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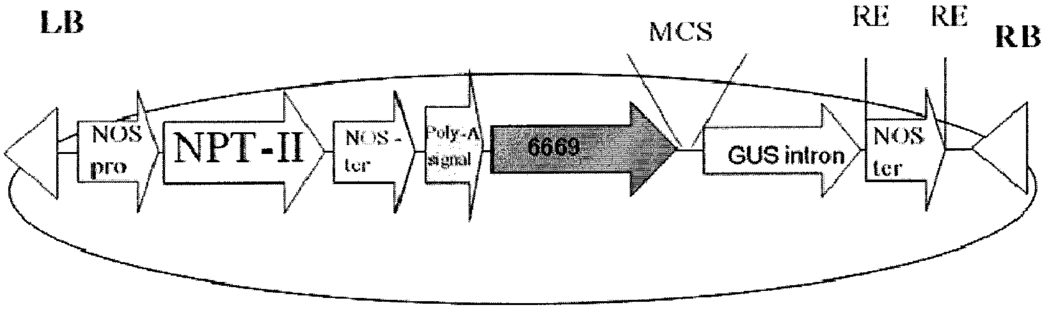
(54) Titre : POLYNUCLEOTIDES ET POLYPEPTIDES ISOLES, ET PROCEDES D'UTILISATION DE CEUX-CI POUR AUGMENTER UN RENDEMENT VEGETAL ET/OU DES CARACTERISTIQUES AGRICOLES

(54) Title: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES, AND METHODS OF USING SAME FOR INCREASING PLANT YIELD AND/OR AGRICULTURAL CHARACTERISTICS



(57) **Abrégé/Abstract:**

Provided are isolated polynucleotides which comprise a nucleic acid sequence at least 80% identical to SEQ ID NO: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739; isolated polypeptides which comprise an amino acid sequence at least 80% homologous to SEQ ID NO: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737, and methods of using same for increasing a yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

ABSTRACT

Provided are isolated polynucleotides which comprise a nucleic acid sequence at least 80% identical to SEQ ID NO: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739; isolated polypeptides which comprise an amino acid sequence at least 80% homologous to SEQ ID NO: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737, and methods of using same for increasing a yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

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ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES, AND METHODS OF USING SAME FOR INCREASING PLANT YIELD AND/OR AGRICULTURAL CHARACTERISTICS

FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to isolated polynucleotides and polypeptides which can increase the yield (e.g., biomass, grain quantity and/or quality), growth rate, vigor, abiotic stress tolerance (ABST), water use efficiency (WUE), 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. 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). In addition, chilling may lead to yield losses and lower product quality through the delayed ripening of maize.

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, 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 levees, 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.

SUMMARY OF THE INVENTION

According to an aspect of some embodiments of the present invention there is provided a method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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 yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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 yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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 yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 246, 240-245, 247-465, 1974-3480, and 3675-3737, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739, wherein said nucleic acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

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: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737, wherein said nucleic acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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 a nucleic acid sequence encoding a polypeptide which comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

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: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737, wherein said amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, 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: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

According to some embodiments of the invention, the nucleic acid sequence is as set forth in SEQ ID NO: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739.

According to some embodiments of the invention, the polynucleotide consists of the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

According to some embodiments of the invention, the nucleic acid sequence encodes an amino acid sequence at least 80% homologous to SEQ ID NO: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737.

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: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

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

According to some embodiments of the invention, the abiotic stress is selected from the group consisting of salinity, drought, water deprivation, 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 method further comprising growing the plant under the abiotic stress.

According to some embodiments of the invention, the method, further comprising growing the plant under nitrogen-limiting conditions.

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.

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:4198) 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:4198) (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 (FIGs. 3A-B), osmotic stress (15% PEG; FIGs. 3C-D) or nitrogen-limiting (FIGs. 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. FIG. 3A – An image of a photograph of plants taken following 10 after transplanting days on agar plates when grown under normal (standard) conditions. FIG. 3B – An image of root analysis of the plants shown in FIG. 3A in which the lengths of the roots measured are represented by arrows. FIG. 3C – An image of a photograph of plants taken following 10 days after transplanting on agar plates, grown under high osmotic (PEG 15%) conditions. FIG. 3D – An image of root analysis of the plants shown in FIG. 3C in which the lengths of the roots measured are represented by arrows. FIG. 3E – An image of a photograph of plants taken following 10 days after transplanting on agar plates, grown under low nitrogen conditions. FIG. 3F – An image of root analysis of the plants shown in FIG. 3E in which the lengths of the roots measured are represented by arrows.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

The present invention, in some embodiments thereof, relates to isolated polynucleotides and polypeptides which can increase yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality abiotic stress tolerance, and/or fertilizer use efficiency (e.g., nitrogen use efficiency) 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 polynucleotides and polypeptides which can be used in increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality abiotic stress tolerance, and/or fertilizer use efficiency (e.g., nitrogen use efficiency) of a plant.

As shown in the Examples section which follows, the present inventors have employed a bioinformatic approach which combines clustering and assembly of sequences from databases of arabidopsis, rice, poplar, brachypodium, soybean, grape, castobean, sorghum and maize and other publicly available plant genomes, expressed sequence tags (ESTs), mRNA sequences, properitary ESTs sequences (Barley, Sorghum), protein and pathway databases, quantitative trait loci (QTL), single nucleotide polymorphism (SNPs) information with a digital expression profile ("electronic Northern Blot") and identified polynucleotides and polypeptides which can increase yield, growth rate, biomass, vigor, tolerance to abiotic stress, nitrogen use efficiency, water use efficiency and fertilizer use efficiency (SEQ ID NOs:1-239 for polynucleotides; SEQ ID NOs:240-465 for polypeptides; Table 1, Example 1). Orthologs from plant species which exhibit at least 80% homology to the identified polypeptides and polynucleotides were also identified (SEQ ID NO:467-1973 for polynucleotides; SEQ ID NOs:1974-3480 for polypeptides; Table 2, Example 1). Selected genes were cloned (Example 7, Tables 26-28), transformed into agrobacterium tumefaciens cells (Example 8) and further into arabidopsis plants (Example 9). Transgenic plants over-expressing the identified polynucleotides were found to exhibit increased seed yield, oil yield, dry weight, fresh weight, root coverage, root length, harvest index, growth rate, rosette area, biomass, oil percentage in seed and weight of 1000 seeds (Examples 10-11; Tables 29-36), and increased tolerance to abiotic stress conditions such as limiting nitrogen conditions (Example 11, Tables 37-38). Thus, the identified polynucleotides and polypeptides of the invention can be used to increase plant's yield, biomass (e.g., of grain or any harvestable plant part with economical value), vigor, growth rate, oil content, fiber yield, fiber quality, tolerance to abiotic stress, nitrogen use efficiency, water use efficiency and/or fertilizer use efficiency.

Thus, according to an aspect of some embodiments of the invention there is provided a method of increasing a yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, water use efficiency, nitrogen use efficiency, fertilizer use efficiency and/or abiotic stress tolerance of a plant.

The method is effected by expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80% identical to SEQ ID NO: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, water use efficiency, nitrogen use efficiency, fertilizer use efficiency and/or abiotic stress tolerance of the plant.

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.

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 phrase "abiotic stress" as used herein refers to any adverse effect on metabolism, growth, reproduction and/or viability of a plant. Accordingly, abiotic stress can be induced by suboptimal environmental growth conditions such as, for example, salinity, water deprivation, flooding, freezing, low or high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, atmospheric pollution or UV irradiation. The implications of abiotic stress are discussed in the Background section.

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

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

As used herein the phrase "fertilizer use efficiency" refers to the 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.

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).

As used herein the phrase "fiber producing plant" refers to plants that share the common feature of having an elongated shape and abundant cellulose in thick cell walls, typically termed as secondary walls. Such walls may or may not be lignified, and the protoplast of such cells may or may be viable at maturity. Such fibers have many industrial uses, for example in lumber and manufactured wood products, paper, textiles, sacking and boxing material, cordage, brushes and brooms, filling and stuffing, caulking, reinforcement of other materials, and manufacture of cellulose derivatives.

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).

According to a preferred embodiment of this aspect of the present invention the fiber producing plant is cotton.

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.

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% or greater increase in plant yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, water use efficiency, nitrogen use efficiency, fertilizer use efficiency and/or abiotic stress tolerance as compared to a native plant [*i.e.*, a plant not modified with the biomolecules (polynucleotide or polypeptides) of the invention, e.g., a non-transformed plant of the same species which is grown under the same growth conditions as the transformed plant].

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 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 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

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 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

According to some embodiments of the invention the exogenous polynucleotide consists of the nucleic acid sequence set forth in SEQ ID NO: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739.

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 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 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: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

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 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: 246, 240-245, 247-465, 1974-3480, 3675-3736 or 3737.

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:

Formula I

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:37 and 43.

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 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 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

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

According to some embodiments of the invention the isolated polynucleotide consists of 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 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: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

According to some embodiments of the invention the isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

According to some embodiments of the invention the isolated polynucleotide is set forth by SEQ ID NO: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, 3738 or 3739.

According to some embodiments of the invention the isolated polynucleotide consists of a nucleic acid sequence selected from the group of SEQ ID NOs: 3487, 1-239, 467-1973, 3481-3486, 3488-3674, and 3738-3739.

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 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 NO: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

According to some embodiments of the invention the amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, water use efficiency, nitrogen use efficiency, fertilizer use efficiency and/or abiotic stress tolerance 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: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

The invention provides an isolated 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 an amino acid sequence selected from the group consisting of SEQ ID NOs: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

According to some embodiments of the invention, the isolated polypeptide is selected from the group consisting of SEQ ID NOs: 246, 240-245, 247-465, 1974-3480, and 3675-3737.

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, cotton and sorghum.

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 capable of directing transcription of the exogenous polynucleotide in the plant cell. Further details of suitable transformation approaches are provided herein below.

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.

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. According to some embodiments of the invention, 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:4196; Odell et al., Nature 313:810-812, 1985); Arabidopsis At6669 promoter (SEQ ID NO:4195; see PCT Publication No. WO04081173A2); Arabidopsis new At6669 promoter (SEQ ID NO:4198); 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., 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), sorghum gamma- kafirin (PMB 32:1029-35, 1996); e.g., the Napin promoter (SEQ ID NO:4197)], embryo specific promoters [e.g., rice OSH1 (Sato et al., Proc. Natl. Acad. Sci. USA, 93: 8117-8122), KNOX (Postma-Haarsma et 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].

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 some embodiments of the 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 (e.g., T-DNA using Agrobacterium tumefaciens or Agrobacterium rhizogenes); see for example, 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. For this reason 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), Gal-on 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 polynucleotide is 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 yield (or other parameters affecting yield such as growth rate, biomass, vigor, content of seeds, oil content and the like), fiber yield and/or quality, water use efficiency, fertilizer use efficiency, nitrogen use efficiency and/or abiotic stress tolerance in plants can involve multiple genes acting additively or in synergy (see, for example, in Quesda et al., Plant Physiol. 130:951-063, 2002), the invention also envisages expressing a plurality of exogenous polynucleotides in a single host plant to thereby achieve superior effect on yield, fiber yield and/or quality, water use efficiency, fertilizer use efficiency, nitrogen use efficiency and/or abiotic stress tolerance.

Expressing a plurality of exogenous polynucleotides in a single host plant can be effected by co-introducing multiple nucleic acid constructs, each including a different exogenous polynucleotide, into a single plant cell. The transformed cell can then be 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 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 yield (e.g., growth rate, biomass, vigor, oil content), fiber yield and/or quality, water use efficiency, fertilizer use efficiency, nitrogen use efficiency and/or abiotic stress tolerance traits, using conventional plant breeding techniques.

