oil_palm|gb166|EL681105	616	616	100	globlastp
2535	LAB268	oil_palm|gb166|EL681189	616	616	100	globlastp
2536	LAB268	oil_palm|gb166|EL682446	616	616	100	globlastp
2537	LAB268	oil_palm|gb166|EL683758	616	616	100	globlastp
2538	LAB268	oil_palm|gb166|EL691023	6435	616	100	glotblastn
2539	LAB268	onion|gb162|CF444612	616	616	100	globlastp
2540	LAB268	papaya|gb165|EX276160	616	616	100	globlastp
2541	LAB268	papaya|gb165|EX278412	6436	616	100	glotblastn
2542	LAB268	papaya|gb165|EX283624	616	616	100	globlastp
2543	LAB268	peanut|gb171|CD037531	616	616	100	globlastp
2544	LAB268	peanut|gb171|CD038462	616	616	100	globlastp
2545	LAB268	peanut|gb171|EE124369	616	616	100	globlastp
2546	LAB268	peanut|gb171|EE124731	616	616	100	globlastp
2547	LAB268	peanut|gb171|EE125784	616	616	100	globlastp
2548	LAB268	peanut|gb171|EE126870	616	616	100	globlastp
2549	LAB268	peanut|gb171|EG373202	616	616	100	globlastp
2550	LAB268	peanut|gb171|EH044313	616	616	100	globlastp
2551	LAB268	pepper|gb171|BM066225	616	616	100	globlastp
2552	LAB268	petunia|gb171|DC241756	616	616	100	globlastp
2553	LAB268	pine|10v1|AW043330	616	616	100	globlastp
2554	LAB268	pine|gb157.2|AW043330	6437	616	100	glotblastn
2555	LAB268	pine|10v1|AW754808	616	616	100	globlastp
2556	LAB268	pine|gb157.2|AW754808	616	616	100	globlastp
2557	LAB268	pine|10v1|BX249832	616	616	100	globlastp
2558	LAB268	pine|gb157.2|BX249832	616	616	100	globlastp
2559	LAB268	pine|10v1|BX254626	616	616	100	globlastp
2560	LAB268	pine|gb157.2|BX254626	616	616	100	globlastp
2561	LAB268	poplar|10v1|AI166092	616	616	100	globlastp
2562	LAB268	poplar|gb170|AI166092	616	616	100	globlastp
2563	LAB268	poplar|10v1|BI071500	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2564	LAB268	poplar|gb170|BI071500	616	616	100	globlastp
2565	LAB268	poplar|10v1|BI119617	616	616	100	globlastp
2566	LAB268	poplar|gb170|BI119617	616	616	100	globlastp
2567	LAB268	poplar|gb170|BI119694	616	616	100	globlastp
2568	LAB268	poplar|10v1|BI121111	616	616	100	globlastp
2569	LAB268	poplar|gb170|BI121111	616	616	100	globlastp
2570	LAB268	poplar|gb170|BU819667	616	616	100	globlastp
2571	LAB268	poplar|10v1|BU819908	616	616	100	globlastp
2572	LAB268	poplar|gb170|BU825016	616	616	100	globlastp
2573	LAB268	poplar|gb170|BU825437	616	616	100	globlastp
2574	LAB268	poplar|10v1|BU829589	616	616	100	globlastp
2575	LAB268	poplar|gb170|BU829589	616	616	100	globlastp
2576	LAB268	poplar|10v1|BU831961	616	616	100	globlastp
2577	LAB268	poplar|gb170|BU831961	616	616	100	globlastp
2578	LAB268	poppy|gb166|FE967969	616	616	100	globlastp
2579	LAB268	poppy|gb166|FG609652	616	616	100	globlastp
2580	LAB268	potato|gb157.2|BM407657	616	616	100	globlastp
2581	LAB268	prunus|gb167|AJ873312	616	616	100	globlastp
2582	LAB268	prunus|gb167|FC865249	616	616	100	globlastp
2583	LAB268	pseudoroegneria|gb167|FF346105	616	616	100	globlastp
2584	LAB268	pseudoroegneria|gb167|FF365552	616	616	100	globlastp
2585	LAB268	pseudoroegneria|gb167|FF365632	616	616	100	globlastp
2586	LAB268	radish|gb164|EV524552	616	616	100	globlastp
2587	LAB268	radish|gb164|EV525864	616	616	100	globlastp
2588	LAB268	radish|gb164|EV529106	616	616	100	globlastp
2589	LAB268	radish|gb164|EW714954	616	616	100	globlastp
2590	LAB268	radish|gb164|EW722342	616	616	100	globlastp
2591	LAB268	radish|gb164|EW725439	6438	616	100	glotblastn
2592	LAB268	radish|gb164|EX764592	616	616	100	globlastp
2593	LAB268	radish|gb164|EX888362	616	616	100	globlastp
2594	LAB268	radish|gb164|EX895689	616	616	100	globlastp
2595	LAB268	radish|gb164|EX902730	616	616	100	globlastp
2596	LAB268	radish|gb164|EY909354	616	616	100	globlastp
2597	LAB268	rice|gb170|OS01G61920	616	616	100	globlastp
2598	LAB268	rice|gb170|OS02G45940	616	616	100	globlastp
2599	LAB268	rice|gb170|OS03G02780	616	616	100	globlastp
2600	LAB268	rice|gb170|OS05G38740	616	616	100	globlastp
2601	LAB268	rice|gb170|OS05G39050	616	616	100	globlastp
2602	LAB268	rice|gb170|OS07G36500	616	616	100	globlastp
2603	LAB268	rice|gb170|OS09G38020	616	616	100	globlastp
2604	LAB268	rice|gb170|OS10G39410	616	616	100	globlastp
2605	LAB268	rose|gb157.2|BI977531	616	616	100	globlastp
2606	LAB268	rose|10v1|BI978035	616	616	100	globlastp
2607	LAB268	rose|gb157.2|BI978035	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2608	LAB268	ryc|gb164|BE495291	616	616	100	globlastp
2609	LAB268	ryc|gb164|BE704952	616	616	100	globlastp
2610	LAB268	rye|gb164|CD453256	6439	616	100	glotblastn
2611	LAB268	senecio|gb170|DY658928	616	616	100	globlastp
2612	LAB268	senecio|gb170|DY659560	616	616	100	globlastp
2613	LAB268	senecio|gb170|DY662328	616	616	100	globlastp
2614	LAB268	senecio|gb170|DY662897	616	616	100	globlastp
2615	LAB268	senecio|gb170|SRR006592S0002545	616	616	100	globlastp
2616	LAB268	sesame|gb157.2|BU668605	616	616	100	globlastp
2617	LAB268	soybean|gb168|AW163944	616	616	100	globlastp
2618	LAB268	soybean|gb168|AW348393	616	616	100	globlastp
2619	LAB268	soybean|gb168|AW574238	616	616	100	globlastp
2620	LAB268	soybean|gb168|AW719271	616	616	100	globlastp
2621	LAB268	soybean|gb168|BE660076	616	616	100	globlastp
2622	LAB268	soybean|gb168|BE660077	616	616	100	globlastp
2623	LAB268	soybean|gb168|BE660078	616	616	100	globlastp
2624	LAB268	soybean|gb168|BM140223	616	616	100	globlastp
2625	LAB268	soybean|gb168|BQ152712	616	616	100	globlastp
2626	LAB268	soybean|gb168|BU548084	616	616	100	globlastp
2627	LAB268	soybean|gb168|CA898697	616	616	100	globlastp
2628	LAB268	soybean|gb168|CA908437	616	616	100	globlastp
2629	LAB268	soybean|gb168|CA908482	616	616	100	globlastp
2630	LAB268	soybean|gb168|CD393765	6440	616	100	glotblastn
2631	LAB268	soybean|gb168|CD418622	616	616	100	globlastp
2632	LAB268	soybean|gb168|CF921561	616	616	100	globlastp
2633	LAB268	spruce|gb162|CO217448	616	616	100	globlastp
2634	LAB268	spruce|gb162|CO222157	616	616	100	globlastp
2635	LAB268	spruce|gb162|CO228093	616	616	100	globlastp
2636	LAB268	spruce|gb162|CO229500	6441	616	100	glotblastn
2637	LAB268	spruce|gb162|ES253514	616	616	100	globlastp
2638	LAB268	spurge|gb161|DV112721	616	616	100	globlastp
2639	LAB268	spurge|gb161|DV113563	616	616	100	globlastp
2640	LAB268	strawberry|gb164|DV439019	616	616	100	globlastp
2641	LAB268	strawberry|gb164|EX657115	616	616	100	globlastp
2642	LAB268	strawberry|gb164|EX665332	616	616	100	globlastp
2643	LAB268	sugarcane|gb157.3|BQ530407	616	616	100	globlastp
2644	LAB268	sugarcane|gb157.3|BQ531627	616	616	100	globlastp
2645	LAB268	sugarcane|gb157.3|BQ533111	616	616	100	globlastp
2646	LAB268	sugarcane|gb157.3|BQ535723	616	616	100	globlastp
2647	LAB268	sugarcane|gb157.3|CA067964	616	616	100	globlastp
2648	LAB268	sugarcane|gb157.3|CA070996	616	616	100	globlastp
2649	LAB268	sugarcane|gb157.3|CA071679	616	616	100	globlastp
2650	LAB268	sugarcane|gb157.3|CA071683	616	616	100	globlastp
2651	LAB268	sugarcane|gb157.3|CA072002	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2652	LAB268	sugarcane|gb157.3|CA072206	616	616	100	globlastp
2653	LAB268	sugarcane|gb157.3|CA072927	616	616	100	globlastp
2654	LAB268	sugarcane|gb157.3|CA073794	616	616	100	globlastp
2655	LAB268	sugarcane|gb157.3|CA077203	616	616	100	globlastp
2656	LAB268	sugarcane|gb157.3|CA078899	616	616	100	globlastp
2657	LAB268	sugarcane|gb157.3|CA080676	616	616	100	globlastp
2658	LAB268	sugarcane|gb157.3|CA081168	616	616	100	globlastp
2659	LAB268	sugarcane|gb157.3|CA082484	616	616	100	globlastp
2660	LAB268	sugarcane|gb157.3|CA087335	616	616	100	globlastp
2661	LAB268	sugarcane|gb157.3|CA103542	616	616	100	globlastp
2662	LAB268	sugarcane|gb157.3|CA112851	616	616	100	globlastp
2663	LAB268	sugarcane|gb157.3|CA115229	616	616	100	globlastp
2664	LAB268	sugarcane|gb157.3|CA116498	616	616	100	globlastp
2665	LAB268	sugarcane|gb157.3|CA118584	616	616	100	globlastp
2666	LAB268	sugarcane|gb157.3|CA136886	616	616	100	globlastp
2667	LAB268	sugarcane|gb157.3|CA138849	616	616	100	globlastp
2668	LAB268	sugarcane|10v1|CA072927	616	616	100	globlastp
2669	LAB268	sugarcane|gb157.3|CA200867	616	616	100	globlastp
2670	LAB268	sugarcane|gb157.3|CA201018	616	616	100	globlastp
2671	LAB268	sugarcane|gb157.3|CA201422	616	616	100	globlastp
2672	LAB268	sugarcane|gb157.3|CA229803	616	616	100	globlastp
2673	LAB268	sugarcane|10v1|BQ531627	616	616	100	globlastp
2674	LAB268	sugarcane|gb157.3|CA230627	616	616	100	globlastp
2675	LAB268	sugarcane|gb157.3|CA236648	616	616	100	globlastp
2676	LAB268	sugarcane|10v1|CA067964	616	616	100	globlastp
2677	LAB268	sunflower|gb162|CD848675	616	616	100	globlastp
2678	LAB268	sunflower|gb162|CD848813	616	616	100	globlastp
2679	LAB268	sunflower|gb162|CD848833	616	616	100	globlastp
2680	LAB268	sunflower|gb162|CD850963	616	616	100	globlastp
2681	LAB268	sunflower|gb162|CD850965	616	616	100	globlastp
2682	LAB268	sunflower|gb162|CD851153	616	616	100	globlastp
2683	LAB268	sunflower|gb162|CD852601	616	616	100	globlastp
2684	LAB268	sunflower|gb162|CD854963	6442	616	100	glotblastn
2685	LAB268	sunflower|gb162|DY917401	6443	616	100	glotblastn
2686	LAB268	sunflower|gb162|DY930625	616	616	100	globlastp
2687	LAB268	sunflower|gb162|DY946300	616	616	100	globlastp
2688	LAB268	sunflower|gb162|DY954323	616	616	100	globlastp
2689	LAB268	sunflower|gb162|EL511221	616	616	100	globlastp
2690	LAB268	switchgrass|gb167|DN141043	616	616	100	globlastp
2691	LAB268	switchgrass|gb167|DN141570	616	616	100	globlastp
2692	LAB268	switchgrass|gb167|DN142502	616	616	100	globlastp
2693	LAB268	switchgrass|gb167|DN143038	616	616	100	globlastp
2694	LAB268	switchgrass|gb167|DN143717	616	616	100	globlastp
2695	LAB268	switchgrass|gb167|DN143995	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2696	LAB268	switchgrass|gb167|DN145911	616	616	100	globlastp
2697	LAB268	switchgrass|gb167|DN146220	616	616	100	globlastp
2698	LAB268	switchgrass|gb167|DN150951	616	616	100	globlastp
2699	LAB268	switchgrass|gb167|FE605474	616	616	100	globlastp
2700	LAB268	switchgrass|gb167|FE616525	616	616	100	globlastp
2701	LAB268	switchgrass|gb167|FE620768	616	616	100	globlastp
2702	LAB268	switchgrass|gb167|FE644523	616	616	100	globlastp
2703	LAB268	switchgrass|gb167|FE647208	616	616	100	globlastp
2704	LAB268	switchgrass|gb167|FL725907	616	616	100	globlastp
2705	LAB268	switchgrass|gb167|FL727674	616	616	100	globlastp
2706	LAB268	tamarix|gb166|CD151503	616	616	100	globlastp
2707	LAB268	tamarix|gb166|CF198776	616	616	100	globlastp
2708	LAB268	tamarix|gb166|EG970851	616	616	100	globlastp
2709	LAB268	tamarix|gb166|EG971166	616	616	100	globlastp
2710	LAB268	tea|10v1|CV013740	616	616	100	globlastp
2711	LAB268	tea|gb171|CV013740	616	616	100	globlastp
2712	LAB268	tea|gb171|CV013760	616	616	100	globlastp
2713	LAB268	tea|10v1|CV013858	616	616	100	globlastp
2714	LAB268	tea|gb171|CV013858	616	616	100	globlastp
2715	LAB268	tea|gb171|CV014033	616	616	100	globlastp
2716	LAB268	tea|10v1|CV014119	616	616	100	globlastp
2717	LAB268	tea|gb171|CV014119	616	616	100	globlastp
2718	LAB268	tea|10v1|CV014596	616	616	100	globlastp
2719	LAB268	tea|gb171|CV014596	616	616	100	globlastp
2720	LAB268	tea|gb171|FE861323	616	616	100	globlastp
2721	LAB268	thellungiella|gb167|BY809845	616	616	100	globlastp
2722	LAB268	thellungiella|gb167|EC599850	616	616	100	globlastp
2723	LAB268	tobacco|gb162|BQ842894	616	616	100	globlastp
2724	LAB268	tobacco|gb162|BQ843064	6444	616	100	glotblastn
2725	LAB268	tobacco|gb162|BQ843158	616	616	100	globlastp
2726	LAB268	tobacco|gb162|BQ843164	616	616	100	globlastp
2727	LAB268	tobacco|gb162|CV016805	616	616	100	globlastp
2728	LAB268	tobacco|gb162|CV017355	6445	616	100	glotblastn
2729	LAB268	tobacco|gb162|CV018990	616	616	100	globlastp
2730	LAB268	tobacco|gb162|CV021089	616	616	100	globlastp
2731	LAB268	tomato|09v1|BG124775	616	616	100	globlastp
2732	LAB268	tomato|gb164|BG124775	616	616	100	globlastp
2733	LAB268	triphysaria|10v1|BM357139	616	616	100	globlastp
2734	LAB268	triphysaria|10v1|BM357221	616	616	100	globlastp
2735	LAB268	triphysaria|gb164|BM357221	616	616	100	globlastp
2736	LAB268	triphysaria|gb164|DR170904	6446	616	100	glotblastn
2737	LAB268	triphysaria|10v1|CB815232	616	616	100	globlastp
2738	LAB268	triphysaria|10v1|EX991298	616	616	100	globlastp
2739	LAB268	triphysaria|10v1|EX994401	616	616	100	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2740	LAB268	triphysaria|10v1|EX999992	616	616	100	globlastp
2741	LAB268	triphysaria|10v1|EX999279	616	616	100	globlastp
2742	LAB268	triphysaria|10v1|EY011518	616	616	100	globlastp
2743	LAB268	triphysaria|10v1|EY019376	616	616	100	globlastp
2744	LAB268	triphysaria|10v1|EY018118	616	616	100	globlastp
2745	LAB268	walnuts|gb166|CB303972	616	616	100	globlastp
2746	LAB268	walnuts|gb166|EL894979	616	616	100	globlastp
2747	LAB268	walnuts|gb166|EL899822	616	616	100	globlastp
2748	LAB268	wheat|gb164|AL815485	6447	616	100	glotblastn
2749	LAB268	wheat|gb164|AL828423	6448	616	100	glotblastn
2750	LAB268	wheat|gb164|BE401770	6449	616	100	glotblastn
2751	LAB268	wheat|gb164|BE402303	616	616	100	globlastp
2752	LAB268	wheat|gb164|BE403687	616	616	100	globlastp
2753	LAB268	wheat|gb164|BE404081	6450	616	100	glotblastn
2754	LAB268	wheat|gb164|BE415777	6451	616	100	glotblastn
2755	LAB268	wheat|gb164|BE415858	616	616	100	globlastp
2756	LAB268	wheat|gb164|BE415872	6452	616	100	glotblastn
2757	LAB268	wheat|gb164|BE415923	6453	616	100	glotblastn
2758	LAB268	wheat|gb164|BE416155	6454	616	100	glotblastn
2759	LAB268	wheat|gb164|BE416248	6455	616	100	glotblastn
2760	LAB268	wheat|gb164|BE419530	616	616	100	globlastp
2761	LAB268	wheat|gb164|BE422926	616	616	100	globlastp
2762	LAB268	wheat|gb164|BE423286	6456	616	100	glotblastn
2763	LAB268	wheat|gb164|BE424653	6457	616	100	glotblastn
2764	LAB268	wheat|gb164|BE427669	6458	616	100	glotblastn
2765	LAB268	wheat|gb164|BE490213	6459	616	100	glotblastn
2766	LAB268	wheat|gb164|BE586199	6460	616	100	glotblastn
2767	LAB268	wheat|gb164|BF199955	6461	616	100	glotblastn
2768	LAB268	wheat|gb164|BF473518	616	616	100	globlastp
2769	LAB268	wheat|gb164|BF484151	616	616	100	globlastp
2770	LAB268	wheat|gb164|BI480019	6462	616	100	glotblastn
2771	LAB268	wheat|gb164|BQ295238	6463	616	100	glotblastn
2772	LAB268	wheat|gb164|CA498443	616	616	100	globlastp
2773	LAB268	wheat|gb164|CA499277	6464	616	100	glotblastn
2774	LAB268	wheat|gb164|CA593119	6465	616	100	glotblastn
2775	LAB268	wheat|gb164|CA603109	6466	616	100	glotblastn
2776	LAB268	wheat|gb164|CA649743	6467	616	100	glotblastn
2777	LAB268	wheat|gb164|CA703450	616	616	100	globlastp
2778	LAB268	wheat|gb164|CA703620	6468	616	100	glotblastn
2779	LAB268	wheat|gb164|CA707912	6469	616	100	glotblastn
2780	LAB268	wheat|gb164|CA728989	6470	616	100	glotblastn
2781	LAB268	wheat|gb164|CA730994	616	616	100	globlastp
2782	LAB268	wheat|gb164|CN009051	6471	616	100	glotblastn
2783	LAB268	zamia|gb166|DY030802	616	616	100	globlastp

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2784	LAB268	zamia|gb166|DY032938	616	616	100	globlastp
2785	LAB268	zamia|gb166|FD767578	616	616	100	globlastp
2786	LAB268	tea|10v1|CV013760	616	616	100	globlastp
2787	LAB268	triphysaria|10v1|BM357495	616	616	100	globlastp
2788	LAB268	barley|10v1|BE413182	616	616	100	globlastp
2789	LAB268	barley|10v1|BE454254	616	616	100	globlastp
2790	LAB268	barley|10v1|BE060192	616	616	100	globlastp
2791	LAB268	barley|10v1|BF627774	616	616	100	globlastp
2792	LAB268	canola|10v1|CD818240	616	616	100	globlastp
2793	LAB268	canola|10v1|CN737593	616	616	100	globlastp
2794	LAB268	lettuce|10v1|DW044538	616	616	100	globlastp
2795	LAB268	lettuce|10v1|DW045072	616	616	100	globlastp
2796	LAB268	lettuce|10v1|DW045694	616	616	100	globlastp
2797	LAB268	lettuce|10v1|AB183301	616	616	100	globlastp
2798	LAB268	lettuce|10v1|DW046403	616	616	100	globlastp
2799	LAB268	lettuce|10v1|DW052423	616	616	100	globlastp
2800	LAB268	lettuce|10v1|DW054176	616	616	100	globlastp
2801	LAB268	lettuce|10v1|DW057506	616	616	100	globlastp
2802	LAB268	lettuce|10v1|DW058399	616	616	100	globlastp
2803	LAB268	lettuce|10v1|DW148044	616	616	100	globlastp
2804	LAB268	lettuce|10v1|DW075886	616	616	100	globlastp
2805	LAB268	poplar|10v1|BU825437	616	616	100	globlastp
2806	LAB268	poplar|10v1|BU819667	616	616	100	globlastp
2807	LAB268	rose|10v1|BI977531	616	616	100	globlastp
2808	LAB268	rose|10v1|EC587236	616	616	100	globlastp
2809	LAB268	sugarcane|10v1|BQ533111	616	616	100	globlastp
2810	LAB268	sugarcane|10v1|BQ530407	616	616	100	globlastp
2811	LAB268	sugarcane|10v1|CA071683	616	616	100	globlastp
2812	LAB268	sugarcane|10v1|CA070996	616	616	100	globlastp
2813	LAB268	sugarcane|10v1|CA072002	616	616	100	globlastp
2814	LAB268	canola|10v1|CD817261	-	616	100	globlastp
2815	LAB268	cichorium|gb171|EH698983	-	616	100	globlastp
2816	LAB268	maize|gb170|AI391820	-	616	100	glotblastn
2817	LAB268	peanut|gb171|EE124716	-	616	100	globlastp
2818	LAB268	poplar|gb170|BU819908	-	616	100	globlastp
2819	LAB268	artemisia|10v1|SRR019254S0012318	6472	616	99.03	glotblastn
2820	LAB268	artemisia|10v1|SRR019254S0027665	6473	616	99.03	glotblastn
2821	LAB268	artemisia|10v1|SRR019254S0111269	6474	616	99.03	glotblastn
2822	LAB268	lettuce|10v1|DW083199	6475	616	99.03	glotblastn
2823	LAB268	nasturtium|10v1|SRR032558S0010849	6476	616	99.03	glotblastn
2824	LAB268	antirrhinum|gb166|AJ792433	6477	616	99.03	glotblastn
2825	LAB268	apple|gb171|CN490774	6478	616	99.03	glotblastn
2826	LAB268	b_rapa|gb162|CX270308	6479	616	99.03	glotblastn
2827	LAB268	barley|gb157SOLEXA|BF259003	6480	616	99.03	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2828	LAB268	lettuce|gb157.2|DW084329	6481	616	99.03	glotblastn
2829	LAB268	nicotiana_benthamiana|gb162|CK990179	6482	616	99.03	glotblastn
2830	LAB268	spikemoss|gb165|DN838885	6483	616	99.03	glotblastn
2831	LAB268	spruce|gb162|DR582087	6484	616	99.03	glotblastn
2832	LAB268	wheat|gb164|AW448482	6485	616	99.03	glotblastn
2833	LAB268	wheat|gb164|CD873027	6486	616	99.03	glotblastn
2834	LAB268	eschscholzia|10v1|SRR014116S0001279	-	616	99.03	glotblastn
2835	LAB268	orobanche|10v1|SRR023189S0057009	-	616	99.03	glotblastn
2836	LAB268	triphysaria|10v1|SRR023500S0028707	-	616	99.03	glotblastn
2837	LAB268	basilicum|10v1|DY336248	-	616	99.03	glotblastn
2838	LAB268	arabidopsis_lyrata|09v1|JGIAL013923	6487	616	99	globlastp
2839	LAB268	artemisia|10v1|GW329205	6488	616	99	globlastp
2840	LAB268	artemisia|10v1|SRR019254S0020910	6489	616	99	globlastp
2841	LAB268	artemisia|10v1|SRR019254S0048488	6489	616	99	globlastp
2842	LAB268	artemisia|10v1|SRR019546S0001094	6490	616	99	globlastp
2843	LAB268	artemisia|10v1|SRR019550S0074110	6489	616	99	globlastp
2844	LAB268	canola|10v1|CD811609	6491	616	99	globlastp
2845	LAB268	chickpea|09v2|GR396286	6492	616	99	globlastp
2846	LAB268	eggplant|10v1|FS000288	6493	616	99	globlastp
2847	LAB268	eggplant|10v1|FS001540	6493	616	99	globlastp
2848	LAB268	jatropha|09v1|GH295594	6494	616	99	globlastp
2849	LAB268	lotus|09v1|BW594671	6495	616	99	globlastp
2850	LAB268	lotus|09v1|LLGO012754	6496	616	99	globlastp
2851	LAB268	medicago|09v1|LLCO512253	6497	616	99	globlastp
2852	LAB268	medicago|09v1|LLCO513425	6498	616	99	globlastp
2853	LAB268	monkeyflower|10v1|GR010633	6499	616	99	globlastp
2854	LAB268	nasturtium|10v1|GH163637	6493	616	99	globlastp
2855	LAB268	nasturtium|10v1|SRR032558S0007001	6493	616	99	globlastp
2856	LAB268	nasturtium|10v1|SRR032558S0014888	6493	616	99	globlastp
2857	LAB268	nasturtium|10v1|SRR032558S0126068	6493	616	99	globlastp
2858	LAB268	orobanche|10v1|SRR023189S0015197	6493	616	99	globlastp
2859	LAB268	orobanche|10v1|SRR023189S0032180	6493	616	99	globlastp
2860	LAB268	orobanche|10v1|SRR023189S0073604	6493	616	99	globlastp
2861	LAB268	pea|09v1|EX571047	6500	616	99	globlastp
2862	LAB268	physcomitrella|10v1|XM001768153	6501	616	99	globlastp
2863	LAB268	physcomitrella|10v1|XM001782794	6502	616	99	globlastp
2864	LAB268	pigeonpea|gb171|GR471516	6503	616	99	globlastp
2865	LAB268	pine|10v1|DR682322	6504	616	99	globlastp
2866	LAB268	pine|10v1|GT259202	6504	616	99	globlastp
2867	LAB268	potato|10v1|BG595694	6493	616	99	globlastp
2868	LAB268	potato|10v1|BM403808	6493	616	99	globlastp
2869	LAB268	rhizophora|10v1|SRR005793S0017626	6505	616	99	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2870	LAB268	solanum_phurcja|09v1|SPHBG123365	6493	616	99	globlastp
2871	LAB268	solanum_phurcja|09v1|SPHBG123501	6493	616	99	globlastp
2872	LAB268	solanum_phureja|09v1|SPHBG123908	6493	616	99	globlastp
2873	LAB268	solanum_phureja|09v1|SPHBG124249	6493	616	99	globlastp
2874	LAB268	solanum_phureja|09v1|SPHBG125424	6493	616	99	globlastp
2875	LAB268	solanum_phureja|09v1|SPHBG125445	6493	616	99	globlastp
2876	LAB268	solanum_phureja|09v1|SPHBG126504	6493	616	99	globlastp
2877	LAB268	solanum_phureja|09v1|SPHBG130199	6493	616	99	globlastp
2878	LAB268	solanum_phureja|09v1|SPHBG627699	6493	616	99	globlastp
2879	LAB268	solanum_phureja|09v1|SPHCRPSP003816	6493	616	99	globlastp
2880	LAB268	solanum_phureja|09v1|SPHCRPSP036363	6493	616	99	globlastp
2881	LAB268	sugarcane|10v1|CA111726	6506	616	99	globlastp
2882	LAB268	tomato|09v1|BG123908	6493	616	99	globlastp
2883	LAB268	tomato|09v1|BG126504	6493	616	99	globlastp
2884	LAB268	tomato|09v1|CN216197	6493	616	99	globlastp
2885	LAB268	tragopogon|10v1|SRR020205S0007187	6507	616	99	globlastp
2886	LAB268	amborella|gb166|CK763863	6489	616	99	globlastp
2887	LAB268	antirrhinum|gb166|AJ799109	6508	616	99	globlastp
2888	LAB268	apple|gb171|CN443956	6509	616	99	globlastp
2889	LAB268	apple|gb171|CN489447	6509	616	99	globlastp
2890	LAB268	apple|gb171|CN490043	6509	616	99	globlastp
2891	LAB268	apple|gb171|CN491079	6509	616	99	globlastp
2892	LAB268	apple|gb171|CN997061	6509	616	99	globlastp
2893	LAB268	apple|gb171|CN997883	6509	616	99	globlastp
2894	LAB268	apple|gb171|CO065741	6509	616	99	globlastp
2895	LAB268	apple|gb171|CO415792	6509	616	99	globlastp
2896	LAB268	apple|gb171|CO416659	6509	616	99	globlastp
2897	LAB268	artemisia|gb164|EY053904	6510	616	99	globlastp
2898	LAB268	avocado|gb164|CK754635	6489	616	99	globlastp
2899	LAB268	b_rapa|gb162|CX271147	6511	616	99	globlastp
2900	LAB268	barley|10v1|BG342998	6512	616	99	globlastp
2901	LAB268	barley|gb157SOLEXA|AL505955	6512	616	99	globlastp
2902	LAB268	barley|gb157SOLEXA|BG416680	6513	616	99	globlastp
2903	LAB268	basilicum|10v1|DY323944	6489	616	99	globlastp
2904	LAB268	centhrus|gb166|EB654992	6514	616	99	globlastp
2905	LAB268	centhrus|gb166|EB665044	6515	616	99	globlastp
2906	LAB268	cynara|gb167|GE589503	6513	616	99	globlastp
2907	LAB268	cynara|gb167|GE601275	6516	616	99	globlastp
2908	LAB268	ginger|gb164|DY362774	6517	616	99	globlastp
2909	LAB268	kiwi|gb166|FG412369	6518	616	99	globlastp
2910	LAB268	kiwi|gb166|FG511349	6519	616	99	globlastp
2911	LAB268	lettuce|10v1|DW049144	6520	616	99	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2912	LAB268	lettuce|gb157.2|DW154476	6521	616	99	globlastp
2913	LAB268	marchantia|gb166|AU081695	6522	616	99	globlastp
2914	LAB268	marchantia|gb166|AU081848	6522	616	99	globlastp
2915	LAB268	marchantia|gb166|BJ849115	6522	616	99	globlastp
2916	LAB268	medicago|gb157.2|AJ498325	6523	616	99	globlastp
2917	LAB268	melon|gb165|AM732498	6524	616	99	globlastp
2918	LAB268	oil_palm|gb166|EY396434	6489	616	99	globlastp
2919	LAB268	onion|gb162|AA451589	6525	616	99	globlastp
2920	LAB268	ostreococcus|gb162|XM001415987	6526	616	99	globlastp
2921	LAB268	ostreococcus|gb162|XM001420298	6526	616	99	globlastp
2922	LAB268	pepper|gb171|AA840708	6493	616	99	globlastp
2923	LAB268	pepper|gb171|AA840801	6493	616	99	globlastp
2924	LAB268	pepper|gb171|BM065365	6493	616	99	globlastp
2925	LAB268	pepper|gb171|BM065900	6493	616	99	globlastp
2926	LAB268	pepper|gb171|BM066186	6493	616	99	globlastp
2927	LAB268	pepper|gb171|BM066215	6493	616	99	globlastp
2928	LAB268	pepper|gb171|BM068037	6493	616	99	globlastp
2929	LAB268	pepper|gb171|CA519950	6493	616	99	globlastp
2930	LAB268	pepper|gb171|GD058514	6493	616	99	globlastp
2931	LAB268	pepper|gb171|GD068989	6493	616	99	globlastp
2932	LAB268	pepper|gb171|GD109617	6493	616	99	globlastp
2933	LAB268	petunia|gb171|AY650011	6527	616	99	globlastp
2934	LAB268	petunia|gb171|FN003085	6528	616	99	globlastp
2935	LAB268	petunia|gb171|FN003987	6504	616	99	globlastp
2936	LAB268	pine|10v1|AA739509	6504	616	99	globlastp
2937	LAB268	pine|gb157.2|AA739509	6504	616	99	globlastp
2938	LAB268	pine|10v1|AW064813	6504	616	99	globlastp
2939	LAB268	pine|gb157.2|AW064813	6504	616	99	globlastp
2940	LAB268	pine|gb157.2|BX250390	6504	616	99	globlastp
2941	LAB268	pine|10v1|CX715301	6504	616	99	globlastp
2942	LAB268	pine|gb157.2|CX715301	6504	616	99	globlastp
2943	LAB268	pine|10v1|BX679616	6504	616	99	globlastp
2944	LAB268	potato|gb157.2|BE923376	6493	616	99	globlastp
2945	LAB268	potato|10v1|BF054460	6493	616	99	globlastp
2946	LAB268	potato|gb157.2|BF054460	6493	616	99	globlastp
2947	LAB268	potato|10v1|BM109083	6493	616	99	globlastp
2948	LAB268	potato|gb157.2|BM405205	6493	616	99	globlastp
2949	LAB268	potato|10v1|BM407657	6489	616	99	globlastp
2950	LAB268	potato|10v1|BQ512707	6493	616	99	globlastp
2951	LAB268	potato|gb157.2|BQ514906	6493	616	99	globlastp
2952	LAB268	potato|10v1|BQ518377	6493	616	99	globlastp
2953	LAB268	radish|gb164|EV536543	6529	616	99	globlastp
2954	LAB268	radish|gb164|EV546187	6530	616	99	globlastp
2955	LAB268	radish|gb164|EV567987	6508	616	99	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2956	LAB268	radish|gb164|EX762693	6531	616	99	globlastp
2957	LAB268	radish|gb164|EX902598	6532	616	99	globlastp
2958	LAB268	rye|gb164|BE493960	6489	616	99	globlastp
2959	LAB268	rye|gb164|BE494160	6489	616	99	globlastp
2960	LAB268	rye|gb164|BE494831	6489	616	99	globlastp
2961	LAB268	rye|gb164|BE495294	6533	616	99	globlastp
2962	LAB268	spruce|gb162|CO215151	6504	616	99	globlastp
2963	LAB268	spruce|gb162|CO237421	6504	616	99	globlastp
2964	LAB268	spruce|gb162|DR481285	6504	616	99	globlastp
2965	LAB268	spruce|gb162|DR495585	6504	616	99	globlastp
2966	LAB268	spruce|gb162|DR575192	6504	616	99	globlastp
2967	LAB268	spurge|gb161|DV113675	6534	616	99	globlastp
2968	LAB268	sugarcane|gb157.3|CA102127	6535	616	99	globlastp
2969	LAB268	sugarcane|gb157.3|CA127979	6536	616	99	globlastp
2970	LAB268	sugarcane|gb157.3|CA128041	6537	616	99	globlastp
2971	LAB268	sugarcane|gb157.3|CA241735	6538	616	99	globlastp
2972	LAB268	sunflower|gb162|CF090846	6491	616	99	globlastp
2973	LAB268	tamarix|gb166|EG971827	6539	616	99	globlastp
2974	LAB268	tobacco|gb162|BQ843074	6540	616	99	globlastp
2975	LAB268	tobacco|gb162|EB683839	6504	616	99	globlastp
2976	LAB268	tomato|09v1|BG123365	6493	616	99	globlastp
2977	LAB268	tomato|09v1|BG123501	6493	616	99	globlastp
2978	LAB268	tomato|gb164|BG123501	6493	616	99	globlastp
2979	LAB268	tomato|gb164|BG123908	6493	616	99	globlastp
2980	LAB268	tomato|09v1|BG124249	6493	616	99	globlastp
2981	LAB268	tomato|gb164|BG124249	6493	616	99	globlastp
2982	LAB268	tomato|09v1|BG125424	6493	616	99	globlastp
2983	LAB268	tomato|09v1|BG125445	6493	616	99	globlastp
2984	LAB268	tomato|gb164|BG125445	6493	616	99	globlastp
2985	LAB268	tomato|09v1|BG126455	6493	616	99	globlastp
2986	LAB268	tomato|09v1|BG130199	6493	616	99	globlastp
2987	LAB268	triphysaria|gb164|BM357139	6541	616	99	globlastp
2988	LAB268	walnuts|gb166|EL892095	6542	616	99	globlastp
2989	LAB268	lettuce|10v1|DW052505	6521	616	99	globlastp
2990	LAB268	potato|10v1|BQ514906	6493	616	99	globlastp
2991	LAB268	rose|10v1|EC586553	6543	616	99	globlastp
2992	LAB268	arabidopsis_lyrata|09v1|CRPALE018329	6544	616	98.1	globlastp
2993	LAB268	artemisia|10v1|SRR019254S0005641	6545	616	98.1	globlastp
2994	LAB268	artemisia|10v1|SRR019254S0085816	6544	616	98.1	globlastp
2995	LAB268	gerbera|09v1|AJ753834	6544	616	98.1	globlastp
2996	LAB268	pine|10v1|GT260140	6546	616	98.1	globlastp
2997	LAB268	potato|10v1|BE923376	6547	616	98.1	globlastp
2998	LAB268	tomato|09v1|BF054460	6548	616	98.1	globlastp