According to some embodiments of the invention, the plant expressing the exogenous polynucleotide(s) is grown under non-stress or normal conditions (e.g., biotic conditions and/or conditions with sufficient water, nutrients such as nitrogen and fertilizer). Such conditions, which depend on the plant being grown, are known to those skilled in the art of agriculture, and are further, described hereinbelow.

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., biomass, growth rate, oil content, fiber yield and/or quality, yield, abiotic stress tolerance, water use efficiency, nitrogen use efficiency and/or fertilizer 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 can be 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.

Plant's growth rate, biomass, yield and/or vigor - Plant vigor can be calculated by the increase in growth parameters such as leaf area, fiber length, rosette diameter, plant fresh weight and the like per time.

The growth rate can be measured using digital analysis of growing plants. For example, images of plants growing in greenhouse on plot basis can be captured every 3 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 also 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

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

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.

Seed yield can be expressed as thousand kernel weight (1000-weight), which is extrapolated from the number of filled seeds counted and their total weight. Hence, an increased 1000-weight may result from an increased seed size and/or seed weight (e.g., increase in embryo size and/or endosperm size). For example, 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

Since the transgenic plants of the invention have increased yield, it is likely that these plants exhibit an increased growth rate (during at least part of their life cycle), relative to the growth rate of corresponding wild type plants at a corresponding stage in their life cycle. The increased growth rate may be specific to one or more parts of a plant (including seeds), or may be throughout substantially the whole plant. A plant having an increased growth rate may also exhibit early flowering. Increased growth rate during the early stages in the life cycle of a plant may reflect enhanced vigor. The increase in growth rate may alter the harvest cycle (early maturing) of a plant allowing plants to be sown later and/or harvested sooner than would otherwise be possible. If the growth rate is sufficiently increased, it may allow for the sowing of further seeds of the same plant species (for example sowing and harvesting of rice plants followed by sowing and harvesting of further rice plants all within one conventional growing period). Similarly, if the growth rate is sufficiently increased, it may allow for the sowing of further seeds of different plants species (for example the sowing and harvesting of rice plants followed by, for example, the sowing and optional harvesting of soybean, potato or any other suitable plant). Harvesting additional times from the same rootstock in the case of some plants may also be possible. Altering the harvest cycle of a plant may lead to an increase in annual biomass production per area (due to an increase in the number of times (say in a year) that any particular plant may be grown and harvested). An increase in growth rate may also allow for the cultivation of transgenic plants in a wider geographical area than their wild-type counterparts, since the territorial limitations for growing a crop are often determined by adverse environmental conditions either at the time of planting (early season) or at the time of harvesting (late season). Such adverse conditions may be avoided if the harvest cycle is shortened. The growth rate may be determined by deriving various parameters from growth curves, such parameters may be: T-Mid (the time taken for plants to reach 50% of their maximal size) and T-90 (time taken for plants to reach 90% of their maximal size).

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.

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.

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, high or low light conditions, 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 with added salt), or by culturing the plants in a hyperosmotic growth medium [e.g., 50% Murashige-Skoog medium (MS medium) with added salt]. 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 chlorosis 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 PEG 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 experiments, the medium is supplemented for example with 50 mM, 100 mM, 200 mM NaCl or 15%, 20% or 25% PEG.

Drought tolerance assay - 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. 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.

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 drought stress tolerant plants

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

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

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

Water use efficiency (WUE) – 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 V:

Formula V

$$RWC = (FW - DW/TW - DW) \times 100$$

Plants that maintain high relative water content (RWC) compared to control lines are considered more tolerant to drought than those exhibiting reduced relative water content. A non limiting example in Arabidopsis is when water uptake by roots matches water loss by transpiration from leaves. Under these circumstances the plant is determined to be under equilibrium and the RWC is about 0.9. When the RWC of transgenic plants decreases significantly less as compared to wild type plants, the transgenic plants are considered more tolerant to drought [Gaxiola et al. PNAS September 25, 2001 vol. 98 no. 20 11444-11449].

Fertilizer use efficiency **-** To analyze whether the transgenic plants are more responsive to fertilizers, plants are grown in agar plates or pots containing growth media with a limited amount of fertilizer (e.g., nitrogen, phosphate, potassium), essentially as described 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, grain and/or seed production. 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 greenness 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. 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 which express the exogenous polynucleotide of the invention to thrive under nutrient restraining conditions. For example, to analyze whether the transgenic Arabidopsis plants are more responsive to phosphate, plants are grown in 250 mM (phosphate deficient conditions) or 1 mM (optimal phosphate concentration). To test the potassium use efficiency, Arabidopsis plants which express the exogenous polynucleotide of the invention are grown in 0.03 mM potassium (potassium deficient conditions) or 3 mM potassium (optimal potassium concentration) essentially as described by Watson et al. Plant Physiol. (1996) 11 1 : 1077-1 083.

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.

Nitrogen use efficiency – To analyze whether the transgenic Arabidopsis plants are more responsive to nitrogen plant are grown in 0.75- 1.5 mM (nitrogen deficient conditions) or 6-10 mM (optimal nitrogen concentration). Plants are allowed to grow for additional 20 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 0.2 mM or 0.05 mM. 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 25 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, 25 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 are used as control.

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).

Thus, the present invention is of high agricultural value for promoting the yield, biomass, growth rate, vigor, water use efficiency, fertilizer use efficiency, nitrogen use efficiency and abiotic stress tolerance of commercially desired crops (e.g., biomass of vegetative organ such as poplar wood, or reproductive organ such as number of seeds or seed biomass).

As used herein the term “about” refers to ± 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.

EXAMPLE 1

IDENTIFYING GENES WHICH IMPROVE YIELD AND AGRONOMICAL IMPORTANT TRAITS IN PLANTS

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

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:***
    - GeneBank 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).
- ***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 yield.

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.

To further investigate and identify putative orthologs of the yield, growth rate, vigor, biomass, growth rate, abiotic stress tolerance (ABST), nitrogen use efficiency (NUE) and fertilizer use efficiency (FUE) genes from other plant species, 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.

Overall, 239 genes were identified to have a major impact on plant yield, growth rate, vigor, biomass, growth rate, oil content, abiotic stress tolerance, 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 1, hereinbelow.

Table 1
Identified genes for increasing yield, growth rate, vigor, biomass, growth rate, oil content, abiotic stress tolerance, nitrogen use efficiency, water use efficiency and fertilizer use efficiency of a plant

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM1	rice|gb157.2|AU058137	rice	1	240
LYM2	rice|gb157.2|AA750140	rice	2	241
LYM3	rice|gb157.2|AU032158	rice	3	242
LYM4	rice|gb157.2|AU082697	rice	4	243
LYM5	rice|gb157.2|AW155107	rice	5	244
LYM6	rice|gb157.2|AW155114	rice	6	245
LYM7	rice|gb157.2|BE039635	rice	7	246
LYM8	rice|gb157.2|BE040233	rice	8	247
LYM9	rice|gb157.2|BE040806	rice	9	248
LYM10	rice|gb157.2|BE230434	rice	10	249
LYM12	rice|gb157.2|BI807331	rice	11	250
LYM13	rice|gb157.2|BM037844	rice	12	251
LYM14	rice|gb157.2|BM038118	rice	13	252
LYM15	rice|gb157.2|CA761603	rice	14	253
LYM16	rice|gb157.2|U38074	rice	15	254
LYM17	rice|gb157.2|AU033038	rice	16	255

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM19	rice|gb157.2|BE040457	rice	17	256
LYM20	rice|gb157.2|BF430570	rice	18	257
LYM21	rice|gb157.2|BI805660	rice	19	258
LYM22	rice|gb157.2|BI808357	rice	20	259
LYM23	rice|gb157.2|AA749984	rice	21	260
LYM24	rice|gb157.2|AF050674	rice	22	261
LYM26	barley|gb157.3|AJ431915	barley	23	262
LYM30	rice|gb157.2|AK100743	rice	24	263
LYM31	rice|gb157.2|AK101734	rice	25	264
LYM32	rice|gb157.2|AK106380	rice	26	265
LYM34	rice|gb157.2|AK107902	rice	27	266
LYM35	rice|gb157.2|AK107934	rice	28	267
LYM36	rice|gb157.2|AK108674	rice	29	268
LYM37	rice|gb157.2|AK111353	rice	30	269
LYM38	barley|gb157.3|AL508889	barley	31	270
LYM40	rice|gb157.2|AU082329	rice	32	271
LYM41	rice|gb157.2|AU096202	rice	33	272
LYM42	rice|gb157.2|AU097348	rice	34	273
LYM43	rice|gb157.2|AU101198	rice	35	274
LYM44	rice|gb157.2|AU172519	rice	36	275
LYM49	maize|gb164|AW331061	maize	37	
LYM51	barley|gb157.3|BE412472	barley	38	276
LYM52	barley|gb157.3|BE422132	barley	39	277
LYM53	maize|gb164|BE511332	maize	40	278
LYM56	barley|gb157.3|BF625411	barley	41	279
LYM57	rice|gb157.2|BI809626	rice	42	280
LYM59	barley|gb157.3|BI952737	barley	43	
LYM61	maize|gb164|BM079029	maize	44	281
LYM62	maize|gb164|BM348041	maize	45	282
LYM66	barley|gb157.3|BU974981	barley	46	283
LYM67	rice|gb157.2|CA763759	rice	47	284
LYM68	rice|gb157.2|CA767240	rice	48	285
LYM69	rice|gb157.2|CA997856	rice	49	286
LYM73	rice|gb157.2|CB683204	rice	50	287
LYM74	maize|gb164|CF075309	maize	51	288
LYM79	maize|gb164|AW191191	maize	52	289
LYM82	barley|gb157.3|AL507706	barley	53	290
LYM83	barley|gb157.3|BI952401	barley	54	291
LYM84	barley|gb157.3|BF622069	barley	55	292
LYM86	rice|gb157.2|AU031857	rice	56	293
LYM88	arabidopsis|gb165|AT2G37750	arabidopsis	57	294
LYM89	arabidopsis|gb165|AT5G67490	arabidopsis	58	295

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM90	barley|gb157.3|AV927104	barley	59	296
LYM91	barley|gb157.3|BE060518	barley	60	297
LYM93	barley|gb157.3|BI955752	barley	61	298
LYM99	barley|gb157.3|BI947870	barley	62	299
LYM95	barley|gb157.3|BI959932	barley	63	300
LYM100	barley|gb157.3|AV912944	barley	64	301
LYM102	rice|gb157.2|CA760613	rice	65	302
LYM103	maize|gb164|CD963970	maize	66	303
LYM105	barley|gb157.3|AL507901	barley	67	304
LYM106	barley|gb157.3|BI954225	barley	68	305
LYM110	maize|gb164|BE552618	maize	69	306
LYM111	maize|gb164|AW053159	maize	70	307
LYM119	maize|gb164|AW498426	maize	71	308
LYM120	rice|gb157.3|BI795677	rice	72	309
LYM122	rice|gb157.3|BI118816	rice	73	310
LYM125	rice|gb157.2|AK108452	rice	74	311
LYM126	rice|gb157.2|AK108969	rice	75	312
LYM127	rice|gb157.2|AU172589	rice	76	313
LYM128	rice|gb157.2|AU172667	rice	77	314
LYM129	rice|gb157.3|BE230206	rice	78	315
LYM130	rice|gb157.3|BF430580	rice	79	316
LYM131	rice|gb157.3|CF309827	rice	80	317
LYM132	rice|gb157.3|BE229876	rice	81	318
LYM134	rice|gb157.2|BI809462	rice	82	319
LYM136	rice|gb157.2|AU093861	rice	83	320
LYM137	barley|gb157.3|AL501911	barley	84	321
LYM140	barley|gb157.3|BF623993	barley	85	322
LYM141	rice|gb157.2|CA761074	rice	86	323
LYM142	barley|gb157.3|CB866504	barley	87	324
LYM143	rice|gb157.3|BI306405	rice	88	325
LYM144	rice|gb157.2|BM420331	rice	89	326
LYM145	rice|gb157.2|AK073109	rice	90	327
LYM148	barley|gb157.3|AL500574	barley	91	328
LYM149	barley|gb157.3|AL509762	barley	92	329
LYM152	arabidopsis|gb165|AT5G57290	arabidopsis	93	330
LYM153	rice|gb157.3|AU066244	rice	94	331
LYM156	barley|gb157.3|BE421631	barley	95	332
LYM157	barley|gb157.3|BE454937	barley	96	333
LYM159	barley|gb157.3|BF259387	barley	97	334
LYM160	barley|gb157.3|BG300909	barley	98	335
LYM161	barley|gb157.3|BG344928	barley	99	336
LYM162	maize|gb164|BG462213	maize	100	337
LYM164	rice|gb157.3|BI805693	rice	101	338