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Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
2999	LAB268	artemisia|gb164|EY035013	6549	616	98.1	globlastp
3000	LAB268	artemisia|gb164|EY037977	6544	616	98.1	globlastp
3001	LAB268	artemisia|gb164|EY056079	6550	616	98.1	globlastp
3002	LAB268	banana|gb167|FL659268	6551	616	98.1	globlastp
3003	LAB268	barley|gb157SOLEXA|BG416840	6552	616	98.1	globlastp
3004	LAB268	cassava|gb164|BM259754	6553	616	98.1	globlastp
3005	LAB268	cryptomeria|gb166|AU299923	6554	616	98.1	globlastp
3006	LAB268	cynara|gb167|GE596075	6555	616	98.1	globlastp
3007	LAB268	lettuce|gb157.2|DW085444	6544	616	98.1	globlastp
3008	LAB268	lettuce|gb157.2|DW123180	6556	616	98.1	globlastp
3009	LAB268	lettuce|gb157.2|DW145765	6556	616	98.1	globlastp
3010	LAB268	lovegrass|gb167|EH187368	6557	616	98.1	globlastp
3011	LAB268	medicago|gb157.2|AL379622	6558	616	98.1	globlastp
3012	LAB268	nicotiana_benthamiana|gb162|CN746600	6559	616	98.1	globlastp
3013	LAB268	petunia|gb171|CV296942	6560	616	98.1	globlastp
3014	LAB268	petunia|gb171|FN008035	6561	616	98.1	globlastp
3015	LAB268	pine|gb157.2|DN611308	6562	616	98.1	globlastp
3016	LAB268	potato|10v1|CK249827	6554	616	98.1	globlastp
3016	LAB268	potato|gb157.2|CK249827	6673	616	93.5	globlastp
3017	LAB268	potato|10v1|CV475517	6563	616	98.1	globlastp
3018	LAB268	pseudorocgncria|gb167|FF366172	6564	616	98.1	globlastp
3019	LAB268	radish|gb164|FD937807	6565	616	98.1	globlastp
3020	LAB268	rye|gb164|BE587390	6566	616	98.1	globlastp
3021	LAB268	sugarcane|gb157.3|CA072969	6567	616	98.1	globlastp
3022	LAB268	sugarcane|gb157.3|CA111743	6568	616	98.1	globlastp
3023	LAB268	sugarcane|gb157.3|CA140464	6569	616	98.1	globlastp
3024	LAB268	walnuts|gb166|EL894813	6570	616	98.1	globlastp
3025	LAB268	zinnia|gb171|AU290856	6544	616	98.1	globlastp
3026	LAB268	pine|10v1|DR694482	6571	616	98.1	globlastp
3027	LAB268	artemisia|10v1|SRR019254S0090211	6572	616	98.06	glotblastn
3028	LAB268	sugarcane|gb157.3|CA116605	6573	616	98.06	glotblastn
3029	LAB268	wheat|gb164|BJ315666	6574	616	98.06	glotblastn
3030	LAB268	wheat|gb164|CA623503	6575	616	98.06	glotblastn
3031	LAB268	wheat|gb164|CA630334	6576	616	98.06	glotblastn
3032	LAB268	artemisia|10v1|SRR019254S0022227	-	616	98.06	glotblastn
3033	LAB268	artemisia|10v1|SRR019254S0216912	-	616	98.06	glotblastn
3034	LAB268	dandelion|gb161|DY840608	-	616	98.06	glotblastn
3035	LAB268	tea|gb171|FE861322	-	616	98.06	glotblastn
3036	LAB268	radish|gb164|EW726563	6577	616	97.2	globlastp
3037	LAB268	avocado|10v1|CO995142	6578	616	97.1	globlastp
3038	LAB268	orobanche|10v1|SRR023495S0084187	6578	616	97.1	globlastp
3039	LAB268	apple|gb171|CN494677	6579	616	97.1	globlastp
3040	LAB268	maize|gb170|LLFL427387	6580	616	97.1	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3041	LAB268	pinc|10v1|CF388178	6581	616	97.1	globlastp
3041	LAB268	pinc|gb157.2|CF388178	6963	616	84.7	globlastp
3042	LAB268	pine|gb157.2|DR694482	6582	616	97.1	globlastp
3043	LAB268	rose|gb157.2|EC586553	6583	616	97.1	globlastp
3044	LAB268	soybean|gb168|CA898703	6584	616	97.1	globlastp
3045	LAB268	sugarcane|gb157.3|CA213810	6585	616	97.1	globlastp
3046	LAB268	tobacco|gb162|AJ633035	6586	616	97.1	globlastp
3047	LAB268	volvox|gb162|BU645998	6587	616	97.1	globlastp
3048	LAB268	volvox|gb162|CBGZ25401FWD	6587	616	97.1	globlastp
3049	LAB268	volvox|gb162|MDLJGIVOLCA1102100	6587	616	97.1	globlastp
3050	LAB268	volvox|gb162|MDLJGIVOLCA1102370	6587	616	97.1	globlastp
3051	LAB268	volvox|gb162|MDLJGIVOLCA155291	6587	616	97.1	globlastp
3052	LAB268	volvox|gb162|MDLJGIVOLCA155542	6587	616	97.1	globlastp
3053	LAB268	volvox|gb162|MDLJGIVOLCA156769	6587	616	97.1	globlastp
3054	LAB268	volvox|gb162|MDLJGIVOLCA163165	6587	616	97.1	globlastp
3055	LAB268	volvox|gb162|MDLJGIVOLCA188140	6587	616	97.1	globlastp
3056	LAB268	zinnia|gb171|DV017431	6588	616	97.1	globlastp
3057	LAB268	artemisia|10v1|SRR019546S0127820	6589	616	97.09	glotblastn
3058	LAB268	artemisia|10v1|SRR019547S0487952	6590	616	97.09	glotblastn
3059	LAB268	artemisia|10v1|SRR019550S0086000	6591	616	97.09	glotblastn
3060	LAB268	gerbera|09v1|AJ755846	6592	616	97.09	glotblastn
3061	LAB268	amborella|gb166|FD427255	6593	616	97.09	glotblastn
3062	LAB268	cotton|gb164|DW484397	6594	616	97.09	glotblastn
3063	LAB268	ipomoea|gb157.2|DV034788	6595	616	97.09	glotblastn
3064	LAB268	rose|gb157.2|EC587467	6596	616	97.09	glotblastn
3065	LAB268	volvox|gb162|MDLJGIVOLCA1103472	6597	616	97.09	glotblastn
3066	LAB268	volvox|gb162|MDLJGIVOLCA1108939	6598	616	97.09	glotblastn
3067	LAB268	basilicum|gb157.3|DY336248	-	616	97.09	glotblastn
3068	LAB268	lettuce|gb157.2|DW049814	6599	616	96.3	globlastp
3069	LAB268	sunflower|gb162|CF088050	6600	616	96.3	globlastp
3070	LAB268	nasturtium|10v1|SRR032563S0097524	6601	616	96.2	globlastp
3071	LAB268	basilicum|gb157.3|DY323944	6602	616	96.2	globlastp
3072	LAB268	monkeyflower|10v1|DV206995	6603	616	96.12	glotblastn
3073	LAB268	oat|10v1|GO585940	6604	616	96.12	glotblastn
3074	LAB268	oat|10v1|GO586224	6605	616	96.12	glotblastn
3075	LAB268	oat|10v1|GO586484	6606	616	96.12	glotblastn
3076	LAB268	oat|10v1|GO586800	6607	616	96.12	glotblastn
3077	LAB268	oat|10v1|CN814783	6608	616	96.12	glotblastn
3078	LAB268	sugarcane|gb157.3|CA082940	6609	616	96.12	glotblastn
3079	LAB268	wheat|gb164|CA617786	6610	616	96.12	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3080	LAB268	wheat|gb164|CA618960	6611	616	96.12	glotblastn
3081	LAB268	sunflower|gb162|DY959162	-	616	96.12	glotblastn
3082	LAB268	artemisia|10v1|SRR019254S0002617	6612	616	96.1	globlastp
3083	LAB268	fescue|gb161|DT686102	6613	616	96.1	globlastp
3084	LAB268	fescue|gb161|DT690378	6614	616	96.1	globlastp
3085	LAB268	senecio|gb170|DY663617	6614	616	96.1	globlastp
3086	LAB268	spurge|gb161|DV116777	6615	616	96.1	globlastp
3087	LAB268	sugarcane|gb157.3|CA226811	6616	616	96.1	globlastp
3088	LAB268	tobacco|gb162|AM838335	6617	616	96.1	globlastp
3089	LAB268	canola|gb161|CX193674	6618	616	95.4	globlastp
3090	LAB268	rye|gb164|BE636849	6619	616	95.4	globlastp
3091	LAB268	triphysaria|gb164|EX999279	6620	616	95.4	globlastp
3092	LAB268	wheat|gb164|BE591511	6621	616	95.4	globlastp
3093	LAB268	canola|gb161|EE502343	6622	616	95.3	globlastp
3094	LAB268	chickpea|09v2|GR398035	6623	616	95.15	glotblastn
3095	LAB268	oat|10v1|CN821564	6624	616	95.15	glotblastn
3096	LAB268	oat|10v1|GO586658	6625	616	95.15	glotblastn
3097	LAB268	oat|10v1|GR332308	6626	616	95.15	glotblastn
3098	LAB268	oat|10v1|GR365369	6627	616	95.15	glotblastn
3099	LAB268	eucalyptus|gb166|CD668166	6628	616	95.15	glotblastn
3100	LAB268	onion|gb162|BI095512	6629	616	95.15	glotblastn
3101	LAB268	pine|gb157.2|AW697623	6630	616	95.15	glotblastn
3102	LAB268	rye|gb164|BE705751	6631	616	95.15	glotblastn
3103	LAB268	sugarcane|gb157.3|CA215987	6632	616	95.15	glotblastn
3104	LAB268	tea|gb171|CV014626	6633	616	95.15	glotblastn
3105	LAB268	triphysaria|gb164|EY019376	6634	616	95.15	glotblastn
3106	LAB268	wheat|gb164|CA620392	6635	616	95.15	glotblastn
3107	LAB268	wheat|gb164|CK202277	6636	616	95.15	glotblastn
3108	LAB268	artemisia|10v1|SRR019254S0011984	6637	616	95.1	globlastp
3109	LAB268	artemisia|10v1|SRR019254S0031076	6638	616	95.1	globlastp
3110	LAB268	artemisia|10v1|SRR019552S0240607	6637	616	95.1	globlastp
3111	LAB268	oat|10v1|GR359321	6639	616	95.1	globlastp
3112	LAB268	liriodendron|gb166|FD495606	6640	616	95.1	globlastp
3113	LAB268	maize|gb170|LLBE512363	6641	616	95.1	globlastp
3114	LAB268	medicago|09v1|LLAJ500188	6642	616	95.1	globlastp
3115	LAB268	medicago|gb157.2|AJ500188	6642	616	95.1	globlastp
3116	LAB268	oat|gb164|CN821564	6643	616	95.1	globlastp
3117	LAB268	rose|gb157.2|EC589151	6644	616	95.1	globlastp
3118	LAB268	wheat|gb164|CA601913	6645	616	95.1	globlastp
3119	LAB268	tobacco|gb162|CN949751	6646	616	94.4	globlastp
3120	LAB268	wheat|gb164|CA652102	6647	616	94.4	globlastp
3121	LAB268	poplar|gb170|CA823688	6648	616	94.3	globlastp
3122	LAB268	wheat|gb164|BG606703	6649	616	94.3	globlastp
3123	LAB268	wheat|gb164|CA711773	6650	616	94.23	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3124	LAB268	artemisia|10v1|SRR019254S0542206	6651	616	94.2	globlastp
3125	LAB268	rhizophora|10v1|SRR005793S0076222	6652	616	94.2	globlastp
3126	LAB268	barley|gb157SOLEXA|BF625158	6653	616	94.2	globlastp
3127	LAB268	barley|gb157SOLEXA|BG417494	6654	616	94.2	globlastp
3128	LAB268	barley|gb157SOLEXA|BI959450	6655	616	94.2	globlastp
3129	LAB268	centaurea|gb166|EH741518	6656	616	94.2	globlastp
3130	LAB268	maize|gb170|LLBE509909	6657	616	94.2	globlastp
3131	LAB268	maize|gb170|LLDN221334	6658	616	94.2	globlastp
3132	LAB268	maize|gb170|LLFL303881	6659	616	94.2	globlastp
3133	LAB268	sugarcane|gb157.3|CA129712	6660	616	94.2	globlastp
3134	LAB268	triphysaria|gb164|EY011518	6661	616	94.2	globlastp
3135	LAB268	triphysaria|gb164|EY133021	6662	616	94.2	globlastp
3136	LAB268	oat|10v1|CN819743	6663	616	94.17	glotblastn
3137	LAB268	oat|10v1|GO586171	6664	616	94.17	glotblastn
3138	LAB268	lettuce|10v1|DW046141	6665	616	94.17	glotblastn
3139	LAB268	lettuce|gb157.2|DW046141	6665	616	94.17	glotblastn
3140	LAB268	lettuce|gb157.2|DW160543	6666	616	94.17	glotblastn
3141	LAB268	lovegrass|gb167|EH194643	6667	616	94.17	glotblastn
3142	LAB268	sunflower|gb162|DY958196	6668	616	94.17	glotblastn
3143	LAB268	ginseng|10v1|GR871574	6669	616	93.6	globlastp
3144	LAB268	medicago|gb157.2|AL366664	6670	616	93.6	globlastp
3145	LAB268	sunflower|gb162|CD851214	6671	616	93.6	globlastp
3146	LAB268	wheat|gb164|CJ880722	6672	616	93.6	globlastp
3147	LAB268	bean|gb167|FE709035	6674	616	93.3	globlastp
3148	LAB268	pine|gb157.2|CN852349	6674	616	93.3	globlastp
3149	LAB268	artemisia|10v1|SRR019254S0003873	6675	616	93.2	globlastp
3150	LAB268	artemisia|10v1|SRR019254S0123773	6676	616	93.2	globlastp
3151	LAB268	artemisia|10v1|SRR019254S0145628	6677	616	93.2	glotblastn
3152	LAB268	barley|10v1|AJ434335	6678	616	93.2	glotblastn
3153	LAB268	oat|10v1|GR358555	6679	616	93.2	globlastp
3154	LAB268	orobanche|10v1|SRR023189S0034388	6676	616	93.2	globlastp
3155	LAB268	barley|gb157SOLEXA|BF258395	6680	616	93.2	globlastp
3156	LAB268	cacao|gb167|CU472310	6681	616	93.2	globlastp
3157	LAB268	cowpea|gb166|FF394656	6682	616	93.2	glotblastn
3158	LAB268	iceplant|gb164|BE035501	6683	616	93.2	glotblastn
3159	LAB268	maize|gb170|LLAW179408	6684	616	93.2	glotblastn
3160	LAB268	maize|gb170|LLCD997639	6685	616	93.2	globlastp
3161	LAB268	maize|gb170|LLFL027196	6686	616	93.2	glotblastn
3162	LAB268	maize|gb170|LLFL303809	6687	616	93.2	glotblastn
3163	LAB268	maize|gb170|LLFL319760	6688	616	93.2	globlastp
3164	LAB268	onion|gb162|ES449597	6675	616	93.2	globlastp
3165	LAB268	peanut|gb171|GO335559	6689	616	93.2	globlastp
3166	LAB268	soybean|gb168|SB2GWP105728	6690	616	93.2	globlastp
3167	LAB268	sugarcane|gb157.3|CA256731	6691	616	93.2	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3168	LAB268	triphysaria|gb164|EX994401	6676	616	93.2	globlastp
3169	LAB268	wheat|gb164|CA608777	6692	616	93.2	glotblastn
3170	LAB268	wheat|gb164|CJ833410	6693	616	93.2	globlastp
3171	LAB268	zinnia|gb171|DV017189	6676	616	93.2	globlastp
3172	LAB268	zinnia|gb171|DV017366	6676	616	93.2	globlastp
3173	LAB268	zinnia|gb171|DV017419	6676	616	93.2	globlastp
3174	LAB268	senecio|gb170|DY661591	-	616	93.2	glotblastn
3175	LAB268	radish|gb164|EV528352	6694	616	92.8	globlastp
3176	LAB268	wheat|gb164|BJ211841	6695	616	92.8	globlastp
3177	LAB268	wheat|gb164|CA729136	6696	616	92.8	globlastp
3178	LAB268	spurge|gb161|BI946403	6697	616	92.6	globlastp
3179	LAB268	maize|gb170|LLBM268739	6698	616	92.3	globlastp
3180	LAB268	ipomoea|gb157.2|EE881854	6699	616	92.23	glotblastn
3180	LAB268	ipomoea_batatas|10v1|EE881854	6702	616	92.2	globlastp
3181	LAB268	maize|gb170|LLEG077297	6700	616	92.23	glotblastn
3182	LAB268	melon|gb165|DV632781	6701	616	92.23	glotblastn
3183	LAB268	salvia|10v1|SRR014553S0015933	6703	616	92.2	globlastp
3184	LAB268	tragopogon|10v1|SRR020205S0178366	6703	616	92.2	globlastp
3185	LAB268	b_rapa|gb162|EX133290	6704	616	92.2	globlastp
3186	LAB268	barley|gb157SOLEXA|BM370668	6705	616	92.2	globlastp
3187	LAB268	cacao|gb167|CU469633	6706	616	92.2	globlastp
3188	LAB268	sugarcane|gb157.3|CA241052	6707	616	92.2	globlastp
3189	LAB268	cotton|gb164|BF270999	6708	616	92	globlastp
3190	LAB268	dandelion|gb161|DY836577	6709	616	92	globlastp
3191	LAB268	radish|gb164|EV529345	6710	616	92	globlastp
3192	LAB268	tomato|gb164|BG130199	6711	616	91.9	globlastp
3193	LAB268	wheat|gb164|CA711406	6712	616	91.9	globlastp
3194	LAB268	artemisia|10v1|EY056079	6713	616	91.3	globlastp
3195	LAB268	canola|10v1|GT085139	6714	616	91.3	globlastp
3196	LAB268	heritiera|10v1|SRR005795S0031594	6715	616	91.3	globlastp
3197	LAB268	oat|10v1|GR361209	6716	616	91.3	globlastp
3198	LAB268	oat|10v1|GR361398	6716	616	91.3	globlastp
3199	LAB268	barley|gb157SOLEXA|CD056360	6716	616	91.3	globlastp
3200	LAB268	bruguiera|gb166|BP939745	6713	616	91.3	globlastp
3201	LAB268	fern|gb171|DK959947	6717	616	91.3	globlastp
3202	LAB268	maize|gb170|LLCF021239	6718	616	91.3	globlastp
3203	LAB268	maize|gb170|LLFL026667	6719	616	91.3	globlastp
3204	LAB268	maize|gb170|LLFL367469	6720	616	91.3	globlastp
3205	LAB268	spruce|gb162|CO210449	6721	616	91.3	globlastp
3206	LAB268	spruce|gb162|CO478069	6716	616	91.3	globlastp
3207	LAB268	spruce|gb162|ES256096	6722	616	91.3	globlastp
3208	LAB268	spruce|gb162|EX306950	6716	616	91.3	globlastp
3209	LAB268	spruce|gb162|EX309778	6723	616	91.3	globlastp
3210	LAB268	sugarcane|gb157.3|CA245664	6724	616	91.3	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3211	LAB268	sugarcane|gb157.3|CA281611	6716	616	91.3	globlastp
3212	LAB268	tamarix|gb166|EG969617	6723	616	91.3	globlastp
3213	LAB268	wheat|gb164|CA686942	6716	616	91.3	globlastp
3214	LAB268	barley|10v1|BE437542	6725	616	91.26	glotblastn
3215	LAB268	tea|10v1|CV013790	6726	616	91.26	glotblastn
3216	LAB268	barley|gb157SOLEXA|BG415721	6727	616	91.26	glotblastn
3217	LAB268	dandelion|gb161|DY836671	6728	616	91.26	glotblastn
3218	LAB268	peanut|gb171|EH043386	6729	616	91.26	glotblastn
3219	LAB268	spruce|gb162|ES249576	6730	616	91.26	glotblastn
3220	LAB268	sunflower|gb162|CF082956	6731	616	91.26	glotblastn
3221	LAB268	volvox|gb162|AW676472	6732	616	91.26	glotblastn
3222	LAB268	wheat|gb164|CA706348	6733	616	91.26	glotblastn
3223	LAB268	wheat|gb164|CJ639897	6734	616	91.26	glotblastn
3224	LAB268	wheat|gb164|DR044938	6735	616	91.26	glotblastn
3225	LAB268	b_juncea|gb164|EVGN00680114742616	6736	616	91.2	globlastp
3226	LAB268	beet|gb162|BI543915	6737	616	91.2	globlastp
3227	LAB268	cassava|gb164|BM260241	6738	616	91.2	globlastp
3228	LAB268	melon|gb165|DV632791	6739	616	91.2	globlastp
3229	LAB268	strawberry|gb164|EX663851	6740	616	91.2	globlastp
3230	LAB268	sunflower|gb162|CD849382	6741	616	91.2	globlastp
3231	LAB268	sunflower|gb162|CD849751	6742	616	91.2	globlastp
3232	LAB268	sunflower|gb162|CD850210	6743	616	91.2	globlastp
3233	LAB268	beet|gb162|BQ588711	6744	616	91.1	globlastp
3234	LAB268	spruce|gb162|EX415867	6745	616	91.1	globlastp
3235	LAB268	potato|gb157.2|BQ518377	6746	616	91	globlastp
3236	LAB268	volvox|gb162|MDLJGIVOLCA178755	6747	616	90.9	globlastp
3237	LAB268	oat|10v1|GR364347	6748	616	90.7	globlastp
3238	LAB268	b_rapa|gb162|EX115114	6749	616	90.4	globlastp
3239	LAB268	dandelion|gb161|DY837249	6750	616	90.4	globlastp
3240	LAB268	oil_palm|gb166|EL681099	6751	616	90.4	globlastp
3241	LAB268	wheat|gb164|AL820678	6752	616	90.4	globlastp
3242	LAB268	wheat|gb164|CA611188	6753	616	90.4	globlastp
3243	LAB268	wheat|gb164|BU672653	6754	616	90.38	glotblastn
3244	LAB268	artemisia|10v1|SRR019254S0032901	6755	616	90.3	globlastp
3245	LAB268	canola|10v1|CD812509	6756	616	90.3	globlastp
3246	LAB268	eschscholzia|10v1|CD480997	6756	616	90.3	globlastp
3247	LAB268	barley|gb157SOLEXA|BI948748	6757	616	90.3	globlastp
3248	LAB268	cacao|gb167|CU614547	6758	616	90.3	globlastp
3249	LAB268	melon|gb165|AM721598	6759	616	90.3	globlastp
3250	LAB268	papaya|gb165|EX272338	6760	616	90.3	globlastp
3251	LAB268	potato|gb157.2|CV492347	6761	616	90.3	globlastp
3252	LAB268	spruce|gb162|ES253259	6762	616	90.3	globlastp
3253	LAB268	sunflower|gb162|CF086418	6763	616	90.3	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3254	LAB268	artemisia|10v1|SRR019254S0030053	-	616	90.29	glotblastn
3255	LAB268	ipomoca_batatas|10v1|DV036726	-	616	90.29	glotblastn
3256	LAB268	ipomoea|gb157.2|DV036726	-	616	90.29	glotblastn
3257	LAB268	sunflower|gb162|CF077698	6764	616	90.1	globlastp
3258	LAB268	artemisia|10v1|SRR019550S0172069	6765	616	89.6	globlastp
3259	LAB268	arabidopsis|gb165|AT2G28740	6766	616	89.6	globlastp
3260	LAB268	cowpea|gb166|FC459371	6767	616	89.6	globlastp
3261	LAB268	fescue|gb161|DT687184	6768	616	89.6	globlastp
3262	LAB268	lettuce|gb157.2|DW045072	6769	616	89.6	globlastp
3263	LAB268	lettuce|gb157.2|DW119855	6770	616	89.6	globlastp
3264	LAB268	lettuce|gb157.2|DW140646	6771	616	89.6	globlastp
3265	LAB268	medicago|gb157.2|AL378431	6772	616	89.6	globlastp
3266	LAB268	wheat|gb164|BE422710	6773	616	89.6	globlastp
3267	LAB268	triphysaria|gb164|BE574792	6774	616	89.52	glotblastn
3268	LAB268	potato|gb157.2|BQ512707	6775	616	89.5	globlastp
3269	LAB268	pseudoroegneria|gb167|FF366170	6776	616	89.5	globlastp
3270	LAB268	wheat|gb164|BQ838511	6777	616	89.5	globlastp
3271	LAB268	eucalyptus|gb166|CT981403	6778	616	89.4	globlastp
3272	LAB268	barley|10v1|BG299823	6779	616	89.32	glotblastn
3273	LAB268	solanum_phureja|09v1|SPHBF054460	6780	616	89.32	glotblastn
3274	LAB268	wheat|gb164|CA607090	6781	616	89.32	glotblastn
3275	LAB268	barley|gb157SOLEXA|BI949366	6782	616	89.32	glotblastn
3276	LAB268	barley|10v1|BM370668	6783	616	89.32	glotblastn
3277	LAB268	lettuce|gb157.2|DW122372	6784	616	89.32	glotblastn
3278	LAB268	maize|gb170|LLFL027108	6785	616	89.32	glotblastn
3279	LAB268	strawberry|gb164|CO817468	6786	616	89.32	glotblastn
3280	LAB268	triphysaria|gb164|EY015990	6787	616	89.32	glotblastn
3281	LAB268	wheat|gb164|CA598647	6788	616	89.32	glotblastn
3282	LAB268	artemisia|10v1|SRR019254S0032449	6789	616	89.3	globlastp
3283	LAB268	barley|10v1|BE455800	6790	616	89.3	globlastp
3284	LAB268	barley|10v1|CV054877	6790	616	89.3	globlastp
3285	LAB268	apple|gb171|EB138544	6791	616	89.3	globlastp
3286	LAB268	bean|gb167|FG229977	6792	616	89.3	globlastp
3287	LAB268	fescue|gb161|DT685923	6793	616	89.3	globlastp
3288	LAB268	oat|10v1|GO586215	6794	616	89.2	globlastp
3289	LAB268	medicago|09v1|LLEL563523	6795	616	89.1	globlastp
3290	LAB268	lettuce|10v1|DW053970	6796	616	88.89	glotblastn
3291	LAB268	b_juncea|gb164|EVGN00255111393429	6797	616	88.8	globlastp
3292	LAB268	cotton|gb164|ES825038	6798	616	88.8	globlastp
3293	LAB268	fescue|gb161|DT686778	6799	616	88.8	globlastp
3294	LAB268	lettuce|gb157.2|DW074962	6800	616	88.8	globlastp
3295	LAB268	medicago|gb157.2|AL366317	6801	616	88.8	globlastp
3296	LAB268	rye|gb164|BE493864	6802	616	88.8	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3297	LAB268	rye|gb164|BE637133	6803	616	88.8	globlastp
3298	LAB268	sunflower|gb162|CD849947	6804	616	88.8	globlastp
3299	LAB268	triphysaria|gb164|BM357495	6805	616	88.8	globlastp
3300	LAB268	radish|gb164|EY934820	6806	616	88.7	globlastp
3301	LAB268	spruce|gb162|DR543346	6807	616	88.7	globlastp
3302	LAB268	tomato|gb164|BG125424	6808	616	88.7	globlastp
3303	LAB268	artemisia|10v1|SRR019254S0000755	6809	616	88.6	globlastp
3304	LAB268	sunflower|gb162|EE652838	6810	616	88.5	globlastp
3305	LAB268	wheat|gb164|CA702608	6811	616	88.5	globlastp
3306	LAB268	barley|gb157SOLEXA|BF624980	6812	616	88.35	glotblastn
3307	LAB268	barley|gb157SOLEXA|BM375641	6813	616	88.35	glotblastn
3308	LAB268	barley|gb157SOLEXA|CV062231	6814	616	88.35	glotblastn
3309	LAB268	cacao|gb167|CU472080	6815	616	88.35	glotblastn
3310	LAB268	maize|gb170|LLFL121319	6816	616	88.35	glotblastn
3311	LAB268	maize|gb170|LLFL290833	6817	616	88.35	glotblastn
3312	LAB268	sugarcane|gb157.3|CA124638	6818	616	88.35	glotblastn
3313	LAB268	sugarcane|gb157.3|CA129028	6819	616	88.35	glotblastn
3314	LAB268	sugarcane|10v1|CA286333	6820	616	88.35	glotblastn
3315	LAB268	sugarcane|gb157.3|CA286333	6820	616	88.35	glotblastn
3316	LAB268	wheat|gb164|BJ309601	6821	616	88.35	glotblastn
3317	LAB268	wheat|gb164|CA607921	6822	616	88.35	glotblastn
3318	LAB268	wheat|gb164|CK170457	6823	616	88.35	glotblastn
3319	LAB268	barley|10v1|BI948748	6824	616	88.3	globlastp
3320	LAB268	barley|10v1|CD056360	6825	616	88.3	globlastp
3321	LAB268	cassava|gb164|DB925963	6826	616	88.3	globlastp
3322	LAB268	cenchrus|gb166|EB661022	6827	616	88.3	globlastp
3323	LAB268	eucalyptus|gb166|CD668068	6828	616	88.3	globlastp
3324	LAB268	prunus|gb167|CB819033	6829	616	88.3	globlastp
3325	LAB268	avocado|gb164|CK754489	6830	616	88	globlastp
3326	LAB268	b_rapa|gb162|L33581	6831	616	88	globlastp
3327	LAB268	cowpea|gb166|FF387598	6832	616	88	globlastp
3328	LAB268	fescue|gb161|DT686507	6833	616	88	globlastp
3329	LAB268	fescue|gb161|DT686700	6834	616	88	globlastp
3330	LAB268	ginger|gb164|DY350509	6835	616	88	globlastp
3331	LAB268	lettuce|gb157.2|DW105457	6836	616	88	globlastp
3332	LAB268	medicago|gb157.2|AL380016	6837	616	88	globlastp
3333	LAB268	radish|gb164|EW714623	6838	616	88	globlastp
3334	LAB268	sunflower|gb162|CD849277	6839	616	88	globlastp
3335	LAB268	sunflower|gb162|CD851055	6840	616	88	globlastp
3336	LAB268	wheat|gb164|BE416157	6841	616	88	globlastp
3337	LAB268	wheat|gb164|BE417363	6842	616	88	globlastp
3338	LAB268	wheat|gb164|BE499108	6843	616	88	globlastp
3339	LAB268	wheat|gb164|BG608114	6844	616	88	globlastp
3340	LAB268	wheat|gb164|CJ646588	6845	616	88	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3341	LAB268	wheat|gb164|CA635795	6846	616	87.5	glotblastn
3342	LAB268	artemisia|10v1|EY032843	6847	616	87.4	globlastp
3343	LAB268	artemisia|10v1|SRR019254S0041967	6847	616	87.4	globlastp
3344	LAB268	kiwi|gb166|FG431516	6848	616	87.4	globlastp
3345	LAB268	nuphar|gb166|CD474059	6849	616	87.4	globlastp
3346	LAB268	pine|gb157.2|DT638657	6850	616	87.4	globlastp
3347	LAB268	sesame|gb157.2|BU667917	6851	616	87.4	globlastp
3348	LAB268	sugarcane|10v1|CA106117	6852	616	87.4	globlastp
3349	LAB268	sugarcane|gb157.3|CA085023	6852	616	87.4	globlastp
3350	LAB268	sugarcane|gb157.3|CA115738	6853	616	87.4	globlastp
3351	LAB268	sugarcane|10v1|CA129028	6854	616	87.4	globlastp
3352	LAB268	sunflower|gb162|BQ974944	6855	616	87.4	globlastp
3353	LAB268	wheat|gb164|CJ578594	6856	616	87.4	globlastp
3354	LAB268	barley|10v1|BE412620	6857	616	87.38	glotblastn
3355	LAB268	b_juncea|gb164|EVGN00529211853307	6858	616	87.3	globlastp
3356	LAB268	fescue|gb161|DT688459	6859	616	87.3	globlastp
3357	LAB268	lotus|gb157.2|CN825630	6860	616	87.3	globlastp
3358	LAB268	radish|gb164|EV527978	6861	616	87.3	globlastp
3359	LAB268	rose|gb157.2|EC588926	6862	616	87.3	globlastp
3360	LAB268	rye|gb164|BE586695	6863	616	87.3	globlastp
3361	LAB268	sunflower|gb162|CD848230	6864	616	87.3	globlastp
3362	LAB268	wheat|gb164|BE415928	6865	616	87.3	globlastp
3363	LAB268	wheat|gb164|BE438441	6866	616	87.3	globlastp
3364	LAB268	wheat|gb164|BE493582	6867	616	87.3	globlastp
3365	LAB268	wheat|gb164|BE518452	6868	616	87.3	globlastp
3366	LAB268	wheat|gb164|BF292946	6869	616	87.3	globlastp
3367	LAB268	wheat|gb164|BJ223844	6870	616	87.3	globlastp
3368	LAB268	avocado|gb164|CK750317	6871	616	87.2	globlastp
3369	LAB268	lettuce|gb157.2|DW052423	6872	616	87.2	globlastp
3370	LAB268	strawberry|gb164|CO817177	6873	616	87	globlastp
3371	LAB268	onion|gb162|BQ579926	6874	616	86.79	glotblastn
3372	LAB268	wheat|gb164|CK168652	6875	616	86.7	globlastp
3373	LAB268	avocado|gb164|CO995142	6876	616	86.6	globlastp
3374	LAB268	b_rapa|gb162|CX267515	6877	616	86.6	globlastp
3375	LAB268	grape|gb160|BQ794122	6878	616	86.6	globlastp
3376	LAB268	lettuce|gb157.2|DW047728	6879	616	86.6	globlastp
3377	LAB268	lettuce|gb157.2|DW059381	6880	616	86.6	globlastp
3378	LAB268	lotus|gb157.2|BW597052	6881	616	86.6	globlastp
3379	LAB268	rye|gb164|BE495019	6882	616	86.6	globlastp
3380	LAB268	spurge|gb161|DV113688	6883	616	86.6	globlastp
3381	LAB268	sunflower|gb162|EE651618	6884	616	86.6	globlastp
3382	LAB268	triphysaria|gb164|EY005632	6885	616	86.6	globlastp
3383	LAB268	wheat|gb164|AL826630	6886	616	86.6	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3384	LAB268	wheat|gb164|BE405172	6887	616	86.6	globlastp
3385	LAB268	wheat|gb164|BE417224	6888	616	86.6	globlastp
3386	LAB268	wheat|gb164|CA618316	6889	616	86.6	globlastp
3387	LAB268	cenchrus|gb166|EB672104	6890	616	86.41	glotblastn
3388	LAB268	maize|gb170|LLFL430119	6891	616	86.41	glotblastn
3389	LAB268	sugarcane|gb157.3|CA241139	6892	616	86.41	glotblastn
3390	LAB268	wheat|gb164|CJ634647	6893	616	86.41	glotblastn
3391	LAB268	canola|10v1|EE455340	6894	616	86.4	globlastp
3392	LAB268	gerbera|09v1|AJ753672	6894	616	86.4	globlastp
3393	LAB268	barley|gb157SOLEXA|BF258586	6895	616	86.4	globlastp
3394	LAB268	barley|gb157SOLEXA|BY850447	6896	616	86.4	globlastp
3395	LAB268	cotton|gb164|BF275139	6897	616	86.4	globlastp
3396	LAB268	fescue|gb161|DT690081	6894	616	86.4	globlastp
3397	LAB268	potato|gb157.2|BM109083	6898	616	86.4	globlastp
3398	LAB268	spruce|gb162|EX375049	6899	616	86.4	globlastp
3399	LAB268	tomato|gb164|BG126455	6900	616	86.4	globlastp
3400	LAB268	artemisia|gb164|EY034318	6901	616	85.8	globlastp
3401	LAB268	artemisia|gb164|EY048377	6902	616	85.8	globlastp
3402	LAB268	bean|gb167|CA898706	6903	616	85.8	globlastp
3403	LAB268	canola|gb161|CD812235	6904	616	85.8	globlastp
3404	LAB268	cowpea|gb166|FC456793	6905	616	85.8	globlastp
3405	LAB268	fescue|gb161|DT689099	6906	616	85.8	globlastp
3406	LAB268	fescue|gb161|DT689969	6907	616	85.8	globlastp
3407	LAB268	grape|gb160|CB970763	6908	616	85.8	globlastp
3408	LAB268	lettuce|gb157.2|DW054334	6909	616	85.8	globlastp
3409	LAB268	lettuce|gb157.2|DW075486	6910	616	85.8	globlastp
3410	LAB268	lettuce|gb157.2|DW105307	6911	616	85.8	globlastp
3411	LAB268	lettuce|gb157.2|DW108025	6912	616	85.8	globlastp
3412	LAB268	rose|gb157.2|EC587851	6913	616	85.8	globlastp
3413	LAB268	sunflower|gb162|CD848228	6914	616	85.8	globlastp
3414	LAB268	sunflower|gb162|CD850844	6915	616	85.8	globlastp
3415	LAB268	sunflower|gb162|CD850923	6916	616	85.8	globlastp
3416	LAB268	wheat|gb164|BE399592	6917	616	85.8	globlastp
3417	LAB268	wheat|gb164|BE405116	6918	616	85.8	globlastp
3418	LAB268	wheat|gb164|BE518109	6919	616	85.8	globlastp
3419	LAB268	wheat|gb164|BJ311599	6920	616	85.8	globlastp
3420	LAB268	wheat|gb164|CA651602	6921	616	85.8	globlastp
3421	LAB268	wheat|gb164|CA718879	6922	616	85.8	globlastp
3422	LAB268	wheat|gb164|CD453642	6923	616	85.8	globlastp
3423	LAB268	rye|gb164|BE494409	6924	616	85.7	globlastp
3424	LAB268	triphysaria|gb164|EX999992	6925	616	85.7	globlastp
3425	LAB268	wheat|gb164|CA622006	6926	616	85.7	globlastp
3426	LAB268	oil_palm|gb166|CN600292	6927	616	85.6	globlastp
3427	LAB268	barley|10v1|CV062231	6928	616	85.44	glotblastn

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3428	LAB268	wheat|gb164|CA624635	6929	616	85.44	glotblastn
3429	LAB268	triphysaria|gb164|EX988310	-	616	85.44	glotblastn
3430	LAB268	artemisia|10v1|SRR019254S0057308	6930	616	85.4	globlastp
3431	LAB268	pea|09v1|EX570524	6931	616	85.4	globlastp
3432	LAB268	pea|09v1|EX570579	6932	616	85.4	globlastp
3433	LAB268	pine|10v1|BX250390	6933	616	85.4	globlastp
3434	LAB268	barley|10v1|BF625158	6934	616	85.4	globlastp
3435	LAB268	poplar|10v1|CV225507	6935	616	85.4	globlastp
3436	LAB268	spruce|gb162|CO224810	6933	616	85.4	globlastp
3437	LAB268	oat|10v1|GO586850	6936	616	85.2	globlastp
3438	LAB268	oat|10v1|GO587649	6937	616	85.2	globlastp
3439	LAB268	oat|10v1|GR328829	6938	616	85.2	globlastp
3440	LAB268	b_oleracea|gb161|ES944086	6939	616	85.1	globlastp
3441	LAB268	b_rapa|gb162|CA991789	6940	616	85.1	globlastp
3442	LAB268	b_rapa|gb162|CX265826	6940	616	85.1	globlastp
3443	LAB268	cotton|gb164|AI728766	6941	616	85.1	globlastp
3444	LAB268	cotton|gb164|BG443736	6942	616	85.1	globlastp
3445	LAB268	dandelion|gb161|DY836046	6943	616	85.1	globlastp
3446	LAB268	dandelion|gb161|DY837761	6944	616	85.1	globlastp
3447	LAB268	ginger|gb164|DY358309	6945	616	85.1	globlastp
3448	LAB268	lettuce|gb157.2|DW072522	6946	616	85.1	globlastp
3449	LAB268	lettuce|gb157.2|DW105156	6947	616	85.1	globlastp
3450	LAB268	lettuce|gb157.2|DW106760	6948	616	85.1	globlastp
3451	LAB268	lettuce|gb157.2|DW170641	6949	616	85.1	globlastp
3452	LAB268	oil_palm|gb166|EL681602	6950	616	85.1	globlastp
3453	LAB268	radish|gb164|EX904649	6951	616	85.1	globlastp
3454	LAB268	radish|gb164|FD936397	6952	616	85.1	globlastp
3455	LAB268	wheat|gb164|BE417597	6953	616	85.1	globlastp
3456	LAB268	wheat|gb164|BE417802	6954	616	85.1	globlastp
3457	LAB268	wheat|gb164|BE422967	6955	616	85.1	globlastp
3458	LAB268	wheat|gb164|BF483140	6956	616	85.1	globlastp
3459	LAB268	wheat|gb164|CA598185	6957	616	85.1	globlastp
3460	LAB268	wheat|gb164|CA707571	6958	616	85.1	globlastp
3461	LAB268	nicotiana_benthamiana|gb162|CN743932	6959	616	85	globlastp
3462	LAB268	spruce|gb162|CO233199	6960	616	85	globlastp
3463	LAB268	tomato|gb164|BG123365	6961	616	85	globlastp
3464	LAB268	kiwi|gb166|FG502449	6962	616	84.9	globlastp
3465	LAB268	sunflower|gb162|EE658389	6964	616	84.7	globlastp
3466	LAB268	maize|gb170|LLAI855380	6965	616	84.68	glotblastn
3467	LAB268	oat|gb164|CN814783	6966	616	84.6	globlastp
3468	LAB268	spruce|gb162|CK434637	6967	616	84.6	globlastp
3469	LAB268	gerbera|09v1|AJ753690	6968	616	84.5	globlastp
3470	LAB268	oat|10v1|GO586105	6969	616	84.5	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3471	LAB268	tragopogon|10v1|SRR020205S0080113	6970	616	84.5	globlastp
3472	LAB268	b_juncea|gb164|EVGN01238609041063	6971	616	84.5	globlastp
3473	LAB268	canola|gb161|EE568160	6972	616	84.5	globlastp
3474	LAB268	cotton|gb164|CD486193	6973	616	84.5	globlastp
3475	LAB268	cycas|gb166|EX921626	6974	616	84.5	globlastp
3476	LAB268	spruce|gb162|DR572882	6975	616	84.5	globlastp
3477	LAB268	wheat|gb164|CV065522	6976	616	84.5	globlastp
3478	LAB268	ipomoea_nil|10v1|BJ573681	6977	616	84.47	glotblastn
3479	LAB268	sugarcane|10v1|CA243313	6978	616	84.47	glotblastn
3480	LAB268	barley|gb157SOLEXA|BF623064	6979	616	84.47	glotblastn
3481	LAB268	maize|gb170|LLFL225872	6980	616	84.47	glotblastn
3482	LAB268	maize|gb170|LLFL375355	6981	616	84.47	glotblastn
3483	LAB268	maize|gb170|LLFL398411	6982	616	84.47	glotblastn
3484	LAB268	sunflower|gb162|CD853795	6983	616	84.47	glotblastn
3485	LAB268	sunflower|gb162|DY929104	6984	616	84.47	glotblastn
3486	LAB268	wheat|gb164|CA627121	6985	616	84.47	glotblastn
3487	LAB268	cotton|gb164|DT458957	6986	616	84.4	globlastp
3488	LAB268	cryptomeria|gb166|BY890130	6987	616	84.4	globlastp
3489	LAB268	fescue|gb161|DT685912	6988	616	84.4	globlastp
3490	LAB268	fescue|gb161|DT685921	6989	616	84.4	globlastp
3491	LAB268	fescue|gb161|DT689498	6990	616	84.4	globlastp
3492	LAB268	lettuce|gb157.2|DW044538	6991	616	84.4	globlastp
3493	LAB268	lettuce|gb157.2|DW045694	6992	616	84.4	globlastp
3494	LAB268	lettuce|gb157.2|DW112493	6993	616	84.4	globlastp
3495	LAB268	lettuce|gb157.2|DW152364	6994	616	84.4	globlastp
3496	LAB268	lotus|gb157.2|CB828182	6995	616	84.4	globlastp
3497	LAB268	oil_palm|gb166|EL681389	6996	616	84.4	globlastp
3498	LAB268	rye|gb164|BE495825	6997	616	84.4	globlastp
3499	LAB268	triphysaria|gb164|CB815232	6998	616	84.4	globlastp
3500	LAB268	wheat|gb164|BE399101	6999	616	84.4	globlastp
3501	LAB268	wheat|gb164|BE400757	7000	616	84.4	globlastp
3502	LAB268	wheat|gb164|BE401940	7001	616	84.4	globlastp
3503	LAB268	wheat|gb164|BE415991	7002	616	84.4	globlastp
3504	LAB268	wheat|gb164|BE416205	7003	616	84.4	globlastp
3505	LAB268	wheat|gb164|BE427056	7004	616	84.4	globlastp
3506	LAB268	wheat|gb164|BE443644	7005	616	84.4	globlastp
3507	LAB268	wheat|gb164|BE498264	7006	616	84.4	globlastp
3508	LAB268	wheat|gb164|BE606944	7007	616	84.4	globlastp
3509	LAB268	wheat|gb164|BQ752653	7008	616	84.4	globlastp
3510	LAB268	wheat|gb164|CA622310	7009	616	84.4	globlastp
3511	LAB268	wheat|gb164|CA701185	7010	616	84.4	globlastp
3512	LAB268	b_oleracea|gb161|EE531495	7011	616	84.3	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3513	LAB268	nicotiana_benthamiana|gb162|ES885671	7012	616	84.3	globlastp
3514	LAB268	spruce|gb162|DV974261	7013	616	84.3	globlastp
3515	LAB268	spruce|gb162|EX317959	7014	616	84.3	globlastp
3516	LAB268	spruce|gb162|EX384965	7015	616	84.3	globlastp
3517	LAB268	maize|gb170|LLFL417329	7016	616	84.1	globlastp
3518	LAB268	monkeyflower|10v1|DV209491	7017	616	83.9	globlastp
3519	LAB268	safflower|gb162|EL398759	7018	616	83.8	globlastp
3520	LAB268	b_juncea|gb164|EVGN00020808423390	7019	616	83.7	globlastp
3521	LAB268	b_juncea|gb164|EVGN00450511902650	7020	616	83.7	globlastp
3522	LAB268	b_rapa|gb162|CV432749	7021	616	83.7	globlastp
3523	LAB268	b_rapa|gb162|CX272811	7022	616	83.7	globlastp
3524	LAB268	cotton|gb164|BE053285	7023	616	83.7	globlastp
3525	LAB268	cotton|gb164|BE053467	7024	616	83.7	globlastp
3526	LAB268	cotton|gb164|DT458659	7025	616	83.7	globlastp
3527	LAB268	cowpea|gb166|FC457316	7026	616	83.7	globlastp
3528	LAB268	fescue|gb161|DT707337	7027	616	83.7	globlastp
3529	LAB268	ginger|gb164|DY358075	7028	616	83.7	globlastp
3530	LAB268	ipomoea|gb157.2|CJ744369	7029	616	83.7	globlastp
3531	LAB268	lettuce|gb157.2|DW148044	7031	616	83.7	globlastp
3532	LAB268	radish|gb164|EV539475	7032	616	83.7	globlastp
3533	LAB268	radish|gb164|EX904372	7033	616	83.7	globlastp
3534	LAB268	sunflower|gb162|CD848280	7034	616	83.7	globlastp
3535	LAB268	sunflower|gb162|CD849983	7035	616	83.7	globlastp
3536	LAB268	wheat|gb164|BE422475	7036	616	83.7	globlastp
3537	LAB268	wheat|gb164|BE423456	7037	616	83.7	globlastp
3538	LAB268	wheat|gb164|BE423794	7038	616	83.7	globlastp
3539	LAB268	wheat|gb164|BE444787	7039	616	83.7	globlastp
3540	LAB268	wheat|gb164|BQ240605	7040	616	83.7	globlastp
3541	LAB268	wheat|gb164|BQ484067	7041	616	83.7	globlastp
3542	LAB268	wheat|gb164|CA633516	7042	616	83.7	globlastp
3543	LAB268	wheat|gb164|CA726043	7043	616	83.7	globlastp
3544	LAB268	wheat|gb164|DR737070	7044	616	83.7	globlastp
3545	LAB268	melon|gb165|AM719080	7045	616	83.6	globlastp
3546	LAB268	radish|gb164|EV547372	7046	616	83.6	globlastp
3547	LAB268	radish|gb164|EV567871	7047	616	83.6	globlastp
3548	LAB268	pea|09v1|EX568838	7048	616	83.5	globlastp
3549	LAB268	pea|09v1|EX570248	7048	616	83.5	globlastp
3550	LAB268	pea|09v1|EX570251	7048	616	83.5	globlastp
3551	LAB268	pea|09v1|EX571338	7049	616	83.5	glotblastn
3552	LAB268	sugarcane|10v1|CA077203	7050	616	83.5	glotblastn
3553	LAB268	artemisia|gb164|EY039119	7051	616	83.5	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3554	LAB268	artemisia|gb164|EY063572	7052	616	83.5	glotblastn
3555	LAB268	barley|gb157SOLEXA|BQ754387	7053	616	83.5	glotblastn
3556	LAB268	canola|gb161|EE545425	7054	616	83.5	glotblastn
3557	LAB268	maize|gb170|LLFL026684	7055	616	83.5	globlastp
3558	LAB268	spruce|gb162|EX403699	7056	616	83.5	globlastp
3559	LAB268	spruce|gb162|EX423558	7057	616	83.5	globlastp
3560	LAB268	sunflower|gb162|CF077380	7058	616	83.5	glotblastn
3561	LAB268	citrus|gb166|EY743876	-	616	83.5	glotblastn
3562	LAB268	canola|gb161|CD812364	7059	616	83.1	globlastp
3563	LAB268	cotton|gb164|DT456196	7060	616	83.1	globlastp
3564	LAB268	cryptomeria|gb166|BY884124	7061	616	83.1	globlastp
3565	LAB268	fescue|gb161|DT685782	7062	616	83.1	globlastp
3566	LAB268	fescue|gb161|DT686722	7063	616	83.1	globlastp
3567	LAB268	ginger|gb164|DY347124	7064	616	83.1	globlastp
3568	LAB268	ipomoea|gb157.2|CB330659	7065	616	83.1	globlastp
3569	LAB268	lettuce|gb157.2|DW104257	7066	616	83.1	globlastp
3570	LAB268	lettuce|gb157.2|DW112662	7067	616	83.1	globlastp
3571	LAB268	radish|gb164|EV569789	7068	616	83.1	globlastp
3572	LAB268	strawberry|gb164|CO817361	7069	616	83.1	globlastp
3573	LAB268	triphysaria|gb164|EY020033	7070	616	83.1	globlastp
3574	LAB268	wheat|gb164|BE416319	7071	616	83.1	globlastp
3575	LAB268	wheat|gb164|BE416450	7072	616	83.1	globlastp
3576	LAB268	wheat|gb164|BE499046	7073	616	83.1	globlastp
3577	LAB268	wheat|gb164|BF200454	7074	616	83.1	globlastp
3578	LAB268	wheat|gb164|BF484135	7075	616	83.1	globlastp
3579	LAB268	wheat|gb164|BU101226	7076	616	83.1	globlastp
3580	LAB268	wheat|gb164|CA597413	7077	616	83.1	globlastp
3581	LAB268	wheat|gb164|CA610380	7078	616	83.1	globlastp
3582	LAB268	wheat|gb164|CA616899	7079	616	83.1	globlastp
3583	LAB268	wheat|gb164|CA639849	7080	616	83.1	globlastp
3584	LAB268	cotton|gb164|CD486080	7081	616	83	globlastp
3585	LAB268	sunflower|gb162|CD848926	7082	616	83	globlastp
3586	LAB268	lettuce|gb157.2|DW120600	7083	616	82.9	globlastp
3587	LAB268	radish|gb164|FD966520	7084	616	82.9	globlastp
3588	LAB268	spikemoss|gb165|FE448582	7085	616	82.9	globlastp
3589	LAB268	spruce|gb162|EX400483	7086	616	82.8	globlastp
3590	LAB268	triphysaria|gb164|EX998942	7087	616	82.8	globlastp
3591	LAB268	wheat|gb164|CA622100	7088	616	82.69	glotblastn
3592	LAB268	apple|gb171|CN578733	7089	616	82.52	glotblastn
3593	LAB268	cotton|gb164|ES837982	7090	616	82.52	glotblastn
3594	LAB268	maize|gb170|LLFL008979	7091	616	82.52	glotblastn
3595	LAB268	sugarcane|10v1|CA234599XX2	7092	616	82.52	glotblastn
3596	LAB268	lolium|10v1|SRR029314S0011890	7093	616	82.5	globlastp
3597	LAB268	orobanche|10v1|SRR023495S0014175	7094	616	82.5	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3598	LAB268	triphysaria|10v1|SRR023500S0019032	7094	616	82.5	globlastp
3599	LAB268	b_rapa|gb162|CA991835	7095	616	82.5	globlastp
3600	LAB268	cichorium|gb171|EH703474	7096	616	82.5	globlastp
3601	LAB268	tea|10v1|GE652467	7097	616	82.5	globlastp
3602	LAB268	tea|gb171|GE652467	7097	616	82.5	globlastp
3603	LAB268	oat|10v1|GO586588	7098	616	82.4	globlastp
3604	LAB268	oat|10v1|GO586968	7099	616	82.4	globlastp
3605	LAB268	arabidopsis|gb165|AT5G59970	7100	616	82.4	globlastp
3606	LAB268	beet|gb162|BI096197	7101	616	82.4	globlastp
3607	LAB268	canola|gb161|CD817261	7102	616	82.4	globlastp
3608	LAB268	fescue|gb161|DT686588	7103	616	82.4	globlastp
3609	LAB268	fescue|gb161|DT687391	7104	616	82.4	globlastp
3610	LAB268	ipomoea|gb157.2|CJ738107	7105	616	82.4	globlastp
3611	LAB268	lettuce|gb157.2|DW075639	7106	616	82.4	globlastp
3612	LAB268	lettuce|gb157.2|DW147673	7107	616	82.4	globlastp
3613	LAB268	lotus|gb157.2|AW163944	7108	616	82.4	globlastp
3614	LAB268	radish|gb164|EV549130	7109	616	82.4	globlastp
3615	LAB268	radish|gb164|EX746739	7110	616	82.4	globlastp
3616	LAB268	rose|gb157.2|EC586164	7111	616	82.4	globlastp
3617	LAB268	rye|gb164|BE704504	7112	616	82.4	globlastp
3618	LAB268	strawberry|gb164|DY670022	7113	616	82.4	globlastp
3619	LAB268	wheat|gb164|BE399555	7114	616	82.4	globlastp
3620	LAB268	wheat|gb164|BE399932	7115	616	82.4	globlastp
3621	LAB268	wheat|gb164|BE415110	7116	616	82.4	globlastp
3622	LAB268	wheat|gb164|BE416325	7117	616	82.4	globlastp
3623	LAB268	wheat|gb164|BE423864	7118	616	82.4	globlastp
3624	LAB268	wheat|gb164|BE424898	7119	616	82.4	globlastp
3625	LAB268	wheat|gb164|BE425234	7120	616	82.4	globlastp
3626	LAB268	wheat|gb164|BG263850	7121	616	82.4	globlastp
3627	LAB268	wheat|gb164|BG275092	7122	616	82.4	globlastp
3628	LAB268	wheat|gb164|CD869572	7123	616	82.4	globlastp
3629	LAB268	cassava|gb164|BM260125	7124	616	82.3	globlastp
3630	LAB268	radish|gb164|FD538823	7125	616	82.3	globlastp
3631	LAB268	spruce|gb162|CO223362	7126	616	82.3	globlastp
3632	LAB268	spruce|gb162|DR570941	7127	616	82.3	globlastp
3633	LAB268	spruce|gb162|EX323253	7128	616	82.3	globlastp
3634	LAB268	triphysaria|gb164|EX991298	7129	616	82.3	globlastp
3635	LAB268	wheat|gb164|CK154925	7130	616	81.8	globlastp
3636	LAB268	barley|gb157SOLEXA|BG344395	7131	616	81.73	glotblastn
3637	LAB268	b_juncea|gb164|EVGN0014140843275 6	7132	616	81.7	globlastp
3638	LAB268	b_rapa|gb162|L33665	7133	616	81.7	globlastp
3639	LAB268	beet|gb162|EG551265	7134	616	81.7	globlastp
3640	LAB268	canola|gb161|CD812509	7135	616	81.7	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3641	LAB268	lettuce|gb157.2|DW054329	7136	616	81.7	globlastp
3642	LAB268	lettuce|gb157.2|DW158082	7137	616	81.7	globlastp
3643	LAB268	radish|gb164|EY903059	7138	616	81.7	globlastp
3644	LAB268	wheat|gb164|AL820085	7139	616	81.7	globlastp
3645	LAB268	wheat|gb164|BE398313	7140	616	81.7	globlastp
3646	LAB268	wheat|gb164|BE415832	7141	616	81.7	globlastp
3647	LAB268	wheat|gb164|BE415870	7142	616	81.7	globlastp
3648	LAB268	wheat|gb164|BE416751	7143	616	81.7	globlastp
3649	LAB268	wheat|gb164|BE417145	7144	616	81.7	globlastp
3650	LAB268	wheat|gb164|BE423800	7145	616	81.7	globlastp
3651	LAB268	wheat|gb164|BE425155	7146	616	81.7	globlastp
3652	LAB268	wheat|gb164|CA605518	7147	616	81.7	globlastp
3653	LAB268	maize|gb170|LLFL325425	7148	616	81.6	globlastp
3654	LAB268	oil_palm|gb166|EL683840	7149	616	81.6	globlastp
3655	LAB268	spruce|gb162|ES665243	7150	616	81.6	globlastp
3656	LAB268	barley|gb157SOLEXA|BM444527	7151	616	81.55	glotblastn
3657	LAB268	maize|gb170|LLCD447518	7152	616	81.55	glotblastn
3658	LAB268	sugarcane|gb157.3|CA107504	7153	616	81.55	glotblastn
3659	LAB268	sugarcane|gb157.3|CA108717	7154	616	81.55	glotblastn
3660	LAB268	jatropha|09v1|FM888435	-	616	81.55	glotblastn
3661	LAB268	triphysaria|gb164|EY012083	-	616	81.55	glotblastn
3662	LAB268	fescue|gb161|DT687241	7155	616	81.5	globlastp
3663	LAB268	radish|gb164|FD580482	7156	616	81.5	globlastp
3664	LAB268	citrus|gb166|EY825373	7157	616	81.1	globlastp
3665	LAB268	fescue|gb161|DT687220	7158	616	81.1	globlastp
3666	LAB268	fescue|gb161|DT688818	7159	616	81.1	globlastp
3667	LAB268	ipomoea|gb157.2|CB330950	7160	616	81.1	globlastp
3668	LAB268	lettuce|gb157.2|DW049144	7161	616	81.1	globlastp
3669	LAB268	rose|gb157.2|EC587324	7162	616	81.1	globlastp
3670	LAB268	wheat|gb164|BE399369	7163	616	81.1	globlastp
3671	LAB268	wheat|gb164|BE416516	7164	616	81.1	globlastp
3672	LAB268	wheat|gb164|BF474715	7165	616	81.1	globlastp
3673	LAB268	wheat|gb164|BM135522	7166	616	81.1	globlastp
3674	LAB268	wheat|gb164|BQ608801	7167	616	81.1	globlastp
3675	LAB268	wheat|gb164|CA593029	7168	616	81.1	globlastp
3676	LAB268	wheat|gb164|CA609335	7169	616	81.1	globlastp
3677	LAB268	pine|gb157.2|DR056167	7170	616	81	globlastp
3678	LAB268	rye|gb164|BE493942	7171	616	81	globlastp
3679	LAB268	soybean|gb168|BM139774	7172	616	81	globlastp
3680	LAB268	wheat|gb164|CA692550	7173	616	81	globlastp
3681	LAB268	wheat|gb164|CA708235	7174	616	81	globlastp
3682	LAB268	fescue|gb161|DT675092	7175	616	80.8	globlastp
3683	LAB268	potato|gb157.2|CV475517	7176	616	80.8	globlastp
3684	LAB268	spruce|gb162|DR481843	7177	616	80.8	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3685	LAB268	sugarcane|gb157.3|CA198373	7178	616	80.8	globlastp
3686	LAB268	pca|09v1|FG532461	7179	616	80.6	globlastp
3687	LAB268	barley|gb157SOLEXA|BF627774	7180	616	80.6	globlastp
3688	LAB268	rose|gb157.2|EC587236	7181	616	80.6	globlastp
3689	LAB268	wheat|gb164|CJ509634	7182	616	80.6	globlastp
3690	LAB268	sesame|10v1|BU667852	7183	616	80.58	glotblastn
3690	LAB268	sesame|gb157.2|BU667852	7184	616	80.58	glotblastn
3691	LAB268	wheat|gb164|DR737618	7185	616	80.58	glotblastn
3692	LAB268	artemisia|10v1|SRR019551S0085700	-	616	80.58	glotblastn
3693	LAB268	b_rapa|gb162|EE523641	7186	616	80.5	globlastp
3694	LAB268	cotton|gb164|BF269451	7187	616	80.5	globlastp
3695	LAB268	fescue|gb161|DT687024	7188	616	80.5	globlastp
3696	LAB268	fescue|gb161|DT687419	7189	616	80.5	globlastp
3697	LAB268	fescue|gb161|DT702542	7190	616	80.5	globlastp
3698	LAB268	iceplant|gb164|BE033998	7191	616	80.5	globlastp
3699	LAB268	wheat|gb164|BE404764	7192	616	80.5	globlastp
3700	LAB268	wheat|gb164|CA484177	7193	616	80.5	globlastp
3701	LAB268	beet|gb162|BE590319	7194	616	80	globlastp
3702	LAB269	sugarcane|gb157.3|CA073377	7195	617	96.2	globlastp
3703	LAB269	sugarcane|gb157.3|CA073918	7196	617	96.2	globlastp
3704	LAB269	sugarcane|gb157.3|CA116132	7195	617	96.2	globlastp
3705	LAB269	sorghum|09v1|SB01G000950	7197	617	95	globlastp
3706	LAB269	sorghum|gb161.crp|BF585848	7197	617	95	globlastp
3707	LAB269	sugarcane|gb157.3|CA073796	7197	617	95	globlastp
3708	LAB269	sugarcane|gb157.3|CA079491	7197	617	95	globlastp
3709	LAB269	sugarcane|gb157.3|CA090885	7197	617	95	globlastp
3710	LAB269	sugarcane|gb157.3|CA242409	7198	617	93.1	globlastp
3711	LAB269	cenchrus|gb166|EB669873	7199	617	92.5	globlastp
3712	LAB269	sugarcane|gb157.3|BU102855	7200	617	92.5	globlastp
3713	LAB269	sugarcane|gb157.3|CA085423	7200	617	92.5	globlastp
3714	LAB269	sugarcane|gb157.3|CA114248	7200	617	92.5	globlastp
3715	LAB269	sugarcane|10v1|CA073377	7201	617	92.45	glotblastn
3716	LAB269	sugarcane|gb157.3|CA071501	7202	617	91.9	globlastp
3717	LAB269	sugarcane|10v1|CA073796	7203	617	91.82	glotblastn
3718	LAB269	sugarcane|10v1|CA088321	7204	617	91.82	glotblastn
3719	LAB269	cotton|gb164|DT556619	7205	617	91.2	globlastp
3720	LAB269	maize|gb170|AA661456	7206	617	91.2	globlastp
3721	LAB269	maize|gb170|AI395882	7205	617	91.2	globlastp
3722	LAB269	sorghum|09v1|SB02G030950	7207	617	91.2	globlastp
3723	LAB269	sorghum|gb161.crp|AI657275	7207	617	91.2	globlastp
3724	LAB269	sugarcane|gb157.3|CA079328	7208	617	91.19	glotblastn
3725	LAB269	sorghum|09v1|SB01G039250	7209	617	90.6	globlastp
3726	LAB269	sorghum|gb161.crp|AI396033	7209	617	90.6	globlastp
3727	LAB269	sugarcane|gb157.3|CA066505	7210	617	90.6	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3728	LAB269	sugarcane|gb157.3|CA071525	7211	617	90.6	globlastp
3729	LAB269	maize|gb170|LLFL026072	7212	617	90	glotblastn
3730	LAB269	sugarcane|gb157.3|CA073176	7213	617	90	globlastp
3731	LAB269	sugarcane|10v1|CA071525	7214	617	89.94	glotblastn
3732	LAB269	sugarcane|gb157.3|CA114685	7215	617	89.94	glotblastn
3733	LAB269	rice|gb170|OS01G31800	7216	617	89.4	globlastp
3734	LAB269	rice|gb170|OS03G17100	7216	617	89.4	globlastp
3735	LAB269	switchgrass|gb167|FE601150	7217	617	89.4	globlastp
3736	LAB269	switchgrass|gb167|FL727559	7218	617	89.4	globlastp
3737	LAB269	maize|gb170|LLEG052954	7219	617	89.38	glotblastn
3738	LAB269	sugarcane|10v1|BU102855	7220	617	89.31	glotblastn
3739	LAB269	sugarcane|10v1|CA071501	7221	617	89.31	glotblastn
3740	LAB269	sugarcane|gb157.3|CA077796	7222	617	89.31	glotblastn
3741	LAB269	sorghum|09v1|SB01G039240	7223	617	88.8	globlastp
3742	LAB269	sorghum|gb161.crp|AI444702	7223	617	88.8	globlastp
3743	LAB269	switchgrass|gb167|FE614567	7224	617	88.8	globlastp
3744	LAB269	sugarcane|gb157.3|CA116578	7225	617	88.75	glotblastn
3745	LAB269	sugarcane|10v1|CA072812	7226	617	88.68	glotblastn
3746	LAB269	maize|gb170|LLCF059749	7227	617	88.68	glotblastn
3747	LAB269	cenchrus|gb166|EB652626	7228	617	88.1	globlastp
3748	LAB269	maize|gb170|AI395995	7229	617	88.1	globlastp
3749	LAB269	maize|gb170|LLDR828188	7230	617	88.1	globlastp
3750	LAB269	maize|gb170|ZMU08225	7230	617	88.1	globlastp
3751	LAB269	switchgrass|gb167|FE599840	7231	617	88.1	globlastp
3752	LAB269	sugarcane|gb157.3|CA123898	7232	617	88.05	glotblastn
3753	LAB269	sugarcane|gb157.3|CA239448	7233	617	88.05	glotblastn
3754	LAB269	millet|09v1|CD724737	7234	617	87.5	glotblastn
3755	LAB269	maize|gb170|AI396033	7235	617	87.5	globlastp
3756	LAB269	switchgrass|gb167|DN151599	7236	617	87.5	globlastp
3757	LAB269	oat|10v1|GO586241	7237	617	87.4	globlastp
3758	LAB269	sugarcane|gb157.3|CA087750	7238	617	87	globlastp
3759	LAB269	sugarcane|gb157.3|CA118440	7239	617	87	globlastp
3760	LAB269	gerbera|09v1|AJ752939	7240	617	86.8	globlastp
3761	LAB269	oat|10v1|CN814889	7241	617	86.8	globlastp
3762	LAB269	sugarcane|gb157.3|CA123779	7242	617	86.79	glotblastn
3763	LAB269	sugarcane|gb157.3|CA101458	7243	617	86.7	globlastp
3764	LAB269	beet|gb162|BQ588291	7244	617	86.2	globlastp
3765	LAB269	fescue|gb161|DT689657	7245	617	86.2	globlastp
3766	LAB269	sugarcane|gb157.3|CA124793	7246	617	86.2	globlastp
3767	LAB269	brachypodium|09v1|DV488718	7247	617	85.7	globlastp
3768	LAB269	brachypodium|gb169|BE401791	7247	617	85.7	globlastp
3769	LAB269	brachypodium|gb169|BI960263	7248	617	85.6	globlastp
3770	LAB269	sugarcane|gb157.3|CA129121	7249	617	85.53	glotblastn
3771	LAB269	switchgrass|gb167|DN140680	7250	617	85.5	globlastp