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM165	maize|gb164|CD439546	maize	102	339
LYM166	wheat|gb164|CJ547519	wheat	103	340
LYM170	rice|gb157.2|AU057403	rice	104	341
LYM172	rice|gb157.2|BE229411	rice	105	342
LYM173	rice|gb157.3|AA751564	rice	106	343
LYM174	sorghum|gb161.crp|AW284303	sorghum	107	344
LYM175	rice|gb157.2|AK060073	rice	108	345
LYM176	rice|gb157.2|BI305434	rice	109	346
LYM178	barley|gb157.3|BE421520	barley	110	347
LYM179	maize|gb164|BE051631	maize	111	348
LYM107	maize|gb164|AW497895	maize	112	349
LYM109	maize|gb169.2|CD984002	maize	113	350
LYM112	maize|gb164|CF038223	maize	114	351
LYM113	maize|gb164|AW257902	maize	115	352
LYM115	maize|gb164|CF646135	maize	116	353
LYM116	maize|gb164|AI964572	maize	117	354
LYM117	maize|gb164|AI739834	maize	118	355
LYM118	maize|gb164|CO518843	maize	119	356
LYM121	rice|gb157.2|AK103124	rice	120	357
LYM123	rice|gb157.2|AI978352	rice	121	358
LYM135	rice|gb157.2|AU101278	rice	122	359
LYM138	rice|gb157.2|BI805497	rice	123	360
LYM146	maize|gb164|AI770878	maize	124	361
LYM147	maize|gb164|AI901828	maize	125	362
LYM154	barley|gb157.3|AV836282	barley	126	363
LYM155	barley|gb157.3|BE412535	barley	127	364
LYM180	barley|gb157.3|AJ476822	barley	128	365
LYM181	barley|gb157.3|AL450622	barley	129	366
LYM182	barley|gb157.3|AL507048	barley	130	367
LYM184	barley|gb157.3|AV833284	barley	131	368
LYM185	barley|gb157.3|AV833969	barley	132	369
LYM186	barley|gb157.3|AV834971	barley	133	370
LYM188	barley|gb157.3|BE438660	barley	134	371
LYM189	barley|gb157.3|BF256192	barley	135	372
LYM192	barley|gb157.3|BF627356	barley	136	373
LYM193	barley|gb157.3|CB858276	barley	137	374
LYM194	barley|gb157.3|CB860975	barley	138	375
LYM196	maize|gb164|AI372352	maize	139	376
LYM197	maize|gb164|AI444704	maize	140	377
LYM198	maize|gb164|AI491323	maize	141	378
LYM201	maize|gb164|AI600670	maize	142	379
LYM203	maize|gb164|AI629486	maize	143	380
LYM204	maize|gb164|AI649791	maize	144	381

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM206	maize|gb164|AI691210	maize	145	382
LYM207	maize|gb164|AI920398	maize	146	383
LYM208	maize|gb164|AI941717	maize	147	384
LYM212	maize|gb164|AW000408	maize	148	385
LYM213	maize|gb164|AW000438	maize	149	386
LYM215	maize|gb164|AW498464	maize	150	387
LYM217	maize|gb164|BE129928	maize	151	388
LYM219	maize|gb164|BE238495	maize	152	389
LYM220	maize|gb164|BG842756	maize	153	390
LYM221	maize|gb164|BI502603	maize	154	391
LYM223	maize|gb164|BM338985	maize	155	392
LYM224	maize|gb164|CA401086	maize	156	393
LYM227	maize|gb164|EC877515	maize	157	394
LYM228	maize|gb164|EC892599	maize	158	395
LYM232	rice|gb157.3|AA750121	rice	159	396
LYM233	rice|gb157.3|AA750182	rice	160	397
LYM234	rice|gb157.3|AA752388	rice	161	398
LYM236	rice|gb157.3|AF155334	rice	162	399
LYM238	rice|gb157.3|AK066551	rice	163	400
LYM239	rice|gb157.3|AU068651	rice	164	401
LYM240	rice|gb157.3|AU069131	rice	165	402
LYM241	rice|gb157.3|AU162998	rice	166	403
LYM242	rice|gb157.3|BE039711	rice	167	404
LYM243	rice|gb157.3|BE228686	rice	168	405
LYM245	rice|gb157.3|BF430828	rice	169	406
LYM248	rice|gb157.3|BQ906571	rice	170	407
LYM249	rice|gb157.3|C25903	rice	171	408
LYM250	rice|gb157.3|CA759158	rice	172	409
LYM251	rice|gb157.3|CA759241	rice	173	410
LYM252	rice|gb157.3|CA759659	rice	174	411
LYM254	rice|gb157.3|CB657978	rice	175	412
LYM255	rice|gb157.3|CF330913	rice	176	413
LYM260	rice|gb157.3|CI581223	rice	177	414
LYM261	rice|gb157.3|D41406	rice	178	415
LYM263	sorghum|gb161.crp|AI622410	sorghum	179	416
LYM183	barley|gb157.3|AL509795	barley	180	417
LYM256	rice|gb157.3|CI004090	rice	181	418
LYM200	maize|gb164|AI586731	maize	182	419
LYM267	maize|gb164|AW231521	maize	183	420
LYM268	rice|gb157.2|BI800054	rice	184	421
LYM270	maize|gb164|AI670268	maize	185	422
LYM271	maize|gb164|CF637107	maize	186	423
LYM272	rice|gb157.2|CA761620	rice	187	424

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM273	rice|gb157.2|BM418692	rice	188	425
LYM274	rice|gb157.2|AK073201	rice	189	426
LYM277	rice|gb157.2|BM038097	rice	190	427
LYM278	barley|gb157.3|BLYTRAA	barley	191	428
LYM283	rice|gb157.2|D23167	rice	192	429
LYM284	rice|gb157.2|BI306331	rice	193	430
LYM285	rice|gb157.2|CB631346	rice	194	431
LYM287	rice|gb157.2|AK102063	rice	195	432
LYM288	rice|gb157.2|BE040927	rice	196	433
LYM289	barley|gb157.3|AV925962	barley	197	434
LYM290	maize|gb164|AA979729	maize	198	435
LYM291	rice|gb157.2|BM037976	rice	199	436
LYM293	rice|gb157.2|AK059161	rice	200	437
LYM38	barley|gb157.3|AL508889	barley	201	438
LYM42	rice|gb157.2|AU097348	rice	202	439
LYM51	barley|gb157.3|BE412472	barley	203	276
LYM52	barley|gb157.3|BE422132	barley	204	277
LYM56	barley|gb157.3|BF625411	barley	205	279
LYM59	barley|gb157.3|BI952737	barley	206	
LYM66	barley|gb157.3|BU974981	barley	207	440
LYM79	maize|gb164|AW191191	maize	208	441
LYM83	barley|gb157.3|BI952401	barley	209	442
LYM90	barley|gb157.3|AV927104	barley	210	296
LYM99	barley|gb157.3|BI947870	barley	211	299
LYM95	barley|gb157.3|BI959932	barley	212	443
LYM148	barley|gb157.3|AL500574	barley	213	328
LYM159	barley|gb157.3|BF259387	barley	214	334
LYM161	barley|gb157.3|BG344928	barley	215	444
LYM166	wheat|gb164|CJ547519	wheat	216	445
LYM175	rice|gb157.2|AK060073	rice	217	446
LYM109	maize|gb164|CD984002	maize	218	447
LYM112	maize|gb164|CF038223	maize	219	448
LYM116	maize|gb164|AI964572	maize	220	354
LYM117	maize|gb164|AI739834	maize	221	449
LYM154	barley|gb157.3|AV836282	barley	222	450
LYM155	barley|gb157.3|BE412535	barley	223	451
LYM180	barley|gb157.3|AJ476822	barley	224	452
LYM181	barley|gb157.3|AL450622	barley	225	453
LYM184	barley|gb157.3|AV833284	barley	226	454
LYM185	barley|gb157.3|AV833969	barley	227	455
LYM186	barley|gb157.3|AV834971	barley	228	370
LYM188	barley|gb157.3|BE438660	barley	229	456
LYM189	barley|gb157.3|BF256192	barley	230	457

Gene Name	*Cluster Name*	*Organism*	*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
LYM192	barley|gb157.3|BF627356	barley	231	458
LYM193	barley|gb157.3|CB858276	barley	232	459
LYM194	barley|gb157.3|CB860975	barley	233	460
LYM219	maize|gb164|BE238495	maize	234	389
LYM221	maize|gb164|BI502603	maize	235	461
LYM228	maize|gb164|EC892599	maize	236	462
LYM250	rice|gb157.3|CA759158	rice	237	463
LYM183	barley|gb157.3|AL509795	barley	238	464
LYM272	rice|gb157.2|CA761620	rice	239	465

Table 1: Provided are the identified genes, their annotation, organism and polynucleotide and polypeptide sequence identifiers.

EXAMPLE 2

IDENTIFICATION OF HOMOLOGOUS SEQUENCES THAT INCREASE YIELD, FIBER YIELD, FIBER QUALITY, GROWTH RATE, BIOMASS, OIL CONTENT, VIGOR, ABST, AND/OR NUE 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 identify putative orthologs of the genes affecting plant yield, oil yield, oil content, seed yield, growth rate, vigor, biomass, abiotic stress tolerance and/or nitrogen use efficiency, 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 the construction of 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.

The search and identification of homologous genes involves the screening of sequence information available, for example, in public databases such as 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 (ortholog) 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 can be 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.

Table 2, hereinbelow, lists a summary of orthologous and homologous sequences of the polynucleotide sequences (SEQ ID NOs:1-239) and polypeptide sequences (SEQ ID NOs:240-465) presented in Table 1 above, which were identified from the databases using the NCBI BLAST software (e.g., using the Blastp and tBlastn algorithms) and needle (EMBOSS package) as being at least 80% homologous to the selected polynucleotides and polypeptides, and which are expected to increase plant yield, seed yield, oil yield, oil content, growth rate, fiber yield, fiber quality, biomass, vigor, ABST and/or NUE of a plant.