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3772	LAB269	switchgrass|gb167|DN141778	7250	617	85.5	globlastp
3773	LAB269	switchgrass|gb167|FE633841	7250	617	85.5	globlastp
3774	LAB269	switchgrass|gb167|FL736645	7250	617	85.5	globlastp
3775	LAB269	sorghum|09v1|SB09G001520	7251	617	85.2	globlastp
3776	LAB269	sorghum|gb161.crp|AW287442	7251	617	85.2	globlastp
3777	LAB269	sugarcane|gb157.3|CA080385	7252	617	85.1	globlastp
3778	LAB269	sugarcane|gb157.3|CA100971	7253	617	85.1	globlastp
3779	LAB269	sugarcane|gb157.3|CA103471	7253	617	85.1	globlastp
3780	LAB269	maize|gb170|T18401	7254	617	85	globlastp
3781	LAB269	oat|10v1|GR358067	7255	617	84.9	globlastp
3782	LAB269	barley|10v1|BQ460682	7256	617	84.9	globlastp
3783	LAB269	barley|gb157SOLEXA|BQ460682	7256	617	84.9	globlastp
3784	LAB269	cassava|09v1|BM259730	7257	617	84.9	globlastp
3785	LAB269	cassava|gb164|BM259730	7257	617	84.9	globlastp
3786	LAB269	liriodendron|gb166|DT579867	7258	617	84.9	globlastp
3787	LAB269	maize|gb170|LLFK966020	7259	617	84.9	globlastp
3788	LAB269	prunus|gb167|DY646167	7260	617	84.9	globlastp
3789	LAB269	lotus|09v1|BG661990	7261	617	84.4	globlastp
3790	LAB269	lotus|gb157.2|BG661990	7261	617	84.4	globlastp
3791	LAB269	oil_palm|gb166|EL681634	7262	617	84.4	globlastp
3792	LAB269	gerbera|09v1|AJ753301	7263	617	84.3	globlastp
3793	LAB269	citrus|gb166|BQ624783	7264	617	84.3	globlastp
3794	LAB269	cowpea|gb166|FC456663	7265	617	84.3	globlastp
3795	LAB269	cowpea|gb166|FC456998	7266	617	84.3	globlastp
3796	LAB269	medicago|09v1|BF643805	7267	617	84.3	globlastp
3797	LAB269	soybean|gb168|CA898616	7268	617	84.3	globlastp
3798	LAB269	artemisia|10v1|EY031915	7269	617	84.28	glotblastn
3799	LAB269	artemisia|10v1|EY075725	7269	617	84.28	glotblastn
3800	LAB269	artemisia|10v1|GW328612	7269	617	84.28	glotblastn
3801	LAB269	artemisia|10v1|GW329305	7269	617	84.28	glotblastn
3802	LAB269	artemisia|10v1|SRR019254S0011741	7269	617	84.28	glotblastn
3803	LAB269	artemisia|10v1|SRR019254S0001774	7269	617	84.28	glotblastn
3804	LAB269	artemisia|gb164|EY031915	7269	617	84.28	glotblastn
3805	LAB269	artemisia|10v1|SRR019254S0002410	7269	617	84.28	glotblastn
3806	LAB269	artemisia|gb164|EY055445	7269	617	84.28	glotblastn
3807	LAB269	lotus|09v1|BI418493	7270	617	84	globlastp
3808	LAB269	lotus|gb157.2|BI418493	7270	617	84	globlastp
3809	LAB269	maize|gb170|BM259143	7271	617	84	globlastp
3810	LAB269	sugarcane|gb157.3|CA071927	7272	617	84	globlastp
3811	LAB269	sugarcane|gb157.3|CA118816	7272	617	84	globlastp
3812	LAB269	spurge|gb161|AF242311	7273	617	83.95	glotblastn
3813	LAB269	castorbean|gb160|EE259198	7274	617	83.8	globlastp
3814	LAB269	castorbean|09v1|EE259198	7274	617	83.8	globlastp
3815	LAB269	cynara|gb167|GE588632	7275	617	83.8	globlastp

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3816	LAB269	maize|gb170|LLAI666147	7276	617	83.8	globlastp
3817	LAB269	onion|gb162|BI095529	7277	617	83.75	glotblastn
3818	LAB269	sugarcane|gb157.3|CA113890	7278	617	83.7	globlastp
3819	LAB269	cichorium|gb171|EH704900	7279	617	83.65	glotblastn
3820	LAB269	gerbera|09v1|AJ756141	7280	617	83.6	globlastp
3821	LAB269	apple|gb171|CN579547	7281	617	83.6	globlastp
3822	LAB269	apple|gb171|CN861500	7282	617	83.6	globlastp
3823	LAB269	beet|gb162|BI543765	7283	617	83.6	globlastp
3824	LAB269	cassava|09v1|BM259833	7284	617	83.6	globlastp
3825	LAB269	cassava|gb164|BM259833	7284	617	83.6	globlastp
3826	LAB269	chestnut|gb170|SRR006295S0009247	7285	617	83.6	globlastp
3827	LAB269	cotton|gb164|BE052224	7286	617	83.6	globlastp
3828	LAB269	cotton|gb164|BE055384	7286	617	83.6	globlastp
3829	LAB269	cotton|gb164|CO110571	7287	617	83.6	globlastp
3830	LAB269	cotton|gb164|DT048656	7286	617	83.6	globlastp
3831	LAB269	oak|gb170|DN950260	7285	617	83.6	globlastp
3832	LAB269	poppy|gb166|FG607964	7288	617	83.6	globlastp
3833	LAB269	soybean|gb168|BE660063	7289	617	83.6	globlastp
3834	LAB269	soybean|gb168|BI273631	7290	617	83.6	globlastp
3835	LAB269	spurge|gb161|AW874994	7291	617	83.6	globlastp
3836	LAB269	wheat|gb164|BQ802458	7292	617	83.6	globlastp
3837	LAB269	strawberry|gb164|DY674860	7293	617	83.3	globlastp
3838	LAB269	cenchrus|gb166|EB656997	7294	617	83.2	globlastp
3839	LAB269	maize|gb170|LLEB406213	7295	617	83.12	glotblastn
3840	LAB269	artemisia|10v1|SRR019254S0013055	7296	617	83.1	globlastp
3841	LAB269	tea|10v1|CV013635	7297	617	83.1	globlastp
3842	LAB269	castorbean|gb160|MDL29154M000210	7298	617	83.1	globlastp
3843	LAB269	castorbean|09v1|EV520334	7298	617	83.1	globlastp
3844	LAB269	ginger|gb164|DY353641	7299	617	83.1	globlastp
3845	LAB269	medicago|gb157.2|BF643805	7300	617	83.1	globlastp
3846	LAB269	sugarcane|gb157.3|CA120528	7301	617	83.1	globlastp
3847	LAB269	tea|gb171|CV013635	7297	617	83.1	globlastp
3848	LAB269	bean|gb167|CA898614	7302	617	83.02	glotblastn
3849	LAB269	iceplant|gb164|BE130702	7303	617	83.02	glotblastn
3850	LAB269	wheat|gb164|AL826759	7304	617	83.02	glotblastn
3851	LAB269	flax|09v1|EU830866	7305	617	83	globlastp
3852	LAB269	orobanche|10v1|SRR023189S0002180	7306	617	83	globlastp
3853	LAB269	cowpea|gb166|FF397354	7307	617	83	globlastp
3854	LAB269	liquorice|gb171|FS254761	7308	617	83	globlastp
3855	LAB269	lotus|09v1|LLAW719911	7309	617	83	globlastp
3856	LAB269	lotus|gb157.2|AW719911	7309	617	83	globlastp
3857	LAB269	pseudoroegneria|gb167|FF340751	7310	617	83	globlastp
3858	LAB269	soybean|gb168|AL377356	7311	617	83	globlastp
3859	LAB269	soybean|gb168|AW348342	7312	617	83	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3860	LAB269	ricc|gb170|OS05G02300	7313	617	82.7	globlastp
3861	LAB269	sugarcanc|10v1|CA080385	7314	617	82.61	glotblastn
3862	LAB269	eschscholzia|10v1|CD480726	7315	617	82.6	globlastp
3863	LAB269	centaurea|gb166|EL932239	7316	617	82.6	globlastp
3864	LAB269	lettuce|10v1|CV700185	7317	617	82.6	globlastp
3865	LAB269	lettuce|gb157.2|CV700185	7317	617	82.6	globlastp
3866	LAB269	lettuce|10v1|DW043988	7317	617	82.6	globlastp
3867	LAB269	lettuce|gb157.2|DW043988	7317	617	82.6	globlastp
3868	LAB269	lettuce|10v1|DW145083	7317	617	82.6	globlastp
3869	LAB269	lettuce|gb157.2|DW145083	7317	617	82.6	globlastp
3870	LAB269	coffea|10v1|DV673276	7318	617	82.5	globlastp
3871	LAB269	eggplant|10v1|FS017038	7319	617	82.5	globlastp
3872	LAB269	ginseng|10v1|DV554362	7320	617	82.5	globlastp
3873	LAB269	avocado|10v1|CV004562	7321	617	82.5	globlastp
3874	LAB269	avocado|gb164|CV004562	7321	617	82.5	globlastp
3875	LAB269	brachypodium|gb169|BE398477	7322	617	82.5	globlastp
3876	LAB269	brachypodium|09v1|DV475962	7323	617	82.5	globlastp
3877	LAB269	brachypodium|gb169|BE400244	7323	617	82.5	globlastp
3878	LAB269	cotton|gb164|BF275621	7324	617	82.5	globlastp
3879	LAB269	cotton|gb164|DR461180	7324	617	82.5	globlastp
3880	LAB269	kiwi|gb166|FG404103	7325	617	82.5	globlastp
3881	LAB269	kiwi|gb166|FG410690	7326	617	82.5	globlastp
3882	LAB269	medicago|09v1|BE239402	7327	617	82.5	globlastp
3883	LAB269	medicago|gb157.2|BE239402	7327	617	82.5	globlastp
3884	LAB269	sunflower|gb162|CD850054	7328	617	82.5	globlastp
3885	LAB269	tca|10v1|FE861646	7329	617	82.5	globlastp
3886	LAB269	tea|gb171|FE861646	7329	617	82.5	globlastp
3887	LAB269	artemisia|10v1|GW329229	7330	617	82.4	globlastp
3888	LAB269	jatropha|09v1|GT228525	7331	617	82.4	globlastp
3889	LAB269	orobanche|10v1|SRR023189S0007626	7332	617	82.4	globlastp
3890	LAB269	grape|gb160|CF209226	7333	617	82.4	globlastp
3891	LAB269	antirrhinum|gb166|AJ568652	7334	617	82.4	globlastp
3892	LAB269	barley|gb157SOLEXA|BQ470520	7335	617	82.4	globlastp
3893	LAB269	bruguiera|gb166|BP941111	7336	617	82.4	globlastp
3894	LAB269	cassava|09v1|FF534531	7337	617	82.4	globlastp
3895	LAB269	clover|gb162|BB902942	7338	617	82.4	globlastp
3896	LAB269	papaya|gb165|EX255877	7339	617	82.4	globlastp
3897	LAB269	peanut|gb171|CD038080	7340	617	82.4	globlastp
3898	LAB269	peanut|gb171|CX018047	7341	617	82.4	globlastp
3899	LAB269	peanut|gb171|EE124672	7342	617	82.4	globlastp
3900	LAB269	poplar|10v1|AI162505	7343	617	82.4	globlastp
3901	LAB269	poplar|gb170|AI162505	7343	617	82.4	globlastp
3902	LAB269	tea|10v1|CV014555	7344	617	82.4	globlastp
3903	LAB269	tea|gb171|CV014555	7344	617	82.4	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3904	LAB269	tragopogon|10v1|SRR020205S0003365	7345	617	82.39	glotblastn
3905	LAB269	cacao|gb167|EH057782	7346	617	82.39	glotblastn
3906	LAB269	canola|10v1|EG020378	7347	617	82.39	glotblastn
3907	LAB269	canola|gb161|EG020378	7348	617	82.39	glotblastn
3908	LAB269	rye|gb164|BE704593	7349	617	82.39	glotblastn
3909	LAB269	artemisia|10v1|SRR019254S0011939	-	617	82.39	glotblastn
3910	LAB269	cichorium|gb171|EH698455	-	617	82.39	glotblastn
3911	LAB269	cucumber|09v1|CK085829	7350	617	82.1	globlastp
3912	LAB269	barley|10v1|BF621287	7351	617	82.1	globlastp
3913	LAB269	barley|gb157SOLEXA|AL508027	7351	617	82.1	globlastp
3914	LAB269	melon|gb165|DV633078	7350	617	82.1	globlastp
3915	LAB269	sugarcane|gb157.3|CA246050	7352	617	82.1	glotblastn
3916	LAB269	wheat|gb164|BE415790	7353	617	82.1	globlastp
3917	LAB269	lettuce|10v1|DW074552	7354	617	82	globlastp
3918	LAB269	brachypodium|09v1|SRR031795S0043037	7355	617	82	globlastp
3919	LAB269	lettuce|gb157.2|DW074552	7354	617	82	globlastp
3920	LAB269	onion|gb162|CF445361	7356	617	82	globlastp
3921	LAB269	sunflower|gb162|CF077703	7357	617	82	globlastp
3922	LAB269	sugarcane|10v1|BQ529676	7358	617	81.99	glotblastn
3923	LAB269	sugarcane|gb157.3|BQ529676	7358	617	81.99	glotblastn
3924	LAB269	eggplant|10v1|AB018242	7359	617	81.9	globlastp
3925	LAB269	cynara|gb167|GE588059	7360	617	81.9	globlastp
3926	LAB269	dandelion|gb161|DY816120	7361	617	81.9	globlastp
3927	LAB269	ginger|gb164|DY366805	7362	617	81.9	globlastp
3928	LAB269	maize|gb170|LLDV025110	7363	617	81.9	globlastp
3929	LAB269	sunflower|gb162|CD848740	7361	617	81.9	globlastp
3930	LAB269	sunflower|gb162|CD850823	7361	617	81.9	globlastp
3931	LAB269	sunflower|gb162|EL460335	7361	617	81.9	globlastp
3932	LAB269	lettuce|10v1|DW076202	7364	617	81.88	glotblastn
3933	LAB269	nasturtium|10v1|SRR032558S0003969	7365	617	81.8	globlastp
3934	LAB269	grape|gb160|CB340156	7366	617	81.8	globlastp
3935	LAB269	barley|10v1|BQ470520	7367	617	81.8	globlastp
3936	LAB269	medicago|09v1|AL384067	7368	617	81.8	globlastp
3937	LAB269	medicago|gb157.2|AL384067	7368	617	81.8	globlastp
3938	LAB269	nuphar|gb166|CD473263	7369	617	81.8	globlastp
3939	LAB269	nuphar|gb166|CD474301	7370	617	81.8	globlastp
3940	LAB269	nuphar|gb166|CD475325	7371	617	81.8	globlastp
3941	LAB269	oil_palm|gb166|CN600853	7372	617	81.8	globlastp
3942	LAB269	oil_palm|gb166|EL682266	7373	617	81.8	globlastp
3943	LAB269	pseudoroegneria|gb167|FF342758	7374	617	81.8	globlastp
3944	LAB269	sesame|10v1|BU667747	7375	617	81.8	globlastp
3945	LAB269	sesame|gb157.2|BU667747	7375	617	81.8	globlastp
3946	LAB269	tamarix|gb166|CF199999	7376	617	81.8	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
3947	LAB269	walnuts|gb166|EL893578	7377	617	81.8	globlastp
3948	LAB269	wheat|gb164|BF475107	7378	617	81.8	globlastp
3949	LAB269	wheat|gb164|BM137700	7379	617	81.8	globlastp
3950	LAB269	pea|09v1|PEAH2A	7380	617	81.76	glotblastn
3951	LAB269	bean|gb167|CA898623	7381	617	81.76	glotblastn
3952	LAB269	lettuce|gb157.2|DW046318	7382	617	81.76	glotblastn
3953	LAB269	lettuce|gb157.2|DW104400	7383	617	81.76	glotblastn
3954	LAB269	lettuce|gb157.2|DW105504	7382	617	81.76	glotblastn
3955	LAB269	lettuce|gb157.2|DW148380	7383	617	81.76	glotblastn
3956	LAB269	lettuce|gb157.2|DW153827	7384	617	81.76	glotblastn
3957	LAB269	maize|gb170|LLBE345313	7385	617	81.76	glotblastn
3958	LAB269	senecio|gb170|DY658597	7386	617	81.76	glotblastn
3959	LAB269	lettuce|10v1|DW104400	7383	617	81.76	glotblastn
3960	LAB269	brachypodium|09v1|SRR031797S0022709	7387	617	81.7	globlastp
3961	LAB269	cotton|gb164|BE055408	7388	617	81.6	globlastp
3962	LAB269	lettuce|gb157.2|DW123638	7389	617	81.6	globlastp
3963	LAB269	avocado|10v1|CK753619	7390	617	81.5	globlastp
3964	LAB269	avocado|gb164|CK753619	7390	617	81.5	globlastp
3965	LAB269	barley|10v1|AJ473557	7391	617	81.5	globlastp
3966	LAB269	barley|gb157SOLEXA|AJ473557	7391	617	81.5	globlastp
3967	LAB269	cichorium|gb171|EH682187	7392	617	81.5	globlastp
3968	LAB269	sugarcane|10v1|CA071927	7314	617	81.48	glotblastn
3969	LAB269	dandelion|gb161|DY834183	7393	617	81.4	globlastp
3970	LAB269	maize|gb170|LLFK947559	7394	617	81.25	glotblastn
3971	LAB269	ginseng|10v1|DV555645	7395	617	81.2	globlastp
3972	LAB269	orobanche|10v1|SRR023189S0008983	7396	617	81.2	globlastp
3973	LAB269	tragopogon|10v1|SRR020205S0018059	7397	617	81.2	globlastp
3974	LAB269	catharanthus|gb166|EG558535	7398	617	81.2	globlastp
3975	LAB269	catharanthus|gb166|EG562453	7399	617	81.2	globlastp
3976	LAB269	catharanthus|gb166|FD416131	7400	617	81.2	globlastp
3977	LAB269	centaurea|gb166|EH753053	7401	617	81.2	globlastp
3978	LAB269	ginger|gb164|DY377650	7402	617	81.2	globlastp
3979	LAB269	kiwi|gb166|FG428941	7403	617	81.2	globlastp
3980	LAB269	safflower|gb162|EL377394	7404	617	81.2	globlastp
3981	LAB269	sunflower|gb162|CD849669	7405	617	81.2	globlastp
3982	LAB269	artemisia|10v1|SRR019254S0001113	7406	617	81.13	glotblastn
3983	LAB269	jatropha|09v1|GT229311	7407	617	81.13	glotblastn
3984	LAB269	nasturtium|10v1|SRR032558S0000657	7408	617	81.13	glotblastn
3985	LAB269	nasturtium|10v1|SRR032558S0008269	7409	617	81.13	glotblastn
3986	LAB269	orobanche|10v1|SRR023189S0017978	7410	617	81.13	glotblastn
3987	LAB269	pea|09v1|EX568943	7411	617	81.13	glotblastn
3988	LAB269	dandelion|gb161|DY840384	7412	617	81.13	glotblastn
3989	LAB269	lettuce|10v1|DW048053	7413	617	81.13	glotblastn

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3990	LAB269	lettuce|gb157.2|DW048053	7413	617	81.13	glotblastn
3991	LAB269	lettuce|gb157.2|DW106082	7414	617	81.13	glotblastn
3992	LAB269	lettuce|gb157.2|DW146506	7414	617	81.13	glotblastn
3993	LAB269	nicotiana_benthamiana|gb162|CN655396	7415	617	81.13	glotblastn
3994	LAB269	rye|gb164|BE586810	7416	617	81.13	glotblastn
3995	LAB269	spurge|gb161|DV157416	7417	617	81.13	glotblastn
3996	LAB269	sunflower|gb162|CD848219	7418	617	81.13	glotblastn
3997	LAB269	barley|10v1|BE455608	7419	617	81.1	globlastp
3998	LAB269	chickpea|09v2|GR401929	7420	617	81.1	globlastp
3999	LAB269	cucumber|09v1|CK085962	7421	617	81.1	globlastp
4000	LAB269	medicago|09v1|AL377356	7422	617	81.1	globlastp
4001	LAB269	medicago|09v1|BF519200	7423	617	81.1	globlastp
4002	LAB269	orobanche|10v1|SRR023189S0010876	7424	617	81.1	globlastp
4003	LAB269	orobanche|10v1|SRR023189S0028654	7425	617	81.1	globlastp
4004	LAB269	pea|09v1|EX569036	7426	617	81.1	globlastp
4005	LAB269	barley|gb157SOLEXA|AL506299	7419	617	81.1	globlastp
4006	LAB269	basilicum|10v1|DY323812	7427	617	81.1	globlastp
4007	LAB269	basilicum|gb157.3|DY323812	7427	617	81.1	globlastp
4008	LAB269	bean|gb167|CA898617	7428	617	81.1	globlastp
4009	LAB269	cacao|gb167|EH057760	7429	617	81.1	globlastp
4010	LAB269	cassava|gb164|DB935361	7430	617	81.1	globlastp
4011	LAB269	cichorium|gb171|DT212229	7431	617	81.1	globlastp
4012	LAB269	clover|gb162|BB937077	7432	617	81.1	globlastp
4013	LAB269	kiwi|gb166|FG403789	7433	617	81.1	globlastp
4014	LAB269	medicago|gb157.2|AW574007	7434	617	81.1	globlastp
4015	LAB269	oak|gb170|CR627534	7435	617	81.1	globlastp
4016	LAB269	peanut|gb171|CX128201	7436	617	81.1	globlastp
4017	LAB269	tobacco|gb162|BQ843038	7437	617	81.1	globlastp
4018	LAB269	triphysaria|10v1|BM356994	7438	617	81.1	globlastp
4019	LAB269	triphysaria|10v1|DR173737	7439	617	81.1	globlastp
4020	LAB269	triphysaria|gb164|EY137032	7439	617	81.1	globlastp
4021	LAB269	wheat|gb164|BE498725	7440	617	81.1	globlastp
4022	LAB269	wheat|gb164|CK202244	7441	617	81.1	globlastp
4023	LAB269	heritiera|10v1|SRR005795S0031964	7442	617	81	globlastp
4024	LAB269	barley|gb157SOLEXA|AL511284	7443	617	81	globlastp
4025	LAB269	lettuce|gb157.2|DW046029	7444	617	81	globlastp
4026	LAB269	barley|10v1|AW983233	7443	617	81	globlastp
4027	LAB269	barley|gb157SOLEXA|AL506114	7445	617	80.98	glotblastn
4028	LAB269	sugarcane|gb157.3|CA200286	7446	617	80.98	glotblastn
4029	LAB269	cleome_gynandra|10v1|SRR015532S0022202	7447	617	80.75	glotblastn
4030	LAB269	artemisia|10v1|EY082330	7448	617	80.7	globlastp
4031	LAB269	artemisia|10v1|EY084850	7448	617	80.7	globlastp

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4032	LAB269	artemisia|10v1|SRR019254S0007700	7448	617	80.7	globlastp
4033	LAB269	artemisia|10v1|SRR019254S0012643	7448	617	80.7	globlastp
4034	LAB269	ipomoea_nil|10v1|BJ554819	7449	617	80.7	globlastp
4035	LAB269	artemisia|10v1|EY039776	7448	617	80.7	globlastp
4036	LAB269	artemisia|gb164|EY082330	7448	617	80.7	globlastp
4037	LAB269	artemisia|gb164|EY084850	7448	617	80.7	globlastp
4038	LAB269	ipomoea|gb157.2|BJ554819	7449	617	80.7	globlastp
4039	LAB269	sunflower|gb162|CD855395	7450	617	80.7	globlastp
4040	LAB269	orobanche|10v1|SRR023189S0001029	7451	617	80.62	glotblastn
4041	LAB269	lettuce|gb157.2|DW076202	7452	617	80.62	glotblastn
4042	LAB269	sorghum|09v1|SB09G022690	7453	617	80.61	glotblastn
4043	LAB269	sorghum|gb161.crp|AW681166	7453	617	80.61	glotblastn
4044	LAB269	cleome_spinosa|10v1|GR932674	7454	617	80.6	globlastp
4045	LAB269	eggplant|10v1|FS000322	7455	617	80.6	globlastp
4046	LAB269	ginseng|10v1|DV553422	7456	617	80.6	globlastp
4047	LAB269	apple|gb171|CN494745	7457	617	80.6	globlastp
4048	LAB269	apple|gb171|CN880302	7458	617	80.6	globlastp
4049	LAB269	centaurea|gb166|EL930888	7459	617	80.6	globlastp
4050	LAB269	centaurea|gb166|EL934894	7460	617	80.6	globlastp
4051	LAB269	rose|10v1|BI978192	7461	617	80.6	globlastp
4052	LAB269	rose|gb157.2|BI978192	7461	617	80.6	globlastp
4053	LAB269	strawberry|gb164|EX664843	7462	617	80.6	globlastp
4054	LAB269	sugarcane|gb157.3|CA112320	7463	617	80.6	globlastp
4055	LAB269	sugarcane|gb157.3|CA193165	7464	617	80.6	globlastp
4056	LAB269	tobacco|gb162|BP192536	7465	617	80.6	globlastp
4057	LAB269	artemisia|10v1|SRR019254S0007762	7466	617	80.5	glotblastn
4058	LAB269	medicago|09v1|AL376385	7467	617	80.5	globlastp
4059	LAB269	monkeyflower|10v1|DV206744	7468	617	80.5	globlastp
4060	LAB269	oat|10v1|GO586644	7469	617	80.5	glotblastn
4061	LAB269	orobanche|10v1|SRR023189S0000458	7470	617	80.5	glotblastn
4062	LAB269	orobanche|10v1|SRR023189S0014080	7471	617	80.5	globlastp
4063	LAB269	pea|09v1|EX571168	7472	617	80.5	glotblastn
4064	LAB269	pea|09v1|EX571270	7473	617	80.5	globlastp
4065	LAB269	triphysaria|10v1|DR176290	7474	617	80.5	globlastp
4066	LAB269	antirrhinum|gb166|AJ558758	7475	617	80.5	glotblastn
4067	LAB269	antirrhinum|gb166|AJ568035	7476	617	80.5	glotblastn
4068	LAB269	barley|gb157SOLEXA|BF625527	7477	617	80.5	glotblastn
4069	LAB269	chestnut|gb170|SRR006295S0011437	7478	617	80.5	globlastp
4070	LAB269	fescue|gb161|DT678950	7479	617	80.5	glotblastn
4071	LAB269	fescue|gb161|DT685753	7480	617	80.5	glotblastn
4072	LAB269	kiwi|gb166|FG403861	7481	617	80.5	globlastp
4073	LAB269	lettuce|gb157.2|DW050465	7482	617	80.5	glotblastn
4074	LAB269	lettuce|10v1|DW074637	7483	617	80.5	glotblastn
4075	LAB269	lettuce|gb157.2|DW074637	7484	617	80.5	glotblastn

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4076	LAB269	lettuce|gb157.2|DW148769	7485	617	80.5	glotblastn
4077	LAB269	liriodendron|gb166|CK748317	7486	617	80.5	glotblastn
4078	LAB269	maize|gb170|LLDQ245995	7487	617	80.5	glotblastn
4079	LAB269	medicago|gb157.2|AL376384	7488	617	80.5	globlastp
4080	LAB269	nicotiana_benthamiana|gb162|CN741779	7489	617	80.5	globlastp
4081	LAB269	petunia|gb171|CV300217	7490	617	80.5	globlastp
4082	LAB269	poppy|gb166|FE967078	7491	617	80.5	glotblastn
4083	LAB269	senecio|gb170|DY658035	7492	617	80.5	globlastp
4084	LAB269	sugarcane|gb157.3|CA124689	7493	617	80.5	globlastp
4085	LAB269	sugarcane|gb157.3|CA214343	7494	617	80.5	glotblastn
4086	LAB269	sunflower|gb162|CD852070	7495	617	80.5	globlastp
4087	LAB269	tobacco|gb162|DV158750	7496	617	80.5	glotblastn
4088	LAB269	triphysaria|gb164|BM356994	7497	617	80.5	globlastp
4089	LAB269	triphysaria|gb164|EY129294	7498	617	80.5	globlastp
4090	LAB269	triphysaria|gb164|EY136702	7499	617	80.5	glotblastn
4091	LAB269	barley|gb157SOLEXA|AL501872	7500	617	80.4	globlastp
4092	LAB269	lettuce|gb157.2|DW080680	7501	617	80.4	globlastp
4093	LAB269	maize|gb170|AI939777	7502	617	80.25	glotblastn
4094	LAB269	triphysaria|gb164|BE574777	7503	617	80.25	glotblastn
4095	LAB269	triphysaria|gb164|EX999662	7504	617	80.25	glotblastn
4096	LAB269	artemisia|10v1|EY082130	7505	617	80.1	globlastp
4097	LAB269	artemisia|10v1|GW328287	7506	617	80.1	globlastp
4098	LAB269	artemisia|10v1|GW328462	7507	617	80.1	globlastp
4099	LAB269	artemisia|10v1|SRR019254S0000360	7508	617	80.1	globlastp
4100	LAB269	artemisia|10v1|SRR019254S0003074	7508	617	80.1	globlastp
4101	LAB269	artemisia|10v1|SRR019254S0042995	7508	617	80.1	globlastp
4102	LAB269	artemisia|10v1|SRR019254S0094458	7506	617	80.1	globlastp
4103	LAB269	artemisia|10v1|SRR019254S0000494	7508	617	80.1	globlastp
4104	LAB269	artemisia|gb164|EY082130	7505	617	80.1	globlastp
4105	LAB269	rice|gb170|OS05G38640	7509	617	80.1	globlastp
4106	LAB269	gerbera|09v1|AJ754996	7510	617	80	globlastp
4107	LAB269	tea|10v1|CV013767	7511	617	80	globlastp
4108	LAB269	cynara|gb167|GE592728	7512	617	80	globlastp
4109	LAB269	radish|gb164|EW726668	7513	617	80	glotblastn
4110	LAB269	safflower|gb162|EL403937	7514	617	80	globlastp
4111	LAB269	sunflower|gb162|CD851052	7515	617	80	globlastp
4112	LAB269	tea|gb171|CV013640	7511	617	80	globlastp
4113	LAB269	tobacco|gb162|BP192693	7516	617	80	globlastp
4114	LAB269	tobacco|gb162|CV018747	7517	617	80	globlastp
4115	LAB270	maize|gb170|AI615043	7518	618	98.1	globlastp
4116	LAB270	maize|gb170|AI586603	7519	618	97.2	globlastp
4117	LAB270	rice|gb170|OS02G55410	7520	618	96.8	globlastp
4118	LAB270	brachypodium|09v1|GT797969	7521	618	93.5	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
4119	LAB270	wheat|gb164|BE400172	7522	618	93.3	globlastp
4120	LAB270	brachypodium|gb169|BE400172	7523	618	93.1	globlastp
4121	LAB270	barley|10v1|AV914416	7524	618	92.9	globlastp
4122	LAB270	barley|gb157SOLEXA|AL507066	7525	618	83.7	globlastp
4123	LAB271	switchgrass|gb167|FE611169	7526	619	92.15	glotblastn
4124	LAB271	switchgrass|gb167|FE600805	7527	619	91.1	globlastp
4125	LAB271	pseudoroegneria|gb167|FF345930	7528	619	80.7	globlastp
4126	LAB271	leymus|gb166|EG378703	7529	619	80.6	globlastp
4127	LAB272	maize|gb170|AW067349	7530	620	94.9	globlastp
4128	LAB272	rice|gb170|OS05G39310	7531	620	92.6	globlastp
4129	LAB272	medicago|09v1|AW256724	7532	620	81	globlastp
4130	LAB272	medicago|gb157.2|AW256724	7532	620	81	globlastp
4131	LAB272	monkeyflower|10v1|CV517019	7533	620	80.6	globlastp
4132	LAB272	soybean|gb168|AW126006	7534	620	80.4	globlastp
4133	LAB272	cassava|09v1|CK643325	7535	620	80.3	globlastp
4134	LAB272	apple|gb171|CK900562	7536	620	80.3	globlastp
4135	LAB272	kiwi|gb166|FG403505	7537	620	80.1	globlastp
4136	LAB272	soybean|gb168|AW256724	7538	620	80.1	globlastp
4137	LAB272	tobacco|gb162|DW002823	7539	620	80.1	globlastp
4138	LAB272	nasturtium|10v1|SRR032558S0007563	7540	620	80	globlastp
4139	LAB274	sugarcane|gb157.3|CA066127	7541	621	94.7	globlastp
4140	LAB274	switchgrass|gb167|FE605626	7542	621	84.7	globlastp
4141	LAB274	brachypodium|09v1|DV477522	7543	621	82.91	glotblastn
4142	LAB274	maize|gb170|CF013850	7544	621	82.6	globlastp
4143	LAB274	leymus|gb166|EG388830	7545	621	82.2	globlastp
4144	LAB274	pseudoroegneria|gb167|FF340314	7546	621	81.2	globlastp
4145	LAB274	wheat|gb164|BE429931	7547	621	80.1	globlastp
4146	LAB275	sugarcane|10v1|BQ535805	7548	622	95.7	globlastp
4147	LAB275	sugarcane|gb157.3|BQ535805	7549	622	95.3	globlastp
4148	LAB275	maize|gb170|AI586596	7550	622	93.1	globlastp
4149	LAB275	maize|gb170|AW129871	7551	622	90.9	globlastp
4150	LAB275	switchgrass|gb167|FE607687	7552	622	89.9	globlastp
4151	LAB276	sorghum|09v1|SB02G003590	7553	623	81.03	glotblastn
4152	LAB276	sorghum|gb161.crp|BE366228	7553	623	81.03	glotblastn
4153	LAB277	sugarcane|10v1|CA074813	7554	624	80.51	glotblastn
4154	LAB278	maize|gb170|AW054293	7555	625	91.3	globlastp
4155	LAB278	switchgrass|gb167|FE626292	7556	625	84.75	glotblastn
4156	LAB278	rice|gb170|OS10G32810	7557	625	82.3	globlastp
4157	LAB279	sugarcane|10v1|CA120192	7558	626	93.2	globlastp
4158	LAB279	sugarcane|gb157.3|CA120192	7559	626	92.6	globlastp
4159	LAB279	maize|gb170|AW355902	7560	626	84.57	glotblastn
4160	LAB279	maize|gb170|LLCO441794	7561	626	82.32	glotblastn
4161	LAB279	switchgrass|gb167|FE649969	7562	626	82.3	globlastp
4162	LAB280	maize|gb170|AW066651	7563	627	81.7	globlastp

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4163	LAB280	maize|gb170|AW289072	7564	627	81.5	globlastp
4164	LAB280	switchgrass|gb167|FE607054	7565	627	80.8	globlastp
4165	LAB281	sugarcane|gb157.3|BQ535213	7566	628	98.1	globlastp
4166	LAB281	switchgrass|gb167|DN141686	7567	628	93.4	globlastp
4167	LAB281	switchgrass|gb167|DN141006	7568	628	92.2	globlastp
4168	LAB281	maize|gb170|AW499357	7569	628	91.8	globlastp
4169	LAB281	rice|gb170|OS03G60080	7570	628	83.9	globlastp
4170	LAB281	maize|gb170|AI668448	7571	628	81.3	globlastp
4171	LAB283	sugarcane|gb157.3|CA075098	7572	630	99.5	globlastp
4172	LAB283	sugarcane|10v1|BQ533910	7572	630	99.5	globlastp
4173	LAB283	sugarcane|gb157.3|BQ533910	7573	630	98.4	globlastp
4174	LAB283	switchgrass|gb167|FE653888	7574	630	98.4	globlastp
4175	LAB283	switchgrass|gb167|FL789395	7575	630	98.4	globlastp
4176	LAB283	rice|gb170|OS03G22180	7576	630	96.3	globlastp
4177	LAB283	brachypodium|09v1|DV476934	7577	630	95.7	globlastp
4178	LAB283	brachypodium|gb169|BE424014	7577	630	95.7	globlastp
4179	LAB283	sorghum|09v1|SB02G042750	7578	630	95.7	globlastp
4180	LAB283	sorghum|gb161.crp|BI096623	7578	630	95.7	globlastp
4181	LAB283	maize|gb170|AI396532	7579	630	95.2	globlastp
4182	LAB283	sugarcane|gb157.3|CA084838	7580	630	95.2	globlastp
4183	LAB283	brachypodium|09v1|GT790399	7581	630	94.7	globlastp
4184	LAB283	maize|gb170|LLEB160472	7582	630	94.7	globlastp
4185	LAB283	sorghum|gb161.crp|AI491551	7583	630	94.7	globlastp
4186	LAB283	switchgrass|gb167|FL770723	7584	630	94.7	globlastp
4187	LAB283	wheat|gb164|CA594043	7585	630	94.7	globlastp
4188	LAB283	maize|gb170|AA030700	7586	630	94.1	globlastp
4189	LAB283	maize|gb170|AI629674	7586	630	94.1	globlastp
4190	LAB283	pseudoroegneria|gb167|FF340152	7587	630	94.1	globlastp
4191	LAB283	sorghum|09v1|SB09G004290	7588	630	94.1	globlastp
4192	LAB283	sugarcane|gb157.3|BQ530487	7588	630	94.1	globlastp
4193	LAB283	wheat|gb164|BE424014	7589	630	94.1	globlastp
4194	LAB283	sugarcane|10v1|BQ530487	7588	630	94.1	globlastp
4195	LAB283	rye|gb164|BE494252	7590	630	93.6	globlastp
4196	LAB283	wheat|gb164|BE422875	7591	630	93.6	globlastp
4197	LAB283	rice|gb170|OS05G06310	7592	630	93.1	globlastp
4198	LAB283	sugarcane|gb157.3|CA080289	7593	630	93.1	globlastp
4199	LAB283	sugarcane|gb157.3|CA094181	7594	630	93.1	globlastp
4200	LAB283	wheat|gb164|BG606257	7595	630	93.05	glotblastn
4201	LAB283	oat|10v1|CN817059	7596	630	93	globlastp
4202	LAB283	wheat|gb164|BE398853	7597	630	93	globlastp
4203	LAB283	wheat|gb164|BE443573	7597	630	93	globlastp
4204	LAB283	lovegrass|gb167|EH188796	7598	630	92.51	glotblastn
4205	LAB283	barley|10v1|BF253836	7599	630	92.5	globlastp
4206	LAB283	barley|gb157SOLEXA|BF253836	7599	630	92.5	globlastp

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4207	LAB283	millet|09v1|EVO454PM013564	7600	630	92	globlastp
4208	LAB283	switchgrass|gb167|DN140847	7601	630	92	globlastp
4209	LAB283	cenchrus|gb166|EB652891	7602	630	91.5	globlastp
4210	LAB283	lovegrass|gb167|DN480250	7603	630	91.5	globlastp
4211	LAB283	switchgrass|gb167|FE612726	7604	630	91.5	globlastp
4212	LAB283	wheat|gb164|CA502712	7605	630	90.4	globlastp
4213	LAB283	brachypodium|09v1|DV477815	7606	630	89.9	globlastp
4214	LAB283	catharanthus|gb166|EG561166	7607	630	89.8	globlastp
4215	LAB283	ginger|gb164|DY346160	7608	630	89.8	globlastp
4216	LAB283	pineapple|10v1|DT336417	7609	630	89.8	globlastp
4217	LAB283	sugarcane|10v1|CA115516	7610	630	89.8	globlastp
4218	LAB283	rice|gb170|OS07G47780	7611	630	89.7	globlastp
4219	LAB283	maize|gb170|LLDQ246011	7612	630	89.4	globlastp
4220	LAB283	wheat|gb164|BE352581	7612	630	89.4	globlastp
4221	LAB283	wheat|gb164|BE404049	7612	630	89.4	globlastp
4222	LAB283	oil_palm|gb166|CN600822	7613	630	89.3	glotblastn
4223	LAB283	banana|gb167|ES433979	7614	630	88.8	globlastp
4224	LAB283	barley|10v1|BG299572	7615	630	88.8	globlastp
4225	LAB283	barley|gb157SOLEXA|AL505846	7615	630	88.8	globlastp
4226	LAB283	fescue|gb161|DT685631	7616	630	88.8	globlastp
4227	LAB283	oil_palm|gb166|EL686178	7617	630	88.8	globlastp
4228	LAB283	pseudoroegneria|gb167|FF343982	7618	630	88.8	globlastp
4229	LAB283	wheat|gb164|BE423765	7619	630	88.8	globlastp
4230	LAB283	lolium|10v1|ES699035	7620	630	88.3	globlastp
4231	LAB283	oat|10v1|GO582808	7621	630	88.3	globlastp
4232	LAB283	leymus|gb166|EG374681	7622	630	88.3	globlastp
4233	LAB283	banana|gb167|FF561221	7623	630	88.2	globlastp
4234	LAB283	cassava|09v1|CK644077	7624	630	88.2	globlastp
4235	LAB283	cassava|gb164|CK644077	7624	630	88.2	globlastp
4236	LAB283	citrus|gb166|BQ623150	7625	630	88.2	globlastp
4237	LAB283	cotton|gb164|DT557850	7626	630	88.2	globlastp
4238	LAB283	sugarcane|gb157.3|CA080288	7627	630	88.2	globlastp
4239	LAB283	cleome_gynandra|10v1|SRR015532S0020282	7628	630	87.7	globlastp
4240	LAB283	cleome_spinosa|10v1|GR931300	7629	630	87.7	globlastp
4241	LAB283	cleome_spinosa|10v1|GR931891	7630	630	87.7	globlastp
4242	LAB283	flax|09v1|EU830561	7631	630	87.7	globlastp
4243	LAB283	jatropha|09v1|GT229173	7632	630	87.7	globlastp
4244	LAB283	amborella|gb166|CD483554	7633	630	87.7	globlastp
4245	LAB283	banana|gb167|FF560367	7634	630	87.7	globlastp
4246	LAB283	cacao|gb167|CA795583	7635	630	87.7	globlastp
4247	LAB283	castorbean|09v1|EE255447	7636	630	87.7	globlastp
4248	LAB283	castorbean|gb160|EE255447	7636	630	87.7	globlastp
4249	LAB283	cotton|gb164|DT046974	7637	630	87.7	globlastp

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4250	LAB283	cotton|gb164|DW232816	7638	630	87.7	globlastp
4251	LAB283	cowpea|gb166|FC459109	7639	630	87.7	globlastp
4252	LAB283	ginger|gb164|DY368354	7640	630	87.7	globlastp
4253	LAB283	grape|gb160|BQ796886	7641	630	87.7	globlastp
4254	LAB283	onion|gb162|CF451866	7642	630	87.7	globlastp
4255	LAB283	papaya|gb165|EX262198	7643	630	87.7	globlastp
4256	LAB283	cleome_gynandra|10v1|SRR015532S0010711	7644	630	87.2	globlastp
4257	LAB283	cleome_spinosa|10v1|SRR015531S0011099	7645	630	87.2	globlastp
4258	LAB283	cucumber|09v1|DV631905	7646	630	87.2	globlastp
4259	LAB283	banana|gb167|FL658404	7647	630	87.2	globlastp
4260	LAB283	cassava|09v1|DV442672	7648	630	87.2	globlastp
4261	LAB283	cassava|gb164|DV442672	7648	630	87.2	globlastp
4262	LAB283	coffea|10v1|DV678801	7649	630	87.2	globlastp
4263	LAB283	coffea|gb157.2|DV678801	7649	630	87.2	globlastp
4264	LAB283	cotton|gb164|AI730706	7650	630	87.2	globlastp
4265	LAB283	cotton|gb164|AI731751	7651	630	87.2	globlastp
4266	LAB283	cotton|gb164|BE052367	7652	630	87.2	globlastp
4267	LAB283	cotton|gb164|BF279005	7650	630	87.2	globlastp
4268	LAB283	papaya|gb165|EX275159	7653	630	87.2	globlastp
4269	LAB283	jatropha|09v1|FM892996	7654	630	87.17	glotblastn
4270	LAB283	chickpea|09v2|AJ004961	7655	630	86.6	globlastp
4271	LAB283	cleome_gynandra|10v1|SRR015532S0008000	7656	630	86.6	globlastp
4272	LAB283	cleome_spinosa|10v1|SRR015531S0003355	7657	630	86.6	globlastp
4273	LAB283	avocado|10v1|CO998684	7658	630	86.6	globlastp
4274	LAB283	avocado|gb164|CO998684	7658	630	86.6	globlastp
4275	LAB283	cassava|09v1|CK648694	7659	630	86.6	globlastp
4276	LAB283	cassava|gb164|CK648694	7660	630	86.6	globlastp
4277	LAB283	grape|gb160|BQ800472	7661	630	86.6	globlastp
4278	LAB283	liquorice|gb171|FS244095	7662	630	86.6	globlastp
4279	LAB283	melon|gb165|DV631905	7663	630	86.6	globlastp
4280	LAB283	onion|gb162|CF436696	7664	630	86.6	globlastp
4281	LAB283	peanut|gb171|CD038311	7665	630	86.6	globlastp
4282	LAB283	peanut|gb171|CD038838	7666	630	86.6	globlastp
4283	LAB283	pineapple|gb157.2|DT336417	7667	630	86.6	globlastp
4284	LAB283	poplar|10v1|AI162670	7668	630	86.6	globlastp
4285	LAB283	arabidopsis_lyrata|09v1|BQ834416	7669	630	86.1	globlastp
4286	LAB283	cleome_gynandra|10v1|SRR015532S0012271	7670	630	86.1	glotblastn
4287	LAB283	cucumber|09v1|DN910478	7671	630	86.1	globlastp
4288	LAB283	nasturtium|10v1|GH163808	7672	630	86.1	globlastp

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4289	LAB283	applc|gb171|CN494008	7673	630	86.1	globlastp
4290	LAB283	applc|gb171|CN864078	7674	630	86.1	globlastp
4291	LAB283	banana|gb167|ES437537	7675	630	86.1	globlastp
4292	LAB283	bean|gb167|CA897668	7676	630	86.1	globlastp
4293	LAB283	bean|gb167|CA897674	7677	630	86.1	globlastp
4294	LAB283	castorbean|09v1|CF981310	7678	630	86.1	globlastp
4295	LAB283	castorbean|gb160|CF981310	7679	630	86.1	glotblastn
4296	LAB283	cotton|gb164|AI730100	7680	630	86.1	globlastp
4297	LAB283	cowpea|gb166|FF383705	7681	630	86.1	globlastp
4298	LAB283	cowpea|gb166|FF384965	7682	630	86.1	globlastp
4299	LAB283	ginger|gb164|DY349506	7683	630	86.1	globlastp
4300	LAB283	grape|gb160|BM437118	7684	630	86.1	globlastp
4301	LAB283	liquorice|gb171|FS244478	7685	630	86.1	globlastp
4302	LAB283	melon|gb165|AM718598	7686	630	86.1	globlastp
4303	LAB283	poplar|gb170|AI162670	7687	630	86.1	globlastp
4304	LAB283	poplar|10v1|AI162871	7688	630	86.1	globlastp
4305	LAB283	poplar|gb170|AI162871	7688	630	86.1	globlastp
4306	LAB283	poplar|10v1|AI163306	7689	630	86.1	globlastp
4307	LAB283	poplar|gb170|AI163306	7689	630	86.1	globlastp
4308	LAB283	poppy|gb166|FE968414	7690	630	86.1	globlastp
4309	LAB283	prunus|gb167|AJ827102	7691	630	86.1	globlastp
4310	LAB283	prunus|gb167|CB822575	7692	630	86.1	globlastp
4311	LAB283	soybean|gb168|AW288068	7693	630	86.1	globlastp
4312	LAB283	walnuts|gb166|EL894571	7694	630	86.1	globlastp
4313	LAB283	wheat|gb164|BQ838809	7695	630	86.1	globlastp
4314	LAB283	ipomoea_nil|10v1|BJ556879	7696	630	85.6	globlastp
4314	LAB283	ipomoea|gb157.2|BJ556879	7696	630	85.6	globlastp
4315	LAB283	orobanche|10v1|SRR023189S0004601	7697	630	85.6	globlastp
4316	LAB283	apple|gb171|CN898032	7698	630	85.6	globlastp
4317	LAB283	citrus|gb166|CB293637	7699	630	85.6	globlastp
4318	LAB283	eucalyptus|gb166|CT982220	7700	630	85.6	globlastp
4319	LAB283	peanut|gb171|EG030272	7701	630	85.6	globlastp
4320	LAB283	soybean|gb168|AW256698	7702	630	85.6	globlastp
4321	LAB283	sunflower|gb162|BU672022	7703	630	85.6	globlastp
4322	LAB283	triphysaria|10v1|BM356765	7704	630	85.1	globlastp
4323	LAB283	triphysaria|10v1|BM356862	7704	630	85.1	globlastp
4324	LAB283	triphysaria|10v1|EX990668	7704	630	85.1	globlastp
4325	LAB283	ipomoea|gb157.2|BJ553202	7705	630	85.03	glotblastn
4326	LAB283	eschscholzia|10v1|CD478146	7706	630	85	globlastp
4327	LAB283	ipomoea_batatas|10v1|CB330344	7707	630	85	globlastp
4328	LAB283	ipomoea_nil|10v1|BJ553202	7708	630	85	globlastp
4329	LAB283	ipomoea_nil|10v1|CJ737673	7709	630	85	globlastp
4330	LAB283	nasturtium|10v1|SRR032558S0018850	7710	630	85	globlastp
4331	LAB283	solanum_phureja|09v1|SPHBG127682	7711	630	85	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
4332	LAB283	arabidopsis|gb165|AT5G27850	7712	630	85	globlastp
4333	LAB283	b_olcracca|gb161|DY025769	7713	630	85	globlastp
4334	LAB283	b_rapa|gb162|DY010000	7713	630	85	globlastp
4335	LAB283	canola|10v1|CN730540	7713	630	85	globlastp
4336	LAB283	canola|gb161|CN730540	7713	630	85	globlastp
4337	LAB283	centaurea|gb166|EH737450	7714	630	85	globlastp
4338	LAB283	cryptomeria|gb166|BW993132	7715	630	85	globlastp
4339	LAB283	cynara|gb167|GE586442	7716	630	85	globlastp
4340	LAB283	ipomoea|gb157.2|CB330344	7707	630	85	globlastp
4341	LAB283	liriodendron|gb166|CK766210	7717	630	85	globlastp
4342	LAB283	petunia|gb171|DY396235	7718	630	85	globlastp
4343	LAB283	poplar|10v1|AI161894	7719	630	85	globlastp
4344	LAB283	poplar|gb170|AI161894	7719	630	85	globlastp
4345	LAB283	radish|gb164|EV537215	7713	630	85	globlastp
4346	LAB283	radish|gb164|EV546651	7713	630	85	globlastp
4347	LAB283	radish|gb164|EV566253	7720	630	85	globlastp
4348	LAB283	radish|gb164|EW718156	7720	630	85	globlastp
4349	LAB283	safflower|gb162|EL395026	7714	630	85	globlastp
4350	LAB283	soybean|gb168|AL376539	7721	630	85	globlastp
4351	LAB283	soybean|gb168|AW684723	7722	630	85	globlastp
4352	LAB283	tobacco|gb162|BQ842820	7723	630	85	globlastp
4353	LAB283	tobacco|gb162|DV158247	7724	630	85	globlastp
4354	LAB283	triphysaria|gb164|BM356862	7725	630	84.6	globlastp
4355	LAB283	gerbera|09v1|AJ750626	7726	630	84.5	globlastp
4356	LAB283	lotus|09v1|BW595275	7727	630	84.5	globlastp
4357	LAB283	pea|09v1|EX568904	7728	630	84.5	globlastp
4358	LAB283	apple|gb171|CN875969	7729	630	84.5	globlastp
4359	LAB283	arabidopsis|gb165|AT3G05590	7730	630	84.5	globlastp
4360	LAB283	b_juncea|gb164|EVGN0103231249082 3	7731	630	84.5	globlastp
4361	LAB283	b_oleracea|gb161|DY028050	7732	630	84.5	globlastp
4362	LAB283	b_rapa|gb162|CX267092	7733	630	84.5	globlastp
4363	LAB283	bean|gb167|CA897690	7734	630	84.5	globlastp
4364	LAB283	canola|10v1|CD818850	7732	630	84.5	globlastp
4365	LAB283	canola|gb161|CD818850	7732	630	84.5	globlastp
4366	LAB283	chestnut|gb170|SRR006295S0003138	7735	630	84.5	globlastp
4367	LAB283	cotton|gb164|BE053784	7736	630	84.5	globlastp
4368	LAB283	fern|gb171|DK952766	7737	630	84.5	globlastp
4369	LAB283	kiwi|gb166|FG397867	7738	630	84.5	globlastp
4370	LAB283	lotus|09v1|LLCN825309	7739	630	84.5	globlastp
4371	LAB283	lotus|gb157.2|CN825309	7739	630	84.5	globlastp
4372	LAB283	oak|gb170|DN951034	7735	630	84.5	globlastp
4373	LAB283	pine|gb157.2|AL750084	7740	630	84.5	globlastp
4374	LAB283	radish|gb164|EX903877	7741	630	84.5	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
4375	LAB283	senecio|gb170|DY658757	7742	630	84.5	globlastp
4376	LAB283	soybean|gb168|BI969217	7743	630	84.5	globlastp
4377	LAB283	soybean|gb168|BI969863	7744	630	84.5	globlastp
4378	LAB283	spruce|gb162|CO234240	7745	630	84.5	globlastp
4379	LAB283	spurge|gb161|BE095307	7746	630	84.5	globlastp
4380	LAB283	sunflower|gb162|CD845836	7747	630	84.5	globlastp
4381	LAB283	sunflower|gb162|CD848533	7748	630	84.5	globlastp
4382	LAB283	thellungiella|gb167|BQ079245	7749	630	84.5	globlastp
4383	LAB283	tobacco|gb162|CV020739	7750	630	84.5	globlastp
4384	LAB283	eschscholzia|10v1|CD477064	7751	630	84.49	glotblastn
4385	LAB283	canola|gb161|CX278684	7752	630	84.49	glotblastn
4386	LAB283	coffea|10v1|DV666712	7753	630	84	globlastp
4387	LAB283	eggplant|10v1|FS007197	7754	630	84	globlastp
4388	LAB283	ipomoea_batatas|10v1|CB330862	7755	630	84	globlastp
4389	LAB283	physcomitrella|10v1|BJ158142	7756	630	84	globlastp
4390	LAB283	physcomitrella|10v1|BJ185019	7757	630	84	globlastp
4391	LAB283	bruguiera|gb166|BP938752	7758	630	84	globlastp
4392	LAB283	cichorium|gb171|EH701900	7759	630	84	globlastp
4393	LAB283	clover|gb162|BB918213	7760	630	84	globlastp
4394	LAB283	dandelion|gb161|DQ160027	7761	630	84	globlastp
4395	LAB283	lettuce|gb157.2|DW045621	7762	630	84	globlastp
4396	LAB283	lettuce|10v1|DW075909	7763	630	84	globlastp
4397	LAB283	lettuce|gb157.2|DW075909	7763	630	84	globlastp
4398	LAB283	lettuce|gb157.2|DW107696	7762	630	84	globlastp
4399	LAB283	lotus|09v1|LLAW720439	7764	630	84	globlastp
4400	LAB283	pine|gb157.2|AW290194	7765	630	84	globlastp
4401	LAB283	potato|gb157.2|AW906174	7766	630	84	globlastp
4402	LAB283	radish|gb164|EV536533	7767	630	84	globlastp
4403	LAB283	radish|gb164|EV536583	7768	630	84	globlastp
4404	LAB283	radish|gb164|EV550169	7769	630	84	globlastp
4405	LAB283	radish|gb164|EV568547	7770	630	84	globlastp
4406	LAB283	radish|gb164|EW716009	7767	630	84	globlastp
4407	LAB283	radish|gb164|EW728074	7767	630	84	globlastp
4408	LAB283	radish|gb164|T25181	7767	630	84	globlastp
4409	LAB283	radish|gb164|T25182	7767	630	84	globlastp
4410	LAB283	safflower|gb162|EL408656	7771	630	84	globlastp
4411	LAB283	tea|10v1|CV013664	7772	630	84	globlastp
4412	LAB283	tea|gb171|CV013664	7772	630	84	globlastp
4413	LAB283	tobacco|gb162|CV016133	7773	630	84	globlastp
4414	LAB283	tobacco|gb162|CV019619	7774	630	84	globlastp
4415	LAB283	tomato|09v1|BG127682	7775	630	84	globlastp
4416	LAB283	tomato|gb164|BG127682	7775	630	84	globlastp
4417	LAB283	triphysaria|gb164|BM356765	7776	630	84	globlastp
4418	LAB283	lettuce|10v1|DW045621	7762	630	84	globlastp

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4419	LAB283	pinc|10v1|AW010654	7765	630	84	globlastp
4420	LAB283	physcomitrella|gb157|BJ158142	7777	630	83.96	glotblastn
4421	LAB283	triphysaria|10v1|EY014546	7778	630	83.5	globlastp
4422	LAB283	beet|gb162|BF011058	7779	630	83.42	glotblastn
4423	LAB283	dandelion|gb161|DY806963	7780	630	83.42	glotblastn
4424	LAB283	physcomitrella|gb157|AW126838	7781	630	83.42	glotblastn
4425	LAB283	physcomitrella|gb157|BG362299	7782	630	83.42	glotblastn
4426	LAB283	arabidopsis_lyrata|09v1|JGIAL022452	7783	630	83.4	globlastp
4427	LAB283	canola|10v1|CD812625	7784	630	83.4	globlastp
4428	LAB283	canola|10v1|CD840995	7785	630	83.4	globlastp
4429	LAB283	ipomoea_batatas|10v1|EE882526	7786	630	83.4	globlastp
4430	LAB283	orobanche|10v1|SRR023189S0022111	7787	630	83.4	globlastp
4431	LAB283	physcomitrella|10v1|AW126838	7788	630	83.4	globlastp
4432	LAB283	physcomitrella|10v1|BG362299	7789	630	83.4	globlastp
4433	LAB283	pigeonpea|gb171|GR466455	7790	630	83.4	globlastp
4434	LAB283	tragopogon|10v1|SRR020205S0015140	7791	630	83.4	globlastp
4435	LAB283	tragopogon|10v1|SRR020205S0106933	7792	630	83.4	globlastp
4436	LAB283	b_juncea|gb164|EVGN00812046100 71	7793	630	83.4	globlastp
4437	LAB283	b_oleracea|gb161|DY025951	7794	630	83.4	globlastp
4438	LAB283	b_oleracea|gb161|DY027454	7784	630	83.4	globlastp
4439	LAB283	b_rapa|gb162|CV432333	7784	630	83.4	globlastp
4440	LAB283	b_rapa|gb162|CV433788	7784	630	83.4	globlastp
4441	LAB283	b_rapa|gb162|L33551	7795	630	83.4	globlastp
4442	LAB283	b_rapa|gb162|L33568	7795	630	83.4	globlastp
4443	LAB283	canola|gb161|CD812625	7784	630	83.4	globlastp
4444	LAB283	canola|10v1|CD814590	7795	630	83.4	globlastp
4445	LAB283	canola|gb161|CD814590	7795	630	83.4	globlastp
4446	LAB283	canola|10v1|CD820367	7795	630	83.4	globlastp
4447	LAB283	canola|gb161|CD820367	7795	630	83.4	globlastp
4448	LAB283	canola|gb161|CX188482	7784	630	83.4	globlastp
4449	LAB283	canola|10v1|T18367	7794	630	83.4	globlastp
4450	LAB283	canola|gb161|T18367	7794	630	83.4	globlastp
4451	LAB283	centaurea|gb166|EH738805	7796	630	83.4	globlastp
4452	LAB283	centaurea|gb166|EH739466	7797	630	83.4	globlastp
4453	LAB283	cichorium|gb171|DT213052	7798	630	83.4	globlastp
4454	LAB283	cynara|gb167|GE588262	7799	630	83.4	globlastp
4455	LAB283	fern|gb171|DK949008	7800	630	83.4	globlastp
4456	LAB283	ipomoea|gb157.2|CJ737673	7801	630	83.4	globlastp
4457	LAB283	lettuce|gb157.2|DW076892	7802	630	83.4	globlastp
4458	LAB283	lettuce|gb157.2|DW145375	7803	630	83.4	globlastp
4459	LAB283	lettuce|gb157.2|DW148040	7804	630	83.4	globlastp
4460	LAB283	nicotiana_benthamiana|gb162|CN745163	7805	630	83.4	globlastp

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4461	LAB283	oak|gb170|DN949820	7806	630	83.4	globlastp
4462	LAB283	pepper|gb171|BM064100	7807	630	83.4	globlastp
4463	LAB283	pepper|gb171|BM068255	7808	630	83.4	globlastp
4464	LAB283	petunia|gb171|CV295039	7809	630	83.4	globlastp
4465	LAB283	petunia|gb171|CV299987	7810	630	83.4	globlastp
4466	LAB283	radish|gb164|EV535201	7811	630	83.4	globlastp
4467	LAB283	radish|gb164|EV551301	7812	630	83.4	globlastp
4468	LAB283	radish|gb164|EY904311	7813	630	83.4	globlastp
4469	LAB283	safflower|gb162|EL374888	7814	630	83.4	globlastp
4470	LAB283	thellungiella|gb167|BY803938	7815	630	83.4	globlastp
4471	LAB283	canola|10v1|CX188482	7784	630	83.4	globlastp
4472	LAB283	ginseng|10v1|CN848661	7816	630	82.9	globlastp
4473	LAB283	physcomitrella|10v1|AW126801	7817	630	82.9	globlastp
4474	LAB283	b_oleracea|gb161|DY026489	7818	630	82.9	globlastp
4475	LAB283	canola|10v1|CD812987	7818	630	82.9	globlastp
4476	LAB283	canola|gb161|CD812987	7818	630	82.9	globlastp
4477	LAB283	chestnut|gb170|SRR006295S0000969	7819	630	82.9	globlastp
4478	LAB283	dandelion|gb161|DY806552	7820	630	82.9	globlastp
4479	LAB283	iceplant|gb164|BE033787	7821	630	82.9	globlastp
4480	LAB283	kiwi|gb166|FG397111	7822	630	82.9	globlastp
4481	LAB283	lettuce|gb157.2|DW046061	7823	630	82.9	globlastp
4482	LAB283	lettuce|gb157.2|DW079832	7824	630	82.9	globlastp
4483	LAB283	lettuce|gb157.2|DW106263	7824	630	82.9	globlastp
4484	LAB283	lettuce|gb157.2|DW108449	7823	630	82.9	globlastp
4485	LAB283	liriodendron|gb166|DT580181	7825	630	82.9	globlastp
4486	LAB283	spikemoss|gb165|DN839616	7826	630	82.9	globlastp
4487	LAB283	spikemoss|gb165|FE445919	7827	630	82.9	globlastp
4488	LAB283	spruce|gb162|CO215472	7828	630	82.9	globlastp
4489	LAB283	sunflower|gb162|EL465100	7829	630	82.9	globlastp
4490	LAB283	zamia|gb166|DY031019	7830	630	82.9	globlastp
4491	LAB283	lettuce|10v1|DW046061	7823	630	82.9	globlastp
4492	LAB283	lettuce|10v1|DW065820	7824	630	82.9	globlastp
4493	LAB283	b_rapa|gb162|BG544074	7831	630	82.89	glotblastn
4494	LAB283	beet|gb162|BQ592402	7832	630	82.89	glotblastn
4495	LAB283	kiwi|gb166|FG418360	7833	630	82.89	glotblastn
4496	LAB283	physcomitrella|gb157|AW126801	7834	630	82.89	glotblastn
4497	LAB283	eggplant|10v1|FS000992	7835	630	82.4	globlastp
4498	LAB283	salvia|10v1|CV164239	7836	630	82.4	globlastp
4499	LAB283	salvia|10v1|SRR014553S0002907	7837	630	82.4	globlastp
4500	LAB283	tragopogon|10v1|SRR020205S0018138	7838	630	82.4	globlastp
4501	LAB283	artemisia|10v1|EY032066	7839	630	82.4	globlastp
4502	LAB283	artemisia|gb164|EY032066	7839	630	82.4	globlastp
4503	LAB283	artemisia|10v1|EY056461	7840	630	82.4	globlastp
4504	LAB283	artemisia|gb164|EY056461	7840	630	82.4	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
4505	LAB283	basilicum|10v1|DY321729	7841	630	82.4	globlastp
4506	LAB283	cichorium|gb171|EH683001	7842	630	82.4	globlastp
4507	LAB283	cycas|gb166|CB088957	7843	630	82.4	globlastp
4508	LAB283	medicago|09v1|AW684723	7844	630	82.4	globlastp
4509	LAB283	medicago|gb157.2|AW684723	7844	630	82.4	globlastp
4510	LAB283	nicotiana_benthamiana|gb162|CN742004	7845	630	82.4	globlastp
4511	LAB283	poppy|gb166|FE964997	7846	630	82.4	globlastp
4512	LAB283	radish|gb164|EW713569	7847	630	82.4	globlastp
4513	LAB283	spruce|gb162|CO231722	7848	630	82.4	globlastp
4514	LAB283	b_juncea|gb164|EVGN00901614231757	7849	630	82.35	glotblastn
4515	LAB283	cynara|gb167|GE588021	7850	630	82.35	glotblastn
4516	LAB283	iceplant|gb164|BE033487	7851	630	82.35	glotblastn
4517	LAB283	medicago|09v1|LLAW256698	7852	630	81.9	globlastp
4518	LAB283	medicago|gb157.2|AW256698	7852	630	81.9	globlastp
4519	LAB283	monkeyflower|10v1|DV207165	7853	630	81.8	globlastp
4520	LAB283	monkeyflower|10v1|DV208950	7854	630	81.8	globlastp
4521	LAB283	salvia|10v1|FE536981	7855	630	81.8	globlastp
4522	LAB283	solanum_phurcja|09v1|SPHBG127027	7856	630	81.8	globlastp
4523	LAB283	antirrhinum|gb166|AJ558493	7857	630	81.8	globlastp
4524	LAB283	antirrhinum|gb166|AJ788113	7858	630	81.8	globlastp
4525	LAB283	clover|gb162|BB923394	7859	630	81.8	globlastp
4526	LAB283	lettuce|gb157.2|DW065820	7860	630	81.8	globlastp
4527	LAB283	potato|gb157.2|BG350906	7856	630	81.8	globlastp
4528	LAB283	potato|gb157.2|BG592372	7856	630	81.8	globlastp
4529	LAB283	potato|10v1|BG350906	7856	630	81.8	globlastp
4530	LAB283	artemisia|gb164|EY033512	7861	630	81.3	globlastp
4531	LAB283	basilicum|gb157.3|DY321729	7862	630	81.3	globlastp
4532	LAB283	liquorice|gb171|FS266383	7863	630	81.3	globlastp
4533	LAB283	marchantia|gb166|C96610	7864	630	81.3	globlastp
4534	LAB283	medicago|09v1|BE249407	7865	630	81.3	globlastp
4535	LAB283	medicago|gb157.2|BE249407	7865	630	81.3	globlastp
4536	LAB283	potato|gb157.2|BG589732	7866	630	81.3	globlastp
4537	LAB283	tomato|09v1|BG127027	7866	630	81.3	globlastp
4538	LAB283	tomato|gb164|BG127027	7866	630	81.3	globlastp
4539	LAB283	artemisia|10v1|EY033512	7867	630	81.28	glotblastn
4540	LAB283	triphysaria|gb164|BM356434	7868	630	80.9	globlastp
4541	LAB283	triphysaria|gb164|EY126952	7869	630	80.9	globlastp
4542	LAB283	triphysaria|10v1|EY133632	7870	630	80.9	globlastp
4543	LAB283	triphysaria|gb164|EY133632	7870	630	80.9	globlastp
4544	LAB283	ginseng|10v1|CN848265	7871	630	80.7	globlastp
4545	LAB283	petunia|gb171|DC244521	7872	630	80.5	globlastp
4546	LAB283	triphysaria|10v1|EY126952	7873	630	80.3	globlastp

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4547	LAB283	triphysaria|10v1|BM356434	7874	630	80.3	globlastp
4548	LAB284	maize|gb170|AW091217	7875	631	89.7	globlastp
4549	LAB286	maize|gb170|AI001359	7876	632	86.6	globlastp
4550	LAB286	sorghum|gb161.crp|CF481271	7877	632	84.11	glotblastn
4551	LAB286	sorghum|09v1|CF481271	7878	632	83.4	globlastp
4552	LAB289	sugarcane|gb157.3|BQ537261	7879	633	99.7	globlastp
4553	LAB289	sugarcane|gb157.3|CA072303	7880	633	99.7	globlastp
4554	LAB289	sugarcane|10v1|BQ537261	7879	633	99.7	globlastp
4555	LAB289	maize|gb170|AI491553	7881	633	97.4	globlastp
4556	LAB289	maize|gb170|BQ294294	7882	633	96.8	globlastp
4557	LAB289	switchgrass|gb167|FE605676	7883	633	95.9	globlastp
4558	LAB289	rice|gb170|OS07G39280	7884	633	94.5	globlastp
4559	LAB289	wheat|gb164|BE470949	7885	633	90	globlastp
4560	LAB289	leymus|gb166|EG384787	7886	633	89.9	globlastp
4561	LAB289	barley|10v1|BE412637	7887	633	89.7	globlastp
4562	LAB289	barley|gb157SOLEXA|BE412637	7887	633	89.7	globlastp
4563	LAB289	brachypodium|gb169|BE412637	7888	633	89.7	globlastp
4564	LAB289	brachypodium|09v1|DV472699	7889	633	89.4	glotblastn
4565	LAB290	sorghum|09v1|SB05G023240	7890	634	97.4	globlastp
4565	LAB290_H0	sorghum|09v1|SB05G023240	7890	688	84.9	globlastp
4566	LAB290	sorghum|gb161.crp|BE363468	7890	634	97.4	globlastp
4566	LAB290 H0	sorghum|gb161.crp|BE363468	7890	688	84.9	globlastp
4567	LAB290	sugarcane|gb157.3|CA084515	7891	634	82.8	globlastp
4567	LAB290_H0	sugarcane|gb157.3|CA084515	7891	688	84.24	glotblastn
4568	LAB290	switchgrass|gb167|DN143335	7892	634	82.1	globlastp
4569	LAB292	sugarcane|10v1|CA065722	7893	635	87.8	globlastp
4570	LAB292	sugarcane|gb157.3|CA065722	7894	635	87.5	globlastp
4571	LAB292	maize|gb170|CB617317	7895	635	83.44	glotblastn
4572	LAB292	maize|gb170|AI901624	7896	635	82.8	globlastp
4573	LAB293	maize|gb170|CD946962	7897	636	88.3	globlastp
4574	LAB296	switchgrass|gb167|FL698667	7898	639	93.55	glotblastn
4575	LAB296	sugarcane|10v1|CA102880	7899	639	92.1	globlastp
4576	LAB296	sugarcane|gb157.3|CA102880	7900	639	89.2	globlastp
4577	LAB296	rice|gb170|OS04G46880	7901	639	86.1	globlastp
4578	LAB296	brachypodium|09v1|SRR031795S0000152	7902	639	85	globlastp
4579	LAB296	brachypodium|gb169|BG262952	7902	639	85	globlastp
4580	LAB296	maize|gb170|LLEU957736	7903	639	85	globlastp
4581	LAB296	maize|gb170|BM259168	7904	639	84.3	globlastp
4582	LAB297	sorghum|gb161.crp|BI098059	7905	640	82.4	globlastp
4583	LAB297	sorghum|09v1|SB05G000860	7906	640	81.9	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
4584	LAB302	maize|gb170|AA979768	7907	644	81.3	glotblastn
4585	LAB302	maize|gb170|LLBE051112	7908	644	81.3	glotblastn
4586	LAB304	maize|gb170|DR813947	7909	646	92.27	glotblastn
4587	LAB304	switchgrass|gb167|FL902445	7910	646	87.63	glotblastn
4588	LAB304	rice|gb170|OS03G03550	7911	646	84.1	glotblastn
4589	LAB304	maize|gb170|CRPZM2N005678	7912	646	83.76	glotblastn
4590	LAB307	soybean|gb168|AW697150	7913	648	91.4	globlastp
4591	LAB307	lotus|09v1|BW594599	7914	648	84.9	globlastp
4592	LAB307	chickpea|09v2|GFXFJ477886X1	7915	648	84.7	globlastp
4593	LAB307	bean|gb167|CV541797	7916	648	84.7	globlastp
4594	LAB307	medicago|09v1|BE325764	7917	648	83.7	globlastp
4595	LAB307	medicago|gb157.2|BE325764	7917	648	83.7	globlastp
4596	LAB307	peanut|gb171|EC365261	7918	648	82.6	globlastp
4597	LAB308	soybean|gb168|BG449301	7919	649	96.3	globlastp
4598	LAB308	cowpea|gb166|AY257179	7920	649	87.9	globlastp
4599	LAB308	medicago|09v1|AW257191	7921	649	83.4	globlastp
4600	LAB309	soybean|gb168|EV263579	7922	650	92.5	globlastp
4601	LAB311	lettuce|gb157.2|DW132299	7923	652	83.5	globlastp
4602	LAB311	lettuce|10v1|DW052365	7924	652	83.5	globlastp
4603	LAB311	lettuce|gb157.2|DW087492	7925	652	83	globlastp
4604	LAB311	lettuce|gb157.2|DW048584	7926	652	82.2	globlastp
4605	LAB311	cichorium|gb171|EH676540	7927	652	80.2	globlastp
4606	LAB311	lettuce|gb157.2|DW117160	7928	652	80	globlastp
4607	LAB312	potato|gb157.2|BG096129	7929	653	98.1	globlastp
4608	LAB312	solanum_phureja|09v1|SPHAF079231	7930	653	97.8	globlastp
4609	LAB312	potato|gb157.2|BQ117749	7931	653	97.8	globlastp
4610	LAB312	eggplant|10v1|FS008591	7932	653	94	globlastp
4611	LAB312	pepper|gb171|BM066919	7933	653	93.4	globlastp
4612	LAB312	tobacco|gb162|AF113545	7934	653	90.5	globlastp
4613	LAB312	potato|10v1|BG096129	7935	653	88.6	globlastp
4614	LAB312	poplar|gb170|AI162953	7936	653	80.7	globlastp
4615	LAB312	poplar|10v1|AI163602	7937	653	80.1	globlastp
4616	LAB312	poplar|10v1|AI162953	7938	653	80.1	globlastp
4617	LAB314	solanum_phureja|09v1|SPHBG627257	7939	654	95.7	globlastp
4618	LAB314	potato|10v1|BE921587	7940	654	95.1	globlastp
4619	LAB314	potato|gb157.2|BE921587	7941	654	92.3	globlastp
4620	LAB314	tobacco|gb162|DW001183	7942	654	83.89	glotblastn
4621	LAB315	potato|10v1|CV503760	7943	655	93.5	globlastp
4622	LAB315	potato|gb157.2|CV503760	7943	655	93.5	globlastp
4623	LAB315	solanum_phureja|09v1|SPHAI487529	7944	655	93	globlastp
4624	LAB317	potato|gb157.2|BG595203	7945	657	98.1	globlastp
4625	LAB317	potato|10v1|BG595203	7946	657	97.8	globlastp
4626	LAB317	eggplant|10v1|FS033756	7947	657	90.8	globlastp
4627	LAB317	solanum_phureja|09v1|SPHAI773737	7948	657	89.7	globlastp

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4628	LAB317	pepper|gb171|CA513828	7949	657	83.6	globlastp
4629	LAB317	nicotiana_benthamiana|gb162|CK284916	7950	657	82.6	globlastp
4630	LAB319	solanum_phureja|09v1|SPHAW032666	7951	659	94.1	globlastp
4631	LAB319	potato|10v1|BG350293	7951	659	94.1	globlastp
4632	LAB319	potato|gb157.2|BG350293	7951	659	94.1	globlastp
4633	LAB319	tobacco|gb162|DW005109	7952	659	82.8	globlastp
4634	LAB319	petunia|gb171|AM489763	7953	659	80.2	globlastp
4635	LAB320	solanum_phureja|09v1|SPHAW979674	7954	660	92.9	globlastp
4636	LAB324	solanum_phureja|09v1|SPHBG628155	7955	662	99.2	globlastp
4637	LAB324	eggplant|10v1|FS000167	7956	662	97.5	globlastp
4638	LAB324	tobacco|gb162|EB424763	7957	662	97.5	globlastp
4639	LAB324	pepper|gb171|CA517713	7958	662	97.1	globlastp
4640	LAB324	petunia|gb171|PETTRNSFB	7959	662	96.7	globlastp
4641	LAB324	coffea|10v1|DV664667	7960	662	94.2	globlastp
4642	LAB324	coffea|gb157.2|DV664667	7960	662	94.2	globlastp
4643	LAB324	ipomoea_nil|10v1|BJ555139	7961	662	90.9	globlastp
4643	LAB324	ipomoea|gb157.2|BJ555139	7961	662	90.9	globlastp
4644	LAB324	grape|gb160|AF373603	7962	662	90.1	globlastp
4645	LAB324	kiwi|gb166|FG414728	7963	662	87.8	globlastp
4646	LAB324	antirrhinum|gb166|AY306142	7964	662	87.7	globlastp
4647	LAB324	castorbean|09v1|EE259386	7965	662	87.6	globlastp
4648	LAB324	prunus|gb167|BU039561	7966	662	87.6	globlastp
4649	LAB324	cucumber|09v1|CD726807	7967	662	87.2	globlastp
4650	LAB324	papaya|gb165|EX248886	7968	662	87.2	globlastp
4651	LAB324	cacao|gb167|CU475790	7969	662	87	globlastp
4652	LAB324	antirrhinum|gb166|AY306140	7970	662	86.8	globlastp
4653	LAB324	antirrhinum|gb166|AY306141	7971	662	86.5	globlastp
4654	LAB324	strawberry|gb164|CO381239	7972	662	86.4	globlastp
4655	LAB324	triphysaria|10v1|SRR023501S0006880	7973	662	86.3	globlastp
4656	LAB324	cassava|09v1|JGICASSAVA45541M1	7974	662	86	globlastp
4657	LAB324	cotton|gb164|BE055122	7975	662	85.6	globlastp
4658	LAB324	apple|gb171|CN445627	7976	662	85.5	globlastp
4659	LAB324	nasturtium|10v1|SRR032558S0070643	7977	662	84.8	globlastp
4660	LAB324	melon|gb165|AM736201	7978	662	84.7	globlastp
4661	LAB324	cotton|gb164|AI725419	7979	662	84.6	globlastp
4662	LAB324	cotton|gb164|BF273794	7979	662	84.6	globlastp
4663	LAB324	citrus|gb166|CB290298	7980	662	84.4	globlastp
4664	LAB324	lotus|09v1|AY770397	7981	662	84.4	globlastp
4665	LAB324	lotus|gb157.2|AY770397	7981	662	84.4	globlastp
4666	LAB324	nasturtium|10v1|SRR032558S0103587	7982	662	83.6	globlastp
4667	LAB324	cichorium|gb171|EH686695	7983	662	83.3	globlastp
4668	LAB324	medicago|09v1|CRPMT000849	7984	662	83.1	globlastp
4669	LAB324	poplar|10v1|BU877006	7985	662	83.1	globlastp