Table 2

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

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
467	LYM2 H5	brachypodium|09v1|DV480246	1974	241	89.1	blastp
468	LYM2 H6	maize|gb170|AW224918	1975	241	86.6	blastp
469	LYM2 H7	millet|09v1|EVO454PM002089	1976	241	87.6	blastp
470	LYM2 H8	sorghum|09v1|SB07G004285	1977	241	86.6	blastp
471	LYM2 H4	switchgrass|gb167|FE606998	1978	241	89.9	blastp
472	LYM2 H5	wheat|gb164|BM136811	1979	241	80.53	tblastn
473	LYM4 H6	barley|gb157SOLEXA|BE438934	1980	243	81.5	blastp
474	LYM4 H7	brachypodium|09v1|DV469575	1981	243	81.5	blastp
475	LYM4 H2	cenchrus|gb166|BM084020	1982	243	83	blastp
476	LYM4 H8	maize|gb170|AI600994	1983	243	82.2	blastp
477	LYM4 H9	maize|gb170|AW054478	1984	243	82.4	blastp
478	LYM4 H10	rice|gb170|OS05G13950	1985	243	94.7	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
479	LYM4 H11	sorghum|09v1|SB03G000920	1986	243	83.2	blastp
480	LYM4 H5	switchgrass|gb167|FL703533	1987	243	83	blastp
481	LYM4 H6	wheat|gb164|BE444991	1988	243	81.3	blastp
482	LYM5 H16	barley|gb157SOLEXA|BI953887	1989	244	90.9	blastp
483	LYM5 H17	brachypodium|09v1|DV474010	1990	244	91.3	blastp
484	LYM5 H3	cenchrus|gb166|EB655978	1991	244	88.19	tblastn
485	LYM5 H4	fescue|gb161|DT688132	1992	244	85.8	blastp
486	LYM5 H5	leymus|gb166|EG394968	1993	244	90.9	blastp
487	LYM5 H18	maize|gb170|AI783290	1994	244	92.1	blastp
488	LYM5 H19	maize|gb170|BG265158	1995	244	92.5	blastp
489	LYM5 H20	rice|gb170|OS02G46660	1996	244	87.8	blastp
490	LYM5 H21	sorghum|09v1|SB04G031180	1997	244	80.3	blastp
491	LYM5 H22	sorghum|09v1|SB06G027060	1998	244	90.9	blastp
492	LYM5 H23	sugarcane|gb157.3|CA118359	1999	244	91.7	blastp
493	LYM5 H12	switchgrass|gb167|FE641223	2000	244	93.3	blastp
494	LYM5 H13	switchgrass|gb167|FL708642	2001	244	92.5	blastp
495	LYM5 H14	wheat|gb164|BE414733	2002	244	90.6	blastp
496	LYM5 H15	wheat|gb164|BE431026	2003	244	91.3	blastp
497	LYM5 H16	wheat|gb164|CA613380	2004	244	90.9	blastp
498	LYM7 H35	b oleracea|gb161|AM057184	2005	246	81.2	blastp
499	LYM7 H36	barley|gb157SOLEXA|BE413128	2006	246	82.6	blastp
500	LYM7 H37	barley|gb157SOLEXA|BF627706	2007	246	95.7	blastp
501	LYM7 H38	brachypodium|09v1|DV468966	2008	246	94.2	blastp
502	LYM7 H39	brachypodium|09v1|DV474806	2009	246	82.6	blastp
503	LYM7 H6	bruguiera|gb166|BP945554	2010	246	81.2	blastp
504	LYM7 H40	canola|gb161|CD811653	2011	246	81.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
505	LYM7 H41	canola|gb161|CD838423	2012	246	81.2	blastp
506	LYM7 H42	cassava|09v1|CK652348	2013	246	82.6	blastp
507	LYM7 H43	castorbean|09v1|XM002532394	2014	246	82.6	blastp
508	LYM7 H44	cucumber|09v1|AM717859	2015	246	82.6	blastp
509	LYM7 H9	eucalyptus|gb166|CB967858	2016	246	81.2	blastp
510	LYM7 H10	kiwi|gb166|FG431017	2017	246	81.2	blastp
511	LYM7 H11	kiwi|gb166|FG521634	2018	246	82.6	blastp
512	LYM7 H12	liriodendron|gb166|FD494835	2019	246	82.6	blastp
513	LYM7 H45	maize|gb170|AI943908	2020	246	82.6	blastp
514	LYM7 H46	maize|gb170|AW282244	2021	246	88.4	blastp
515	LYM7 H47	maize|gb170|LLAI855232	2022	246	82.61	tblastn
516	LYM7 H48	maize|gb170|LLDN209190	2023	246	82.61	tblastn
517	LYM7 H49	millet|09v1|EVO454PM003641	2024	246	91.3	blastp
518	LYM7 H50	millet|09v1|EVO454PM019125	2025	246	81.2	blastp
519	LYM7 H16	oat|gb164|CN817490	2026	246	88.4	blastp
520	LYM7 H17	oat|gb164|CN819643	2027	246	82.6	blastp
521	LYM7 H51	poplar|gb170|BI069446	2028	246	81.2	blastp
522	LYD97 H18	poplar|gb170|BI123662	2029	246	81.2	blastp
523	LYM7 H20	rye|gb164|BE496021	2030	246	94.2	blastp
524	LYM7 H21	rye|gb164|BE587226	2031	246	81.2	blastp
525	LYM7 H52	sorghum|09v1|SB05G003875	2032	246	88.4	blastp
526	LYM7 H53	sugarcane|gb157.3|CA079082	2033	246	89.9	blastp
527	LYM7 H54	sugarcane|gb157.3|CA158782	2034	246	81.2	blastp
528	LYM7 H25	switchgrass|gb167|DN149707	2035	246	82.6	blastp
529	LYM7 H26	switchgrass|gb167|FE644021	2036	246	84.1	blastp
530	LYM7 H27	switchgrass|gb167|FE657215	2037	246	80	blastp
531	LYM7 H28	switchgrass|gb167|FE658413	2038	246	88.4	blastp
532	LYM7 H29	switchgrass|gb167|FL689692	2039	246	88.4	blastp
533	LYM7 H30	wheat|gb164|BE404350	2040	246	81.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
534	LYM7 H31	wheat|gb164|BE414371	2041	246	84.1	blastp
535	LYM7 H32	wheat|gb164|BE430017	2042	246	94.2	blastp
536	LYM7 H33	wheat|gb164|BE444058	2043	246	95.7	blastp
537	LYM7 H34	wheat|gb164|BE444789	2044	246	82.6	blastp
538	LYM7 H35	wheat|gb164|CA598363	2045	246	95.7	blastp
539	LYM8 H7	arabidopsis lyrata|09v1|JGIAL008627	2046	247	80.2	blastp
540	LYM8 H8	arabidopsis lyrata|09v1|JGIAL021400	2047	247	83.3	blastp
541	LYM8 H1	arabidopsis|gb165|AT3G03110	2048	247	80.6	blastp
542	LYM8 H2	arabidopsis|gb165|AT5G17020	2049	247	82.9	blastp
543	LYM8 H9	brachypodium|09v1|GT774368	2050	247	95.6	blastp
544	LYM8 H10	castorbean|09v1|EE255045	2051	247	84.2	blastp
545	LYM8 H11	chestnut|gb170|SRR006295S0059698	2052	247	85.7	blastp
546	LYM8 H12	cucumber|09v1|GD174631	2053	247	84.5	blastp
547	LYM8 H13	lotus|09v1|BP043858	2054	247	83.8	blastp
548	LYM8 H14	lotus|09v1|BP071708	2055	247	83.6	blastp
549	LYM8 H15	maize|gb170|AA030709	2056	247	92.1	blastp
550	LYM8 H16	maize|gb170|AI621522	2057	247	92.2	blastp
551	LYM8 H17	medicago|09v1|BE205102	2058	247	83.5	blastp
552	LYM8 H18	medicago|09v1|BM779128	2059	247	83.9	blastp
553	LYM8 H19	poplar|gb170|BI127444	2060	247	84.8	blastp
554	LYM8 H20	poplar|gb170|BU837911	2061	247	85	blastp
555	LYM8 H21	rice|gb170|OS03G64080	2062	247	99.72	tblastn
556	LYM8 H22	solanum phureja|09v1|SPHBG128228	2063	247	83.2	blastp
557	LYM8 H23	sorghum|09v1|SB01G000490	2064	247	93.9	blastp
558	LYM8 H24	sorghum|09v1|SB02G009800	2065	247	89	blastp
559	LYM8 H6	soybean|gb168|BE205102	2066	247	82.98	tblastn

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
560	LYM8 H7	soybean|gb168|BE823809	2067	247	81.6	blastp
561	LYM8 H25	tomato|09v1|BG128228	2068	247	83.33	tblastn
562	LYM9 H0	lolium|09v1|AU245599	2069	248	80.1	blastp
563	LYM10 H1	antirrhinum|gb166|AJ786992	2070	249	89.9	blastp
564	LYM10 H207	apple|gb171|CN443929	2071	249	91.3	blastp
565	LYM10 H208	apple|gb171|CN489763	2072	249	91.3	blastp
566	LYM10 H209	apple|gb171|CN874192	2073	249	87	blastp
567	LYM10 H210	arabidopsis lyrata|09v1|JGIAL017989	2074	249	85.5	blastp
568	LYM10 H211	arabidopsis lyrata|09v1|JGIAL025614	2075	249	91.3	blastp
569	LYM10 H212	arabidopsis lyrata|09v1|JGIAL029470	2076	249	91.3	blastp
570	LYM10 H7	arabidopsis|gb165|AT3G48570	2077	249	85.5	blastp
571	LYM10 H8	arabidopsis|gb165|AT4G24920	2078	249	91.3	blastp
572	LYM10 H9	arabidopsis|gb165|AT5G50460	2079	249	91.3	blastp
573	LYM10 H10	artemisia|gb164|EX980216	2080	249	88.4	blastp
574	LYM10 H11	b juncea|gb164|EVGN00323614690486	2081	249	85.5	blastp
575	LYM10 H12	b juncea|gb164|EVGN00357611620134	2082	249	81.16	tblastn
576	LYM10 H13	b juncea|gb164|EVGN00407015981886	2083	249	91.3	blastp
577	LYM10 H14	b juncea|gb164|EVGN01046711722157	2084	249	91.3	blastp
578	LYM10 H15	b juncea|gb164|EVGN01350404310247	2085	249	91.3	tblastn
579	LYM10 H16	b juncea|gb164|EVGN01826229072660	2086	249	91.3	blastp
580	LYM10 H17	b juncea|gb164|EVGN10412810992898	2087	249	86.3	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
581	LYM10 H18	b juncea|gb164|EVGN19578802581818	2088	249	81.2	blastp
582	LYM10 H19	b oleracea|gb161|AM059639	2089	249	91.3	blastp
583	LYM10 H20	b oleracea|gb161|EH414574	2090	249	91.3	blastp
584	LYM10 H21	b oleracea|gb161|EH427198	2091	249	81.7	blastp
585	LYM10 H22	b rapa|gb162|BG544908	2092	249	91.3	blastp
586	LYM10 H23	b rapa|gb162|DY010003	2093	249	91.3	blastp
587	LYM10 H24	b rapa|gb162|EE524434	2094	249	91.3	tblastn
588	LYM10 H25	b rapa|gb162|L35825	2095	249	91.3	blastp
589	LYM10 H26	banana|gb167|DN239748	2096	249	94.2	blastp
590	LYM10 H27	banana|gb167|ES432517	2097	249	95.7	blastp
591	LYM10 H28	banana|gb167|FL649789	2098	249	95.7	blastp
592	LYM10 H29	banana|gb167|FL658161	2099	249	94.2	blastp
593	LYM10 H213	barley|gb157SOLEXA|AJ433765	2100	249	100	blastp
594	LYM10 H214	barley|gb157SOLEXA|BE412470	2101	249	100	blastp
595	LYM10 H215	barley|gb157SOLEXA|BF254576	2102	249	98.6	blastp
596	LYM10 H216	barley|gb157SOLEXA|BF257015	2103	249	100	blastp
597	LYM10 H34	bean|gb167|CA907476	2104	249	92.75	tblastn
598	LYM10 H35	bean|gb167|CA907483	2105	249	94.2	blastp
599	LYM10 H217	beech|gb170|SRR006293S0011456	2106	249	92.8	blastp
600	LYM10 H218	beech|gb170|SRR006294S0008365	2107	249	88.4	blastp
601	LYM10 H219	brachypodium|09v1|DV469126	2108	249	100	blastp
602	LYM10 H220	brachypodium|09v1|GT803631	2109	249	92.8	blastp
603	LYM10 H38	bruguiera|gb166|BP941922	2110	249	95.7	blastp
604	LYM10 H39	bruguiera|gb166|BP944773	2111	249	95.7	blastp
605	LYM10 H40	cacao|gb167|CU471529	2112	249	94.2	blastp