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4670	LAB324	monkeyflower|10v1|DV209383	7986	662	82.7	globlastp
4671	LAB324	lettuce|10v1|DY978967	7987	662	82.4	globlastp
4672	LAB324	dandelion|gb161|DY812927	7988	662	82	globlastp
4673	LAB324	poplar|10v1|BU876142	7989	662	81.9	globlastp
4674	LAB324	poplar|gb170|BU876142	7989	662	81.9	globlastp
4675	LAB324	soybean|gb168|BE822733	7990	662	81.8	globlastp
4676	LAB324	soybean|gb168|BI970422	7991	662	81.4	globlastp
4677	LAB324	walnuts|gb166|CB303585	7992	662	81.3	globlastp
4678	LAB324	peanut|gb171|AY517932	7993	662	80.7	globlastp
4679	LAB324	sunflower|gb162|DY928057	7994	662	80	glotblastn
4680	LAB325	potato|gb157.2|BQ514801	7995	663	94.5	glotblastn
4681	LAB325	solanum_phureja|09v1|SPHBG630481	7996	663	94.2	globlastp
4682	LAB325	potato|10v1|BQ514801	7997	663	94.2	globlastp
4683	LAB325	potato|gb157.2|BM108612	7998	663	88.4	globlastp
4684	LAB325	pepper|gb171|BM060738	7999	663	82.4	globlastp
4685	LAB326	potato|10v1|BE922713	8000	664	82	globlastp
4686	LAB327	solanum_phureja|09v1|SPHBI934696	8001	665	99.5	globlastp
4687	LAB327	tobacco|gb162|GFXX79005X1	8002	665	97.8	globlastp
4688	LAB327	cucumber|09v1|AA660065	8003	665	95.2	globlastp
4689	LAB327	citrus|gb166|CB293061	8004	665	95.2	globlastp
4690	LAB327	cassava|09v1|CK642375	8005	665	94.4	globlastp
4691	LAB327	cassava|gb164|CK642375	8005	665	94.4	globlastp
4692	LAB327	liriodendron|gb166|DT580890	8006	665	94.4	globlastp
4693	LAB327	poplar|10v1|AI163141	8007	665	94.4	globlastp
4694	LAB327	poplar|gb170|AI163141	8007	665	94.4	globlastp
4695	LAB327	spurge|gb161|BI975260	8008	665	94.4	globlastp
4696	LAB327	cucumber|09v1|DV632499	8009	665	94.2	globlastp
4697	LAB327	castorbean|09v1|EE255332	8010	665	94.2	globlastp
4698	LAB327	castorbean|gb160|EE255332	8010	665	94.2	globlastp
4699	LAB327	grape|gb160|BQ793182	8011	665	94.2	globlastp
4700	LAB327	strawberry|gb164|CO381092	8012	665	94.2	globlastp
4701	LAB327	cotton|gb164|AI726446	8013	665	93.9	globlastp
4702	LAB327	cotton|gb164|AI730198	8014	665	93.9	globlastp
4703	LAB327	grape|gb160|CB917904	8015	665	93.9	globlastp
4704	LAB327	liriodendron|gb166|CO998849	8016	665	93.9	globlastp
4705	LAB327	walnuts|gb166|CV195060	8017	665	93.9	globlastp
4706	LAB327	cleome_spinosa|10v1|GR932329	8018	665	93.7	globlastp
4707	LAB327	eschscholzia|10v1|CD476730	8019	665	93.7	globlastp
4708	LAB327	nasturtium|10v1|GH163469	8020	665	93.7	globlastp
4709	LAB327	nasturtium|10v1|SRR032558S0000854	8021	665	93.7	globlastp
4710	LAB327	nasturtium|10v1|SRR032558S0006059	8022	665	93.7	globlastp
4711	LAB327	citrus|gb166|CF417897	8023	665	93.7	globlastp
4712	LAB327	oil_palm|gb166|CN600175	8024	665	93.7	globlastp
4713	LAB327	sunflower|gb162|CD851809	8025	665	93.7	globlastp

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4714	LAB327	monkeyflower|10v1|DV208648	8026	665	93.5	globlastp
4715	LAB327	solanum_phurcja|09v1|SPHBG134543	8027	665	93.5	globlastp
4716	LAB327	apple|gb171|AY347787	8028	665	93.5	globlastp
4717	LAB327	apple|gb171|CN581798	8029	665	93.5	globlastp
4718	LAB327	aquilegia|10v1|DR937723	8030	665	93.5	globlastp
4719	LAB327	aquilegia|gb157.3|DR937723	8030	665	93.5	globlastp
4720	LAB327	avocado|10v1|CV003076	8031	665	93.5	globlastp
4721	LAB327	avocado|gb164|CV003076	8031	665	93.5	globlastp
4722	LAB327	cacao|gb167|CU473741	8032	665	93.5	globlastp
4723	LAB327	cotton|gb164|AI727813	8033	665	93.5	globlastp
4724	LAB327	nicotiana_benthamiana|gb162|CN743455	8034	665	93.5	globlastp
4725	LAB327	poplar|10v1|BI120621	8035	665	93.5	globlastp
4726	LAB327	poplar|gb170|BI120621	8035	665	93.5	globlastp
4727	LAB327	potato|gb157.2|BF460248	8027	665	93.5	globlastp
4728	LAB327	tobacco|gb162|AJ632823	8036	665	93.5	globlastp
4729	LAB327	tobacco|gb162|X79138	8037	665	93.5	globlastp
4730	LAB327	tomato|09v1|BG127387	8038	665	93.5	globlastp
4731	LAB327	tomato|gb164|AI637390	8038	665	93.5	globlastp
4732	LAB327	tomato|09v1|BG134543	8027	665	93.5	globlastp
4733	LAB327	tomato|gb164|BG134543	8027	665	93.5	globlastp
4734	LAB327	solanum_phurcja|09v1|SPHEG016197	8039	665	93.2	globlastp
4735	LAB327	apple|gb171|CN494642	8040	665	93.2	globlastp
4736	LAB327	cichorium|gb171|DT212028	8041	665	93.2	globlastp
4737	LAB327	clover|gb162|BB939080	8042	665	93.2	globlastp
4738	LAB327	grape|gb160|BM437878	8043	665	93.2	globlastp
4739	LAB327	lettuce|gb157.2|DW070872	8044	665	93.2	globlastp
4740	LAB327	oak|gb170|CU640723	8045	665	93.2	globlastp
4741	LAB327	oil_palm|gb166|ES323934	8046	665	93.2	globlastp
4742	LAB327	peanut|gb171|CD037791	8047	665	93.2	globlastp
4743	LAB327	potato|gb157.2|BF052374	8048	665	93.2	globlastp
4744	LAB327	potato|gb157.2|BG350562	8048	665	93.2	globlastp
4745	LAB327	prunus|gb167|BU046232	8049	665	93.2	globlastp
4746	LAB327	soybean|gb168|AJ388958	8050	665	93.2	globlastp
4747	LAB327	soybean|gb168|AW690650	8051	665	93.2	globlastp
4748	LAB327	soybean|gb168|AW697016	8051	665	93.2	globlastp
4749	LAB327	tobacco|gb162|CV019594	8052	665	93.2	globlastp
4750	LAB327	solanum_phureja|09v1|SPHAI637390	8053	665	93	globlastp
4751	LAB327	apple|gb171|CN495362	8054	665	93	globlastp
4752	LAB327	artemisia|10v1|EY045818	8055	665	93	globlastp
4753	LAB327	cassava|09v1|FF380298	8056	665	93	globlastp
4754	LAB327	chestnut|gb170|SRR006295S0000341	8057	665	93	globlastp
4755	LAB327	chestnut|gb170|SRR006295S0005786	8058	665	93	globlastp
4756	LAB327	cotton|gb164|BE054566	8059	665	93	globlastp

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4757	LAB327	lcttucc|10v1|DW089577	8060	665	93	globlastp
4758	LAB327	lotus|09v1|LLBG662143	8061	665	93	globlastp
4759	LAB327	medicago|09v1|AA660688	8062	665	93	globlastp
4760	LAB327	medicago|gb157.2|AA660688	8062	665	93	globlastp
4761	LAB327	melon|gb165|DV632499	8063	665	93	globlastp
4762	LAB327	oak|gb170|DB996889	8064	665	93	globlastp
4763	LAB327	papaya|gb165|AM903981	8065	665	93	globlastp
4764	LAB327	pepper|gb171|CA515957	8066	665	93	globlastp
4765	LAB327	poplar|gb170|BU871877	8067	665	93	globlastp
4766	LAB327	prunus|gb167|BU039863	8068	665	93	globlastp
4767	LAB327	soybean|gb168|AL370120	8069	665	93	globlastp
4768	LAB327	sunflower|gb162|BU672037	8070	665	93	globlastp
4769	LAB327	sunflower|gb162|CD849909	8071	665	93	globlastp
4770	LAB327	tobacco|gb162|CV016269	8072	665	93	globlastp
4771	LAB327	poplar|10v1|AI163175	8073	665	93	globlastp
4772	LAB327	coffea|10v1|DV665562	8074	665	92.8	globlastp
4773	LAB327	coffea|gb157.2|DV665562	8074	665	92.8	globlastp
4774	LAB327	cleome_gynandra|10v1|SRR015532S0001004	8075	665	92.7	globlastp
4775	LAB327	cacao|gb167|EH057828	8076	665	92.7	globlastp
4776	LAB327	castorbean|09v1|EE258638	8077	665	92.7	globlastp
4777	LAB327	castorbean|gb160|EE258638	8077	665	92.7	globlastp
4778	LAB327	cichorium|gb171|DT211464	8078	665	92.7	globlastp
4779	LAB327	cowpea|gb166|FC457491	8079	665	92.7	globlastp
4780	LAB327	kiwi|gb166|FG403474	8080	665	92.7	globlastp
4781	LAB327	medicago|09v1|BE239304	8081	665	92.7	globlastp
4782	LAB327	medicago|gb157.2|BE239304	8081	665	92.7	globlastp
4783	LAB327	petunia|gb171|CV293104	8082	665	92.7	globlastp
4784	LAB327	poplar|10v1|BU871877	8083	665	92.7	globlastp
4785	LAB327	soybean|gb168|AA660688	8084	665	92.7	globlastp
4786	LAB327	soybean|gb168|AL379116	8085	665	92.7	globlastp
4787	LAB327	soybean|gb168|BI420953	8086	665	92.7	globlastp
4788	LAB327	strawberry|gb164|CO380304	8087	665	92.7	globlastp
4789	LAB327	cassava|09v1|JGICASSAVA37390VALIDM1	8088	665	92.5	globlastp
4790	LAB327	pea|09v1|CD859558	8089	665	92.5	globlastp
4791	LAB327	artemisia|gb164|EY045818	8090	665	92.5	globlastp
4792	LAB327	artemisia|10v1|EY084194	8091	665	92.5	globlastp
4793	LAB327	artemisia|gb164|EY084194	8091	665	92.5	globlastp
4794	LAB327	bean|gb167|CA898099	8092	665	92.5	globlastp
4795	LAB327	ginger|gb164|DY344990	8093	665	92.5	globlastp
4796	LAB327	prunus|gb167|BU039728	8094	665	92.5	globlastp
4797	LAB327	soybean|gb168|AW586495	8095	665	92.5	globlastp
4798	LAB327	soybean|gb168|CD415289	8096	665	92.5	globlastp

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4799	LAB327	tomato|09v1|BG135965	8097	665	92.5	globlastp
4800	LAB327	tomato|gb164|BG135965	8097	665	92.5	globlastp
4801	LAB327	jatropha|09v1|GO247020	8098	665	92.3	globlastp
4802	LAB327	cowpea|gb166|FF382852	8099	665	92.3	globlastp
4803	LAB327	cowpea|gb166|FF394250	8100	665	92.3	globlastp
4804	LAB327	lotus|09v1|BI420953	8101	665	92.3	globlastp
4805	LAB327	lotus|gb157.2|BI420953	8101	665	92.3	globlastp
4806	LAB327	oak|gb170|CU656288	8102	665	92.3	globlastp
4807	LAB327	potato|10v1|BE924067	8103	665	92.3	globlastp
4808	LAB327	tobacco|gb162|X79137	8104	665	92.3	globlastp
4809	LAB327	canola|10v1|CD836425	8105	665	92.3	globlastp
4810	LAB327	arabidopsis_lyrata|09v1|JGIAL004953	8106	665	92	globlastp
4811	LAB327	arabidopsis_lyrata|09v1|JGIAL009850	8107	665	92	globlastp
4812	LAB327	monkeyflower|10v1|DV206993	8108	665	92	globlastp
4813	LAB327	oat|10v1|GO586168	8109	665	92	globlastp
4814	LAB327	arabidopsis|gb165|AT3G13920	8110	665	92	globlastp
4815	LAB327	canola|gb161|CD823763	8111	665	92	globlastp
4816	LAB327	cenchrus|gb166|EB653990	8112	665	92	globlastp
4817	LAB327	chestnut|gb170|SRR006295S0005347	8113	665	92	globlastp
4818	LAB327	kiwi|gb166|FG403265	8114	665	92	globlastp
4819	LAB327	maize|gb170|ZMU73459	8115	665	92	globlastp
4820	LAB327	medicago|09v1|AW256944	8116	665	92	globlastp
4821	LAB327	medicago|gb157.2|AW256944	8116	665	92	globlastp
4822	LAB327	pepper|gb171|BM065705	8117	665	92	globlastp
4823	LAB327	sorghum|09v1|SB10G028940	8118	665	92	globlastp
4824	LAB327	sorghum|gb161.crp|ZMU73459	8118	665	92	globlastp
4825	LAB327	sugarcane|gb157.3|AA525682	8119	665	92	globlastp
4826	LAB327	switchgrass|gb167|FE602797	8120	665	92	globlastp
4827	LAB327	oat|10v1|GO581813	8121	665	91.8	globlastp
4828	LAB327	b_oleracea|gb161|AM386369	8122	665	91.8	globlastp
4829	LAB327	b_oleracea|gb161|AM387779	8123	665	91.8	globlastp
4830	LAB327	b_rapa|gb162|BQ790684	8123	665	91.8	globlastp
4831	LAB327	barley|10v1|BE427740	8124	665	91.8	globlastp
4832	LAB327	barley|gb157SOLEXA|BE427740	8124	665	91.8	globlastp
4833	LAB327	bean|gb167|CA898100	8125	665	91.8	globlastp
4834	LAB327	brachypodium|09v1|DV470402	8126	665	91.8	globlastp
4835	LAB327	brachypodium|gb169|Z21510	8126	665	91.8	globlastp
4836	LAB327	canola|gb161|CD813607	8123	665	91.8	globlastp
4837	LAB327	canola|gb161|CD822634	8127	665	91.8	globlastp
4838	LAB327	canola|gb161|CD836953	8123	665	91.8	globlastp
4839	LAB327	cowpea|gb166|FF382264	8128	665	91.8	globlastp
4840	LAB327	kiwi|gb166|FG397118	8129	665	91.8	globlastp
4841	LAB327	lotus|09v1|BP036168	8130	665	91.8	globlastp
4842	LAB327	maize|gb170|AF007580	8131	665	91.8	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
4843	LAB327	soybean|gb168|CA783189	8132	665	91.8	globlastp
4844	LAB327	sugarcane|gb157.3|CA071075	8133	665	91.8	globlastp
4845	LAB327	switchgrass|gb167|FE602798	8134	665	91.8	globlastp
4846	LAB327	triphysaria|10v1|BE574917	8135	665	91.8	globlastp
4847	LAB327	wheat|gb164|BE398943	8136	665	91.8	globlastp
4848	LAB327	wheat|gb164|BE400861	8137	665	91.8	globlastp
4849	LAB327	wheat|gb164|BE402776	8136	665	91.8	globlastp
4850	LAB327	wheat|gb164|Z21510	8124	665	91.8	globlastp
4851	LAB327	sugarcane|10v1|CA071075	8133	665	91.8	globlastp
4852	LAB327	orobanche|10v1|SRR023189S0018945	8138	665	91.5	globlastp
4853	LAB327	arabidopsis|gb165|AT1G54270	8139	665	91.5	globlastp
4854	LAB327	barley|gb157SOLEXA|BE411837	8140	665	91.5	globlastp
4855	LAB327	canola|gb161|DY030421	8141	665	91.5	globlastp
4856	LAB327	canola|gb161|EG020438	8141	665	91.5	globlastp
4857	LAB327	cotton|gb164|AI728255	8142	665	91.5	globlastp
4858	LAB327	millet|09v1|DQ013263	8143	665	91.5	globlastp
4859	LAB327	rice|gb170|OS02G05330	8144	665	91.5	globlastp
4860	LAB327	sorghum|09v1|SB04G003390	8145	665	91.5	globlastp
4861	LAB327	sorghum|gb161.crp|ZMU17979	8145	665	91.5	globlastp
4862	LAB327	barley|10v1|BE411837	8140	665	91.5	globlastp
4863	LAB327	canola|10v1|EE456605	8146	665	91.5	globlastp
4864	LAB327	artemisia|gb164|EY063986	8147	665	91.3	globlastp
4865	LAB327	canola|10v1|CD822634	8148	665	91.3	globlastp
4866	LAB327	canola|10v1|DY002101	8148	665	91.3	globlastp
4867	LAB327	leymus|gb166|CD808554	8149	665	91.3	globlastp
4868	LAB327	rice|gb170|OS06G48750	8150	665	91.3	globlastp
4869	LAB327	millet|gb161|DQ013263	8151	665	91.1	globlastp
4870	LAB327	lettuce|gb157.2|DW047925	8152	665	91.04	glotblastn
4871	LAB327	cowpea|gb166|FC458343	8153	665	91	globlastp
4872	LAB327	maize|gb170|LLZMU17979	8154	665	91	globlastp
4873	LAB327	b_oleracea|gb161|GFXAF180356X1	8155	665	90.8	globlastp
4874	LAB327	bean|gb167|CA905627	8156	665	90.8	globlastp
4875	LAB327	canola|10v1|CD837669	8157	665	90.8	globlastp
4876	LAB327	canola|gb161|CD837669	8157	665	90.8	globlastp
4877	LAB327	cenchrus|gb166|BM084681	8158	665	90.8	globlastp
4878	LAB327	nuphar|gb166|CD474917	8159	665	90.8	globlastp
4879	LAB327	triphysaria|10v1|BE574926	8160	665	90.8	globlastp
4880	LAB327	triphysaria|gb164|BE574926	8161	665	90.6	globlastp
4881	LAB327	monkeyflower|10v1|DV210546	8162	665	90.3	globlastp
4882	LAB327	cycas|gb166|CB088419	8163	665	90.3	globlastp
4883	LAB327	poplar|gb170|BU814784	8164	665	90.1	globlastp
4884	LAB327	millet|09v1|EVO454PM015209	8165	665	89.6	globlastp
4885	LAB327	pea|09v1|AY167671	8166	665	89.6	globlastp
4886	LAB327	potato|10v1|BF460248	8167	665	89.6	globlastp

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4887	LAB327	potato|10v1|BG350562	8168	665	89.6	globlastp
4888	LAB327	safflower|gb162|EL375669	8169	665	89.59	glotblastn
4889	LAB327	canola|10v1|CD813607	8170	665	89.5	globlastp
4890	LAB327	canola|10v1|CD836953	8171	665	89.3	globlastp
4891	LAB327	aquilegia|10v1|DR917189	8172	665	89.3	globlastp
4892	LAB327	aquilegia|gb157.3|DR917189	8172	665	89.3	globlastp
4893	LAB327	iceplant|gb164|BE036146	8173	665	89.3	globlastp
4894	LAB327	triphysaria|10v1|EY006504	8174	665	89.1	globlastp
4895	LAB327	lettuce|gb157.2|DW104332	8175	665	88.9	globlastp
4896	LAB327	physcomitrella|10v1|AW145733	8176	665	88.6	globlastp
4897	LAB327	cacao|gb167|CU512667	8177	665	88.6	globlastp
4898	LAB327	marchantia|gb166|C96517	8178	665	88.6	globlastp
4899	LAB327	physcomitrella|gb157|AW145733	8176	665	88.6	globlastp
4900	LAB327	pine|10v1|AA556416	8179	665	88.6	globlastp
4901	LAB327	pine|gb157.2|AA556416	8179	665	88.6	globlastp
4902	LAB327	spruce|gb162|CO218039	8180	665	88.6	globlastp
4903	LAB327	canola|10v1|DY030421	8181	665	88.5	globlastp
4904	LAB327	arabidopsis_lyrata|09v1|JGIAL007533	8182	665	88.4	globlastp
4905	LAB327	arabidopsis|gb165|AT1G72730	8183	665	88.4	globlastp
4906	LAB327	canola|10v1|EG020438	8184	665	88.1	globlastp
4907	LAB327	lolium|10v1|AU250857	8185	665	87.9	globlastp
4908	LAB327	physcomitrella|10v1|AW477079	8186	665	87.9	globlastp
4909	LAB327	physcomitrella|10v1|BG409334	8187	665	87.9	globlastp
4910	LAB327	physcomitrella|gb157|AW477079	8186	665	87.9	globlastp
4911	LAB327	physcomitrella|gb157|BG409334	8187	665	87.9	globlastp
4912	LAB327	centaurea|gb166|EH763543	8188	665	87.7	globlastp
4913	LAB327	physcomitrella|10v1|AJ225463	8189	665	87.7	globlastp
4914	LAB327	lovegrass|gb167|DN483216	8190	665	87.7	globlastp
4915	LAB327	physcomitrella|gb157|AW561235	8189	665	87.7	globlastp
4916	LAB327	tomato|09v1|CRPSP014772	8191	665	87.4	globlastp
4917	LAB327	castorbean|09v1|XM002524260	8192	665	87.4	globlastp
4918	LAB327	castorbean|gb160|MDL29863M001062	8192	665	87.4	globlastp
4919	LAB327	canola|gb161|CD826344	8193	665	87.2	globlastp
4920	LAB327	b_rapa|gb162|EX037330	8194	665	87	globlastp
4921	LAB327	spikemoss|gb165|FE431394	8195	665	86.7	globlastp
4922	LAB327	spikemoss|gb165|FE439012	8195	665	86.7	globlastp
4923	LAB327	cotton|gb164|AI055309	8196	665	86.4	globlastp
4924	LAB327	catharanthus|gb166|EG558000	8197	665	86.2	globlastp
4925	LAB327	canola|10v1|CD826344	8198	665	85.3	globlastp
4926	LAB327	artemisia|10v1|EY063986	8199	665	85.2	globlastp
4927	LAB327	spikemoss|gb165|FE428260	8200	665	85.2	globlastp
4928	LAB327	bean|gb167|CA905225	8201	665	85	globlastp
4929	LAB327	b_rapa|gb162|CV650421	8202	665	84.8	globlastp
4930	LAB327	orobanche|10v1|SRR023189S0021240	8203	665	84.5	glotblastn

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4931	LAB327	pinc|10v1|AI812354	8204	665	84.5	globlastp
4932	LAB327	pinc|gb157.2|AI812354	8204	665	84.5	globlastp
4933	LAB327	pine|10v1|AW011098	8205	665	84.5	globlastp
4934	LAB327	pine|gb157.2|AW011098	8205	665	84.5	globlastp
4935	LAB327	radish|gb164|EV540574	8206	665	84.5	globlastp
4936	LAB327	iceplant|gb164|BE034440	8207	665	84.3	globlastp
4937	LAB327	spruce|gb162|CO242602	8208	665	84.3	globlastp
4938	LAB327	mesostigma|gb166|DN254955	8209	665	84	globlastp
4939	LAB327	peanut|gb171|CD038335	8210	665	84	globlastp
4940	LAB327	spruce|gb162|CK444474	8211	665	84	globlastp
4941	LAB327	spruce|gb162|CO216603	8212	665	83.8	globlastp
4942	LAB327	chlamydomonas|gb162|AI670453	8213	665	83.5	globlastp
4943	LAB327	pine|10v1|AA557094	8214	665	83.5	globlastp
4944	LAB327	pine|gb157.2|AA557094	8214	665	83.5	globlastp
4945	LAB327	volvox|gb162|AI670453	8215	665	82.5	globlastp
4946	LAB327	dandelion|gb161|DY820664	8216	665	82.08	glotblastn
4947	LAB327	b_rapa|gb162|CX267240	8217	665	81.2	globlastp
4948	LAB327	switchgrass|gb167|FE601743	8218	665	81.1	globlastp
4949	LAB327	ostreococcus|gb162|XM001418935	8219	665	80.6	globlastp
4950	LAB327	pseudoroegneria|gb167|FF346170	8220	665	80.6	globlastp
4951	LAB327	sugarcane|10v1|AA525682	8221	665	80.1	globlastp
4952	LAB329	solanum_phureja|09v1|SPHAA076679	8222	666	81	globlastp
4953	LAB329	potato|gb157.2|BG600407	8222	666	81	globlastp
4954	LAB335	pseudoroegneria|gb167|FF348025	8223	667	98.18	glotblastn
4955	LAB335	wheat|gb164|BE430022	8224	667	97.4	globlastp
4956	LAB335	barley|gb157SOLEXA|AL502372	8225	667	97.1	globlastp
4957	LAB335	barley|10v1|BE420777XX1	8225	667	97.1	globlastp
4958	LAB335	brachypodium|09v1|DV477130	8226	667	86.2	globlastp
4959	LAB335	rice|gb170|OS06G33710	8227	667	84.2	globlastp
4960	LAB335	switchgrass|gb167|FE658978	8228	667	82.5	globlastp
4961	LAB335	brachypodium|gb169|BE430022	8229	667	82.3	globlastp
4962	LAB335	switchgrass|gb167|FE632114	8230	667	82	globlastp
4963	LAB335	switchgrass|gb167|DN143077	8231	667	81.9	globlastp
4964	LAB335	sorghum|09v1|SB10G020570	8232	667	81.7	globlastp
4965	LAB335	sorghum|gb161.crp|AI977976	8232	667	81.7	globlastp
4966	LAB335	maize|gb170|AI649774	8233	667	81.2	globlastp
4967	LAB335	sorghum|09v1|SB04G009230	8234	667	80.8	globlastp
4968	LAB335	sorghum|gb161.crp|AI987556	8234	667	80.8	globlastp
4969	LAB335	sorghum|09v1|SB04G001510	8235	667	80.46	glotblastn
4970	LAB335	sorghum|gb161.crp|BE918485	8235	667	80.46	glotblastn
4971	LAB336	wheat|gb164|CK211137	8236	668	98.67	glotblastn
4972	LAB336	barley|10v1|BE213707	8237	668	89.3	globlastp
4973	LAB336	barley|gb157SOLEXA|BE213707	8237	668	89.3	globlastp
4974	LAB336	barley|10v1|BE193842	8238	668	86.7	globlastp

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4975	LAB336	barley|gb157SOLEXA|BE193842	8238	668	86.7	globlastp
4976	LAB337	wheat|gb164|BE605188	8239	669	98.5	globlastp
4977	LAB337	wheat|gb164|CA711145	8240	669	97.1	globlastp
4978	LAB337	barley|10v1|BI947303	8241	669	95.6	globlastp
4979	LAB337	barley|gb157SOLEXA|BI947303	8241	669	95.6	globlastp
4980	LAB337	pseudoroegneria|gb167|FF341367	8242	669	92.8	globlastp
4981	LAB339	wheat|gb164|BM138484	8243	670	97.9	globlastp
4982	LAB339	pseudoroegneria|gb167|FF344192	8244	670	95.4	globlastp
4983	LAB339	barley|10v1|AV835301	8245	670	95.2	globlastp
4984	LAB339	barley|gb157SOLEXA|AL501112	8245	670	95.2	globlastp
4985	LAB339	oat|10v1|GR350608	8246	670	89.8	globlastp
4986	LAB340	brachypodium|09v1|GT766551	8247	671	82.91	glotblastn
4987	LAB342	lolium|10v1|ES699371	8248	672	86	globlastp
4988	LAB342	barley|10v1|AW982420	8249	672	82	globlastp
4989	LAB342	barley|gb157SOLEXA|AW982420	8250	672	80.86	glotblastn
4990	LAB343	b_rapa|gb162|DY013496	8251	673	95.6	globlastp
4991	LAB343	canola|gb161|CD831099	8252	673	94.4	globlastp
4992	LAB343	radish|gb164|EV526960	8253	673	86.7	globlastp
4993	LAB343	radish|gb164|EV546393	8254	673	85.7	globlastp
4994	LAB343	canola|gb161|DY023342	8255	673	85.5	globlastp
4995	LAB343	canola|10v1|EG019883	8256	673	85.1	globlastp
4996	LAB343	canola|10v1|EE483904	8257	673	85.1	globlastp
4997	LAB343	canola|gb161|EE483904	8257	673	85.1	globlastp
4998	LAB343	radish|gb164|EV529074	8258	673	84.5	globlastp
4999	LAB343	canola|10v1|DY023342	8259	673	84.34	glotblastn
5000	LAB343	arabidopsis|gb165|AT3G07880	8260	673	84	globlastp
5001	LAB343	radish|gb164|EX770997	8261	673	83.3	globlastp
5002	LAB343	arabidopsis_lyrata|09v1|JGIAL009219	8262	673	83.1	globlastp
5003	LAB343	radish|gb164|EW713645	8263	673	80.7	globlastp
5004	LAB344	sugarcane|10v1|CA081767	8264	674	84.4	globlastp
5005	LAB344	sugarcane|gb157.3|CA075762	8265	674	83.41	glotblastn
5006	LAB344	sorghum|gb161.crp|BE917776	8266	674	81.4	globlastp
5007	LAB344	sorghum|09v1|SB06G029650	8266	674	81.4	globlastp
5008	LAB344	sugarcane|gb157.3|CA075840	8267	674	80.95	glotblastn
5009	LAB349	soybean|gb168|BE824094	8268	679	89.3	globlastp
5010	LAB352	barley|gb157SOLEXA|BF628371	8269	681	98.1	globlastp
5011	LAB352	barley|10v1|BF628371	8269	681	98.1	globlastp
5012	LAB352	leymus|gb166|EG375949	8270	681	97.5	globlastp
5013	LAB352	brachypodium|09v1|DV478509	8271	681	80.7	globlastp
5014	LAB353	barley|10v1|BM816694	8272	682	85.9	globlastp
5015	LAB353	barley|gb157SOLEXA|BM816694	8272	682	85.9	globlastp
5016	LAB355	barley|10v1|AV908964	8273	683	91.6	globlastp
5017	LAB355	barley|gb157SOLEXA|AV908964	8273	683	91.6	globlastp
5018	LAB355	wheat|gb164|BE499690	8274	683	84.7	globlastp

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5019	LAB355	ricc|gb170|OS08G38780	8275	683	83.7	globlastp
5020	LAB355	brachypodium|gb169|BE494994	8276	683	82.3	globlastp
5021	LAB355	brachypodium|09v1|GFXAM072969X2	8276	683	82.3	globlastp
5022	LAB355	sorghum|09v1|SB02G027870	8277	683	82.2	globlastp
5023	LAB355	sorghum|gb161.crp|BF507008	8277	683	82.2	globlastp
5024	LAB355	barley|gb157SOLEXA|BM100516	8278	683	81.8	globlastp
5025	LAB355	maize|gb170|AI783410	8279	683	81.7	globlastp
5026	LAB355	sorghum|09v1|SB07G028600	8280	683	81.6	globlastp
5027	LAB355	maize|gb170|AI372324	8281	683	81.6	globlastp
5028	LAB355	sorghum|gb161.crp|AI372324	8280	683	81.6	globlastp
5029	LAB367	b_oleracea|gb161|DY025911	8282	684	97.2	globlastp
5030	LAB367	thellungiella|gb167|BY818625	8283	684	95.8	globlastp
5031	LAB367	arabidopsis_lyrata|09v1|JGIAL015133	8284	684	93.71	glotblastn
5032	LAB367	arabidopsis|gb165|AT2G38880	8284	684	93.71	glotblastn
5033	LAB367	radish|gb164|EV527174	8285	684	89.5	globlastp
5034	LAB367	cleome_gynandra|10v1|SRR015532S0028391	8286	684	84.6	globlastp
5035	LAB381	poplar|gb170|BI129814	8287	685	94.86	glotblastn
5036	LAB381	cassava|gb164|CK645876	8288	685	90.8	globlastp
5037	LAB381	castorbean|gb160|EG665628	8289	685	90.8	glotblastn
5038	LAB381	castorbean|09v1|EG665628	8290	685	90.8	globlastp
5039	LAB381	citrus|gb166|CB290512	8291	685	85.7	globlastp
5040	LAB381	nasturtium|10v1|SRR032558S0015243	8292	685	85.1	globlastp
5041	LAB381	cotton|gb164|AI728916	8293	685	81.1	globlastp
5042	LAB383	soybean|gb168|BE821922	8294	686	95.9	globlastp
5043	LAB383	medicago|09v1|AL387357	8295	686	85.1	globlastp
5044	LAB55	rye|gb164|BF145456	8296	690	93.48	glotblastn
5045	LAB55	millet|09v1|EVO454PM000227	8297	690	86.96	glotblastn
5046	LAB55	wheat|gb164|CA484197	8298	690	84.8	globlastp
5047	LAB55	fescue|gb161|DT713184	8299	690	83.7	glotblastn
5048	LAB55	wheat|gb164|CK208158	8300	690	83.7	glotblastn
5049	LAB72	papaya|gb165|EX239264	8301	694	82.35	glotblastn
5050	LAB72	citrus|gb166|CK740017	8302	694	80.95	glotblastn
5051	LAB72	castorbean|09v1|XM002510905	8303	694	80.88	glotblastn
5052	LAB72	castorbean|gb160|MDL30147M014220	8303	694	80.88	glotblastn
5053	LAB72	cassava|gb164|DV447303	8304	694	80.51	glotblastn
5054	LAB120	pepper|gb171|CA522804	8305	700	86.3	globlastp
5055	LAB120	solanum_phureja|09v1|SPHAK320985	8306	700	81.23	glotblastn
5056	LAB120	nasturtium|10v1|SRR032558S0243931	8307	700	80	glotblastn
5057	LAB221	sorghum|09v1|SB02G038960	8308	711	86.7	globlastp
5058	LAB221	sorghum|gb161.crp|SBGWP022909	8308	711	86.7	globlastp
5059	LAB221	maize|gb170|AW231650	8309	711	85.1	globlastp
5060	LAB293	maize|gb170|AI629471	8310	715	89.2	globlastp

Polyn. SEQ ID NO:	*Hom. to Gene Name*	*Cluster name*	*Polyp. SEQ ID NO:*	*Hom. to SEQ ID NO:*	*% Glob. identity*	*Algor.*
5061	LAB293	ricc|gb170|OS08G33740	8311	715	86.7	glotblastn
5062	LAB293	brachypodium|09v1|GT829942	8312	715	85.22	glotblastn
5063	LAB293	brachypodium|gb169|BF257470	8313	715	84.1	globlastp
5064	LAB293	switchgrass|gb167|FE656679	8314	715	83.5	globlastp
5065	LAB293	wheat|gb164|CA627636	8315	715	82.5	globlastp
5066	LAB300	sorghum|09v1|SB05G002450	8316	719	95.7	glotblastn
5067	LAB300	sorghum|gb161.crp|BF421813	8316	719	95.7	glotblastn
5068	LAB300	maize|gb170|AW120452	8317	719	92.47	glotblastn
5069	LAB300	sugarcane|10v1|BU103524	8318	719	92.47	glotblastn
5070	LAB300	sugarcane|gb157.3|BU103524	8319	719	92.47	glotblastn
5071	LAB300	maize|gb170|BQ035158	8320	719	90.32	glotblastn
5072	LAB300	switchgrass|gb167|FE618131	8321	719	87.1	glotblastn
5073	LAB300	millet|09v1|EVO454PM051167	8322	719	86.02	glotblastn
5074	LAB300	rice|gb170|OS12G04290	8323	719	86.02	glotblastn
5075	LAB300	switchgrass|gb167|DN141039	8324	719	86.02	glotblastn
5076	LAB300	rice|gb170|OS11G04520	8325	719	84.95	glotblastn
5077	LAB300	oat|10v1|GR349530	8326	719	82.8	glotblastn
5078	LAB300	brachypodium|09v1|GT778679	8327	719	80.65	glotblastn
5079	LAB300	brachypodium|gb169|BE496864	8328	719	80.65	glotblastn
5080	LAB300	wheat|gb164|BE416393	8329	719	80.65	glotblastn
5081	LAB311	cichorium|gb171|DT211930	8330	721	83.71	glotblastn
5082	LAB311	dandelion|gb161|DY828396	8331	721	81.47	glotblastn
5083	LAB316	petunia|gb171|CV292888	8332	723	87.61	glotblastn
5084	LAB316	triphysaria|10v1|DR175232	8333	723	83	glotblastn
5085	LAB316	grape|gb160|CF213593	8334	723	82.66	glotblastn
5086	LAB316	cotton|gb164|AI726514	8335	723	82.08	glotblastn
5087	LAB316	coffea|10v1|DV665545	8336	723	81.84	glotblastn
5088	LAB316	bean|gb167|CA910091	8337	723	81.79	glotblastn
5089	LAB316	castorbean|09v1|XM002530954	8338	723	81.79	glotblastn
5090	LAB316	castorbean|gb160|MDL29847M000246	8338	723	81.79	glotblastn
5091	LAB316	soybean|gb168|BI969411	8339	723	81.5	glotblastn
5092	LAB316	soybean|gb168|CA910091	8340	723	81.5	glotblastn
5093	LAB316	tragopogon|10v1|SRR020205S0000615	8341	723	81.21	glotblastn
5094	LAB316	chestnut|gb170|SRR006295S0002034	8342	723	81.21	glotblastn
5095	LAB316	citrus|gb166|CF507005	8343	723	81.21	glotblastn
5096	LAB316	cucumber|09v1|DN910234	8344	723	80.98	glotblastn
5097	LAB316	coffea|gb157.2|DV665545	8345	723	80.98	glotblastn
5098	LAB316	lotus|09v1|BP037753	8346	723	80.92	glotblastn
5099	LAB316	cichorium|gb171|EH673760	8347	723	80.92	glotblastn
5100	LAB316	sunflower|gb162|DY925338	8348	723	80.92	glotblastn
5101	LAB316	sunflower|gb162|DY932981	8349	723	80.92	glotblastn
5102	LAB316	artemisia|10v1|EY089946	8350	723	80.64	glotblastn
5103	LAB316	artemisia|gb164|EY089946	8351	723	80.35	glotblastn
5104	LAB323	potato|gb157.2|AW907080	8352	725	89.24	glotblastn

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5105	LAB326	pcppcr|gb171|CA514118	8353	726	92.28	glotblastn
5106	LAB326	solanum_phurcja|09v1|SPHAI776997	8354	726	91.95	glotblastn
5107	LAB326	potato|10v1|BG886798	8355	726	90.9	globlastp
5108	LAB326	petunia|gb171|CV298273	8356	726	89.04	glotblastn
5109	LAB326	artemisia|gb164|EY085224	8357	726	81.46	glotblastn
5110	LAB326	artemisia|10v1|SRR019254S0002302	8358	726	80.74	glotblastn
5111	LAB326	lettuce|10v1|DW065639	8359	726	80.5	globlastp
5112	LAB327	poppy|gb166|FG606884	8360	727	99.01	glotblastn
5113	LAB327	canola|10v1|CD823763	8361	727	98.02	glotblastn
5114	LAB327	eggplant|10v1|FS002516	8362	727	98.02	glotblastn
5115	LAB327	eggplant|10v1|FS018078	8363	727	98.02	glotblastn
5116	LAB327	sorghum|09v1|SLXL50010512D1	8364	727	98.02	glotblastn
5117	LAB327	tomato|09v1|AI484526	8365	727	98.02	glotblastn
5118	LAB327	tomato|09v1|BQ118912	8366	727	98.02	glotblastn
5119	LAB327	b_juncea|gb164|EVGN0138283171021 9	8367	727	98.02	glotblastn
5120	LAB327	b_oleracea|gb161|AM386836	8368	727	98.02	glotblastn
5121	LAB327	canola|gb161|DY002101	8369	727	98.02	glotblastn
5122	LAB327	canola|gb161|EE413610	8370	727	98.02	glotblastn
5123	LAB327	canola|gb161|EE440622	8371	727	98.02	glotblastn
5124	LAB327	canola|gb161|EE456605	8372	727	98.02	glotblastn
5125	LAB327	canola|gb161|EE460641	8373	727	98.02	glotblastn
5126	LAB327	cassava|09v1|CK644469	8374	727	98.02	glotblastn
5127	LAB327	cassava|gb164|CK644469	8375	727	98.02	glotblastn
5128	LAB327	cotton|gb164|BF271275	8376	727	98.02	glotblastn
5129	LAB327	petunia|gb171|CV299604	8377	727	98.02	glotblastn
5130	LAB327	potato|gb157.2|CK270482	8378	727	98.02	glotblastn
5131	LAB327	radish|gb164|EV527546	8379	727	98.02	glotblastn
5132	LAB327	radish|gb164|EX888568	8380	727	98.02	glotblastn
5133	LAB327	walnuts|gb166|CV195688	8381	727	98.02	glotblastn
5134	LAB327	b_rapa|gb162|AB012653	8382	727	98	globlastp
5135	LAB327	nicotiana_benthamiana|gb162|CN7431 93	8383	727	98	globlastp
5136	LAB327	cleome_spinosa|10v1|SRR015531S000 0653	8384	727	97.03	glotblastn
5137	LAB327	cucumber|09v1|DN909393	8385	727	97.03	glotblastn
5138	LAB327	eggplant|10v1|FS018763	8386	727	97.03	glotblastn
5139	LAB327	eschscholzia|10v1|SRR014116S000554 1	8387	727	97.03	glotblastn
5140	LAB327	ipomoea_nil|10v1|BJ567233	8388	727	97.03	glotblastn
5140	LAB327	ipomoea|gb157.2|BJ567233	8388	727	97.03	glotblastn
5141	LAB327	rhizophora|10v1|SRR005792S0001643	8389	727	97.03	glotblastn
5142	LAB327	rhizophora|10v1|SRR005793S0006109	8390	727	97.03	glotblastn
5143	LAB327	solanum_phureja|09v1|SPHBQ118912	8391	727	97.03	glotblastn

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5144	LAB327	solanum_phurcja|09v1|SPHCV492300	8392	727	97.03	glotblastn
5145	LAB327	tomato|09v1|CV492300	8393	727	97.03	glotblastn
5146	LAB327	b_juncea|gb164|EVGN00146809031110	8394	727	97.03	glotblastn
5147	LAB327	banana|gb167|FF562462	8395	727	97.03	glotblastn
5148	LAB327	barley|gb157SOLEXA|BJ449692	8396	727	97.03	glotblastn
5149	LAB327	eucalyptus|gb166|CU396200	8397	727	97.03	glotblastn
5150	LAB327	ginger|gb164|DY353207	8398	727	97.03	glotblastn
5151	LAB327	leymus|gb166|CD808996	8399	727	97.03	glotblastn
5152	LAB327	maize|gb170|CD441688	8400	727	97.03	glotblastn
5153	LAB327	oil_palm|gb166|AY040227	8401	727	97.03	glotblastn
5154	LAB327	pineapple|10v1|DT337548	8402	727	97.03	glotblastn
5155	LAB327	poplar|gb170|AI163175	8403	727	97.03	glotblastn
5156	LAB327	potato|gb157.2|CK267835	8404	727	97.03	glotblastn
5157	LAB327	pseudoroegneria|gb167|FF343365	8405	727	97.03	glotblastn
5158	LAB327	radish|gb164|EV536307	8406	727	97.03	glotblastn
5159	LAB327	sorghum|gb161.crp|SBGWP053010	8407	727	97.03	glotblastn
5160	LAB327	tobacco|gb162|DW001412	8408	727	97.03	glotblastn
5161	LAB327	wheat|gb164|BE412017	8409	727	97.03	glotblastn
5162	LAB327	wheat|gb164|BF293084	8410	727	97.03	glotblastn
5163	LAB327	wheat|gb164|CD491106	8411	727	97.03	glotblastn
5164	LAB327	banana|gb167|FL665731	8412	727	97	globlastp
5165	LAB327	arabidopsis_lyrata|09v1|CRPALE014458	8413	727	96.04	glotblastn
5166	LAB327	chickpea|09v2|GR399685	8414	727	96.04	glotblastn
5167	LAB327	cleome_spinosa|10v1|SRR015531S0018590	8415	727	96.04	glotblastn
5168	LAB327	cleome_spinosa|10v1|SRR015531S0034249	8416	727	96.04	glotblastn
5169	LAB327	ipomoea_nil|10v1|BJ566333	8417	727	96.04	glotblastn
5169	LAB327	ipomoea|gb157.2|BJ566333	8417	727	96.04	glotblastn
5170	LAB327	lettuce|10v1|DW070872	8418	727	96.04	glotblastn
5171	LAB327	millet|09v1|EVO454PM002075	8419	727	96.04	glotblastn
5172	LAB327	pigeonpea|gb171|GR471472	8420	727	96.04	glotblastn
5173	LAB327	pigeonpea|gb171|GR473022	8421	727	96.04	glotblastn
5174	LAB327	salvia|10v1|CV162812	8422	727	96.04	glotblastn
5175	LAB327	salvia|10v1|CV163214	8423	727	96.04	glotblastn
5176	LAB327	solanum_phureja|09v1|SPHCRPSP044068	8424	727	96.04	glotblastn
5177	LAB327	banana|gb167|FL664451	8425	727	96.04	glotblastn
5178	LAB327	basilicum|10v1|DY325098	8426	727	96.04	glotblastn
5179	LAB327	basilicum|gb157.3|DY325098	8426	727	96.04	glotblastn
5180	LAB327	centaurea|gb166|EL931474	8427	727	96.04	glotblastn
5181	LAB327	cichorium|gb171|EH685996	8428	727	96.04	glotblastn

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5182	LAB327	melon|gb165|AM713503	8429	727	96.04	glotblastn
5183	LAB327	peanut|gb171|EG030107	8430	727	96.04	glotblastn
5184	LAB327	sugarcane|gb157.3|CA073323	8431	727	96.04	glotblastn
5185	LAB327	switchgrass|gb167|FE605806	8432	727	96.04	glotblastn
5186	LAB327	zamia|gb166|CB095911	8433	727	96.04	glotblastn
5187	LAB327	eschscholzia|10v1|SRR014116S0006563	8434	727	96	globlastp
5188	LAB327	basilicum|gb157.3|DY326229	8435	727	96	globlastp
5188	LAB327	basilicum|10v1|DY326229	8486	727	91.5	globlastp
5189	LAB327	brachypodium|09v1|CRPBD012820	8436	727	95.05	glotblastn
5190	LAB327	chickpea|09v2|GR394209	8437	727	95.05	glotblastn
5191	LAB327	gerbera|09v1|AJ753152	8438	727	95.05	glotblastn
5192	LAB327	lotus|09v1|BG662143	8439	727	95.05	glotblastn
5193	LAB327	nasturtium|10v1|SRR032558S0020815	8440	727	95.05	glotblastn
5194	LAB327	oat|10v1|GR349416	8441	727	95.05	glotblastn
5195	LAB327	orobanche|10v1|SRR023189S0012423	8442	727	95.05	glotblastn
5196	LAB327	pea|09v1|FG529035	8443	727	95.05	glotblastn
5197	LAB327	physcomitrella|10v1|PHPCRP010667	8444	727	95.05	glotblastn
5198	LAB327	pigeonpea|gb171|GR466365	8445	727	95.05	glotblastn
5199	LAB327	bean|gb167|CA898102	8446	727	95.05	glotblastn
5200	LAB327	clover|gb162|BB907933	8447	727	95.05	glotblastn
5201	LAB327	cynara|gb167|GE599288	8448	727	95.05	glotblastn
5202	LAB327	onion|gb162|CF439850	8449	727	95.05	glotblastn
5203	LAB327	pineapple|10v1|DT335927	8450	727	95.05	glotblastn
5204	LAB327	pineapple|gb157.2|DT335927	8451	727	95.05	glotblastn
5205	LAB327	sunflower|gb162|BQ914361	8452	727	95.05	glotblastn
5206	LAB327	basilicum|10v1|DY341441	8453	727	94.06	glotblastn
5207	LAB327	eggplant|10v1|FS002029	8454	727	94.06	glotblastn
5208	LAB327	ipomoea_batatas|10v1|CO500259	8455	727	94.06	glotblastn
5209	LAB327	medicago|09v1|AL370119	8456	727	94.06	glotblastn
5210	LAB327	physcomitrella|10v1|PHPCRP016239	8457	727	94.06	glotblastn
5211	LAB327	tragopogon|10v1|SRR020205S0006730	8458	727	94.06	glotblastn
5212	LAB327	amborella|gb166|CO999518	8459	727	94.06	glotblastn
5213	LAB327	basilicum|gb157.3|DY341441	8453	727	94.06	glotblastn
5214	LAB327	beet|gb162|BF011040	8460	727	94.06	glotblastn
5215	LAB327	canola|10v1|EV041917	8461	727	94.06	glotblastn
5216	LAB327	canola|gb161|EV041917	8462	727	94.06	glotblastn
5217	LAB327	cichorium|gb171|EH679514	8463	727	94.06	glotblastn
5218	LAB327	dandelion|gb161|DY832440	8464	727	94.06	glotblastn
5219	LAB327	petunia|gb171|CV297073	8465	727	94.06	glotblastn
5220	LAB327	sunflower|gb162|EL421491	8466	727	94.06	glotblastn
5221	LAB327	triphysaria|gb164|DR176592	8467	727	94.06	glotblastn
5222	LAB327	walnuts|gb166|CV195670	8468	727	94.06	glotblastn
5223	LAB327	tomato|gb164|BG735245	8469	727	93.1	globlastp