Nucl. SEQ ID NO:	***Gene Name***	***cluster name***	***Polyp. SEQ ID NO:***	***Homolog. to SEQ ID NO:***	***% global identity***	***Algor.***
606	LYM10 H41	cacao|gb167|CU480597	2113	249	84.1	blastp
607	LYM10 H42	cacao|gb167|CU493298	2114	249	89.9	blastp
608	LYM10 H43	canola|gb161|CD813231	2115	249	91.3	tblastn
609	LYM10 H44	canola|gb161|CD817528	2116	249	91.3	tblastn
610	LYM10 H45	canola|gb161|CD820075	2117	249	91.3	tblastn
611	LYM10 H46	canola|gb161|CD824239	2118	249	91.3	tblastn
612	LYM10 H47	canola|gb161|CD838062	2119	249	86.3	blastp
613	LYM10 H48	canola|gb161|CD840808	2120	249	91.3	blastp
614	LYM10 H49	canola|gb161|CN732434	2121	249	91.3	tblastn
615	LYM10 H50	canola|gb161|DW999288	2122	249	91.3	blastp
616	LYM10 H51	canola|gb161|EE434176	2123	249	84.1	blastp
617	LYM10 H52	canola|gb161|EE464036	2124	249	87	blastp
618	LYM10 H221	cassava|09v1|CK642225	2125	249	94.2	blastp
619	LYM10 H222	cassava|09v1|DV455717	2126	249	94.2	blastp
620	LYM10 H223	cassava|09v1|FF380389	2127	249	94.2	blastp
621	LYM10 H224	castorbean|09v1|EG664279	2128	249	92.8	blastp
622	LYM10 H225	castorbean|09v1|XM002509459	2129	249	91.3	blastp
623	LYM10 H58	catharanthus|gb166|EG560643	2130	249	91.3	blastp
624	LYM10 H59	catharanthus|gb166|FD416462	2131	249	91.3	blastp
625	LYM10 H60	catharanthus|gb166|FD420164	2132	249	92.8	blastp
626	LYM10 H61	centaurea|gb166|EH747070	2133	249	87	blastp
627	LYM10 H62	centaurea|gb166|EH788831	2134	249	89.9	blastp
628	LYM10 H226	chestnut|gb170|SRR006295S0002470	2135	249	95.7	blastp
629	LYM10 H227	chestnut|gb170|SRR006295S0013318	2136	249	92.8	blastp
630	LYM10 H228	cichorium|gb171|FL673304	2137	249	85.51	tblastn
631	LYM10 H63	citrus|gb166|CF417520	2138	249	91.3	blastp
632	LYM10 H64	coffea|gb157.2|DV666460	2139	249	91.3	blastp

Nucl. SEQ ID NO:	***Gene Name***	***cluster name***	***Polyp. SEQ ID NO:***	***Homolog. to SEQ ID NO:***	***% global identity***	***Algor.***
633	LYM10H65	coffea|gb157.2|DV676797	2140	249	89.86	tblastn
634	LYM10H66	cotton|gb164|BE052198	2141	249	94.2	blastp
635	LYM10H67	cotton|gb164|BQ404833	2142	249	95.7	blastp
636	LYM10H68	cotton|gb164|BQ407407	2143	249	92.8	blastp
637	LYM10H69	cotton|gb164|CK640593	2144	249	95.7	blastp
638	LYM10H70	cotton|gb164|DT052759	2145	249	88	blastp
639	LYM10H71	cotton|gb164|DT574061	2146	249	80.7	blastp
640	LYM10H72	cowpea|gb166|FF386543	2147	249	94.2	blastp
641	LYM10H73	cowpea|gb166|FF389357	2148	249	94.2	tblastn
642	LYM10H74	cryptomeria|gb166|BP174192	2149	249	89.9	blastp
643	LYM10H75	cryptomeria|gb166|BP174931	2150	249	88.6	blastp
644	LYM10H229	cucumber|09v1|AM715093	2151	249	88.41	tblastn
645	LYM10H230	cucumber|09v1|AM720495	2152	249	98.6	blastp
646	LYM10H231	cucumber|09v1|DN909507	2153	249	95.7	blastp
647	LYM10H76	cycas|gb166|CB091499	2154	249	88.4	blastp
648	LYM10H77	cynara|gb167|GE589284	2155	249	88.4	blastp
649	LYM10H78	dandelion|gb161|DY811008	2156	249	88.41	tblastn
650	LYM10H79	dandelion|gb161|DY839599	2157	249	89.86	tblastn
651	LYM10H80	eucalyptus|gb166|CD669252	2158	249	92.8	blastp
652	LYM10H232	fern|gb171|DK961389	2159	249	88.4	blastp
653	LYM10H81	fescue|gb161|DT702292	2160	249	100	tblastn
654	LYM10H82	fescue|gb161|DT704458	2161	249	100	tblastn
655	LYM10H233	flax|09v1|EU829193	2162	249	92.8	blastp
656	LYM10H234	gerbera|09v1|AJ761193	2163	249	89.9	blastp
657	LYM10H235	gerbera|09v1|AJ765913	2164	249	84.1	blastp
658	LYM10H83	ginger|gb164|DY368424	2165	249	95.65	tblastn
659	LYM10H84	ginger|gb164|DY382125	2166	249	94.2	blastp

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660	LYM10H85	grape|gb160|BQ793552	2167	249	91.3	blastp
661	LYM10H86	grape|gb160|CA809997	2168	249	91.3	blastp
662	LYM10H87	iceplant|gb164|AI943423	2169	249	88.4	blastp
663	LYM10H88	ipomoea|gb157.2|BJ553479	2170	249	89.86	tblastn
664	LYM10H89	ipomoea|gb157.2|CB329955	2171	249	88.41	tblastn
665	LYM10H90	ipomoea|gb157.2|CJ751960	2172	249	88.4	blastp
666	LYM10H236	jatropha|09v1|GO247649	2173	249	94.2	blastp
667	LYM10H91	kiwi|gb166|FG397070	2174	249	89.9	blastp
668	LYM10H92	kiwi|gb166|FG477805	2175	249	95.7	blastp
669	LYM10H93	lettuce|gb157.2|DW047717	2176	249	88.4	blastp
670	LYM10H94	lettuce|gb157.2|DW051281	2177	249	89.9	blastp
671	LYM10H95	lettuce|gb157.2|DW080235	2178	249	82.61	tblastn
672	LYM10H96	lettuce|gb157.2|DW101958	2179	249	88.4	blastp
673	LYM10H97	lettuce|gb157.2|DW123456	2180	249	88.41	tblastn
674	LYM10H237	liquorice|gb171|FS242287	2181	249	94.2	blastp
675	LYM10H98	liriodendron|gb166|FD495465	2182	249	95.7	blastp
676	LYM10H99	liriodendron|gb166|FD500844	2183	249	94.2	blastp
677	LYM10H238	lolium|09v1|AU247819	2184	249	98.6	blastp
678	LYM10H239	lotus|09v1|CB827059	2185	249	92.8	blastp
679	LYM10H240	lotus|09v1|DN652280	2186	249	89.9	blastp
680	LYM10H102	lovegrass|gb167|DN482980	2187	249	98.6	blastp
681	LYM10H241	maize|gb170|AI001340	2188	249	97.1	blastp
682	LYM10H242	maize|gb170|AI665512	2189	249	98.6	blastp
683	LYM10H243	maize|gb170|AI677195	2190	249	97.1	blastp
684	LYM10H244	maize|gb170|LLAI619401	2191	249	97.1	blastp
685	LYM10H245	maize|gb170|LLCF003156	2192	249	81.16	tblastn
686	LYM10H246	maize|gb170|LLDQ245943	2193	249	98.6	blastp

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687	LYM10 H247	maize|gb170|W21637	2194	249	98.6	blastp
688	LYM10 H109	marchantia|gb166|BJ844102	2195	249	87	blastp
689	LYM10 H248	medicago|09v1|AA660461	2196	249	94.2	blastp
690	LYM10 H249	medicago|09v1|AW287868	2197	249	94.2	blastp
691	LYM10 H250	medicago|09v1|LLBQ138650	2198	249	85.5	blastp
692	LYM10 H112	melon|gb165|AM715093	2199	249	94.2	tblastn
693	LYM10 H113	melon|gb165|AM720495	2200	249	98.55	tblastn
694	LYM10 H114	melon|gb165|DV631710	2201	249	95.7	blastp
695	LYM10 H251	millet|09v1|CD724432	2202	249	98.6	blastp
696	LYM10 H252	monkeyflower|09v1|DV208117	2203	249	91.3	blastp
697	LYM10 H116	nuphar|gb166|CD472502	2204	249	97.1	blastp
698	LYM10 H253	oak|gb170|SRR006307S0013335	2205	249	94.2	blastp
699	LYM10 H254	oak|gb170|SRR006307S0023745	2206	249	92.75	tblastn
700	LYM10 H117	oil palm|gb166|EL684180	2207	249	92.8	blastp
701	LYM10 H118	onion|gb162|BQ580148	2208	249	97.1	blastp
702	LYM10 H119	papaya|gb165|EX279251	2209	249	89.9	blastp
703	LYM10 H255	peanut|gb171|EE124530	2210	249	94.2	blastp
704	LYM10 H256	peanut|gb171|EE126680	2211	249	94.2	blastp
705	LYM10 H257	peanut|gb171|EG028825	2212	249	81.2	blastp
706	LYM10 H258	peanut|gb171|EG373993	2213	249	94.2	blastp
707	LYM10 H259	pepper|gb171|CA516679	2214	249	91.3	blastp
708	LYM10 H260	pepper|gb171|GD053770	2215	249	89.9	blastp
709	LYM10 H261	petunia|gb171|AF049933	2216	249	87	blastp
710	LYM10 H262	petunia|gb171|EB174381	2217	249	87	blastp
711	LYM10 H263	physcomitrella|10v1|AW145358	2218	249	81.2	blastp
712	LYM10 H264	physcomitrella|10v1|BG361572	2219	249	81.2	blastp
713	LYM10 H133	pine|gb157.2|AL750813	2220	249	91.3	blastp

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714	LYM10H134	pine|gb157.2|AW064895	2221	249	91.3	blastp
715	LYM10H135	pine|gb157.2|AW226488	2222	249	89.9	blastp
716	LYM10H265	poplar|gb170|BI127745	2223	249	92.8	blastp
717	LYM10H266	poplar|gb170|BU824190	2224	249	92.8	blastp
718	LYM10H267	poplar|gb170|BU862632	2225	249	92.8	blastp
719	LYM10H139	poppy|gb166|FE965009	2226	249	88.4	blastp
720	LYM10H140	poppy|gb166|FE966430	2227	249	92.8	blastp
721	LYM10H141	potato|gb157.2|BG350890	2228	249	91.3	blastp
722	LYM10H142	potato|gb157.2|BG589211	2229	249	89.86	tblastn
723	LYM10H143	potato|gb157.2|BG592598	2230	249	89.86	tblastn
724	LYM10H144	potato|gb157.2|BQ516058	2231	249	91.3	blastp
725	LYM10H145	prunus|gb167|BU039566	2232	249	92.8	blastp
726	LYM10H146	prunus|gb167|BU046783	2233	249	87	blastp
727	LYM10H147	radish|gb164|EV526354	2234	249	91.3	tblastn
728	LYM10H148	radish|gb164|EV528390	2235	249	91.3	blastp
729	LYM10H149	radish|gb164|EV536273	2236	249	91.3	blastp
730	LYM10H150	radish|gb164|EV545751	2237	249	91.3	tblastn
731	LYM10H151	radish|gb164|EV548721	2238	249	91.3	blastp
732	LYM10H152	radish|gb164|EV550488	2239	249	91.3	blastp
733	LYM10H153	radish|gb164|EV567397	2240	249	85.5	blastp
734	LYM10H154	radish|gb164|EW713425	2241	249	89.9	blastp
735	LYM10H155	radish|gb164|FD570559	2242	249	89.9	blastp
736	LYM10H268	rice|gb170|OS06G44374	2243	249	95.7	blastp
737	LYM10H157	rose|gb157.2|BI978198	2244	249	91.3	tblastn
738	LYM10H158	rose|gb157.2|EC589842	2245	249	92.75	tblastn
739	LYM10H159	safflower|gb162|EL393855	2246	249	88.41	tblastn
740	LYM10H160	safflower|gb162|EL511136	2247	249	89.9	blastp

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741	LYM10H269	senecio|gb170|CO553399	2248	249	88.4	blastp
742	LYM10H161	sesame|gb157.2|BU669069	2249	249	91.3	tblastn
743	LYM10H270	solanum phureja|09v1|SPHAI483617	2250	249	89.9	blastp
744	LYM10H271	solanum phureja|09v1|SPHBG127130	2251	249	91.3	blastp
745	LYM10H272	sorghum|09v1|SB04G005280	2252	249	98.6	blastp
746	LYM10H273	sorghum|09v1|SB10G026000	2253	249	97.1	blastp
747	LYM10H164	soybean|gb168|AA660461	2254	249	94.2	blastp
748	LYM10H165	soybean|gb168|AW472512	2255	249	92.8	blastp
749	LYM10H166	soybean|gb168|BU544187	2256	249	94.2	blastp
750	LYM10H167	spikemoss|gb165|DN838422	2257	249	85.51	tblastn
751	LYM10H168	spruce|gb162|CO216979	2258	249	91.3	blastp
752	LYM10H169	spruce|gb162|CO217020	2259	249	91.3	blastp
753	LYM10H170	spurge|gb161|DV112655	2260	249	84.1	blastp
754	LYM10H171	spurge|gb161|DV120263	2261	249	86.5	blastp
755	LYM10H172	strawberry|gb164|CO380171	2262	249	91.3	tblastn
756	LYM10H173	strawberry|gb164|EX664646	2263	249	92.8	blastp
757	LYM10H274	sugarcane|gb157.3|CA072778	2264	249	97.1	blastp
758	LYM10H275	sugarcane|gb157.3|CA087927	2265	249	98.6	blastp
759	LYM10H276	sugarcane|gb157.3|CA103056	2266	249	98.6	blastp
760	LYM10H177	sunflower|gb162|BU015373	2267	249	89.86	tblastn
761	LYM10H178	sunflower|gb162|CD849625	2268	249	88.4	blastp
762	LYM10H179	sunflower|gb162|CD851122	2269	249	88.41	tblastn
763	LYM10H180	switchgrass|gb167|DN145554	2270	249	98.6	blastp
764	LYM10H181	switchgrass|gb167|FE633347	2271	249	97.1	blastp
765	LYM10H182	switchgrass|gb167|FE639131	2272	249	98.6	blastp
766	LYM10H183	switchgrass|gb167|FL720694	2273	249	95.7	blastp

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767	LYM10 H184	tamarix|gb166|EG968743	2274	249	85.5	blastp
768	LYM10 H185	tamarix|gb166|EG969152	2275	249	88.4	blastp
769	LYM10 H277	tea|gb171|FF682807	2276	249	95.7	blastp
770	LYM10 H186	thellungiella|gb167|BI698898	2277	249	91.3	blastp
771	LYM10 H187	thellungiella|gb167|EC599088	2278	249	91.3	blastp
772	LYM10 H188	tobacco|gb162|CV020564	2279	249	81.8	blastp
773	LYM10 H189	tobacco|gb162|CV021149	2280	249	80.8	blastp
774	LYM10 H190	tobacco|gb162|CV021577	2281	249	91.3	tblastn
775	LYM10 H191	tobacco|gb162|EB426093	2282	249	91.3	tblastn
776	LYM10 H192	tobacco|gb162|EB447225	2283	249	89.9	blastp
777	LYM10 H278	tomato|09v1|AI483617	2284	249	89.9	blastp
778	LYM10 H279	tomato|09v1|BG127130	2285	249	91.3	tblastn
779	LYM10 H195	triphysaria|gb164|EX988147	2286	249	81.6	blastp
780	LYM10 H196	walnuts|gb166|CB304079	2287	249	98.6	blastp
781	LYM10 H197	wheat|gb164|BE423226	2288	249	100	tblastn
782	LYM10 H198	wheat|gb164|BE423858	2289	249	100	tblastn
783	LYM10 H199	wheat|gb164|BE445139	2290	249	98.55	tblastn
784	LYM10 H200	wheat|gb164|BE604834	2291	249	98.55	tblastn
785	LYM10 H201	wheat|gb164|BF473482	2292	249	100	tblastn
786	LYM10 H202	wheat|gb164|BF474814	2293	249	98.55	tblastn
787	LYM10 H203	wheat|gb164|BI479895	2294	249	98.55	tblastn
788	LYM10 H204	wheat|gb164|CA619357	2295	249	86.96	tblastn
789	LYM10 H205	wheat|gb164|CA619965	2296	249	91.3	tblastn
790	LYM10 H206	wheat|gb164|CA627315	2297	249	83.8	blastp
791	LYM10 H207	wheat|gb164|DR737205	2298	249	85.51	tblastn
792	LYM13 H3	brachypodium|09v1|GT794488	2299	251	80.6	blastp
793	LYM13 H4	maize|gb170|T12684	2300	251	84.5	blastp

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794	LYM13 H5	sorghum|09v1|SB01G049950	2301	251	84.5	blastp
795	LYM13 H3	switchgrass|gb167|FE634401	2302	251	84.53	tblastn
796	LYM14 H1	aquilegia|gb157.3|DR927713	2303	252	81.1	blastp
797	LYM14 H31	arabidopsis lyrata|09v1|JGIAL009556	2304	252	80.7	blastp
798	LYM14 H32	arabidopsis lyrata|09v1|JGIAL020254	2305	252	80.4	blastp
799	LYM14 H2	arabidopsis|gb165|AT3G11320	2306	252	80.4	blastp
800	LYM14 H3	arabidopsis|gb165|AT5G05820	2307	252	80.4	blastp
801	LYM14 H4	artemisia|gb164|EY034514	2308	252	81.7	blastp
802	LYM14 H33	brachypodium|09v1|GT762844	2309	252	96	blastp
803	LYM14 H7	canola|gb161|DY024685	2310	252	81.1	blastp
804	LYM14 H34	cassava|09v1|CK650018	2311	252	80.1	blastp
805	LYM14 H35	castorbean|09v1|EG659029	2312	252	80.43	tblastn
806	LYM14 H8	centaurea|gb166|EH712821	2313	252	80.1	blastp
807	LYM14 H36	cichorium|gb171|EH688253	2314	252	80.7	blastp
808	LYM14 H11	cotton|gb164|AA659984	2315	252	80.43	tblastn
809	LYM14 H37	cucumber|09v1|DN910737	2316	252	80.75	tblastn
810	LYM14 H12	ginger|gb164|DY358976	2317	252	83.3	blastp
811	LYM14 H13	iceplant|gb164|AI822835	2318	252	80.75	tblastn
812	LYM14 H14	lettuce|gb157.2|DW158376	2319	252	82.3	tblastn
813	LYM14 H15	leymus|gb166|CD809180	2320	252	95	blastp
814	LYM14 H38	maize|gb170|AI783260	2321	252	93.8	blastp
815	LYM14 H39	maize|gb170|AI941675	2322	252	95.1	blastp
816	LYM14 H18	melon|gb165|AM713763	2323	252	80.5	tblastn
817	LYM14 H40	monkeyflower|09v1|GO959633	2324	252	80.12	tblastn
818	LYM14 H41	monkeyflower|09v1|GR111000	2325	252	80.12	tblastn
819	LYM14 H19	papaya|gb165|EX261125	2326	252	81.1	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
820	LYM14 H20	radish|gb164|EW723681	2327	252	81.37	tblastn
821	LYM14 H42	solanum phureja|09v1|SPHBG628013	2328	252	80.1	blastp
822	LYM14 H43	sorghum|09v1|SB01G038730	2329	252	96	blastp
823	LYM14 H44	sorghum|09v1|SB02G044050	2330	252	86	blastp
824	LYM14 H23	soybean|gb168|AW560935	2331	252	80.1	blastp
825	LYM14 H25	spikemoss|gb165|FE434307	2332	252	81.06	tblastn
826	LYM14 H45	sugarcane|gb157.3|CA079818	2333	252	84.2	blastp
827	LYM14 H46	sugarcane|gb157.3|CA150518	2334	252	93.85	tblastn
828	LYM14 H29	sunflower|gb162|EL484937	2335	252	80.75	tblastn
829	LYM14 H30	switchgrass|gb167|DN143407	2336	252	95.4	blastp
830	LYM14 H47	tomato|09v1|BG628013	2337	252	80.1	blastp
831	LYM14 H31	wheat|gb164|BE416003	2338	252	83.6	blastp
832	LYM15 H4	brachypodium|09v1|DV476162	2339	253	80.2	blastp
833	LYM15 H2	pseudoroegneria|gb167|FF343970	2340	253	82	blastp
834	LYM15 H3	wheat|gb164|BE213295	2341	253	81.4	blastp
835	LYM15 H4	wheat|gb164|BE496833	2342	253	81.4	blastp
836	LYM16 H9	barley|gb157SOLEXA|BE421507	2343	254	90.9	blastp
837	LYM16 H10	brachypodium|09v1|DV475217	2344	254	92.7	blastp
838	LYM16 H3	fescue|gb161|DT691110	2345	254	93.9	blastp
839	LYM16 H11	lolium|09v1|AU246876	2346	254	84.1	blastp
840	LYD199	maize|gb170|BI423687	2347	254	82.9	blastp
841	LYM16 H12	maize|gb170|LLFL254633	2348	254	81.1	tblastn
842	LYM16 H5	pseudoroegneria|gb167|FF355494	2349	254	92.1	blastp
843	LYM16 H6	rye|gb164|BE494944	2350	254	90.24	tblastn
844	LYM16 H7	wheat|gb164|BE216981	2351	254	91.5	blastp
845	LYM16 H8	wheat|gb164|BE416071	2352	254	90.9	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
846	LYM16 H9	wheat|gb164|BE418113	2353	254	91.5	blastp
847	LYM17 H6	barley|gb157SOLEXA|BE602651	2354	255	83.3	blastp
848	LYM17 H7	sugarcane|gb157.3|CA152022	2355	255	80.3	blastp
849	LYM17 H3	wheat|gb164|BE406565	2356	255	85.6	blastp
850	LYM17 H4	wheat|gb164|BE429209	2357	255	85.6	blastp
851	LYM17 H5	wheat|gb164|BE490714	2358	255	86.4	blastp
852	LYM17 H6	wheat|gb164|BQ803198	2359	255	85.6	blastp
853	LYM19 H10	barley|gb157SOLEXA|AL506367	2360	256	86	blastp
854	LYM19 H11	brachypodium|09v1|DV476339	2361	256	87.2	blastp
855	LYM19 H3	leymus|gb166|EG387247	2362	256	84.8	blastp
856	LYM19 H5	pseudoroegneria|gb167|FF352256	2363	256	86.9	blastp
857	LYM19 H12	sorghum|09v1|SB05G009990	2364	256	82.6	blastp
858	LYM19 H7	switchgrass|gb167|FE603507	2365	256	83.6	blastp
859	LYM19 H8	wheat|gb164|BE398692	2366	256	82.7	blastp
860	LYM19 H9	wheat|gb164|BE585979	2367	256	86.28	tblastn
861	LYM19 H10	wheat|gb164|BU672325	2368	256	81.4	blastp
862	LYM20 H9	barley|gb157SOLEXA|AL450927	2369	257	86.3	blastp
863	LYM20 H10	brachypodium|09v1|DV479896	2370	257	89.1	blastp
864	LYM20 H11	castorbean|09v1|XM002519056	2371	257	80	blastp
865	LYM20 H12	maize|gb170|AI857236	2372	257	90.1	blastp
866	LYM20 H5	pseudoroegneria|gb167|FF343142	2373	257	89	blastp
867	LYM20 H13	sorghum|09v1|SB01G009140	2374	257	89.7	blastp
868	LYM20 H14	sugarcane|gb157.3|CA072511	2375	257	83.9	blastp
869	LYM20 H8	switchgrass|gb167|FE654910	2376	257	84.5	blastp
870	LYM20 H9	wheat|gb164|BE411982	2377	257	88.6	blastp
871	LYM21 H1	banana|gb167|FF557436	2378	258	80.9	blastp
872	LYM21 H2	banana|gb167|FF559448	2379	258	80.9	blastp