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5224	LAB327	solanum_phurcja|09v1|SPHCRPSP014772	8470	727	93.07	glotblastn
5225	LAB327	antirrhinum|gb166|AJ789472	8471	727	93.07	glotblastn
5226	LAB327	clover|gb162|BB909848	8472	727	93.07	glotblastn
5227	LAB327	cynara|gb167|GE598198	8473	727	93.07	glotblastn
5228	LAB327	fern|gb171|DK952436	8474	727	93.07	glotblastn
5229	LAB327	radish|gb164|EV545321	8475	727	93.07	glotblastn
5230	LAB327	radish|gb164|EW731903	8476	727	93.07	glotblastn
5231	LAB327	thellungiella|gb167|BY800754	8477	727	92.5	globlastp
5232	LAB327	avocado|10v1|CO996828	8478	727	92.08	glotblastn
5233	LAB327	medicago|09v1|LLAL381370	8479	727	92.08	glotblastn
5234	LAB327	solanum_phureja|09v1|SPHCRPSP026105	8480	727	92.08	glotblastn
5235	LAB327	tomato|09v1|CRPSP026105	8480	727	92.08	glotblastn
5236	LAB327	brachypodium|09v1|DV469797	8481	727	92.08	glotblastn
5237	LAB327	brachypodium|gb169|BE400316	8481	727	92.08	glotblastn
5238	LAB327	lettuce|10v1|DW047925	8482	727	92.08	glotblastn
5239	LAB327	nuphar|gb166|CD474327	8483	727	92.08	glotblastn
5240	LAB327	triphysaria|gb164|EY006504	8484	727	92.08	glotblastn
5241	LAB327	zinnia|gb171|AU305761	8485	727	92.08	glotblastn
5242	LAB327	ginseng|10v1|GR871242	8487	727	91.1	globlastp
5243	LAB327	chickpea|09v2|GR915554	8488	727	91.09	glotblastn
5244	LAB327	gerbera|09v1|AJ754459	8489	727	91.09	glotblastn
5245	LAB327	b_oleracea|gb161|ES940987	8490	727	91.09	glotblastn
5246	LAB327	jatropha|09v1|FM891968	8491	727	90.1	globlastp
5247	LAB327	canola|gb161|CD836727	8492	727	90.1	glotblastn
5248	LAB327	cassava|gb164|DB943271	8493	727	90.1	globlastp
5249	LAB327	mesostigma|gb166|EC727138	8494	727	90.1	glotblastn
5250	LAB327	antirrhinum|gb166|AJ559628	8495	727	89.7	globlastp
5251	LAB327	arabidopsis_lyrata|09v1|CRPALE015090	8496	727	89.11	glotblastn
5252	LAB327	soybean|gb168|SB2GWP031146	8497	727	88.12	glotblastn
5253	LAB327	rhizophora|10v1|SRR005793S0029492	8498	727	87.7	globlastp
5254	LAB327	cacao|gb167|CU583493	8499	727	87.13	glotblastn
5255	LAB327	senecio|gb170|SRR006594S0009563	8500	727	87.13	glotblastn
5256	LAB327	soybean|gb168|ES612478	8501	727	87.13	glotblastn
5257	LAB327	salvia|10v1|SRR014553S0018208	8502	727	86.8	globlastp
5258	LAB327	kiwi|gb166|FG403299	8503	727	86.6	globlastp
5259	LAB327	lettuce|gb157.2|DW044074	8504	727	86.4	globlastp
5260	LAB327	lettuce|10v1|DW044074	8504	727	86.4	globlastp
5261	LAB327	castorbean|09v1|CRPRC009201	8505	727	86.14	glotblastn
5262	LAB327	fern|gb171|DK945838	8506	727	86.14	glotblastn
5263	LAB327	cryptomeria|gb166|AU066365	8507	727	85.7	globlastp
5264	LAB327	lettuce|10v1|BQ847691	8508	727	85.5	globlastp

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5265	LAB327	fcscuc|gb161|DT674428	8509	727	85.2	globlastp
5266	LAB327	fcscuc|gb161|DT704683	8509	727	85.2	globlastp
5267	LAB327	ginger|gb164|DY352710	8510	727	85.2	globlastp
5268	LAB327	ginger|gb164|DY367029	8511	727	85.1	globlastp
5269	LAB327	lettuce|gb157.2|BQ846927	8512	727	84.8	globlastp
5270	LAB327	chickpea|09v2|FL512356	8513	727	84.3	globlastp
5271	LAB327	beet|gb162|EG549666	8514	727	84.3	globlastp
5272	LAB327	castorbean|09v1|XM002516046	8515	727	84.16	glotblastn
5273	LAB327	castorbean|gb160|MDL29739M003574	8515	727	84.16	glotblastn
5274	LAB327	cryptomeria|gb166|BP175684	8516	727	83.5	globlastp
5275	LAB327	lotus|gb157.2|BP036168	8517	727	83.5	globlastp
5276	LAB327	triphysaria|10v1|EY154847	8518	727	83.17	glotblastn
5277	LAB327	triphysaria|gb164|EY154847	8519	727	83.17	glotblastn
5278	LAB327	wheat|gb164|BQ242360	8520	727	83.17	glotblastn
5279	LAB327	ipomoea_batatas|10v1|DV038154	8521	727	82.6	globlastp
5280	LAB327	ginger|gb164|DY357739	8522	727	82.6	globlastp
5281	LAB327	potato|gb157.2|EG016197	8523	727	82.6	globlastp
5281	LAB327	potato|10v1|EG016197	8527	727	81.9	globlastp
5282	LAB327	eucalyptus|gb166|CB967721	8524	727	82.2	globlastp
5283	LAB327	thellungiella|gb167|BY825969	8525	727	82.2	globlastp
5284	LAB327	pea|09v1|FG534024	8526	727	82.1	globlastp
5285	LAB327	maize|gb170|LLCD985621	8528	727	81.19	glotblastn
5286	LAB327	oat|10v1|SRR020744S0068207	8529	727	80.6	globlastp
5287	LAB327	tragopogon|10v1|SRR020205S0002992	8530	727	80.2	glotblastn
5288	LAB327	b_juncea|gb164|EVGN1522842471194 9	8531	727	80.2	globlastp
5289	LAB327	sunflower|gb162|EL434559	8532	727	80.2	glotblastn
5290	LAB327	canola|10v1|CD836727	8533	727	80	globlastp
5291	LAB327	ipomoea|gb157.2|BJ569764	8534	727	80	globlastp
5292	LAB348	maize|gb170|EB407478	8535	728	90.7	globlastp
5293	LAB348	maize|gb170|DR814793	8536	728	87	globlastp
5294	LAB381	poplar|10v1|BI129814	8537	730	93.2	globlastp
5295	LAB381	cassava|09v1|CK645876	8538	730	91.3	globlastp
5296	LAB381	cucumber|09v1|EB715836	8539	730	81.1	globlastp
5297	LAB65	barley|10v1|BG368928	8540	735	81.73	glotblastn
5298	LAB73	cassava|09v1|CK649713	8541	736	81.7	globlastp
5299	LAB73	cacao|gb167|CU476966	8542	736	81.1	globlastp
5300	LAB73	cotton|gb164|AI725704	8543	736	80.5	globlastp
5301	LAB73	poplar|10v1|BU861781	8544	736	80.2	globlastp
5302	LAB73	poplar|10v1|CV230194	8545	736	80.18	glotblastn
5303	LAB108	maize|gb170|BM661010	8546	738	94.28	glotblastn
5304	LAB108	rice|gb170|OS12G12260	8547	738	84.7	globlastp
5305	LAB108	brachypodium|09v1|DV482604	8548	738	83.7	globlastp
5306	LAB108	brachypodium|gb169|BF474193	8548	738	83.7	globlastp

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5307	LAB108	barley|10v1|BG300035	8549	738	81.9	globlastp
5308	LAB123	tomato|09v1|BG889563	8550	739	94.1	globlastp
5309	LAB125	solanum_phureja|09v1|SPHBG124210	8551	741	88.8	globlastp
5310	LAB126	solanum_phureja|09v1|SPHBG126148	8552	742	96.5	globlastp
5311	LAB138	brachypodium|gb169|BE426494	8553	744	86.9	globlastp
5312	LAB138	brachypodium|09v1|SRR031795S0016784	8554	744	86.6	globlastp
5313	LAB138	rice|gb170|OS09G35680	8555	744	83.4	globlastp
5314	LAB157	maize|gb170|AW424421	8556	746	92.5	globlastp
5315	LAB157	rice|gb170|OS11G31570	8557	746	85.4	globlastp
5316	LAB157	brachypodium|09v1|SRR031797S0018936	8558	746	84.5	globlastp
5317	LAB157	wheat|gb164|CJ625105	8559	746	81.4	globlastp
5318	LAB164	switchgrass|gb167|FL925553	8560	748	92.9	globlastp
5319	LAB164	leymus|gb166|EG389112	8561	748	90.6	globlastp
5320	LAB164	rice|gb170|OS08G02070	8562	748	90.5	globlastp
5321	LAB164	maize|gb170|EG075778	8563	748	90.2	globlastp
5322	LAB164	maize|gb170|BM379409	8564	748	89	globlastp
5323	LAB164	wheat|gb164|BE445505	8565	748	88.8	globlastp
5324	LAB164	brachypodium|09v1|SRR031797S0001217	8566	748	84.5	globlastp
5325	LAB190	arabidopsis_lyrata|09v1|JGIAL027834	8567	753	89.3	globlastp
5326	LAB206	wheat|gb164|BE430173	8568	754	91.6	globlastp
5327	LAB206	wheat|gb164|BE591206	8568	754	91.6	globlastp
5328	LAB206	wheat|gb164|BE493558	8569	754	90.9	globlastp
5329	LAB206	wheat|gb164|BG313801	8570	754	90.9	globlastp
5330	LAB206	oat|10v1|GR360139	8571	754	87.7	globlastp
5331	LAB207	barley|gb157SOLEXA|AJ470859	8572	755	87.2	globlastp
5332	LAB207	barley|gb157SOLEXA|BI947011	8573	755	87.2	globlastp
5333	LAB207	barley|10v1|BI947011	8573	755	87.2	globlastp
5334	LAB207	wheat|gb164|BE399070	8574	755	83	globlastp
5335	LAB207	wheat|gb164|BG312816	8575	755	82.22	glotblastn
5336	LAB207	wheat|gb164|BE425222	8576	755	81.67	glotblastn
5337	LAB207	wheat|gb164|BE420315	8577	755	81.46	glotblastn
5338	LAB207	wheat|gb164|BE425435	8578	755	80.66	glotblastn
5339	LAB207	wheat|gb164|CD937530	8579	755	80.6	globlastp
5340	LAB207	wheat|gb164|BE426035	8580	755	80.3	globlastp
5341	LAB207	wheat|gb164|BE492138	8581	755	80.11	glotblastn
5342	LAB210	leymus|gb166|EG389322	8582	756	82.6	glotblastn
5343	LAB210	wheat|gb164|BE403306	8583	756	82.6	globlastp
5344	LAB210	wheat|gb164|BM134945	8584	756	82.4	globlastp
5345	LAB210	wheat|gb164|CA596301	8585	756	82.1	globlastp
5346	LAB210	wheat|gb164|BE499093	8586	756	82	globlastp
5347	LAB210	barley|10v1|BF621975	8587	756	80.5	globlastp

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5348	LAB210	barley|gb157SOLEXA|BF621975	8587	756	80.5	globlastp
5349	LAB210	brachypodium|gb169|BE403306	8588	756	80.3	globlastp
5350	LAB212	rice|gb170|OS06G46900	8589	757	83.8	globlastp
5351	LAB213	wheat|gb164|BF473141	8590	758	93.4	globlastp
5352	LAB213	wheat|gb164|BF474599	8591	758	93.4	globlastp
5353	LAB213	wheat|gb164|BQ743375	8592	758	93.4	globlastp
5354	LAB213	leymus|gb166|EG374734	8593	758	92.1	globlastp
5355	LAB213	oat|10v1|GO594668	8594	758	82.6	globlastp
5356	LAB213	wheat|gb164|BE426266	8595	758	82.4	globlastp
5357	LAB213	brachypodium|09v1|DV469105	8596	758	81	globlastp
5358	LAB213	brachypodium|gb169|BE426266	8596	758	81	globlastp
5359	LAB222	sorghum|09v1|SB04G034760	8597	761	83.6	globlastp
5360	LAB271	sugarcane|10v1|BU103128	8598	763	95.9	globlastp
5361	LAB271	sugarcane|gb157.3|BU103128	8598	763	95.9	globlastp
5362	LAB271	maize|gb170|AI649483	8599	763	94.6	globlastp
5363	LAB271	rice|gb170|OS01G66120	8600	763	84.2	globlastp
5364	LAB271	wheat|gb164|BE414854	8601	763	83	globlastp
5365	LAB271	wheat|gb164|BE414877	8602	763	82.7	globlastp
5366	LAB271	brachypodium|09v1|DV475081	8603	763	82.5	globlastp
5367	LAB271	brachypodium|gb169|BE414854	8603	763	82.5	globlastp
5368	LAB271	oat|10v1|GR323587	8604	763	81.8	globlastp
5369	LAB271	leymus|gb166|EG379378	8605	763	81.4	globlastp
5370	LAB271	barley|10v1|BF625713	8606	763	80.6	globlastp
5371	LAB271	barley|gb157SOLEXA|AL507776	8606	763	80.6	globlastp
5372	LAB294	maize|gb170|AW267317	8607	765	88.9	globlastp
5373	LAB295	maize|gb170|AI987279	8608	766	90.99	glotblastn
5374	LAB297	maize|gb170|AI939833	8609	768	82.9	globlastp
5375	LAB298	maize|gb170|BM267212	8610	769	91.2	globlastp
5376	LAB299	sugarcane|10v1|CA067401	8611	770	95.8	globlastp
5377	LAB299	sugarcane|gb157.3|CA067401	8612	770	95.8	globlastp
5378	LAB306	soybean|gb168|BU549205	8613	772	86.3	globlastp
5379	LAB306	cowpea|gb166|FF387950	8614	772	80.2	globlastp
5380	LAB316	solanum_phureja|09v1|SPHAI773156	8615	775	95.2	globlastp
5381	LAB316	tomato|09v1|BG125377	8616	775	86.6	globlastp
5382	LAB316	tomato|gb164|BG125377	8616	775	86.6	globlastp
5383	LAB316	tobacco|gb162|AJ718731	8617	775	86.1	globlastp
5384	LAB316	potato|gb157.2|BI405340	8618	775	85.9	globlastp
5385	LAB316	potato|10v1|BF459737	8619	775	85.7	globlastp
5386	LAB316	solanum_phureja|09v1|SPHBG125377	8620	775	85	globlastp
5387	LAB316	triphysaria|gb164|DR175232	8621	775	81.7	globlastp
5388	LAB316	triphysaria|10v1|DR171145	8622	775	81.5	globlastp
5389	LAB316	poplar|10v1|AI166150	8623	775	81.25	glotblastn
5390	LAB316	poplar|gb170|AI166150	8623	775	81.25	glotblastn
5391	LAB316	cassava|09v1|CK649108	8624	775	80.9	globlastp

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5392	LAB316	orobanchc|10v1|SRR023189S0001256	8625	775	80.8	globlastp
5393	LAB316	grapc|gb160|CB342294	8626	775	80.5	globlastp
5394	LAB316	lotus|09v1|GO026464	8627	775	80.3	globlastp
5395	LAB316	lettuce|10v1|DW047539	8628	775	80.1	globlastp
5396	LAB316	lettuce|gb157.2|DW047539	8628	775	80.1	globlastp
5397	LAB318	solanum_phureja|09v1|SPHAI899075	8629	777	95.1	globlastp
5398	LAB318	potato|10v1|BG596620	8630	777	94.9	globlastp
5399	LAB326	potato|gb157.2|BG350058	8631	778	97.5	globlastp
5400	LAB326	potato|10v1|BG350058	8631	778	97.5	globlastp
5401	LAB326	tomato|09v1|BG129901	8632	778	97.2	globlastp
5402	LAB326	potato|gb157.2|BE920131	8633	778	96.4	globlastp
5403	LAB326	solanum_phureja|09v1|SPHBG642701	8634	778	96.3	globlastp
5404	LAB326	potato|10v1|BG887005	8635	778	95.72	glotblastn
5405	LAB326	solanum_phureja|09v1|SPHBG123720	8636	778	95.71	glotblastn
5406	LAB326	potato|gb157.2|BF053757	8637	778	95.31	glotblastn
5407	LAB326	potato|10v1|BF153565	8638	778	94.7	globlastp
5408	LAB326	potato|gb157.2|BF153565	8638	778	94.7	globlastp
5409	LAB326	potato|gb157.2|BE922713	8639	778	94.64	glotblastn
5410	LAB326	solanum_phureja|09v1|SPHBG626585	8640	778	94.3	globlastp
5411	LAB326	pepper|gb171|AF081215	8641	778	93.6	globlastp
5412	LAB326	tobacco|gb162|GFXAB008200X1	8642	778	93.1	globlastp
5413	LAB326	solanum_phureja|09v1|SPHGFXX63103X1	8643	778	93.08	glotblastn
5414	LAB326	solanum_phureja|09v1|SPHAW031670	8644	778	93.07	glotblastn
5415	LAB326	tobacco|gb162|TOBPAL1	8645	778	90.2	globlastp
5416	LAB326	tobacco|gb162|X78269	8646	778	89.9	globlastp
5417	LAB326	potato|10v1|BG095888	8647	778	89.6	globlastp
5418	LAB326	potato|gb157.2|BG095888	8647	778	89.6	globlastp
5419	LAB326	solanum_phureja|09v1|SPHBG626799	8648	778	89.1	globlastp
5420	LAB326	solanum_phureja|09v1|SPHCV498380	8649	778	88.5	globlastp
5421	LAB326	ipomoea_nil|10v1|GFXAF325496X1	8650	778	88.4	globlastp
5422	LAB326	tomato|09v1|BG626799	8651	778	88.4	globlastp
5423	LAB326	ipomoea|gb157.2|IPBPALA	8652	778	86.8	globlastp
5424	LAB326	catharanthus|gb166|AB042520	8653	778	86.5	globlastp
5425	LAB326	castorbean|09v1|EE260559	8654	778	85.2	globlastp
5426	LAB326	castorbean|gb160|EE260559	8654	778	85.2	globlastp
5427	LAB326	sunflower|gb162|CD846484	8655	778	85.2	globlastp
5428	LAB326	ipomoea_batatas|10v1|IPBPAL	8656	778	85	globlastp
5428	LAB326	ipomoea|gb157.2|IPBPAL	8656	778	85	globlastp
5429	LAB326	ipomoea_batatas|10v1|IPBPALA	8657	778	84.7	globlastp
5430	LAB326	cotton|gb164|BF276718	8658	778	84.7	globlastp
5431	LAB326	cynara|gb167|GFXAM418586X1	8659	778	84.7	globlastp
5432	LAB326	artemisia|10v1|EY085223	8660	778	84.6	globlastp
5433	LAB326	cassava|09v1|AF383150	8661	778	84.6	globlastp

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5434	LAB326	cassava|gb164|AF383150	8662	778	84.5	globlastp
5435	LAB326	basilicum|10v1|DY321950	8663	778	84.3	globlastp
5436	LAB326	basilicum|gb157.3|DY322602	8663	778	84.3	globlastp
5437	LAB326	lettuce|gb157.2|CV700169	8664	778	84.21	glotblastn
5438	LAB326	artemisia|10v1|EY060660	8665	778	84.2	globlastp
5439	LAB326	basilicum|10v1|DY321580	8666	778	84.2	globlastp
5440	LAB326	lettuce|10v1|CV700169	8667	778	84.1	globlastp
5441	LAB326	jatropha|09v1|GFXDQ883805X1	8668	778	84	globlastp
5442	LAB326	poplar|10v1|AI166477	8669	778	83.9	globlastp
5443	LAB326	cotton|gb164|BE051903	8670	778	83.9	globlastp
5444	LAB326	beet|gb162|BI543368	8671	778	83.6	globlastp
5445	LAB326	citrus|gb166|CLU43338	8672	778	83.6	globlastp
5446	LAB326	salvia|10v1|CV165552	8673	778	83.6	globlastp
5447	LAB326	aquilegia|10v1|DR912258	8674	778	83.6	globlastp
5448	LAB326	monkeyflower|10v1|GO944801	8675	778	83.54	glotblastn
5449	LAB326	castorbean|09v1|EG660464	8676	778	83.5	globlastp
5450	LAB326	grape|gb160|BQ793161	8677	778	83.5	globlastp
5451	LAB326	grape|gb160|X75967	8678	778	83.5	globlastp
5452	LAB326	apple|gb171|X68126	8679	778	83.4	globlastp
5453	LAB326	poplar|10v1|POPPALGA	8680	778	83.4	globlastp
5454	LAB326	citrus|gb166|CF832012	8681	778	83.3	globlastp
5455	LAB326	prunus|gb167|AF036948	8682	778	83.3	globlastp
5456	LAB326	cacao|gb167|CF974594	8683	778	83.2	globlastp
5457	LAB326	cynara|gb167|GFXAM418560X1	8684	778	83.2	globlastp
5458	LAB326	medicago|09v1|AI737513	8685	778	83.2	globlastp
5459	LAB326	grape|gb160|BQ796207	8686	778	83.1	globlastp
5460	LAB326	citrus|gb166|BE208887	8687	778	82.8	globlastp
5461	LAB326	cotton|gb164|BG443220	8688	778	82.8	globlastp
5462	LAB326	soybean|gb168|PHVPAL	8689	778	82.8	globlastp
5463	LAB326	cassava|09v1|DB927918	8690	778	82.7	globlastp
5464	LAB326	nasturtium|10v1|GH164221	8691	778	82.7	globlastp
5465	LAB326	poplar|10v1|AI166713	8692	778	82.7	globlastp
5466	LAB326	tea|10v1|AY694188	8693	778	82.7	globlastp
5467	LAB326	cassava|09v1|AY036011	8694	778	82.6	globlastp
5468	LAB326	soybean|gb168|BG835821	8695	778	82.5	globlastp
5469	LAB326	monkeyflower|10v1|GO944409	8696	778	82.4	globlastp
5470	LAB326	clover|gb162|AB236800	8697	778	82.3	globlastp
5471	LAB326	cassava|09v1|JGICASSAVA14518M1	8698	778	82.2	globlastp
5472	LAB326	poplar|10v1|BI131326	8699	778	82.2	globlastp
5473	LAB326	lotus|09v1|AW720528	8700	778	82.1	globlastp
5474	LAB326	petunia|gb171|CV294118	8701	778	82	globlastp
5475	LAB326	lotus|09v1|CB826853	8702	778	81.9	globlastp
5476	LAB326	pea|09v1|CD858906	8703	778	81.7	globlastp
5477	LAB326	soybean|gb168|AA660545	8704	778	81.7	globlastp

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5478	LAB326	soybean|gb168|S46988	8705	778	81.6	globlastp
5479	LAB326	canola|10v1|AA960723	8706	778	81.5	globlastp
5480	LAB326	nasturtium|10v1|SRR032558S0014671	8707	778	81.5	globlastp
5481	LAB326	bean|gb167|CA914521	8708	778	81.44	glotblastn
5482	LAB326	chestnut|gb170|SRR006295S0000016	8709	778	81.4	globlastp
5483	LAB326	triphysaria|10v1|EX991935	8710	778	81.28	glotblastn
5484	LAB326	coffea|10v1|AF218453	8711	778	81.2	globlastp
5485	LAB326	nasturtium|10v1|GH168296	8712	778	81.2	globlastp
5486	LAB326	tomato|09v1|BG132153	8713	778	81.1	globlastp
5487	LAB326	canola|10v1|CD828744	8714	778	81	globlastp
5488	LAB326	cucumber|09v1|AF529240	8715	778	81	globlastp
5489	LAB326	pea|09v1|GFXPEAPAL2X1	8716	778	81	globlastp
5490	LAB326	cucumber|09v1|AM715693	8717	778	80.9	globlastp
5491	LAB326	lotus|09v1|BP085550	8718	778	80.9	globlastp
5492	LAB326	oak|gb170|AY443341	8719	778	80.9	globlastp
5493	LAB326	solanum_phureja|09v1|SPHBG132153	8720	778	80.9	globlastp
5494	LAB326	soybean|gb168|BE352696	8721	778	80.9	globlastp
5495	LAB326	castorbean|09v1|XM002529368	8722	778	80.8	globlastp
5496	LAB326	clover|gb162|DQ073808	8723	778	80.8	globlastp
5497	LAB326	cucumber|09v1|AI563248	8724	778	80.8	globlastp
5498	LAB326	arabidopsis|gb165|AT2G37040	8725	778	80.6	globlastp
5499	LAB326	grape|gb160|CB975210	8726	778	80.6	globlastp
5500	LAB326	cucumber|09v1|AM715202	8727	778	80.58	glotblastn
5501	LAB326	arabidopsis_lyrata|09v1|JGIAL014871	8728	778	80.5	globlastp
5502	LAB326	citrus|gb166|CF417508	8729	778	80.5	globlastp
5503	LAB326	lotus|09v1|AB283035	8730	778	80.44	glotblastn
5504	LAB326	canola|10v1|GFXAY795077X1	8731	778	80.2	globlastp
5505	LAB326	canola|10v1|CD829602	8732	778	80.17	glotblastn
5506	LAB326	cotton|gb164|AA659954	8733	778	80.17	glotblastn
5507	LAB326	tea|10v1|FE942976	8734	778	80.17	glotblastn
5508	LAB339	brachypodium|09v1|DV469561	8735	779	81.3	globlastp
5509	LAB383	bean|gb167|FE898132	8736	782	86.21	glotblastn

Table 54: Provided are the homologous polypeptides (polypep.) and polynucleotides (polynucl.) of the genes for increasing abiotic stress tolerance, yield, growth rate, vigor, oil content, biomass, nitrogen use efficiency, water use efficiency and fertilizer use efficiency genes of a plant which are listed in Table 53 above. Homology was calculated as % of identity over the aligned sequences. The query sequences were polynucleotide and polypeptides depicted in Table 53 above, and the subject sequences are protein and polynucleotide sequences identified in the database based on greater than 80 % global identity to the query nucleotide and/or polypeptide sequences. Hom. = Homology; Glob. = Global; Algor. = Algorithm.

The output of the functional genomics approach described herein is a set of genes highly predicted to improve ABST, yield and/or other agronomic important traits such as growth rate, vigor, biomass, growth rate, oil content, nitrogen use efficiency, water use efficiency and fertilizer use efficiency of a plant by increasing their expression. Although each gene is predicted to have its own impact, modifying the mode of expression of more than one gene is expected to provide an additive or synergistic effect on the plant yield and/or other agronomic important yields performance. Altering the expression of each gene described here alone or set of genes together increases the overall yield and/or other agronomic important traits, hence expects to increase agricultural productivity.

EXAMPLE 11

GENE CLONING AND GENERATION OF BINARY VECTORS FOR PLANT EXPRESSION

To validate their role in improving ABST, yield, growth rate, biomass, vigor, oil content, WUE, NUE and/or FUE selected genes were over-expressed in plants, as follows.

Cloning strategy

Selected genes from those presented in Examples 4 and 5 hereinabove are 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 analyzed to identify the entire open reading frame by comparing the results of several translation algorithms to known proteins from other plant species.

In order to clone the full-length cDNAs, reverse transcription (RT) followed by polymerase chain reaction (PCR; RT-PCR) is performed on total RNA extracted from leaves, roots or other plant tissues, growing under normal conditions. Total RNA extraction, production of cDNA and PCR amplification is performed using standard protocols described elsewhere (Sambrook J., E.F. Fritsch, and T. Maniatis. 1989. Molecular Cloning. A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratory Press, New York.) which are well known to those skilled in the art. PCR products are purified using PCR purification kit (Qiagen)

Usually, 2 sets of primers are prepared for the amplification of each gene, via nested PCR (if required). Both sets of primers are used for amplification on cDNA. In case no product is obtained, a nested PCR reaction is performed. Nested PCR is performed by amplification of 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 are 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, an 8-12 bp extension is added to the 5' 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 such that the digested cDNA is inserted in the sense direction into the binary vector utilized for transformation.

PCR products are digested with the restriction endonucleases (New England BioLabs Inc) according to the sites designed in the primers. Each digested PCR product is inserted into a high copy vector pBlue-script KS plasmid vector [pBlue-script KS plasmid vector, or pUC19 (New England BioLabs Inc], or into plasmids originated from these vectors. In case of the high copy vector originated from pBlue-script KS plasmid vector (pGXN or pGXNa), the PCR product is inserted in the high copy plasmid upstream to the NOS terminator (SEQ ID NO:8737) originated from pBI 101.3 binary vector (GenBank Accession No. U12640, nucleotides 4356 to 4693) and downstream to the 35S promoter. In other cases (pKSJ_6669a or pUC19_pr6669), the At6669 promoter (SEQ ID NO:8741) is already cloned into the pBlue-script KS or pUC19 respectively, so the gene is introduced downstream of the promoter.

Sequencing of the inserted genes is performed, using the ABI 377 sequencer (Applied Biosystems). In some cases, after confirming the sequences of the cloned genes, the cloned cDNA accompanied/ or not with the NOS terminator is introduced into a modified pGI binary vector containing the At6669 promoter via digestion with appropriate restriction endonucleases (the cloned gene replaces the GUI gene). In other cases the cloned cDNA accompanied with the At6669 promoter is introduced into a pGI vector (that does not contain the At6669 promoter). In any case the insert is followed by

single copy of the NOS terminator (SEQ ID NO:8737). The digested products and the linearized plasmid vector are ligated using T4 DNA ligase enzyme (Roche, Switzerland).

Several DNA sequences of the selected genes are synthesized by GeneArt. Synthetic DNA is designed in silico. Suitable restriction enzymes sites are added to the cloned sequences at the 5' end and at the 3' end to enable later cloning into the desired binary vector.

The pPI plasmid vector is constructed by inserting a synthetic poly-(A) signal sequence, originating from pGL3 basic plasmid vector (Promega, GenBank Accession No. U47295; nucleotides 4658-4811) into the *Hind*III restriction site of the binary vector pBI101.3 (Clontech, GenBank Accession No. U12640). pGI (Figure 1) is similar to pPI, but the original gene in the backbone is GUS-Intron and not GUS.

The modified pGI vector (pQFN or pQYN_6669) is a modified version of the pGI vector in which the cassette is inverted between the left and right borders so the gene and its corresponding promoter are close to the right border and the NPTII gene is close to the left border.

At6669, the *Arabidopsis thaliana* promoter sequence (SEQ ID NO:8741) is inserted in the modified pGI binary vector, upstream to the cloned genes, followed by DNA ligation and binary plasmid extraction from positive *E. coli* colonies, as described above. Colonies are analyzed by PCR using the primers covering the insert which are designed to span the introduced promoter and gene. Positive plasmids are identified, isolated and sequenced.

Selected genes cloned by the present inventors are provided in Table 55 below.

Table 55
Genes cloned in High copy number plasmids

Gene Name	*High copy plasmid*	*Organism*	*Primers used SEQ ID NOs:*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LAB190	pKS(Pks_J)	Arabidopsis thaliana Kondara	8903, 8904	360	753
LAB191	pGXN (pKG+Nos+35S)	Arabidopsis thaliana Kondara	8905, 8905, 8906, 8907	361	567
LAB53	pKS(Pks_J)	BARLEY Hordeum vulgare L. ND	9148, 9149	275	474
LAB54	Topo B	BARLEY Hordeum vulgare L. Manit	9150, 9151	276	732
LAB55	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	9152, 9153, 9154, 9155	277	733
LAB56*				278	477
LAB197	Topo B	BARLEY Hordeum vulgare L. Manit	8908, 8909	362	570
LAB121	pKS(Pks_J)	TOMATO Lycopersicum ND ND	8770, 8771, 8772, 8773	312	516
LAB124	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8778, 8778, 8779, 8780	315	740
LAB131	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8798, 8799	322	526
LAB58	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	9156, 9157, 9158, 9159	279	478
LAB206	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	8912, 8912, 8913, 8914	364	754
LAB207	pKS(Pks_J)	BARLEY Hordeum vulgare L. ND	8915, 8916	365	755
LAB64	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. ND	9160, 9161, 9162, 9163	220	734
LAB210	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	8917, 8918, 8919, 8920	366	756
LAB211*				367	575
LAB213	pGXNa	BARLEY Hordeum vulgare L. Manit	8925, 8926	369	758
LAB65	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	9164, 9165, 9166, 9167	280	735
LAB170	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8852, 8853, 8854, 8855	344	549
LAB67	Topo B	Brachypodiums distachyon ND	9168, 9169	281	481
LAB68	pGXN (pKG+Nos+35S)	Brachypodiums distachyon ND	9170, 9171, 9172, 9173	282	482
LAB69	pGXN (pKG+Nos+35S)	Brachypodiums distachyon ND	9174, 9175, 9176, 9177	283	483
LAB70	pKS(Pks_J)	CANOLA Brassica napus ND	9178, 9179	284	484
LAB217	Topo B	COTTON Gossypium hirsutum Akala	8927, 8928	370	578
LAB218	pKS(Pks_J)	COTTON Gossypium hirsutum Akala	8929, 8929, 8930, 8931	371	759
LAB73	pKS(Pks_J)	GRAPE Vitis vinifera ND(rcd glob (rcd) x salt	9180, 9181	285	736

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		krik)			
LAB74	pKS(Pks_J)	MAIZE Zea mays L. B73	9182, 9183	286	488
LAB220*				372	580
LAB222	pKS(Pks_J)	MAIZE Zea mays L. OH43	8935, 8936	374	761
LAB204	pKS(Pks_J)	BARLEY Hordeum vulgare L. ND	8910, 8911	363	571
LAB228*				376	585
LAB229*				377	586
LAB230	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8939, 8940	378	587
LAB231	Topo B	RICE Oryza sativa L. Japonica Nipponbare	8941, 8942	379	588
LAB232	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8943, 8944	380	589
LAB234*				381	591
LAB235*				382	592
LAB236*				383	593
LAB237*				384	594
LAB247	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica Nipponbare	8957, 8958	390	600
LAB221	pKS(Pks_J)	MAIZE Zea mays L. B73	8932, 8932, 8933, 8934	373	760
LAB249	pKS(Pks_J)	RICE Oryza sativa L. Japonica LEMONT	8959, 8960	391	601
LAB147*				327	532
LAB250	Topo B	RICE Oryza sativa L. Japonica ND	8961, 8962	392	602
LAB225	Topo B	RICE Oryza sativa L. Japonica LEMONT	8937, 8938	375	584
LAB252*				393	603
LAB86	pGXNa	RICE Oryza sativa L. Japonica ND	9194, 9195, 9196, 9197	292	495
LAB253*				394	604
LAB254	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8963, 8964	395	605
LAB255	Topo B	RICE Oryza sativa L. Japonica ND	8965, 8966, 8967, 8968	396	762
LAB258	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	8969, 8970	397	607
LAB259	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	8971, 8972	398	608
LAB260*				399	609
LAB238	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8945, 8946, 8947, 8948	385	595
LAB262	pGXNa	RICE Oryza sativa L. Japonica ND	8975, 8976	401	611
LAB263	pGXNa	RICE Oryza sativa L. Japonica ND	8977, 8978	402	612
LAB264*				403	613

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LAB89	Topo B	RICE Oryza sativa L. Japonica ND	9200, 9201	294	737
LAB145	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8806, 8807, 8808, 8809	326	531
LAB265	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8979, 8980	404	614
LAB240	Topo B	RICE Oryza sativa L. Japonica Nipponbare	8949, 8950	386	596
LAB261	Topo B	RICE Oryza sativa L. Japonica ND	8973, 8974	400	610
LAB269	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8985, 8985, 8986, 8987	407	617
LAB167	pKS(Pks_J)	Sorghum bicolor ND	8846, 8847	342	749
LAB267	Topo B	Sorghum bicolor ND	8981, 8982	405	615
LAB268	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8983, 8984	406	616
LAB270	pKS(Pks_J)	Sorghum bicolor ND	8988, 8989	408	618
LAB271	Topo B	Sorghum bicolor ND	8990, 8991	409	763
LAB169	pKS(Pks_J)	Sorghum bicolor ND	8848, 8849, 8850, 8851	343	548
LAB272	Topo B	Sorghum bicolor ND	8992, 8993	410	620
LAB171	pKS(Pks_J)	Sorghum bicolor ND	8856, 8857	345	550
LAB97	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9208, 9209, 9210, 9211	230	501
LAB274	Topo B	Sorghum bicolor ND	8994, 8995	411	621
LAB98*				298	502
LAB275	Topo B	Sorghum bicolor ND	8996, 8997	412	622
LAB172	pKS(Pks_J)	Sorghum bicolor ND	8858, 8859	346	551
LAB276_H0*				470	687
LAB277	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8998, 8999	413	624
LAB101	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8743, 8744	299	503
LAB278	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9000, 9001, 9002, 9003	414	625
LAB102*				300	504
LAB279	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9004, 9005	415	626
LAB175	pGXNa	Sorghum bicolor ND	8860, 8861, 8862, 8863	347	553
LAB152	pKS(Pks_J)	Sorghum bicolor ND	8810, 8811	328	533
LAB153	pKS(Pks_J)	Sorghum bicolor ND	8812, 8813, 8814, 8815	329	534
LAB154	pKS(Pks_J)	Sorghum bicolor ND	8816, 8817, 8818, 8819	330	535
LAB280	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9006, 9007, 9008, 9009	416	627
LAB281	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9010, 9011	417	628

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LAB282	pKS(Pks_J)	Sorghum bicolor ND	9012, 9013	418	629
LAB106**	Topo B	Sorghum bicolor Monsanto S5	8745, 8746	301	505
LAB283	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9014, 9015	419	630
LAB107	Topo B	Sorghum bicolor ND	8747, 8748	302	506
LAB284	pKS(Pks_J)	Sorghum bicolor ND	9016, 9017	420	631
LAB286	pKS(Pks_J)	Sorghum bicolor ND	9018, 9019, 9020, 9021	421	632
LAB109	pKS(Pks_J)	Sorghum bicolor ND	8751, 8752	304	508
LAB335	Topo B	WHEAT Triticum aestivum L. ND	9104, 9105	453	667
LAB289	pKS(Pks_J)	Sorghum bicolor ND	9022, 9023, 9024, 9025	422	633
LAB290_H0*				471	688
LAB291**	TopoB	Sorghum bicolor ND	9026, 9027	473	
LAB292	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9028, 9029	423	635
LAB293	Topo B	Sorghum bicolor ND	9030, 9031	254	764
LAB294	Topo B	Sorghum bicolor ND	9032, 9033	424	765
LAB166	Topo B	Sorghum bicolor ND	8844, 8845	341	546
LAB156	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8820, 8821, 8822	331	745
LAB295	Topo B	Sorghum bicolor ND	9034, 9035	425	766
LAB157	pKS(Pks_J)	Sorghum bicolor ND	8823, 8824	332	746
LAB158	pKS(Pks_J)	Sorghum bicolor ND	8825, 8826	333	747
LAB296	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9036, 9037	426	767
LAB159	pKS(Pks_J)	Sorghum bicolor ND	8827, 8828, 8829, 8830	334	539
LAB110	pGXNa	Sorghum bicolor ND	8753, 8754, 8755, 8756	305	509
LAB160	pKS(Pks_J)	Sorghum bicolor ND	8831, 8832	335	540
LAB297	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9038, 9039	427	768
LAB298	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9040, 9041, 9042, 9043	428	769
LAB161	pKS(Pks_J)	Sorghum bicolor ND	8833, 8834	336	541
LAB299	pKS(Pks_J)	Sorghum bicolor ND	9044, 9045	429	770
LAB176	Topo B	Sorghum bicolor ND	8864, 8865, 8866, 8867	348	554
LAB300	Topo B	Sorghum bicolor ND	9046, 9047, 9048, 9049	430	771
LAB336	pKS(Pks_J)	WHEAT Triticum aestivum L. ND	9106, 9106, 9107, 9108	454	668
LAB302	pKS(Pks_J)	Sorghum bicolor ND	9050, 9051	431	644

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LAB303	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	9052, 9053	432	645
LAB162	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8835, 8836	337	542
LAB163	pKS(Pks_J)	Sorghum bicolor ND	8837, 8838	338	543
LAB164	pKS(Pks_J)	Sorghum bicolor ND	8839, 8840	339	748
LAB177	Topo B	Sorghum bicolor ND	8868, 8869, 8870, 8871	349	555
LAB165	pGXN (pKG+Nos+35S)	Sorghum bicolor ND	8841, 8842, 8843	340	545
LAB306**	pGXN (pKG+Nos+35S)	SOYBEAN Glycine max 58-261	9054, 9055	433	772
LAB307	pKS(Pks_J)	SOYBEAN Glycine max 58-261	9056, 9057	434	648
LAB308	pKS(Pks_J)	SOYBEAN Glycine max 58-261	9058, 9059, 9060, 9061	435	649
LAB309	Topo B	SOYBEAN Glycine max 58-261	9062, 9063	436	650
LAB310	pGXN (pKG+Nos+35S)	SOYBEAN Glycine max 58-261	9064, 9065	437	651
LAB311	pGXN (pKG+Nos+35S)	SUNFLOWER Helianthus annuus ND	9066, 9067	438	773
LAB113	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8757, 8758, 8759, 8760	306	510
LAB312	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9068, 9069	439	653
LAB314	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9070, 9071	440	774
LAB315	Topo B	TOMATO Lycopersicum esculentum M82	9072, 9073	441	655
LAB115	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	8761, 8762	307	511
LAB178	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8872, 8872, 8873, 8874	350	556
LAB116*				308	512
LAB117	Topo B	TOMATO Lycopersicum esculentum M82	8763, 8764	309	513
LAB119	Topo B	TOMATO Lycopersicum esculentum M82	8765, 8766, 8767	310	514
LAB316	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9074, 9074, 9075, 9076	442	775
LAB317	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	9077, 9078	443	776
LAB318	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9079, 9080, 9081, 9082	444	777
LAB319	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	9083, 9084, 9085, 9086	445	659
LAB120	pGXNa	TOMATO Lycopersicum esculentum M82	8768, 8769	311	515
LAB122	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	8774, 8775	313	517
LAB123	Topo B	TOMATO Lycopersicum ND ND	8776, 8777	314	739
LAB320	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9087, 9088, 9089, 9090	446	660
LAB125	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	8781, 8782	316	741
LAB126	Topo B	TOMATO Lycopersicum esculentum M82	8783, 8784	317	742
LAB127	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8785, 8786	318	522

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LAB128	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum ND ND	8787, 8788, 8789, 8790	319	523
LAB129	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8791, 8791, 8792, 8793	320	524
LAB323	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	9091, 9092, 9093, 9094	447	661
LAB130	Topo B	TOMATO Lycopersicum esculentum M82	8794, 8795, 8796, 8797	321	525
LAB80	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica Nipponbare	9184, 9184, 9185, 9185	287	490
LAB324	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	9095, 9096	448	662
LAB133	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	8800, 8801	323	527
LAB325	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9097, 9098	449	663
LAB326	pGXN (pKG+Nos+35S)	TOMATO Lycopersicum esculentum M82	9099, 9100	450	778
LAB327	pKS(Pks_J)	TOMATO Lycopersicum esculentum M82	9101, 9103	451	665
LAB329*				452	666
LAB88	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica Nipponbare	9198, 9199	293	496
LAB137	pKS(Pks_J)	WHEAT Triticum aestivum L. EYAL	8802, 8803	324	743
LAB92	pKS(Pks_J)	Sorghum bicolor ND	9202, 9203	295	498
LAB138	Topo B	WHEAT Triticum aestivum L. EYAL	8804, 8805	325	744
LAB93	pKS(Pks_J)	Sorghum bicolor ND	9204, 9205	296	499
LAB94	pKS(Pks_J)	Sorghum bicolor ND	9206, 9207	297	500
LAB337	pKS(Pks_J)	WHEAT Triticum aestivum L. ND	9109, 9110, 9111, 9112	455	669
LAB339	pKS(Pks_J)	WHEAT Triticum aestivum L. ND	9113, 9114	456	779
LAB179	pKS(Pks_J)	WHEAT Triticum aestivum L. ND	8875, 8875, 8876, 8877	351	557
LAB342*				457	672
LAB343	pGXNa	CANOLA Brassica napus ND	9115, 9116	458	673
LAB344*				459	674
LAB345	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica LEMONT	9117, 9118	460	675
LAB346	pKS(Pks_J)	RICE Oryza sativa L. Japonica LEMONT	9119, 9120	461	780
LAB347_H0*				472	689
LAB348	pKS(Pks_J)	Sorghum bicolor ND	9121, 9122, 9123, 9124	205	678
LAB349	pKS(Pks_J)	SOYBEAN Glycine max 58-261	9125, 9125, 9126, 9127	462	679
LAB351*				463	680
LAB352	pKS(Pks_J)	WHEAT Triticum aestivum L. EYAL	9128, 9129	464	781
LAB353	Topo B	WHEAT Triticum aestivum L. ND	9130, 9131	465	682

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LAB355	pGXN (pKG+Nos+35S)	Brachypodiums distachyon ND	9132, 9133, 9134, 9135	466	683
LAB367	Topo B	CANOLA Brassica napus ND	9136, 9137, 9138, 9139	467	684
LAB381	pGXN (pKG+Nos+35S)	POPLAR Populus ND ND	9140, 9141, 9142, 9143	468	685
LAB383	pKS(Pks_J)	SOYBEAN Glycine max 58-261	9144, 9145, 9146, 9147	469	782
LAB181	pKS(Pks_J)	Arabidopsis thaliana Kondara	8878, 8879, 8880, 8881	352	558
LAB182	pKS(Pks_J)	Arabidopsis thaliana Kondara	8882, 8883, 8884, 8885	353	750
LAB183	pKS(Pks_J)	Arabidopsis thaliana Kondara	8886, 8887, 8888, 8889	354	560
LAB108	Topo B	Sorghum bicolor ND	8749, 8750	303	738
LAB185	Topo B	Arabidopsis thaliana Kondara	8890, 8891	355	561
LAB186	pKS(Pks_J)	Arabidopsis thaliana Kondara	8892, 8893	356	562
LAB187	pKS(Pks_J)	Arabidopsis thaliana Kondara	8894, 8895, 8896, 8897	357	751
LAB188	pGXN (pKG+Nos+35S)	Arabidopsis thaliana Kondara	8898, 8899, 8900, 8900	358	564
LAB189	Topo B	Arabidopsis thaliana Kondara	8901, 8902	359	752
LAB81	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	9186, 9187	288	491
LAB82	Topo B	RICE Oryza sativa L. Japonica LEMONT	9188, 9188, 9189, 9189	289	492
LAB212	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	8921, 8922, 8923, 8924	368	757
LAB241*				387	597
LAB242	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8951, 8952, 8953, 8954	388	598
LAB83	pGXNa	RICE Oryza sativa L. Japonica ND	9190, 9191	290	493
LAB243	pKS(Pks_J)	RICE Oryza sativa L. Japonica Nipponbare	8955, 8956	389	599
LAB84	Topo B	RICE Oryza sativa L. Japonica LEMONT	9192, 9193	291	494

Table 55. "Polyn." – Polynucleotide; "Polyp." – polypeptide. For cloning of each gene at least 2 primers were used: Forward (Fwd) or Reverse (Rev). In some cases, 4 primers were used: External forward (EF), External reverse (ER), nested forward (NF) or nested reverse (NR). The sequences of the primers used for cloning the genes are provided in the sequence listing.

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EXAMPLE 12

TRANSFORMING AGROBACTERIUM TUMEFACIENS CELLS WITH BINARY VECTORS HARBORING THE POLYNUCLEOTIDES OF THE INVENTION

Each of the binary vectors described in Example 11 above are used to transform *Agrobacterium* cells. Two additional binary constructs, having only the At6669 or the 35S promoter or no additional promoter are used as negative controls.

The binary vectors are introduced to *Agrobacterium tumefaciens* GV301, or LB4404 competent cells (about 10^9 cells/mL) by electroporation. The electroporation is performed using a MicroPulser electroporator (Biorad), 0.2 cm cuvettes (Biorad) and EC-2 electroporation program (Biorad). The treated cells are cultured in LB liquid medium at 28 °C for 3 hours, then plated over LB agar supplemented with gentamycin (50 mg/L; for *Agrobacterium* strains GV301) or streptomycin (300 mg/L; for *Agrobacterium* strain LB4404) and kanamycin (50 mg/L) at 28 °C for 48 hours. *Abrobacterium* colonies, which are developed on the selective media, are further analyzed by PCR using the primers designed to span the inserted sequence in the pPI plasmid. The resulting PCR products are isolated and sequenced to verify that the correct polynucleotide sequences of the invention are properly introduced to the *Agrobacterium* cells.

EXAMPLE 13

TRANSFORMATION OF ARABIDOPSIS THALIANA PLANTS WITH THE POLYNUCLEOTIDES OF THE INVENTION

Arabidopsis thaliana Columbia plants (T_0 plants) are transformed using the Floral Dip procedure described by Clough and Bent ,1998 (Floral dip: a simplified method for Agrobacterium-mediated transformation of Arabidopsis thaliana. Plant J 16:735-43) and by Desfeux et al., 2000 (Female Reproductive Tissues Are the Primary Target of Agrobacterium-Mediated Transformation by the Arabidopsis Floral-Dip Method. Plant Physiol, July 2000, Vol. 123, pp. 895-904), with minor modifications. Briefly, T_0 Plants are sown in 250 ml pots filled with wet peat-based growth mix. The pots are 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 hour light/dark cycles. The T0 plants are ready for transformation six days before anthesis.

Single colonies of *Agrobacterium* carrying the binary constructs, are generated as described in Example 3 above. Colonies are cultured in LB medium supplemented with kanamycin (50 mg/L) and gentamycin (50 mg/L). The cultures are incubated at 28 °C for 48 hours under vigorous shaking and then centrifuged at 4000 rpm for 5 minutes. The pellets comprising the *Agrobacterium* cells are re-suspended in a transformation medium containing half-strength (2.15 g/L) Murashige-Skoog (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 T_0 plants is performed by inverting each plant into an *Agrobacterium* suspension, such that the above ground plant tissue is submerged for 3-5 seconds. Each inoculated T_0 plant is immediately placed in a plastic tray, then covered with clear plastic dome to maintain humidity and is kept in the dark at room temperature for 18 hours, to facilitate infection and transformation. Transformed (transgenic) plants are then uncovered and transferred to a greenhouse for recovery and maturation. The transgenic T_0 plants are grown in the greenhouse for 3-5 weeks until siliques are brown and dry. Seeds are harvested from plants and kept at room temperature until sowing.

For generating T_1 and T_2 transgenic plants harboring the genes, seeds collected from transgenic T_0 plants are surface-sterilized by soaking in 70 % ethanol for 1 minute, followed by soaking in 5 % sodium hypochloride and 0.05 % triton 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 carbenicylin (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 T_1 *Arabidopsis* plants are transferred to a fresh culture plates for another week of incubation. Following incubation the T_1 plants are removed from culture plates and planted in growth mix contained in 250 ml pots. The transgenic plants are allowed to grow in a greenhouse to maturity. Seeds harvested from T_1 plants are cultured and grown to maturity as T_2 plants under the same conditions as used for culturing and growing the T_1 plants.

EXAMPLE 14

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

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., 1.5% PEG) is used to simulate the osmotic stress conditions resembling the high osmolarity found during drought stress.

Surface sterilized seeds are 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 are 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 are carefully transferred to plates containing 1.5% 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 are analyzed from each construct. Plants expressing the polynucleotides of the invention are compared to the average measurement of the control plants (empty vector or GUS reporter gene under the same promoter) used in the same experiment.

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, is used for capturing images of plantlets sawn in agar plates.

The image capturing process is repeated every 3-4 days starting at day 1 till day 10 (see for example the images in Figures 3A-F).

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

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).

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 XVI, XVII and XVIII.

Formula XVI: Relative growth rate of leaf area = Regression coefficient of leaf area along time course.

Formula XVII: Relative growth rate of root coverage = Regression coefficient of root coverage along time course.

Formula XVIII: Relative growth rate of root length = Regression coefficient of root length along time course.

At the end of the experiment, plantlets are removed from the media and weighed for the determination of plant fresh weight. Plantlets are then dried for 24 hours at 60 °C, and weighed again to measure plant dry weight for later statistical analysis. Growth rate is determined by comparing the leaf area coverage, root coverage and root length, between each couple of sequential photographs, and results are 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, is 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 are 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 are compared to those obtained from control plants. To identify outperforming genes and constructs, results from the independent transformation events tested are analyzed separately. To evaluate the effect of a gene event over a control the data is analyzed by Student's t-test and the p value is calculated. Results are 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 genes presented in Tables 56-59 showed a significant improvement in plant ABST since they produced larger plant biomass (plant fresh and dry weight and leaf area) in T2 generation (Tables 27-28) or T1 generation (Tables 29-30) when grown under osmotic stress conditions, compared to control plants. The genes were cloned under the regulation of a constitutive promoter (At6669; SEQ ID NO:8741). The evaluation of each gene was carried out by testing the performance of different number of events. Some of the genes were evaluated in more than one tissue culture assay. The results obtained in these second experiments were significantly positive as well.

Table 56
Genes showing improved plant performance under osmotic stress conditions (T2 generation)

Gene Name	*Event #*	*Plant Biomass Fresh Weight [gr.]*			*Gene Name*	*Event #*	*Plant Biomass Dry Weight [gr.]*		
		Ave.	*p-val.*	*% Incr.*			*Ave.*	*p-val.*	*% Incr.*
LAB115	27281.2	0.146	0.283	47	LAB115	27281.2	0.0082	0.218	66
LAB115	27282.3	0.102	0.883	2	LAB115	27282.3	0.0054	0.511	10
LAB115	27284.3	0.112	0.137	12	LAB115	27284.3	0.0061	0.138	23
LAB115	27285.2	0.164	0.011	65	LAB115	27285.2	0.0078	0.008	59
LAB123	28282.3	0.114	0.267	14	LAB123	28282.3	0.0061	0.049	24
LAB123	28283.1	.		.	LAB123	28283.1	0.0051	0.853	3
LAB123	28284.2	.		.	LAB123	28284.2	0.0059	0.124	21
LAB123	28285.2	0.134	0.004	35	LAB123	28285.2	0.0069	0.004	40
LAB183	27452.2	0.120	0.419	20	LAB183	27452.2	0.0071	0.231	45
LAB183	27453.1	.		.	LAB183	27453.1	0.0053	0.497	7
LAB189	28163.2	0.101	0.871	1	LAB189	28163.2	0.0052	0.631	5
LAB189	28165.2	.		.	LAB189	28165.2	0.0057	0.436	16
LAB212	28041.1	0.110	0.619	11	LAB212	28041.1	0.0062	0.453	26
LAB212	28042.1	0.138	0.001	39	LAB212	28042.1	0.0066	0.250	33
LAB212	28043.2	0.130	0.441	30	LAB212	28043.2	0.0061	0.500	24
LAB212	28044.2	.		.	LAB212	28044.2	0.0057	0.290	15
LAB217	28033.2	0.128	0.405	28	LAB217	28033.2	0.0089	0.164	82
LAB217	28034.1	0.118	0.596	18	LAB217	28034.1	0.0068	0.424	37
LAB326	28053.2	0.148	0.240	49	LAB326	28053.2	0.0079	0.141	61
LAB326	28054.1	.		.	LAB326	28054.1	0.0061	0.154	24
LAB326	28056.2	0.111	0.381	12	LAB326	28056.2	0.0054	0.645	10
LAB326	28056.3	0.108	0.481	8	LAB326	28056.3	.		.
CONT	-	0.100	-	0	CONT	-	0.0049	-	0

LAB115	27281.3	.		.	LAB115	27281.3	0.0058	0.789	7
LAB115	27284.3	0.142	0.047	38	LAB115	27284.3	0.0072	0.038	35
LAB115	27285.1	0.161	0.199	56	LAB115	27285.1	0.0094	0.221	76
LAB123	28281.1	0.330	0.002	220	LAB123	28281.1	0.0212	0.005	296
LAB123	28282.3	0.145	0.169	40	LAB123	28282.3	0.0071	0.004	33
LAB123	28283.1	0.198	0.203	92	LAB123	28283.1	0.0116	0.132	116
LAB123	28284.1	0.197	0.000	91	LAB123	28284.1	0.0122	0.000	128
LAB123	28285.2	0.209	0.002	103	LAB123	28285.2	0.0117	0.011	118
LAB183	27453.4	0.165	0.021	60	LAB183	27453.4	0.0095	0.061	78
LAB189	28163.2	0.128	0.283	24	LAB189	28163.2	.		.
LAB189	28165.2	0.118	0.605	14	LAB189	28165.2	.		.
LAB189	28166.2	0.138	0.378	34	LAB189	28166.2	0.0072	0.489	34
LAB189	28166.5	0.121	0.577	17	LAB189	28166.5	0.0064	0.559	20
LAB206	30011.2	0.110	0.586	7	LAB206	30011.2	0.0080	0.015	49
LAB206	30012.4	0.153	0.013	48	LAB206	30012.4	0.0075	0.002	40
LAB206	30012.7	0.129	0.308	25	LAB206	30012.7	0.0059	0.516	10
LAB206	30012.8	0.109	0.717	6	LAB206	30012.8	0.0066	0.153	23
LAB212	28041.1	.		.	LAB212	28041.1	0.0056	0.684	4
LAB212	28042.1	0.105	0.904	2	LAB212	28042.1	.		.
LAB212	28045.1	0.129	0.073	25	LAB212	28045.1	0.0067	0.117	26
LAB217	28033.2	0.216	0.001	110	LAB217	28033.2	0.0110	0.010	105
LAB217	28034.1	0.164	0.225	59	LAB217	28034.1	0.0089	0.092	65
LAB217	28034.3	0.128	0.054	24	LAB217	28034.3	0.0066	0.099	24
LAB217	28035.1	0.199	0.169	93	LAB217	28035.1	0.0107	0.174	100
LAB217	28036.1	0.145	0.207	40	LAB217	28036.1	0.0084	0.137	57
LAB250	30251.2	0.135	0.198	31	LAB250	30251.2	0.0076	0.199	41
LAB250	30252.1	0.117	0.146	14	LAB250	30252.1	0.0069	0.109	29
LAB250	30254.3	0.116	0.543	12	LAB250	30254.3	0.0056	0.768	5
LAB314	29292.4	0.109	0.774	5	LAB314	29292.4	.		.
LAB314	29292.6	0.123	0.024	19	LAB314	29292.6	0.0070	0.007	31
LAB314	29294.1	0.117	0.471	14	LAB314	29294.1	0.0059	0.471	10
LAB326	28052.4	0.117	0.478	14	LAB326	28052.4	0.0060	0.373	13
LAB326	28056.3	0.122	0.125	19	LAB326	28056.3	0.0061	0.234	14
LAB351	30112.1	0.128	0.297	24	LAB351	30112.1	0.0068	0.059	28
LAB351	30115.1	.		.	LAB351	30115.1	0.0063	0.228	17
LAB351	30115.3	0.116	0.167	13	LAB351	30115.3	0.0057	0.679	6
LAB93	28271.3	0.146	0.159	42	LAB93	28271.3	0.0079	0.208	47
LAB93	28271.4	0.130	0.375	27	LAB93	28271.4	0.0062	0.354	16
LAB93	28272.3	0.211	0.017	104	LAB93	28272.3	0.0131	0.020	144
LAB93	28274.2	0.133	0.165	29	LAB93	28274.2	0.0079	0.040	47
LAB93	28274.3	0.121	0.335	18	LAB93	28274.3	0.0064	0.374	20
CONT	-	0.103	-	0	CONT	-	0.0054	-	0
LAB106	30031.4	0.096	0.702	3	LAB106	30031.4	0.0061	0.062	29
LAB106	30032.1	0.146	0.082	56	LAB106	30032.1	0.0077	0.060	64
LAB106	30032.2	0.141	0.072	51	LAB106	30032.2	0.0089	0.012	89
LAB206	30011.7	0.118	0.325	26	LAB206	30011.7	0.0063	0.123	33
LAB206	30012.4	.		.	LAB206	30012.4	0.0055	0.410	17
LAB206	30012.8	0.114	0.336	22	LAB206	30012.8	0.0059	0.306	24
LAB207	28842.1	0.099	0.729	6	LAB207	28842.1	0.0053	0.466	13
LAB207	28842.5	0.112	0.377	19	LAB207	28842.5	0.0061	0.314	30
LAB207	28843.3	0.114	0.372	22	LAB207	28843.3	0.0076	0.009	61

LAB207	28843.5	0.099	0.737	5	LAB207	28843.5	0.0057	0.266	22
LAB218	29432.2	0.111	0.057	19	LAB218	29432.2	0.0062	0.119	31
LAB218	29433.4	.		.	LAB218	29433.4	0.0048	0.888	2
LAB218	29434.3	0.108	0.651	15	LAB218	29434.3	0.0066	0.416	40
LAB250	30252.1	0.104	0.743	11	LAB250	30252.1	0.0052	0.307	11
LAB250	30253.1	0.134	0.228	43	LAB250	30253.1	0.0080	0.133	69
LAB250	30254.1	.		.	LAB250	30254.1	0.0050	0.729	6
LAB252	30291.4	0.120	0.199	29	LAB252	30291.4	0.0067	0.119	43
LAB252	30292.3	0.193	0.012	106	LAB252	30292.3	0.0109	0.030	131
LAB309	30052.2	0.117	0.264	24	LAB309	30052.2	0.0065	0.211	39
LAB309	30052.3	0.138	0.142	48	LAB309	30052.3	0.0084	0.030	78
LAB314	29292.4	0.118	0.099	26	LAB314	29292.4	0.0077	0.002	64
LAB314	29292.6	0.124	0.057	32	LAB314	29292.6	0.0061	0.199	29
LAB314	29294.1	0.151	0.015	61	LAB314	29294.1	0.0081	0.002	73
LAB314	29295.2	0.141	0.183	51	LAB314	29295.2	0.0072	0.012	53
LAB346	29442.2	.		.	LAB346	29442.2	0.0052	0.289	11
LAB346	29442.4	0.101	0.427	8	LAB346	29442.4	0.0054	0.338	14
LAB346	29443.2	0.111	0.561	18	LAB346	29443.2	0.0060	0.371	27
LAB346	29445.3	0.139	0.073	48	LAB346	29445.3	0.0080	0.013	70
LAB351	30111.2	0.118	0.182	26	LAB351	30111.2	0.0073	0.006	55
LAB351	30114.2	0.138	0.011	47	LAB351	30114.2	0.0079	0.000	68
LAB82	30181.3	0.095	0.964	1	LAB82	30181.3	0.0055	0.388	18
LAB84	30161.4	0.159	0.013	69	LAB84	30161.4	0.0086	0.017	83
LAB84	30162.2	0.104	0.672	11	LAB84	30162.2	0.0071	0.142	51
LAB84	30162.4	0.172	0.061	84	LAB84	30162.4	0.0110	0.040	135
LAB84	30163.4	0.150	0.059	60	LAB84	30163.4	0.0091	0.036	94
LAB84	30164.2	0.166	0.093	77	LAB84	30164.2	0.0109	0.015	132
CONT	-	0.094	-	0	CONT	-	0.0047	-	0
LAB110	30571.3	0.135	0.251	37	LAB110	30571.3	0.0058	0.274	34
LAB110	30572.1	.		.	LAB110	30572.1	0.0045	0.870	4
LAB110	30573.2	0.129	0.058	31	LAB110	30573.2	0.0060	0.113	40
LAB110	30574.2	0.140	0.115	42	LAB110	30574.2	0.0069	0.005	61
LAB117	27291.1	0.109	0.361	11	LAB117	27291.1	0.0050	0.565	16
LAB117	27291.5	0.150	0.092	53	LAB117	27291.5	0.0063	0.292	47
LAB117	27293.1	0.221	0.034	125	LAB117	27293.1	0.0086	0.090	100
LAB117	27296.1	0.135	0.109	37	LAB117	27296.1	0.0067	0.262	55
LAB124	30431.1	0.115	0.255	17	LAB124	30431.1	0.0066	0.093	53
LAB124	30434.1	0.148	0.174	51	LAB124	30434.1	0.0059	0.510	36
LAB124	30434.3	0.149	0.140	52	LAB124	30434.3	0.0067	0.200	55
LAB124	30435.2	0.154	0.027	57	LAB124	30435.2	0.0059	0.045	37
LAB125	30581.3	0.113	0.154	15	LAB125	30581.3	0.0053	0.486	24
LAB125	30583.1	0.110	0.469	12	LAB125	30583.1	0.0047	0.789	8
LAB125	30583.2	0.123	0.131	26	LAB125	30583.2	0.0052	0.335	21
LAB156	30401.4	.		.	LAB156	30401.4	0.0056	0.440	31
LAB156	30402.2	0.135	0.030	38	LAB156	30402.2	0.0071	0.043	66
LAB156	30405.3	0.112	0.285	14	LAB156	30405.3	0.0047	0.468	9
LAB228	30081.4	0.109	0.508	11	LAB228	30081.4	.		.
LAB228	30082.3	.		.	LAB228	30082.3	0.0048	0.724	11
LAB228	30084.3	0.129	0.105	31	LAB228	30084.3	0.0052	0.458	20
LAB275	30361.2	0.136	0.073	38	LAB275	30361.2	.		.
LAB275	30361.3	0.154	0.120	57	LAB275	30361.3	0.0074	0.050	73

LAB275	30366.4	0.110	0.642	12	LAB275	30366.4	0.0052	0.304	20
LAB276_H0	30331.1	0.161	0.037	64	LAB276_H0	30331.1	0.0068	0.006	58
LAB276_H0	30331.4	.		.	LAB276_H0	30331.4	0.0045	0.823	4
LAB276_H0	30333.3	0.116	0.381	18	LAB276_H0	30333.3	0.0049	0.305	14
LAB276_H0	30333.7	0.124	0.080	26	LAB276_H0	30333.7	0.0051	0.474	19
LAB277	30651.2	0.099	0.947	1	LAB277	30651.2	0.0051	0.406	18
LAB277	30652.3	0.117	0.222	19	LAB277	30652.3	0.0052	0.226	21
LAB277	30652.5	0.114	0.152	16	LAB277	30652.5	0.0053	0.160	23
LAB277	30653.1	0.134	0.044	36	LAB277	30653.1	0.0077	0.014	79
LAB278	30411.4	0.170	0.051	73	LAB278	30411.4	0.0072	0.159	68
LAB278	30412.1	0.109	0.649	11	LAB278	30412.1	.		.
LAB278	30413.3	0.110	0.417	12	LAB278	30413.3	0.0046	0.816	7
LAB278	30414.1	.		.	LAB278	30414.1	0.0048	0.454	12
LAB278	30414.2	0.143	0.210	46	LAB278	30414.2	0.0069	0.010	60
LAB281	30741.1	0.101	0.808	3	LAB281	30741.1	0.0046	0.872	7
LAB281	30742.1	0.102	0.761	4	LAB281	30742.1	0.0043	0.996	0
LAB281	30742.4	0.114	0.304	16	LAB281	30742.4	0.0054	0.178	25
LAB282	30751.3	0.125	0.264	27	LAB282	30751.3	0.0054	0.558	26
CONT	-	0.098	-	0	CONT	-	0.0043	-	0
LAB110	30571.3	0.116	0.620	12	LAB110	30571.3	0.0058	0.431	16
LAB110	30572.1	0.112	0.694	7	LAB110	30572.1	0.0053	0.541	7
LAB110	30572.2	0.195	0.023	87	LAB110	30572.2	0.0105	0.000	112
LAB110	30573.2	0.107	0.871	3	LAB110	30573.2	0.0060	0.255	20
LAB110	30574.2	0.157	0.070	51	LAB110	30574.2	0.0080	0.036	61
LAB117	27291.2	0.132	0.221	26	LAB117	27291.2	0.0071	0.052	43
LAB117	27293.1	0.194	0.019	87	LAB117	27293.1	0.0118	0.015	136
LAB117	27296.1	0.141	0.043	36	LAB117	27296.1	0.0072	0.014	45
LAB124	30432.3	.		.	LAB124	30432.3	0.0053	0.511	7
LAB124	30434.1	0.105	0.958	1	LAB124	30434.1	0.0061	0.236	22
LAB125	30581.3	0.136	0.288	31	LAB125	30581.3	0.0062	0.564	24
LAB125	30582.2	.		.	LAB125	30582.2	0.0055	0.568	11
LAB125	30584.2	0.175	0.053	68	LAB125	30584.2	0.0095	0.042	91
LAB156	30401.4	0.107	0.826	3	LAB156	30401.4	0.0069	0.019	39
LAB156	30403.4	.		.	LAB156	30403.4	0.0054	0.392	9
LAB156	30405.3	0.141	0.156	35	LAB156	30405.3	0.0069	0.207	38
LAB228	30082.3	0.169	0.034	62	LAB228	30082.3	0.0090	0.010	81
LAB228	30084.3	0.126	0.354	21	LAB228	30084.3	0.0055	0.469	10
LAB228	30084.4	0.121	0.309	17	LAB228	30084.4	.		.
LAB275	30361.2	.		.	LAB275	30361.2	0.0053	0.664	7
LAB275	30361.3	0.110	0.816	6	LAB275	30361.3	.		.
LAB275	30363.1	0.115	0.529	10	LAB275	30363.1	0.0062	0.161	24
LAB275	30363.4	0.105	0.956	1	LAB275	30363.4	0.0053	0.591	7
LAB275	30366.4	.		.	LAB275	30366.4	0.0057	0.391	14
LAB276_H0	30331.1	0.146	0.350	40	LAB276_H0	30331.1	0.0076	0.303	53
LAB276_H0	30331.4	0.199	0.000	91	LAB276_H0	30331.4	0.0090	0.006	81

LAB277	30652.3	0.107	0.890	3	LAB277	30652.3	0.0057	0.313	15
LAB277	30652.6	0.140	0.063	34	LAB277	30652.6	0.0075	0.093	51
LAB277	30653.1	.		.	LAB277	30653.1	0.0053	0.591	6
LAB278	30411.4	0.108	0.835	4	LAB278	30411.4	0.0052	0.668	5
LAB278	30413.3	0.139	0.350	33	LAB278	30413.3	0.0081	0.087	64
LAB278	30414.1	0.161	0.018	54	LAB278	30414.1	0.0089	0.016	80
LAB278	30414.2	0.115	0.699	11	LAB278	30414.2	.		.
LAB281	30742.4	.		.	LAB281	30742.4	0.0054	0.674	8
LAB282	30752.2	0.114	0.698	9	LAB282	30752.2	.		.
LAB282	30753.4	0.108	0.781	4	LAB282	30753.4	0.0067	0.022	34
CONT	-	0.104	-	0	CONT	-	0.0050	-	0
LAB106	30031.4	0.125	0.409	18	LAB106	30031.4	0.0071	0.363	22
LAB106	30032.1	0.113	0.759	6	LAB106	30032.1	0.0072	0.133	24
LAB106	30034.1	0.131	0.426	24	LAB106	30034.1	0.0071	0.507	22
LAB106	30035.2	0.120	0.546	13	LAB106	30035.2	0.0073	0.332	25
LAB127	30811.4	.		.	LAB127	30811.4	0.0059	0.970	1
LAB127	30814.2	0.116	0.708	9	LAB127	30814.2	.		.
LAB128	28074.1	0.121	0.510	14	LAB128	28074.1	0.0061	0.808	5
LAB128	28074.3	0.125	0.198	17	LAB128	28074.3	0.0067	0.220	15
LAB128	28075.2	0.142	0.032	33	LAB128	28075.2	0.0080	0.018	37
LAB207	28842.1	.		.	LAB207	28842.1	0.0061	0.815	5
LAB207	28842.5	0.108	0.937	1	LAB207	28842.5	0.0067	0.474	14
LAB207	28845.1	0.114	0.289	7	LAB207	28845.1	.		.
LAB218	29431.3	0.109	0.860	3	LAB218	29431.3	0.0061	0.877	4
LAB218	29432.2	0.110	0.813	4	LAB218	29432.2	0.0063	0.766	8
LAB218	29434.3	0.126	0.133	19	LAB218	29434.3	0.0072	0.218	23
LAB252	30291.1	0.116	0.745	9	LAB252	30291.1	.		.
LAB252	30292.3	0.169	0.144	59	LAB252	30292.3	0.0097	0.167	66
LAB252	30292.4	0.128	0.371	20	LAB252	30292.4	0.0075	0.341	28
LAB309	30052.2	.		.	LAB309	30052.2	0.0061	0.820	4
LAB309	30052.3	0.132	0.281	24	LAB309	30052.3	0.0077	0.164	32
LAB309	30054.2	0.166	0.017	56	LAB309	30054.2	0.0090	0.025	54
LAB309	30056.1	.		.	LAB309	30056.1	0.0063	0.542	8
LAB337	27265.2	0.130	0.204	22	LAB337	27265.2	0.0069	0.302	17
LAB346	29442.2	0.146	0.187	38	LAB346	29442.2	0.0081	0.114	38
LAB346	29443.2	0.113	0.757	6	LAB346	29443.2	0.0059	0.954	1
LAB346	29445.6	0.136	0.046	28	LAB346	29445.6	0.0079	0.042	36
LAB80	30671.2	0.108	0.907	2	LAB80	30671.2	.		.
LAB80	30673.2	0.140	0.089	32	LAB80	30673.2	0.0081	0.046	39
LAB80	30675.2	0.140	0.020	32	LAB80	30675.2	0.0064	0.217	9
LAB80	30675.5	0.115	0.622	8	LAB80	30675.5	0.0060	0.886	2
LAB84	30162.4	0.123	0.546	15	LAB84	30162.4	0.0067	0.483	15
LAB84	30164.2	0.138	0.257	30	LAB84	30164.2	0.0072	0.464	23
CONT	-	0.106	-	0	CONT	-	0.0058	-	0
LAB127	30811.4	0.157	0.614	9	LAB127	30811.4	.		.
LAB127	30812.1	0.156	0.350	9	LAB127	30812.1	0.0079	0.827	4
LAB127	30813.2	0.151	0.835	5	LAB127	30813.2	.		.
LAB128	28071.2	0.159	0.790	11	LAB128	28071.2	.		.
LAB128	28075.2	0.144	0.957	1	LAB128	28075.2	.		.
LAB147	31104.1	.		.	LAB147	31104.1	0.0080	0.740	6
LAB147	31104.2	0.189	0.086	32	LAB147	31104.2	.		.

LAB147	31105.6	0.152	0.735	6	LAB147	31105.6	0.0078	0.844	3
LAB147	31105.7	0.155	0.776	8	LAB147	31105.7	.		.
LAB186	31001.4	0.271	0.083	89	LAB186	31001.4	0.0144	0.084	91
LAB186	31002.1	0.226	0.141	58	LAB186	31002.1	0.0122	0.083	61
LAB186	31004.1	0.174	0.098	21	LAB186	31004.1	0.0084	0.652	11
LAB186	31004.2	0.164	0.328	15	LAB186	31004.2	.		.
LAB197	31083.1	0.194	0.254	35	LAB197	31083.1	.		.
LAB197	31084.3	0.222	0.117	55	LAB197	31084.3	0.0107	0.014	41
LAB197	31085.3	0.162	0.546	13	LAB197	31085.3	0.0081	0.739	7
LAB315	31061.1	0.156	0.689	9	LAB315	31061.1	0.0078	0.878	3
LAB315	31061.2	0.154	0.621	7	LAB315	31061.2	.		.
LAB315	31063.1	0.161	0.561	13	LAB315	31063.1	0.0078	0.904	2
LAB317	30951.4	0.159	0.281	11	LAB317	30951.4	0.0077	0.903	1
LAB317	30953.1	0.145	0.936	1	LAB317	30953.1	.		.
LAB324	30961.1	0.150	0.865	5	LAB324	30961.1	.		.
LAB325	30971.4	0.155	0.431	8	LAB325	30971.4	0.0078	0.835	3
LAB325	30972.2	0.238	0.126	66	LAB325	30972.2	0.0133	0.075	75
LAB325	30973.1	0.207	0.285	44	LAB325	30973.1	0.0107	0.209	41
LAB325	30975.1	0.155	0.399	8	LAB325	30975.1	0.0090	0.166	19
LAB325	30975.4	0.199	0.406	39	LAB325	30975.4	0.0104	0.429	38
LAB67	31021.4	0.147	0.787	3	LAB67	31021.4	.		.
LAB67	31022.1	0.219	0.024	53	LAB67	31022.1	0.0121	0.000	60
LAB67	31023.3	0.145	0.949	1	LAB67	31023.3	0.0083	0.660	9
LAB80	30671.2	0.160	0.744	12	LAB80	30671.2	.		.
CONT	-	0.143	-	0	CONT	-	0.0076	-	0
LAB147	31103.2	0.145	0.051	135	LAB147	31103.2	0.0066	0.094	85
LAB147	31104.1	0.094	0.037	52	LAB147	31104.1	0.0058	0.001	63
LAB147	31104.2	0.098	0.011	58	LAB147	31104.2	0.0058	0.083	63
LAB147	31105.6	0.119	0.003	92	LAB147	31105.6	0.0071	0.004	100
LAB147	31105.7	0.085	0.145	38	LAB147	31105.7	0.0061	0.001	71
LAB178	30631.2	0.076	0.259	23	LAB178	30631.2	0.0042	0.414	20
LAB178	30632.1	0.124	0.145	100	LAB178	30632.1	0.0067	0.098	90
LAB178	30633.3	0.115	0.006	86	LAB178	30633.3	0.0062	0.002	76
LAB178	30633.4	0.140	0.004	127	LAB178	30633.4	0.0081	0.012	130
LAB178	30635.1	0.077	0.253	24	LAB178	30635.1	0.0046	0.083	29
LAB186	31001.4	0.113	0.052	84	LAB186	31001.4	0.0063	0.054	78
LAB186	31002.1	0.095	0.064	54	LAB186	31002.1	0.0057	0.019	61
LAB186	31003.1	0.156	0.001	153	LAB186	31003.1	0.0091	0.000	156
LAB186	31004.1	0.112	0.028	82	LAB186	31004.1	0.0057	0.038	61
LAB186	31004.2	0.111	0.119	80	LAB186	31004.2	0.0054	0.106	54
LAB197	31081.3	0.080	0.045	30	LAB197	31081.3	0.0049	0.078	38
LAB197	31083.1	0.064	0.858	4	LAB197	31083.1	.		.
LAB197	31084.3	0.081	0.170	32	LAB197	31084.3	0.0048	0.120	35
LAB197	31084.4	0.103	0.014	67	LAB197	31084.4	0.0054	0.001	52
LAB197	31085.3	0.089	0.082	43	LAB197	31085.3	0.0046	0.186	30
LAB247	28091.4	0.108	0.039	75	LAB247	28091.4	0.0054	0.024	52
LAB247	28093.2	0.089	0.255	45	LAB247	28093.2	0.0051	0.105	44
LAB247	28094.1	0.081	0.018	31	LAB247	28094.1	0.0047	0.007	34
LAB247	28094.3	0.098	0.006	59	LAB247	28094.3	0.0055	0.000	54
LAB247	28095.4	0.070	0.509	13	LAB247	28095.4	.		.
LAB314	29292.4	.		.	LAB314	29292.4	0.0040	0.541	12

LAB314	29292.6	0.082	0.036	33	LAB314	29292.6	0.0045	0.168	28
LAB314	29294.1	0.072	0.455	16	LAB314	29294.1	0.0039	0.612	10
LAB314	29294.2	0.083	0.007	35	LAB314	29294.2	0.0038	0.539	6
LAB314	29295.1	0.083	0.134	34	LAB314	29295.1	0.0045	0.425	27
LAB315	31061.1	0.067	0.342	9	LAB315	31061.1	.		.
LAB315	31061.2	0.142	0.000	130	LAB315	31061.2	0.0084	0.000	136
LAB315	31063.1	0.110	0.051	78	LAB315	31063.1	0.0065	0.053	83
LAB315	31064.3	0.112	0.030	81	LAB315	31064.3	0.0060	0.001	68
LAB315	31065.4	0.086	0.118	40	LAB315	31065.4	0.0042	0.110	20
LAB317	30952.2	0.125	0.016	102	LAB317	30952.2	0.0073	0.010	106
LAB317	30952.3	0.124	0.001	101	LAB317	30952.3	0.0071	0.000	102
LAB317	30953.1	0.109	0.131	76	LAB317	30953.1	0.0061	0.048	73
LAB317	30953.4	0.073	0.075	19	LAB317	30953.4	0.0043	0.132	20
LAB317	30954.4	0.113	0.006	84	LAB317	30954.4	0.0067	0.051	89
LAB324	30961.1	0.133	0.011	115	LAB324	30961.1	0.0072	0.010	104
LAB324	30962.2	0.117	0.120	90	LAB324	30962.2	0.0046	0.170	31
LAB324	30963.1	0.104	0.106	68	LAB324	30963.1	0.0064	0.069	80
LAB324	30965.2	0.101	0.070	64	LAB324	30965.2	0.0054	0.011	53
LAB324	30965.3	0.092	0.013	48	LAB324	30965.3	0.0056	0.010	59
LAB325	30971.4	0.120	0.001	94	LAB325	30971.4	0.0078	0.000	119
LAB325	30972.2	0.119	0.001	92	LAB325	30972.2	0.0064	0.098	81
LAB325	30973.1	0.094	0.303	52	LAB325	30973.1	0.0050	0.311	40
LAB325	30975.2	0.107	0.081	74	LAB325	30975.2	0.0058	0.091	65
LAB325	30975.4	0.115	0.010	86	LAB325	30975.4	0.0060	0.051	70
LAB54	28133.1	0.075	0.119	21	LAB54	28133.1	0.0039	0.423	10
LAB54	28133.4	0.222	0.000	260	LAB54	28133.4	0.0125	0.000	253
LAB54	28134.1	0.106	0.000	72	LAB54	28134.1	0.0062	0.005	76
LAB54	28136.1	0.082	0.125	33	LAB54	28136.1	0.0041	0.157	16
LAB54	28136.2	0.146	0.067	137	LAB54	28136.2	0.0095	0.073	167
LAB67	31021.4	0.071	0.293	16	LAB67	31021.4	0.0042	0.195	19
LAB67	31022.1	0.145	0.007	136	LAB67	31022.1	0.0100	0.002	183
LAB67	31022.6	0.083	0.011	34	LAB67	31022.6	0.0061	0.002	73
LAB67	31023.3	0.130	0.043	110	LAB67	31023.3	0.0068	0.016	91
LAB67	31023.4	0.072	0.140	16	LAB67	31023.4	0.0044	0.040	25
LAB68	29331.5	0.070	0.431	13	LAB68	29331.5	0.0045	0.153	27
LAB68	29335.1	0.075	0.644	21	LAB68	29335.1	0.0036	0.919	2
LAB68	29335.3	.		.	LAB68	29335.3	0.0038	0.486	8
LAB73	30151.1	0.067	0.434	8	LAB73	30151.1	0.0036	0.835	2
LAB73	30152.1	0.094	0.050	53	LAB73	30152.1	0.0053	0.024	50
LAB73	30152.2	0.093	0.188	50	LAB73	30152.2	0.0059	0.126	66
LAB73	30153.1	0.096	0.057	55	LAB73	30153.1	0.0050	0.078	42
LAB73	30154.3	0.067	0.367	8	LAB73	30154.3	0.0040	0.289	13
LAB74	28451.3	0.137	0.080	123	LAB74	28451.3	0.0079	0.156	122
LAB74	28452.1	0.089	0.181	44	LAB74	28452.1	0.0042	0.150	17
LAB74	28452.2	0.125	0.003	103	LAB74	28452.2	0.0079	0.002	123
LAB74	28453.5	0.096	0.235	55	LAB74	28453.5	.		.
LAB74	28454.1	0.126	0.016	105	LAB74	28454.1	0.0070	0.007	99
CONT	-	0.062	-	0	CONT	-	0.0035	-	0
LAB133	28833.2	0.138	0.206	36	LAB133	28833.2	0.0051	0.039	60
LAB133	28833.5	0.107	0.720	5	LAB133	28833.5	0.0042	0.111	31
LAB158	29412.1	0.131	0.230	30	LAB158	29412.1	0.0041	0.117	28

LAB158	29414.3	0.103	0.920	2	LAB158	29414.3	0.0037	0.229	16
LAB158	29415.1	0.107	0.788	5	LAB158	29415.1	0.0052	0.003	63
LAB160	29312.1	0.107	0.708	5	LAB160	29312.1	0.0044	0.105	38
LAB160	29314.2	0.109	0.777	7	LAB160	29314.2	0.0036	0.737	12
LAB160	29315.2	.		.	LAB160	29315.2	0.0041	0.282	28
LAB160	29315.3	0.108	0.693	7	LAB160	29315.3	0.0038	0.472	18
LAB162	29341.2	.		.	LAB162	29341.2	0.0039	0.140	23
LAB162	29342.6	0.108	0.623	7	LAB162	29342.6	0.0039	0.274	21
LAB162	29344.1	.		.	LAB162	29344.1	0.0054	0.006	68
LAB177	29422.1	0.119	0.394	17	LAB177	29422.1	0.0054	0.080	71
LAB177	29424.3	0.146	0.139	44	LAB177	29424.3	0.0062	0.038	93
LAB177	29424.4	.		.	LAB177	29424.4	0.0034	0.622	8
LAB177	29425.1	0.103	0.950	1	LAB177	29425.1	0.0040	0.088	25
LAB179	29301.4	0.147	0.437	45	LAB179	29301.4	0.0045	0.065	42
LAB179	29302.4	.		.	LAB179	29302.4	0.0038	0.298	19
LAB179	29303.2	0.176	0.001	74	LAB179	29303.2	0.0088	0.001	177
LAB179	29304.3	.		.	LAB179	29304.3	0.0033	0.880	4
LAB179	29304.4	0.145	0.178	43	LAB179	29304.4	0.0080	0.055	150
LAB185	28172.4	.		.	LAB185	28172.4	0.0037	0.324	17
LAB185	28174.2	0.108	0.640	7	LAB185	28174.2	0.0038	0.584	19
LAB185	28175.2	.		.	LAB185	28175.2	0.0040	0.208	26
LAB185	28175.3	0.112	0.656	11	LAB185	28175.3	0.0054	0.046	68
LAB210	28331.3	.		.	LAB210	28331.3	0.0042	0.205	31
LAB210	28333.2	0.112	0.651	11	LAB210	28333.2	.		.
LAB210	28335.3	0.200	0.019	98	LAB210	28335.3	0.0089	0.056	179
LAB254	28811.1	0.114	0.521	12	LAB254	28811.1	0.0034	0.613	8
LAB254	28814.1	.		.	LAB254	28814.1	0.0046	0.039	43
LAB254	28814.5	0.119	0.496	17	LAB254	28814.5	0.0061	0.019	90
LAB254	28815.3	0.137	0.163	36	LAB254	28815.3	0.0057	0.042	78
LAB254	28815.4	0.145	0.017	43	LAB254	28815.4	0.0050	0.091	57
LAB293	29232.2	0.118	0.261	16	LAB293	29232.2	0.0047	0.193	48
LAB293	29233.2	0.127	0.251	25	LAB293	29233.2	0.0042	0.034	33
LAB293	29233.3	0.121	0.215	19	LAB293	29233.3	0.0043	0.035	34
LAB293	29233.4	.		.	LAB293	29233.4	0.0039	0.284	21
LAB293	29235.4	.		.	LAB293	29235.4	0.0034	0.810	6
LAB297	29272.1	.		.	LAB297	29272.1	0.0036	0.493	12
LAB297	29272.5	.		.	LAB297	29272.5	0.0038	0.507	19
LAB297	29273.1	0.139	0.235	37	LAB297	29273.1	0.0063	0.066	97
LAB297	29273.4	0.128	0.532	26	LAB297	29273.4	0.0038	0.355	19
LAB297	29275.1	0.196	0.006	93	LAB297	29275.1	0.0080	0.045	151
LAB310	28181.3	0.102	0.993	0	LAB310	28181.3	0.0035	0.600	9
LAB310	28182.2	.		.	LAB310	28182.2	0.0039	0.171	22
LAB310	28183.3	.		.	LAB310	28183.3	0.0043	0.234	34
LAB318	28101.5	.		.	LAB318	28101.5	0.0042	0.254	33
LAB318	28101.7	0.152	0.095	50	LAB318	28101.7	0.0060	0.118	88
LAB318	28104.3	.		.	LAB318	28104.3	0.0042	0.211	31
LAB327	29221.2	0.134	0.213	32	LAB327	29221.2	0.0041	0.525	28
LAB327	29221.5	.		.	LAB327	29221.5	0.0037	0.230	16
LAB327	29221.6	0.106	0.751	4	LAB327	29221.6	0.0040	0.345	24
LAB327	29221.8	0.123	0.412	21	LAB327	29221.8	0.0060	0.076	89
LAB327	29225.4	0.106	0.799	4	LAB327	29225.4	.		.