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873	LYM21 H27	barley|gb157SOLEXA|BE437461	2380	258	88.2	blastp
874	LYM21 H28	brachypodium|09v1|DV488150	2381	258	95.5	blastp
875	LYM21 H29	brachypodium|09v1|GT760558	2382	258	97.3	blastp
876	LYM21 H5	cenchrus|gb166|EB655115	2383	258	91.8	blastp
877	LYM21 H6	fescue|gb161|DT680631	2384	258	90	blastp
878	LYM21 H7	kiwi|gb166|FG405276	2385	258	81.8	blastp
879	LYM21 H8	leymus|gb166|CN465770	2386	258	88.2	blastp
880	LYM21 H30	lolium|09v1|AU250288	2387	258	90	blastp
881	LYM21 H9	lovegrass|gb167|DN480337	2388	258	92.7	blastp
882	LYM21 H31	maize|gb170|AI586459	2389	258	93.6	blastp
883	LYM21 H32	millet|09v1|EVO454PM000432	2390	258	95.5	blastp
884	LYM21 H33	millet|09v1|EVO454PM000947	2391	258	91.8	blastp
885	LYM21 H12	pineapple|gb157.2|CO731607	2392	258	82.73	tblastn
886	LYM21 H34	rice|gb170|OS02G47320	2393	258	87.27	tblastn
887	LYM21 H35	sorghum|09v1|SB02G006170	2394	258	93.6	blastp
888	LYM21 H36	sorghum|09v1|SB06G027500	2395	258	95.5	blastp
889	LYM21 H37	sugarcane|gb157.3|BQ529660	2396	258	93.6	blastp
890	LYM21 H38	sugarcane|gb157.3|BQ535381	2397	258	92.7	blastp
891	LYM21 H39	sugarcane|gb157.3|CA118830	2398	258	87.3	blastp
892	LYM21 H19	switchgrass|gb167|DN151016	2399	258	93.6	blastp
893	LYM21 H20	switchgrass|gb167|FL722429	2400	258	94.5	blastp
894	LYM21 H21	switchgrass|gb167|FL936988	2401	258	95.5	blastp
895	LYM21 H22	tobacco|gb162|AM791579	2402	258	88.2	blastp
896	LYM21 H23	wheat|gb164|BE352632	2403	258	89.1	blastp
897	LYM21 H24	wheat|gb164|BE402792	2404	258	89.1	blastp
898	LYM21 H25	wheat|gb164|BE492575	2405	258	89.09	tblastn
899	LYM21 H26	wheat|gb164|CA484575	2406	258	94.5	blastp

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900	LYM21 H27	wheat|gb164|CA616609	2407	258	92.73	tblastn
901	LYM24 H1	fescue|gb161|DT681171	2408	261	80.61	tblastn
902	LYM24 H2	leymus|gb166|CD808623	2409	261	80.5	blastp
903	LYM24 H8	maize|gb170|AI621440	2410	261	81	blastp
904	LYM24 H9	pseudoroegneria|gb167|FF349814	2411	261	80	blastp
905	LYM24 H10	sorghum|09v1|SB03G044280	2412	261	83.1	blastp
906	LYM24 H11	sugarcane|gb157.3|CA072633	2413	261	82.6	blastp
907	LYM24 H6	switchgrass|gb167|DN144637	2414	261	84.6	blastp
908	LYM24 H7	switchgrass|gb167|DN145452	2415	261	85.6	blastp
909	LYM24 H8	wheat|gb164|BE425900	2416	261	80	tblastn
910	LYM26 H1	wheat|gb164|BE398903	2417	262	88.6	blastp
911	LYM30 H5	brachypodium|09v1|SRR031799S0073966	2418	263	86.5	blastp
912	LYM30 H6	maize|gb170|AW520185	2419	263	85.8	blastp
913	LYM30 H7	maize|gb170|AW927689	2420	263	85	blastp
914	LYM30 H8	rice|gb170|OS11G02580	2421	263	99.2	blastp
915	LYM30 H9	rice|gb170|OS12G02510	2422	263	87.7	blastp
916	LYM30 H10	sorghum|09v1|SB05G001250	2423	263	86.1	blastp
917	LYM30 H5	switchgrass|gb167|FL796240	2424	263	80.16	tblastn
918	LYM31 H1	rice|gb170|OS12G02710	2425	264	97.9	blastp
919	LYM35 H5	brachypodium|09v1|SRR031798S0189278	2426	267	80	blastp
920	LYM35 H6	maize|gb170|BM416880	2427	267	89.7	blastp
921	LYM35 H7	sorghum|09v1|SB06G031730	2428	267	86.7	blastp
922	LYM35 H8	sugarcane|gb157.3|CA105471	2429	267	87.5	blastp
923	LYM35 H4	switchgrass|gb167|FL939819	2430	267	89.9	blastp
924	LYM35 H5	wheat|gb164|BE500504	2431	267	86.1	blastp
925	LYM42 H0	rice|gb170|OS01G41120	2432	273	96.7	blastp
925	LYM42 H0	rice|gb170|OS01G41120	2432	439	99.83	tblastn

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926	LYM43 H1	rice|gb170|OS12G02800	2433	274	91.4	blastp
927	LYM52 H1	b rapa|gb162|EX068270	2434	277	94.5	blastp
928	LYM52 H2	fescue|gb161|CK802823	2435	277	84.4	blastp
929	LYM52 H3	leymus|gb166|EG379466	2436	277	96.3	blastp
930	LYM52 H10	maize|gb170|BE130094	2437	277	80	blastp
931	LYM52 H11	maize|gb170|LLBE056010	2438	277	81	blastp
932	LYM52 H12	rice|gb170|OS04G51792	2439	277	81.4	blastp
933	LYM52 H13	sorghum|09v1|SB06G027870	2440	277	82.5	blastp
934	LYM52 H14	sugarcane|gb157.3|AA577629	2441	277	84.47	tblastn
935	LYM52 H8	switchgrass|gb167|DN147335	2442	277	82.65	tblastn
936	LYM52 H9	wheat|gb164|BG909259	2443	277	94.5	blastp
937	LYM52 H10	wheat|gb164|BG909493	2444	277	95.1	blastp
938	LYM56 H9	brachypodium|09v1|SRR031795S0049724	2445	279	85.9	blastp
939	LYM56 H10	maize|gb170|AI711954	2446	279	80.14	tblastn
940	LYM56 H2	pseudoroegneria|gb167|FF341776	2447	279	87.9	blastp
941	LYM56 H11	rice|gb170|OS03G45720	2448	279	80.1	blastp
942	LYM56 H12	sorghum|09v1|SB01G012840	2449	279	81	blastp
943	LYM56 H13	sugarcane|gb157.3|BQ533995	2450	279	80.14	tblastn
944	LYM56 H6	switchgrass|gb167|FE631693	2451	279	84.5	blastp
945	LYM56 H7	switchgrass|gb167|FL782747	2452	279	83.1	blastp
946	LYM56 H8	wheat|gb164|BE404207	2453	279	88.7	blastp
947	LYM56 H9	wheat|gb164|CD912963	2454	279	87.8	blastp
948	LYM57 H0	brachypodium|09v1|DV475724	2455	280	81.1	blastp
949	LYM62 H1	sorghum|09v1|SB10G012150	2456	282	88.9	blastp
950	LYM66 H1	wheat|gb164|BE403932	2457	283	83	blastp
950	LYM66 H1	wheat|gb164|BE403932	2457	440	83	blastp
951	LYM66 H2	wheat|gb164|BE405409	2458	283	90.4	blastp

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951	LYM66 H2	wheat|gb164|BE405409	2458	440	90.4	blastp
952	LYM66 H3	wheat|gb164|CA600263	2459	283	90.1	blastp
952	LYM66 H3	wheat|gb164|CA600263	2459	440	90.1	blastp
953	LYM69 H0	rice|gb170|OS07G42520	2460	286	98.3	blastp
954	LYM73 H6	brachypodium|09v1|DV481090	2461	287	95.8	blastp
955	LYM73 H7	maize|gb170|AW256155	2462	287	93.7	blastp
956	LYM73 H8	sorghum|09v1|SB07G004300	2463	287	94.3	blastp
957	LYM73 H9	sugarcane|gb157.3|CA117425	2464	287	94.3	blastp
958	LYM73 H5	switchgrass|gb167|DN145973	2465	287	94.6	blastp
959	LYM73 H6	wheat|gb164|AF289257S1	2466	287	92.67	tblastn
960	LYM79 H3	brachypodium|09v1|SRR031800S0005207	2467	289	83.8	blastp
961	LYM79 H4	millet|09v1|EVO454PM011117	2468	441	82.72	tblastn
962	LYM79 H5	sorghum|09v1|SB10G012140	2469	289	93	blastp
962	LYM79 H5	sorghum|09v1|SB10G012140	2469	441	93.75	tblastn
963	LYM79 H1	switchgrass|gb167|FE598528	2470	289	90.6	blastp
963	LYM79 H1	switchgrass|gb167|FE598528	2470	441	91.1	tblastn
964	LYM79 H2	switchgrass|gb167|FL957870	2471	441	86.6	tblastn
965	LYM79 H3	wheat|gb164|BE590518	2472	289	80	blastp
965	LYM79 H3	wheat|gb164|BE590518	2472	441	83.33	tblastn
966	LYM82 H1	banana|gb167|FF561962	2473	290	82.1	blastp
967	LYM82 H12	brachypodium|09v1|GT816645	2474	290	94.1	blastp
968	LYM82 H2	leymus|gb166|EG384073	2475	290	97.9	blastp
969	LYM82 H13	maize|gb170|AW181152	2476	290	90.6	blastp
970	LYM82 H4	melon|gb165|AM718213	2477	290	80.21	tblastn
971	LYM82 H14	millet|09v1|EVO454PM002754	2478	290	82.99	tblastn
972	LYM82 H5	pseudoroegneria|gb167|FF352234	2479	290	99	blastp
973	LYM82 H15	rice|gb170|OS06G04460	2480	290	91	blastp