LAB335	27311.2	.		.	LAB335	27311.2	0.0039	0.602	21
LAB335	27314.1	.		.	LAB335	27314.1	0.0036	0.440	12
LAB335	27314.2	0.157	0.170	55	LAB335	27314.2	0.0071	0.014	122
LAB335	27315.4	0.114	0.690	13	LAB335	27315.4	0.0040	0.425	25
CONT	-	0.101	-	0	CONT	-	0.0032	-	0
LAB102	30312.2	0.112	0.439	27	LAB102	30312.2	0.0072	0.146	76
LAB102	30312.4	0.102	0.425	16	LAB102	30312.4	0.0061	0.077	51
LAB102	30313.2	0.111	0.004	25	LAB102	30313.2	0.0056	0.080	37
LAB102	30313.3	0.114	0.356	30	LAB102	30313.3	0.0066	0.152	61
LAB102	30314.3	0.093	0.495	5	LAB102	30314.3	0.0042	0.791	4
LAB126	30201.3	0.132	0.088	50	LAB126	30201.3	0.0074	0.089	82
LAB126	30202.3	0.136	0.056	55	LAB126	30202.3	0.0068	0.018	67
LAB126	30203.3	0.159	0.020	80	LAB126	30203.3	0.0106	0.019	160
LAB126	30205.1	0.159	0.019	80	LAB126	30205.1	0.0095	0.022	134
LAB126	30205.3	0.132	0.005	50	LAB126	30205.3	0.0076	0.000	86
LAB165	30231.1	0.148	0.224	68	LAB165	30231.1	0.0078	0.146	91
LAB165	30232.1	0.108	0.336	22	LAB165	30232.1	0.0063	0.015	56
LAB165	30233.1	0.166	0.009	89	LAB165	30233.1	0.0101	0.016	147
LAB165	30235.1	0.096	0.362	9	LAB165	30235.1	0.0053	0.158	30
LAB167	27321.3	0.107	0.571	21	LAB167	27321.3	0.0045	0.727	11
LAB167	27321.4	0.139	0.019	58	LAB167	27321.4	0.0095	0.000	133
LAB167	27321.6	0.098	0.449	11	LAB167	27321.6	0.0064	0.012	57
LAB167	27324.1	0.120	0.185	36	LAB167	27324.1	0.0063	0.053	55
LAB220	30321.4	0.195	0.001	121	LAB220	30321.4	0.0115	0.004	182
LAB220	30322.3	.		.	LAB220	30322.3	0.0041	0.952	1
LAB220	30323.1	0.102	0.108	15	LAB220	30323.1	0.0048	0.228	18
LAB220	30324.4	0.147	0.157	67	LAB220	30324.4	0.0080	0.050	97
LAB241	30212.2	.		.	LAB241	30212.2	0.0056	0.087	38
LAB241	30213.1	0.112	0.393	27	LAB241	30213.1	0.0067	0.100	64
LAB268	30392.2	0.197	0.023	123	LAB268	30392.2	0.0100	0.003	145
LAB268	30395.1	0.164	0.012	86	LAB268	30395.1	0.0091	0.000	124
LAB280	30041.1	0.199	0.021	126	LAB280	30041.1	0.0116	0.007	185
LAB280	30044.1	0.209	0.033	137	LAB280	30044.1	0.0114	0.030	180
LAB280	30045.1	0.089	0.967	0	LAB280	30045.1	0.0048	0.476	17
LAB280	30045.3	0.126	0.096	42	LAB280	30045.3	0.0076	0.042	86
LAB289	30371.2	0.094	0.707	7	LAB289	30371.2	0.0051	0.362	26
LAB289	30371.4	0.118	0.083	34	LAB289	30371.4	0.0060	0.151	47
LAB289	30371.6	0.125	0.022	42	LAB289	30371.6	0.0082	0.000	102
LAB289	30375.2	0.269	0.004	205	LAB289	30375.2	0.0157	0.002	287
LAB289	30375.3	0.149	0.032	69	LAB289	30375.3	0.0091	0.017	124
LAB303	30423.4	0.096	0.544	9	LAB303	30423.4	0.0059	0.148	45
LAB303	30424.3	0.121	0.015	37	LAB303	30424.3	0.0069	0.002	69
LAB303	30425.3	0.166	0.107	88	LAB303	30425.3	0.0074	0.006	81
CONT	-	0.088	-	0	CONT	-	0.0041	-	0
LAB303	30421.2	.		.	LAB303	30421.2	0.0039	0.573	10
LAB303	30421.3	0.073	0.942	1	LAB303	30421.3	0.0039	0.461	10
LAB303	30423.4	0.120	0.005	65	LAB303	30423.4	0.0057	0.083	60
LAB303	30425.3	0.082	0.255	13	LAB303	30425.3	0.0043	0.153	21
LAB311	30221.4	0.083	0.198	14	LAB311	30221.4	0.0048	0.009	36
LAB311	30222.2	0.088	0.298	21	LAB311	30222.2	0.0051	0.054	43
LAB311	30223.4	0.138	0.000	89	LAB311	30223.4	0.0070	0.006	99

LAB311	30224.2	0.084	0.519	15	LAB311	30224.2	0.0050	0.250	41
LAB344	30092.3	0.123	0.009	70	LAB344	30092.3	0.0074	0.000	110
LAB344	30093.3	0.136	0.343	87	LAB344	30093.3	0.0065	0.239	84
LAB344	30096.1	.		.	LAB344	30096.1	0.0037	0.753	5
LAB344	30096.3	0.112	0.217	54	LAB344	30096.3	0.0070	0.138	98
LAB355	29281.3	0.191	0.038	163	LAB355	29281.3	0.0102	0.066	187
LAB355	29282.1	0.074	0.850	2	LAB355	29282.1	0.0047	0.205	34
LAB355	29282.2	0.184	0.082	153	LAB355	29282.2	0.0097	0.077	174
LAB355	29282.3	0.099	0.018	36	LAB355	29282.3	0.0049	0.008	38
LAB355	29283.1	0.082	0.468	13	LAB355	29283.1	0.0050	0.045	42
LAB367	30171.3	0.119	0.083	64	LAB367	30171.3	0.0086	0.010	143
LAB367	30172.3	.		.	LAB367	30172.3	0.0036	0.940	2
LAB367	30173.1	0.084	0.568	16	LAB367	30173.1	0.0046	0.192	31
LAB367	30173.3	0.107	0.267	48	LAB367	30173.3	0.0059	0.198	66
LAB367	30174.1	0.097	0.406	33	LAB367	30174.1	0.0045	0.322	28
LAB381	30351.4	0.118	0.056	63	LAB381	30351.4	0.0071	0.072	101
LAB381	30352.2	0.170	0.008	134	LAB381	30352.2	0.0091	0.017	158
LAB381	30352.4	0.110	0.213	52	LAB381	30352.4	0.0063	0.044	77
LAB381	30354.2	0.135	0.067	86	LAB381	30354.2	0.0058	0.000	65
LAB381	30356.1	0.102	0.001	41	LAB381	30356.1	0.0065	0.001	85
LAB383	28111.1	.		.	LAB383	28111.1	0.0042	0.386	19
LAB383	28111.3	0.172	0.052	136	LAB383	28111.3	0.0086	0.049	142
LAB383	28111.4	0.131	0.208	81	LAB383	28111.4	0.0077	0.166	116
LAB383	28115.2	0.114	0.137	56	LAB383	28115.2	0.0057	0.073	62
LAB64	30271.2	0.185	0.065	154	LAB64	30271.2	0.0089	0.027	152
LAB64	30272.1	0.123	0.006	70	LAB64	30272.1	0.0068	0.032	92
LAB64	30273.2	0.181	0.056	149	LAB64	30273.2	0.0104	0.025	194
LAB64	30274.2	.		.	LAB64	30274.2	0.0040	0.287	14
LAB64	30274.3	0.089	0.313	22	LAB64	30274.3	0.0044	0.384	24
LAB65	30302.1	0.129	0.039	77	LAB65	30302.1	0.0070	0.033	97
LAB65	30304.3	.		.	LAB65	30304.3	0.0043	0.171	20
LAB92	29321.2	0.113	0.112	55	LAB92	29321.2	0.0067	0.013	89
LAB92	29322.1	0.110	0.005	52	LAB92	29322.1	0.0067	0.004	89
LAB92	29323.2	0.108	0.000	49	LAB92	29323.2	0.0052	0.078	48
LAB92	29324.2	0.118	0.081	62	LAB92	29324.2	0.0073	0.076	106
LAB92	29325.1	.		.	LAB92	29325.1	0.0038	0.815	6
CONT	-	0.073	-	0	CONT	-	0.0035	-	0
LAB172	30852.3	0.101	0.426	35	LAB172	30852.3	0.0051	0.198	37
LAB172	30852.4	0.088	0.247	17	LAB172	30852.4	0.0048	0.052	29
LAB172	30853.4	0.143	0.246	91	LAB172	30853.4	0.0073	0.204	96
LAB172	30854.1	0.091	0.194	22	LAB172	30854.1	0.0052	0.143	39
LAB172	30854.4	0.105	0.022	39	LAB172	30854.4	0.0063	0.003	68
LAB188	30722.2	0.130	0.116	73	LAB188	30722.2	0.0076	0.059	105
LAB188	30723.3	0.110	0.250	47	LAB188	30723.3	0.0056	0.121	49
LAB188	30724.1	.		.	LAB188	30724.1	0.0039	0.613	5
LAB188	30724.2	0.084	0.754	12	LAB188	30724.2	0.0039	0.893	4
LAB243	27101.1	0.104	0.016	38	LAB243	27101.1	0.0059	0.001	58
LAB243	30872.1	0.139	0.105	85	LAB243	30872.1	0.0071	0.092	92
LAB243	30873.2	0.130	0.081	74	LAB243	30873.2	0.0062	0.160	68
LAB243	30873.4	0.192	0.008	157	LAB243	30873.4	0.0107	0.014	188
LAB270	30591.2	0.103	0.120	38	LAB270	30591.2	0.0064	0.033	72

LAB270	30595.1	0.103	0.174	37	LAB270	30595.1	0.0051	0.228	37
LAB270	30595.2	0.091	0.280	22	LAB270	30595.2	0.0056	0.020	52
LAB291	31851.2	0.128	0.096	71	LAB291	31851.2	0.0071	0.022	91
LAB291	31851.3	0.226	0.008	201	LAB291	31851.3	0.0141	0.000	280
LAB291	31852.4	0.134	0.055	79	LAB291	31852.4	0.0074	0.126	98
LAB291	31853.3	0.185	0.008	147	LAB291	31853.3	0.0112	0.001	202
LAB291	31854.4	0.111	0.000	48	LAB291	31854.4	0.0057	0.065	53
LAB295	31861.3	0.171	0.030	129	LAB295	31861.3	0.0096	0.020	159
LAB295	31863.1	0.144	0.066	93	LAB295	31863.1	0.0077	0.001	107
LAB295	31864.3	0.143	0.148	90	LAB295	31864.3	0.0077	0.126	107
LAB295	31864.4	0.176	0.097	135	LAB295	31864.4	0.0100	0.050	169
LAB295	31865.1	0.099	0.059	32	LAB295	31865.1	0.0061	0.006	65
LAB323	30381.4	0.211	0.035	182	LAB323	30381.4	0.0102	0.031	174
LAB323	30383.1	0.080	0.822	7	LAB323	30383.1	.		.
LAB323	30383.2	0.113	0.005	51	LAB323	30383.2	0.0070	0.025	89
LAB347_H0	30441.1	0.091	0.140	21	LAB347_H0	30441.1	0.0050	0.054	33
LAB347_H0	30443.4	.		.	LAB347_H0	30443.4	0.0049	0.014	32
LAB347_H0	30444.1	0.101	0.046	34	LAB347_H0	30444.1	0.0060	0.056	62
LAB347_H0	30444.3	0.139	0.033	86	LAB347_H0	30444.3	0.0080	0.020	114
LAB55	30023.1	0.125	0.018	66	LAB55	30023.1	0.0063	0.002	68
LAB55	30023.3	0.084	0.587	12	LAB55	30023.3	0.0043	0.300	16
LAB55	30025.3	0.097	0.166	30	LAB55	30025.3	0.0053	0.145	42
LAB55	30025.4	0.084	0.336	12	LAB55	30025.4	0.0050	0.095	35
LAB94	30681.4	0.081	0.354	9	LAB94	30681.4	.		.
LAB94	30682.2	0.098	0.050	31	LAB94	30682.2	0.0048	0.162	30
CONT	-	0.075	-	0	CONT	-	0.0037	-	0
LAB243	30873.2	0.169	0.470	15	LAB243	30873.2	0.0090	0.378	19
LAB291	31851.3	0.185	0.193	26	LAB291	31851.3	0.0093	0.351	23
LAB291	31854.4	0.170	0.545	16	LAB291	31854.4	0.0098	0.254	30
LAB295	31863.1	0.164	0.622	12	LAB295	31863.1	0.0076	0.960	1
CONT	-	0.147	-	0	CONT	-	0.0075	-	0

Table 56. "CONT." – Control; "Ave." – Average; "% Incr." = % increment; "p-val." – p-value.

Table 57

Genes showing improved plant performance under osmotic stress conditions (T2 generation)

Gene Name	*Event #*	*Leaf Area [cm2]*		
		Ave.	*p-value*	*% Incr.*
LAB115	27281.2	0.492581	0.550029	7.5041
LAB115	27284.3	0.491238	0.409865	7.2108
LAB115	27285.2	0.600376	0.073903	31.0299
LAB123	28282.3	0.474588	0.719054	3.5772
LAB123	28285.2	0.541201	0.064459	18.1151
LAB183	27452.2	0.535593	0.26164	16.8911

LAB189	28163.2	0.475895	0.665098	3.8623
LAB212	28042.1	0.606956	0.001791	32.4661
LAB212	28043.2	0.566207	0.144842	23.5726
LAB217	28033.2	0.548179	0.401974	19.6381
LAB217	28034.1	0.537861	0.409899	17.3863
LAB326	28053.2	0.609536	0.219758	33.029
LAB326	28054.1	0.470813	0.733727	2.7531
LAB326	28056.2	0.487388	0.656455	6.3708
CONTROL	-	0.458198	-	0
LAB115	27281.3	0.405226	0.470403	21.0703
LAB115	27284.3	0.40826	0.250554	21.9768
LAB115	27285.1	0.456307	0.165822	36.3319
LAB123	28281.1	0.931889	0.001103	178.423
LAB123	28282.3	0.517971	0.022203	54.7555
LAB123	28283.1	0.664148	0.046241	98.4293
LAB123	28284.1	0.569157	0.00031	70.0485
LAB123	28285.2	0.666459	0.000298	99.1196
LAB183	27453.1	0.344789	0.624562	3.0136
LAB183	27453.4	0.541672	0.008339	61.8367
LAB189	28163.2	0.34512	0.849484	3.1124
LAB189	28164.2	0.352018	0.794778	5.1734
LAB189	28166.2	0.521153	0.28994	55.7063
LAB189	28166.5	0.351799	0.77102	5.108
LAB206	30011.2	0.438581	0.000145	31.0361
LAB206	30012.4	0.424324	0.071649	26.7764
LAB206	30012.8	0.416905	0.242639	24.5598
LAB212	28041.1	0.348075	0.812788	3.9954
LAB212	28045.1	0.389928	0.072483	16.4997
LAB217	28033.2	0.589107	0.005534	76.009
LAB217	28034.1	0.490329	0.081787	46.4968
LAB217	28034.3	0.407859	0.183291	21.857
LAB217	28035.1	0.564533	0.058804	68.6669
LAB217	28036.1	0.487975	0.113276	45.7935
LAB250	30251.2	0.477266	0.047278	42.594
LAB250	30252.1	0.432266	0.262131	29.1493
LAB250	30253.1	0.340796	0.878908	1.8205
LAB250	30254.3	0.373202	0.5178	11.5024
LAB314	29292.6	0.458433	0.044845	36.9673
LAB314	29294.1	0.347632	0.624312	3.8628
LAB326	28052.4	0.384941	0.281381	15.0098
LAB326	28056.3	0.391255	0.200582	16.8962
LAB351	30112.1	0.393817	0.362382	17.6617
LAB351	30114.2	0.335987	0.943057	0.3836
LAB351	30115.1	0.39702	0.230711	18.6186
LAB351	30115.3	0.357745	0.58414	6.8844
LAB93	28271.3	0.452625	0.293431	35.2318
LAB93	28271.4	0.366399	0.508579	9.4699
LAB93	28272.3	0.609827	0.005631	82.1995
LAB93	28274.2	0.424391	0.351458	26.7964
LAB93	28274.3	0.397579	0.073034	18.7858
CONTROL	-	0.334703	-	0

LAB106	30031.4	0.433242	0.809753	1.1617
LAB106	30032.1	0.604263	0.010781	41.0951
LAB106	30032.2	0.613151	0.0449	43.1703
LAB206	30011.7	0.511335	0.123124	19.3964
LAB206	30012.4	0.48376	0.52015	12.9576
LAB206	30012.8	0.493725	0.26732	15.2845
LAB207	28842.1	0.492689	0.215245	15.0426
LAB207	28842.5	0.50988	0.138254	19.0566
LAB207	28843.3	0.592716	0.009049	38.3988
LAB207	28843.5	0.462581	0.470746	8.0124
LAB218	29432.2	0.497758	0.003533	16.2261
LAB218	29434.3	0.480693	0.592747	12.2414
LAB250	30252.1	0.433915	0.888913	1.3189
LAB250	30253.1	0.572333	0.112403	33.6393
LAB252	30291.4	0.539245	0.082946	25.9132
LAB252	30292.3	0.728927	0.015284	70.2039
LAB309	30052.2	0.53437	0.082382	24.7749
LAB309	30052.3	0.638199	0.104583	49.0189
LAB314	29292.4	0.548978	0.108212	28.1859
LAB314	29292.6	0.514209	0.296004	20.0673
LAB314	29294.1	0.587109	0.078976	37.0896
LAB314	29295.2	0.589143	0.166901	37.5644
LAB346	29442.2	0.430409	0.91403	0.5001
LAB346	29442.4	0.473001	0.011265	10.4454
LAB346	29443.2	0.509608	0.408925	18.993
LAB346	29445.3	0.607803	0.000412	41.9217
LAB351	30111.2	0.582071	0.0824	35.9131
LAB351	30114.2	0.547015	0.000989	27.7275
LAB82	30181.3	0.446253	0.782242	4.1997
LAB84	30161.4	0.620047	0.036393	44.7806
LAB84	30162.2	0.463221	0.57883	8.1618
LAB84	30162.4	0.75909	0.037918	77.2469
LAB84	30163.4	0.586299	0.079822	36.9004
LAB84	30164.2	0.725831	0.053685	69.481
CONTROL	-	0.428267	-	0
LAB110	30571.3	0.536832	0.044102	27.9731
LAB110	30572.1	0.434081	0.758985	3.4786
LAB110	30573.2	0.544723	0.103607	29.8541
LAB110	30574.2	0.585938	0.013378	39.6793
LAB117	27291.1	0.48302	0.248833	15.145
LAB117	27291.5	0.673927	0.049242	60.6545
LAB117	27293.1	0.751263	0.028464	79.0904
LAB117	27296.1	0.644995	0.051948	53.7576
LAB124	30431.1	0.576713	0.135159	37.4802
LAB124	30432.3	0.444879	0.450955	6.0528
LAB124	30434.1	0.457703	0.644762	9.1099
LAB124	30434.3	0.619718	0.007451	47.732
LAB124	30435.2	0.547173	0.036318	30.4383
LAB125	30581.3	0.479091	0.164977	14.2083
LAB125	30583.1	0.430392	0.690373	2.5993
LAB125	30583.2	0.545187	0.155513	29.9648

LAB156	30401.4	0.493363	0.266154	17.6106
LAB156	30402.2	0.629655	0.000094	50.1008
LAB156	30403.1	0.514312	0.056065	22.6047
LAB156	30403.4	0.46755	0.029832	11.4572
LAB156	30405.3	0.445987	0.413778	6.317
LAB228	30084.3	0.504385	0.066816	20.2383
LAB275	30361.3	0.634276	0.037049	51.2024
LAB275	30363.1	0.440686	0.640677	5.0533
LAB275	30363.4	0.464658	0.276712	10.7678
LAB275	30366.4	0.452122	0.170325	7.7794
LAB276_H0	30331.1	0.743994	0.017181	77.3576
LAB276_H0	30333.3	0.503326	0.057465	19.9858
LAB276_H0	30333.7	0.475515	0.143282	13.3561
LAB277	30651.2	0.462981	0.211085	10.368
LAB277	30652.3	0.49313	0.182928	17.5553
LAB277	30652.5	0.533964	0.000193	27.2893
LAB277	30653.1	0.628786	0.023225	49.8937
LAB278	30411.4	0.535183	0.146022	27.5801
LAB278	30412.1	0.476332	0.200056	13.5508
LAB278	30413.3	0.51687	0.184518	23.2144
LAB278	30414.2	0.476043	0.459745	13.4819
LAB281	30741.1	0.567167	0.046979	35.2046
LAB281	30742.1	0.472732	0.275046	12.6926
LAB281	30742.4	0.479067	0.303987	14.2028
LAB281	30743.4	0.462929	0.058307	10.3556
LAB282	30751.3	0.580444	0.000653	38.3695
LAB282	30754.2	0.436443	0.767815	4.0418
CONTROL	-	0.419488	-	0
LAB110	30572.2	0.779042	0	69.3998
LAB110	30573.2	0.489878	0.48067	6.5221
LAB110	30574.2	0.568641	0.081905	23.6488
LAB117	27291.2	0.604603	0.14437	31.4685
LAB117	27293.1	0.749335	0.04519	62.9401
LAB117	27296.1	0.676169	0.061711	47.0304
LAB124	30434.1	0.55654	0.201147	21.0176
LAB125	30581.3	0.602427	0.172697	30.9956
LAB125	30584.2	0.721511	0.022792	56.8898
LAB156	30401.4	0.593774	0.055292	29.1138
LAB156	30403.4	0.471576	0.799002	2.5424
LAB156	30405.3	0.571045	0.084402	24.1715
LAB228	30082.3	0.71399	0.02019	55.2544
LAB228	30084.4	0.484567	0.488401	5.3672
LAB275	30361.3	0.472891	0.841761	2.8283
LAB275	30363.1	0.525901	0.116218	14.3553
LAB275	30363.4	0.467866	0.86448	1.7356
LAB276_H0	30331.1	0.579806	0.411028	26.0765
LAB276_H0	30331.4	0.741702	0.00215	61.2803
LAB276_H0	30333.7	0.473788	0.763189	3.0234
LAB277	30652.3	0.484435	0.511735	5.3385
LAB277	30652.6	0.565196	0.018512	22.8997
LAB277	30653.1	0.47342	0.696594	2.9435

LAB278	30411.4	0.468236	0.911304	1.8163
LAB278	30413.3	0.587589	0.249059	27.769
LAB278	30414.1	0.663996	0.004889	44.3835
LAB278	30414.2	0.551584	0.076912	19.9398
LAB282	30752.2	0.469438	0.794792	2.0775
LAB282	30753.4	0.504913	0.260512	9.7915
CONTROL	-	0.459884	-	0
LAB106	30031.4	0.465433	0.455329	12.0166
LAB106	30035.2	0.470797	0.287758	13.3077
LAB127	30811.4	0.441931	0.628879	6.3604
LAB128	28075.2	0.526959	0.020352	26.8242
LAB207	28842.1	0.46412	0.580757	11.7007
LAB207	28842.5	0.429851	0.860162	3.453
LAB218	29431.3	0.459688	0.719811	10.634
LAB218	29433.4	0.449736	0.497642	8.2388
LAB218	29434.3	0.430604	0.645537	3.6343
LAB252	30292.3	0.623292	0.209372	50.0088
LAB252	30292.4	0.522909	0.283602	25.8496
LAB309	30052.3	0.541754	0.078526	30.3849
LAB309	30054.2	0.500653	0.061998	20.4932
LAB309	30056.1	0.44214	0.703517	6.4107
LAB337	27265.1	0.429209	0.830246	3.2986
LAB337	27265.2	0.508096	0.309374	22.2844
LAB346	29442.2	0.493886	0.450987	18.8644
LAB346	29443.2	0.430175	0.841819	3.531
LAB346	29445.6	0.460336	0.327389	10.79
LAB80	30673.2	0.45865	0.250836	10.3843
CONTROL	-	0.415503	-	0
LAB127	30811.4	0.565154	0.670346	4.469
LAB127	30812.1	0.542791	0.977218	0.3352
LAB128	28075.2	0.545578	0.946077	0.8503
LAB147	31104.1	0.589211	0.508254	8.916
LAB147	31104.2	0.58599	0.520365	8.3205
LAB147	31105.6	0.585524	0.426867	8.2344
LAB186	31001.4	0.839527	0.062035	55.187
LAB186	31002.1	0.684112	0.110027	26.4585
LAB186	31004.1	0.610187	0.324353	12.7934
LAB186	31004.2	0.567542	0.64125	4.9103
LAB197	31084.3	0.685466	0.042039	26.7087
LAB315	31061.1	0.575347	0.735246	6.3531
LAB315	31063.1	0.630407	0.129457	16.531
LAB317	30951.4	0.577024	0.521638	6.6632
LAB325	30971.4	0.573235	0.624246	5.9628
LAB325	30972.2	0.851595	0.087823	57.4178
LAB325	30973.1	0.684022	0.173355	26.4418
LAB325	30975.1	0.595892	0.190482	10.1509
LAB325	30975.4	0.751681	0.271172	38.9485
LAB67	31021.4	0.610333	0.289083	12.8203
LAB67	31022.1	0.924785	0.000412	70.947
CONTROL	-	0.540978	-	0
LAB147	31103.2	0.424483	0.148617	55.16

LAB147	31104.1	0.331882	0.140152	21.3119
LAB147	31104.2	0.329353	0.194598	20.3874
LAB147	31105.6	0.377447	0.061911	37.967
LAB147	31105.7	0.376588	0.131288	37.6531
LAB178	30632.1	0.36229	0.053255	32.4266
LAB178	30633.3	0.398419	0.007803	45.633
LAB178	30633.4	0.388219	0.030637	41.9045
LAB186	31001.4	0.368203	0.013186	34.5882
LAB186	31002.1	0.29727	0.537463	8.6603
LAB186	31003.1	0.455729	0.014611	66.5811
LAB186	31004.1	0.345937	0.265102	26.4492
LAB186	31004.2	0.37409	0.232684	36.74
LAB197	31081.3	0.33295	0.18789	21.7021
LAB197	31084.3	0.2826	0.833002	3.2981
LAB197	31084.4	0.387674	0.012062	41.7054
LAB197	31085.3	0.288729	0.783107	5.5382
LAB247	28091.4	0.300824	0.528273	9.9592
LAB247	28094.3	0.316522	0.370158	15.6975
LAB314	29292.6	0.342382	0.07535	25.1499
LAB314	29294.1	0.301714	0.424111	10.2847
LAB314	29295.1	0.278065	0.918831	1.6402
LAB315	31061.2	0.499781	0.000044	82.6835
LAB315	31063.1	0.411009	0.033191	50.2351
LAB315	31064.3	0.376237	0.029749	37.5248
LAB317	30952.2	0.331162	0.349316	21.0487
LAB317	30952.3	0.368499	0.089009	34.6963
LAB317	30953.1	0.357199	0.153688	30.5658
LAB317	30954.4	0.36408	0.076628	33.0811
LAB324	30961.1	0.372431	0.137357	36.1338
LAB324	30963.1	0.392933	0.007852	43.6277
LAB325	30971.4	0.363026	0.070271	32.6958
LAB325	30972.2	0.433389	0.015891	58.4154
LAB325	30973.1	0.287165	0.819366	4.9666
LAB325	30975.2	0.370916	0.248236	35.5799
LAB325	30975.4	0.379836	0.038539	38.8402
LAB54	28133.4	0.707245	0.002196	158.517
LAB54	28134.1	0.376218	0.039459	37.5179
LAB54	28136.1	0.328516	0.29264	20.0816
LAB54	28136.2	0.452787	0.018803	65.5058
LAB67	31022.1	0.498288	0.001131	82.1376
LAB67	31022.6	0.291578	0.751845	6.5798
LAB67	31023.3	0.368188	0.022824	34.5827
LAB67	31023.4	0.316952	0.464277	15.8545
LAB73	30152.1	0.375887	0.132887	37.3968
LAB73	30152.2	0.333882	0.159834	22.0429
LAB73	30153.1	0.326093	0.419964	19.196
LAB73	30154.3	0.286529	0.837266	4.7342
LAB74	28451.3	0.501417	0.109506	83.2814
LAB74	28452.2	0.424729	0.009466	55.2498
LAB74	28454.1	0.434273	0.015961	58.7385
CONTROL	-	0.273578	-	0

LAB133	28833.2	0.340892	0.307997	28.4461
LAB133	28833.5	0.350463	0.066523	32.0524
LAB158	29411.4	0.27109	0.844626	2.1451
LAB158	29412.1	0.313925	0.128663	18.285
LAB158	29414.3	0.323587	0.287175	21.9259
LAB158	29415.1	0.34563	0.060786	30.2313
LAB160	29312.1	0.35934	0.195939	35.3974
LAB160	29314.2	0.316955	0.215346	19.4269
LAB160	29315.2	0.291906	0.5666	9.9885
LAB160	29315.3	0.307959	0.352371	16.0371
LAB162	29341.2	0.30474	0.23163	14.8241
LAB162	29342.6	0.306514	0.295222	15.4926
LAB162	29344.1	0.309558	0.392925	16.6396
LAB177	29422.1	0.37312	0.138235	40.5894
LAB177	29424.3	0.465361	0.000998	75.3455
LAB177	29424.4	0.295326	0.455037	11.277
LAB177	29425.1	0.305501	0.373557	15.1112
LAB179	29301.4	0.310381	0.187689	16.9499
LAB179	29302.4	0.278489	0.71477	4.9331
LAB179	29303.2	0.535918	0.000056	101.931
LAB179	29304.3	0.285557	0.585268	7.5964
LAB179	29304.4	0.451377	0.095538	70.0761
LAB185	28172.4	0.296704	0.36514	11.7963
LAB185	28174.2	0.300332	0.409349	13.1636
LAB185	28175.2	0.275723	0.75459	3.8907
LAB185	28175.3	0.373945	0.013285	40.9004
LAB210	28331.3	0.268941	0.931731	1.3356
LAB210	28333.2	0.270266	0.902819	1.8348
LAB210	28333.3	0.288473	0.445704	8.6949
LAB210	28335.3	0.564833	0.020279	112.826
LAB254	28811.1	0.268492	0.939413	1.1663
LAB254	28814.1	0.357772	0.018758	34.8064
LAB254	28814.5	0.39131	0.019069	47.4433
LAB254	28815.3	0.387161	0.034381	45.8802
LAB254	28815.4	0.270657	0.933994	1.9821
LAB293	29232.2	0.406393	0.003783	53.1268
LAB293	29233.2	0.357082	0.021152	34.5464
LAB293	29233.3	0.379649	0.010432	43.0494
LAB293	29233.4	0.292564	0.532652	10.2366
LAB293	29235.4	0.32746	0.073601	23.3851
LAB297	29272.1	0.303931	0.219252	14.5195
LAB297	29272.5	0.296343	0.335333	11.6604
LAB297	29273.1	0.377014	0.074132	42.0567
LAB297	29273.4	0.303932	0.279946	14.5198
LAB297	29275.1	0.532931	0.019069	100.805
LAB310	28181.3	0.269727	0.875424	1.6315
LAB310	28182.2	0.287101	0.48576	8.1781
LAB310	28183.3	0.309661	0.340925	16.6786
LAB318	28101.5	0.34235	0.082062	28.9956
LAB318	28101.7	0.402919	0.167773	51.8174
LAB318	28103.2	0.27395	0.80926	3.2228

LAB327	29221.2	0.307034	0.409976	15.6887
LAB327	29221.5	0.270627	0.845487	1.9708
LAB327	29221.6	0.294868	0.444921	11.1045
LAB327	29221.8	0.332527	0.174214	25.2943
LAB327	29225.4	0.305729	0.27926	15.1968
LAB335	27314.1	0.270331	0.855608	1.8594
LAB335	27314.2	0.421045	0.078989	58.6473
LAB335	27315.4	0.277605	0.695396	4.6001
CONTROL	-	0.265397	-	0
LAB102	30312.2	0.50226	0.206938	37.3278
LAB102	30312.4	0.459183	0.056697	25.5498
LAB102	30313.2	0.407305	0.148632	11.3651
LAB102	30313.3	0.464043	0.123122	26.8785
LAB102	30314.3	0.384391	0.664152	5.1002
LAB126	30201.3	0.52265	0.090536	42.9028
LAB126	30202.3	0.513024	0.053463	40.2709
LAB126	30203.3	0.660007	0.000202	80.4589
LAB126	30205.1	0.661736	0.001306	80.9316
LAB126	30205.3	0.562359	0.002691	53.7601
LAB165	30231.1	0.511656	0.215715	39.8968
LAB165	30233.1	0.673653	0.005304	84.1899
LAB165	30235.1	0.475754	0.023038	30.0806
LAB167	27321.3	0.379056	0.739059	3.6413
LAB167	27321.4	0.606661	0.000378	65.873
LAB167	27324.1	0.42178	0.191715	15.3229
LAB220	30321.4	0.607839	0.007405	66.195
LAB220	30323.1	0.382251	0.576082	4.515
LAB220	30324.4	0.514024	0.177971	40.5444
LAB241	30212.2	0.408671	0.235301	11.7385
LAB241	30213.1	0.453615	0.139154	24.0273
LAB268	30392.2	0.678247	0.001036	85.446
LAB268	30395.1	0.676646	0.000737	85.0084
LAB280	30041.1	0.683636	0.001593	86.9196
LAB280	30044.1	0.740357	0.011918	102.428
LAB280	30045.3	0.527843	0.053506	44.3228
LAB289	30371.2	0.40623	0.45811	11.0712
LAB289	30371.4	0.510303	0.045482	39.5268
LAB289	30371.6	0.55547	0.000021	51.8763
LAB289	30375.2	0.95694	0.000018	161.646
LAB289	30375.3	0.576548	0.021054	57.6395
LAB303	30423.4	0.374413	0.835659	2.3718
LAB303	30424.3	0.493246	0.019303	34.8631
LAB303	30425.3	0.552681	0.017897	51.1139
CONTROL	-	0.365738	-	0
LAB303	30421.3	0.409815	0.459042	7.1327
LAB303	30423.4	0.511628	0.104157	33.7482
LAB303	30425.3	0.397345	0.593949	3.8729
LAB311	30221.4	0.493731	0.001631	29.0699
LAB311	30222.2	0.396091	0.738882	3.5449
LAB311	30223.2	0.390541	0.877991	2.0941
LAB311	30223.4	0.613702	0.000012	60.4324

LAB311	30224.2	0.449738	0.351201	17.5692
LAB344	30092.3	0.650905	0.007121	70.1579
LAB344	30093.3	0.547598	0.296794	43.1514
LAB344	30096.1	0.41722	0.228144	9.0685
LAB344	30096.3	0.633404	0.143779	65.5827
LAB355	29281.3	0.802823	0.016162	109.872
LAB355	29282.1	0.422846	0.359207	10.5391
LAB355	29282.2	0.774576	0.026067	102.488
LAB355	29282.3	0.457924	0.050532	19.7091
LAB355	29283.1	0.448685	0.301707	17.294
LAB367	30171.3	0.647676	0.001533	69.3137
LAB367	30173.3	0.502382	0.279815	31.3314
LAB367	30174.1	0.39441	0.835721	3.1056
LAB381	30351.4	0.591703	0.043368	54.6813
LAB381	30352.2	0.757606	0.004948	98.0513
LAB381	30352.4	0.611105	0.078322	59.7532
LAB381	30354.2	0.513489	0.083253	34.2347
LAB381	30356.1	0.592023	0.074526	54.7651
LAB383	28111.1	0.445096	0.048898	16.3558
LAB383	28111.3	0.775069	0.018554	102.616
LAB383	28111.4	0.643364	0.081276	68.1865
LAB383	28115.2	0.588124	0.0627	53.7456
LAB383	28115.5	0.385958	0.908397	0.8962
LAB64	30271.2	0.722862	0.001659	88.9687
LAB64	30272.1	0.550807	0.010269	43.9904
LAB64	30273.2	0.802716	0.019671	109.844
LAB64	30274.2	0.397548	0.760272	3.9258
LAB64	30274.3	0.408149	0.657566	6.6972
LAB65	30302.1	0.56794	0.006719	48.4693
LAB92	29321.2	0.537178	0.048359	40.4276
LAB92	29322.1	0.502934	0.001099	31.4755
LAB92	29323.2	0.501246	0.057879	31.0344
LAB92	29324.2	0.514598	0.207781	34.5247
CONTROL	-	0.38253	-	0
LAB172	30852.3	0.41849	0.412983	13.3029
LAB172	30853.4	0.492365	0.468212	33.3039
LAB172	30854.1	0.400971	0.379062	8.5595
LAB172	30854.4	0.386082	0.506231	4.5286
LAB188	30722.2	0.484092	0.119059	31.064
LAB188	30723.3	0.44229	0.173446	19.7464
LAB243	27101.1	0.514793	0.079918	39.3761
LAB243	30872.1	0.379162	0.778531	2.6551
LAB243	30873.2	0.444948	0.211592	20.466
LAB243	30873.4	0.740696	0.071643	100.537
LAB270	30591.2	0.437632	0.36711	18.4854
LAB270	30595.1	0.44216	0.032356	19.7111
LAB270	30595.2	0.395473	0.303151	7.071
LAB291	31851.2	0.45086	0.247337	22.0667
LAB291	31851.3	0.865096	0.013718	134.218
LAB291	31852.4	0.596448	0.10691	61.4835
LAB291	31853.3	0.747476	0.006986	102.373

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS COMPREND PLUS D'UN TOME.

CECI EST LE TOME __1___ DE __2 __

NOTE: Pour les tomes additionels, veillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE THAN ONE VOLUME.

THIS IS VOLUME __1___ OF __2___

NOTE: For additional volumes please contact the Canadian Patent Office.

WHAT IS CLAIMED IS:

1. A method of screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity, comprising:

(a) expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80% identical to SEQ ID NO: 343, wherein said nucleic acid sequence increases tolerance to salinity stress, growth rate, biomass and/or photosynthetic capacity of the plant, and

(b) selecting plants resulting from step (a) for an increased tolerance to a salinity stress, an increased growth rate, an increased biomass and/or an increased photosynthetic capacity as compared to a non-transformed plant which is grown under the same growth conditions,

thereby screening the plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity.

2. A method of screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity, comprising:

(a) expressing within the plant an exogenous polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 343, 75, and 1221-1233, and

(b) selecting plants resulting from step (a) for an increased tolerance to salinity stress, an increased growth rate, an increased biomass and/or an increased photosynthetic capacity as compared to a non-transformed plant which is grown under the same growth conditions,

thereby screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity.

3. A method of screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity, comprising:

(a) over-expressing within the plant a polypeptide at least 80% identical to SEQ ID NO:548, wherein said polypeptide increases tolerance to salinity stress, growth rate, biomass and/or photosynthetic capacity of the plant, and

Date Reçue/Date Received 2020-05-07

(b) selecting plants resulting from step (a) for an increased tolerance to a salinity stress, an increased growth rate, an increased biomass and/or an increased photosynthetic capacity as compared to a non-transformed plant which is grown under the same growth conditions,

thereby screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity.

4. A method of screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity, comprising:

(a) over-expressing within the plant a polypeptide selected from the group consisting of SEQ ID NOs: 548, and 5893-5904, and

(b) selecting plants resulting from step (a) for an increased tolerance to a salinity stress, an increased growth rate, an increased biomass and/or an increased photosynthetic capacity as compared to a non-transformed plant which is grown under the same growth conditions,

thereby screening plants for increased tolerance to salinity stress, yield, biomass, growth rate, and/or photosynthetic capacity.

5. The method of claim 3, wherein said polypeptide is expressed from a nucleic acid sequence as set forth in SEQ ID NO: 343, 75, 1221-1232 or 1233.

6. The method of claim 3, wherein said polypeptide is expressed from a nucleic acid sequence as set forth in SEQ ID NO: 75, 343, 1221, 1222, 1223, 1224, 1225, 1226, or 1227.

7. The method of claim 1, wherein said nucleic acid sequence encodes the amino acid sequence set forth in SEQ ID NO:548.

8. The method of claim 3, wherein said polypeptide is at least 85% identical to SEQ ID NO:548.

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9. The method of claim 3, wherein said polypeptide is at least 90% identical to SEQ ID NO:548.

10. The method of claim 3, wherein said polypeptide is at least 95% identical to SEQ ID NO:548.

11. The method of claim 3, wherein said polypeptide is at least 97% identical to SEQ ID NO:548.

12. The method of claim 3, wherein said polypeptide is set forth in SEQ ID NO:548.

13. The method of claim 5 or claim 6, wherein said nucleic acid sequence encodes the amino acid sequence selected from the group consisting of SEQ ID NOs:548, and 5893-5904.

14. The method of claim 1 or claim 2, further comprising growing the plant expressing said exogenous polynucleotide and selected for increased tolerance to salinity stress under the salinity stress.

Date Reçue/Date Received 2020-05-07

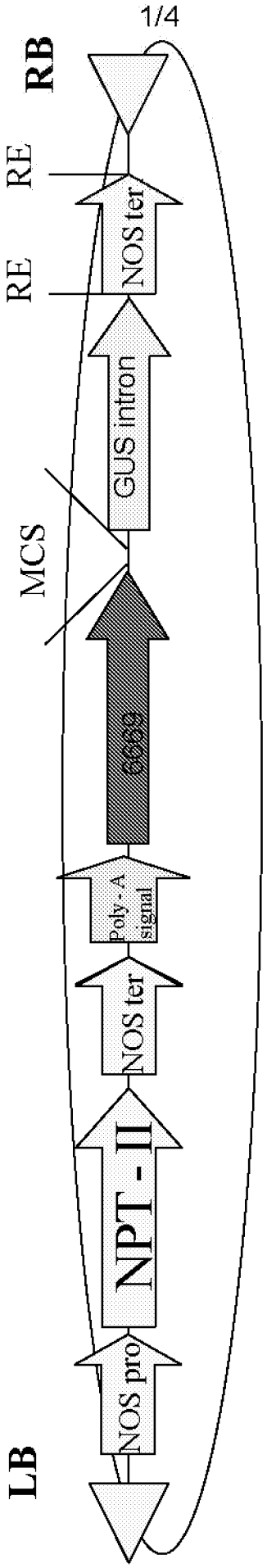

RB
RE
RE
NOS ter
GUS intron
MCS
G099
Poly - A signal
NOS ter
NPT - II
NOS pro
LB

FIG. 1

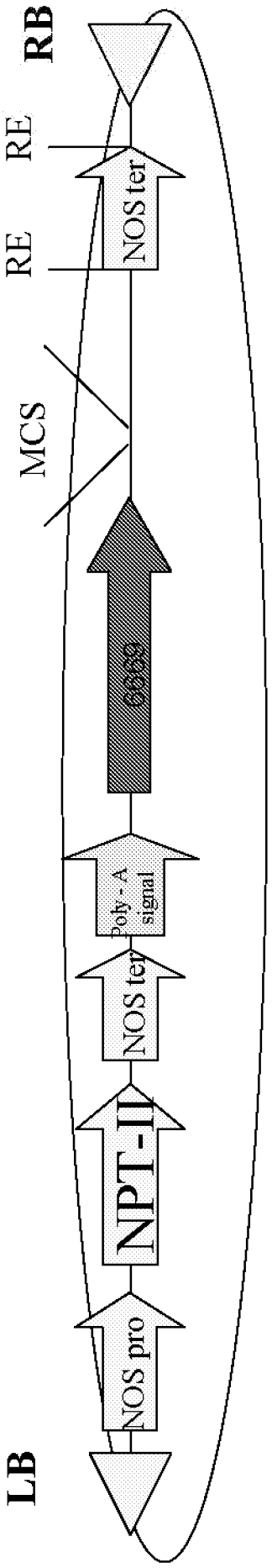


FIG. 2

Normal conditions

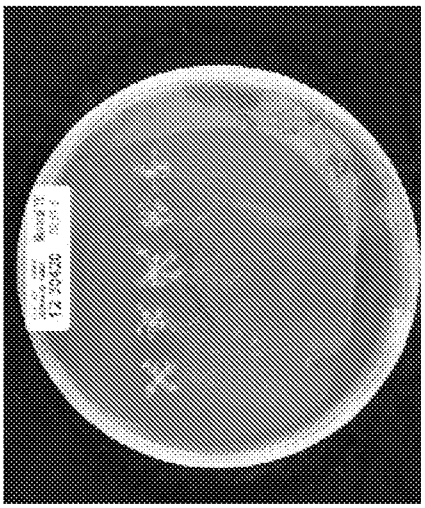


FIG. 3A

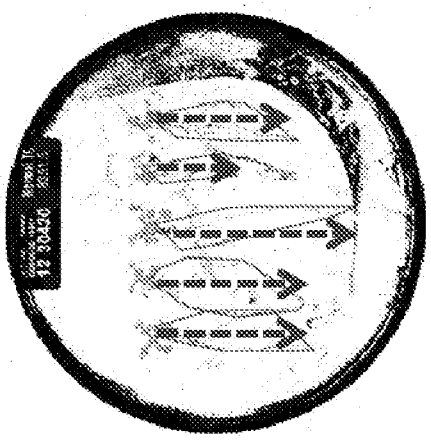


FIG. 3B

Osmotic stress (15 % PEG)

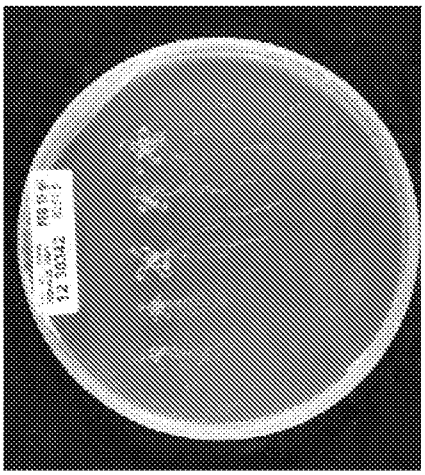


FIG. 3C

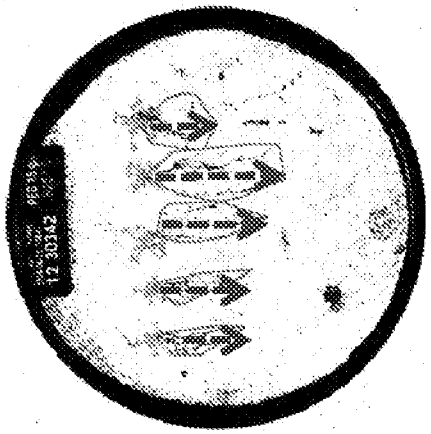


FIG. 3D

Nitrogen limiting conditions

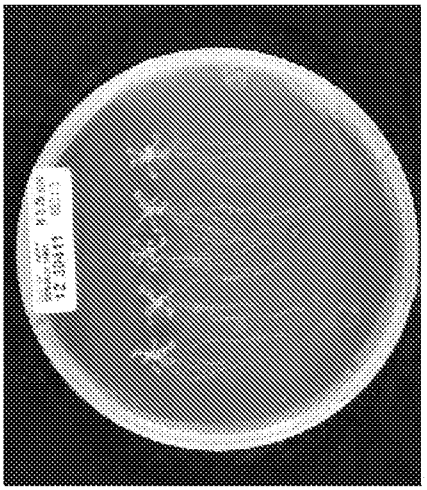


FIG. 3E

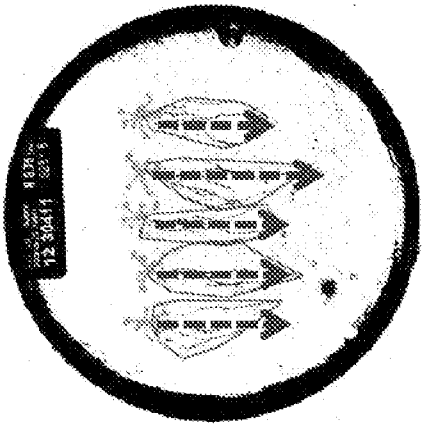


FIG. 3F

FIG. 3

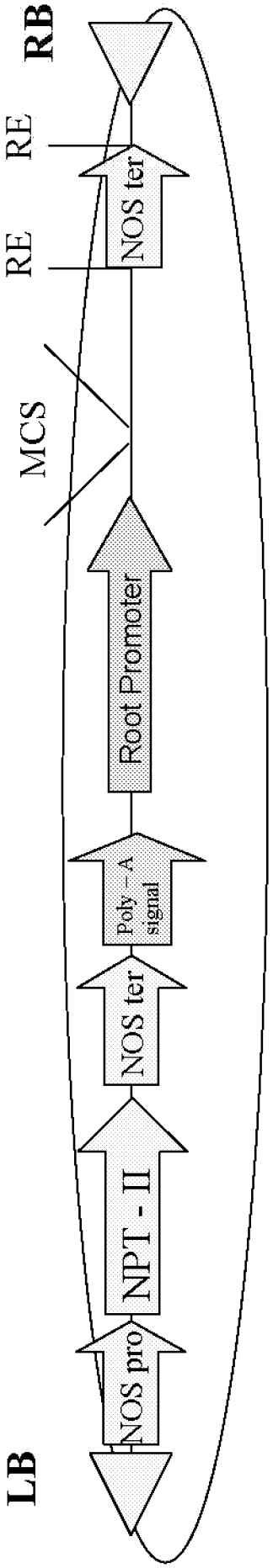

RB
RE
RE
NOS ter
MCS
Root Promoter
Poly – A signal
NOS ter
NPT - II
NOS pro
LB

FIG. 4