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974	LYM82 H16	sorghum|09v1|SB10G002420	2481	290	90.3	blastp
975	LYM82 H8	soybean|gb168|CA921223	2482	290	80.21	tblastn
976	LYM82 H17	sugarcane|gb157.3|BU102729	2483	290	90.3	blastp
977	LYM82 H10	switchgrass|gb167|FL744837	2484	290	89.6	blastp
978	LYM82 H11	wheat|gb164|BE403842	2485	290	99	blastp
979	LYM82 H12	wheat|gb164|CA660788	2486	290	99	blastp
980	LYM83 H8	brachypodium|09v1|SRR031797S0009670	2487	291	86.5	blastp
980	LYM83 H8	brachypodium|09v1|SRR031797S0009670	2487	442	86.1	blastp
981	LYM83 H9	lolium|09v1|ES699086	2488	291	84.84	tblastn
981	LYM83 H9	lolium|09v1|ES699086	2488	442	84.43	tblastn
982	LYM83 H10	maize|gb170|AI665347	2489	291	82.4	blastp
982	LYM83 H10	maize|gb170|AI665347	2489	442	82.4	blastp
983	LYM83 H3	pseudoroegneria|gb167|FF354990	2490	291	97.5	blastp
983	LYM83 H3	pseudoroegneria|gb167|FF354990	2490	442	97.1	blastp
984	LYM83 H11	rice|gb170|OS05G45300	2491	291	81.6	blastp
984	LYM83 H11	rice|gb170|OS05G45300	2491	442	81.1	blastp
985	LYM83 H12	sorghum|09v1|SB09G026370	2492	291	82	blastp
985	LYM83 H12	sorghum|09v1|SB09G026370	2492	442	81.6	blastp
986	LYM83 H6	switchgrass|gb167|DN149383	2493	291	84	blastp
986	LYM83 H6	switchgrass|gb167|DN149383	2493	442	83.6	blastp
987	LYM83 H7	wheat|gb164|BE516715	2494	291	94.7	blastp
987	LYM83 H7	wheat|gb164|BE516715	2494	442	94.3	blastp
988	LYM83 H8	wheat|gb164|BF428688	2495	291	95.1	blastp
988	LYM83 H8	wheat|gb164|BF428688	2495	442	94.7	blastp
989	LYM84 H8	brachypodium|09v1|SRR031795S0021840	2496	292	92.8	blastp
990	LYM84 H9	maize|gb170|AW282161	2497	292	82.8	blastp
991	LYM84 H10	maize|gb170|LLDQ245778	2498	292	98.7	blastp

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992	LYM84 H4	pseudoroegneria|gb167|FF355744	2499	292	98.3	blastp
993	LYM84 H11	rice|gb170|OS03G41612	2500	292	84.58	tblastn
994	LYM84 H12	sorghum|09v1|SB01G014640	2501	292	82.9	blastp
995	LYM84 H7	switchgrass|gb167|FE652995	2502	292	81.3	blastp
996	LYM84 H8	wheat|gb164|BE417697	2503	292	95.1	blastp
997	LYM88 H0	arabidopsis lyrata|09v1|JGIAL014996	2504	294	91.5	blastp
998	LYM89 H5	arabidopsis lyrata|09v1|JGIAL031299	2505	295	86.36	tblastn
999	LYM89 H2	canola|gb161|CD812018	2506	295	81.8	blastp
1000	LYM89 H3	canola|gb161|CD821897	2507	295	81.8	blastp
1001	LYM89 H4	radish|gb164|EW732798	2508	295	81.65	tblastn
1002	LYM89 H5	radish|gb164|EX749702	2509	295	80.7	blastp
1003	LYM90 H3	brachypodium|09v1|DV488904	2510	296	83.2	blastp
1004	LYM90 H2	wheat|gb164|BQ242151	2511	296	94.6	blastp
1005	LYM90 H3	wheat|gb164|BQ244922	2512	296	94.6	blastp
1006	LYM91 H1	rye|gb164|BE494176	2513	297	82.5	blastp
1007	LYM91 H2	wheat|gb164|BE400659	2514	297	85.4	blastp
1008	LYM91 H3	wheat|gb164|CA593112	2515	297	86.27	tblastn
1009	LYM93 H1	wheat|gb164|BE401535	2516	298	93.6	blastp
1010	LYM93 H2	wheat|gb164|BE418047	2517	298	93.6	blastp
1011	LYM93 H3	wheat|gb164|CA624071	2518	298	84.6	blastp
1012	LYM93 H4	wheat|gb164|CA678405	2519	298	94.55	tblastn
1013	LYM93 H5	wheat|gb164|CJ920171	2520	298	88.7	blastp
1014	LYM99 H2	brachypodium|09v1|DV482533	2521	299	86.8	blastp
1015	LYM99 H2	wheat|gb164|AL818990	2522	299	94.12	tblastn
1016	LYM100 H1	wheat|gb164|BE399036	2523	301	89.5	blastp
1017	LYM103 H2	sorghum|09v1|SB03G004410	2524	303	89.69	tblastn

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1018	LYM103 H3	sugarcane|gb157.3|CA078686	2525	303	89.69	tblastn
1019	LYM103 H2	switchgrass|gb167|FL877864	2526	303	87	blastp
1020	LYM105 H5	barley|gb157SOLEXA|BQ461657	2527	304	90.9	blastp
1021	LYM105 H2	pseudoroegneria|gb167|FF366339	2528	304	90.5	blastp
1022	LYM105 H3	wheat|gb164|BE405330	2529	304	90	blastp
1023	LYM105 H4	wheat|gb164|BE637936	2530	304	91.8	blastp
1024	LYM105 H5	wheat|gb164|BQ743875	2531	304	89.4	blastp
1025	LYM106 H8	brachypodium|09v1|DV476632	2532	305	80.7	blastp
1026	LYM106 H9	maize|gb170|LLDQ245927	2533	305	97.9	blastp
1027	LYM106 H3	pseudoroegneria|gb167|FF347837	2534	305	96.5	blastp
1028	LYM106 H4	rye|gb164|BE586535	2535	305	90.3	blastp
1029	LYM106 H5	spruce|gb162|DR543563	2536	305	84.72	tblastn
1030	LYM106 H6	wheat|gb164|BE443195	2537	305	96.5	blastp
1031	LYM106 H7	wheat|gb164|BE445264	2538	305	97.9	blastp
1032	LYM106 H8	wheat|gb164|BF485098	2539	305	97.2	blastp
1033	LYM110 H1	sugarcane|gb157.3|CA204413	2540	306	84.3	tblastn
1034	LYM111 H7	brachypodium|09v1|GT765731	2541	307	80.96	tblastn
1035	LYM111 H1	cenchrus|gb166|EB657665	2542	307	87.6	blastp
1036	LYM111 H8	maize|gb170|AI941545	2543	307	89.9	blastp
1037	LYM111 H9	rice|gb170|OS01G57066	2544	307	81.5	blastp
1038	LYM111 H10	sorghum|09v1|SB03G036350	2545	307	91.5	blastp
1039	LYM111 H11	sorghum|09v1|SB05G023720	2546	307	93.1	tblastn
1040	LYM111 H12	sugarcane|gb157.3|CA072460	2547	307	89.38	tblastn
1041	LYM111 H7	switchgrass|gb167|FL711377	2548	307	90.8	blastp
1042	LYM119 H1	sorghum|09v1|SB05G003680	2549	308	93.8	blastp
1043	LYM122 H1	brachypodium|09v1|DV469739	2550	310	84.5	blastp
1044	LYM122 H1	pseudoroegneria|gb167|FF350527	2551	310	82.53	tblastn

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1045	LYM129 H2	brachypodium|09v1|SRR031795S0005798	2552	315	80.4	blastp
1046	LYM129 H3	maize|gb170|BQ486269	2553	315	82.8	blastp
1047	LYM129 H4	sorghum|09v1|SB03G044510	2554	315	81.6	blastp
1048	LYM129 H2	switchgrass|gb167|FE643628	2555	315	80.6	blastp
1049	LYM130 H1	leymus|gb166|EG377985	2556	316	80.2	blastp
1050	LYM130 H2	rice|gb170|OS05G04380	2557	316	99.4	blastp
1051	LYM130 H2	wheat|gb164|BE414767	2558	316	80.8	blastp
1052	LYM131 H1	aquilegia|gb157.3|DR917618	2559	317	81.2	blastp
1053	LYM131 H13	barley|gb157SOLEXA|AL450948	2560	317	83	blastp
1054	LYM131 H14	brachypodium|09v1|DV479902	2561	317	85.3	blastp
1055	LYM131 H15	maize|gb170|AI861327	2562	317	90.8	blastp
1056	LYM131 H16	maize|gb170|AW129826	2563	317	82.8	blastp
1057	LYM131 H17	maize|gb170|AW453172	2564	317	91.7	blastp
1058	LYM131 H18	rice|gb170|OS08G12750	2565	317	85.1	blastp
1059	LYM131 H19	sorghum|09v1|SB06G027970	2566	317	91.5	blastp
1060	LYM131 H20	sorghum|09v1|SB07G006320	2567	317	81	blastp
1061	LYM131 H21	sugarcane|gb157.3|CA068895	2568	317	91.5	blastp
1062	LYM131 H11	switchgrass|gb167|FE607026	2569	317	81.7	blastp
1063	LYM131 H12	switchgrass|gb167|FL708944	2570	317	91.49	tblastn
1064	LYM131 H13	wheat|gb164|BE412257	2571	317	83.7	blastp
1065	LYM134 H0	rice|gb170|OS04G56990	2572	319	98.8	blastp
1066	LYM137 H2	amborella|gb166|CK758151	2573	321	85.1	blastp
1067	LYM137 H3	antirrhinum|gb166|AJ788115	2574	321	83.7	blastp
1068	LYM137 H4	antirrhinum|gb166|AJ791024	2575	321	83	blastp
1069	LYM137 H5	antirrhinum|gb166|AJ793144	2576	321	83.01	tblastn
1070	LYM137 H217	apple|gb171|CN445333	2577	321	81	blastp
1071	LYM137 H218	apple|gb171|CN489019	2578	321	82.4	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1072	LYM137 H219	apple|gb171|CN491888	2579	321	81.8	blastp
1073	LYM137 H10	aquilegia|gb157.3|DT729599	2580	321	82.7	blastp
1074	LYM137 H220	arabidopsis lyrata|09v1|BQ834082	2581	321	81.8	blastp
1075	LYM137 H221	arabidopsis lyrata|09v1|BQ834260	2582	321	80.5	blastp
1076	LYM137 H222	arabidopsis lyrata|09v1|JGIAL015196	2583	321	80.5	blastp
1077	LYM137 H11	arabidopsis|gb165|AT3G55280	2584	321	81.2	blastp
1078	LYM137 H12	artemisia|gb164|EY035831	2585	321	85	blastp
1079	LYM137 H13	avocado|gb164|CO995706	2586	321	85.3	blastp
1080	LYM137 H14	avocado|gb164|CV460574	2587	321	84.6	blastp
1081	LYM137 H15	b juncea|gb164|EVGN00185312102498	2588	321	83.8	blastp
1082	LYM137 H16	b juncea|gb164|EVGN00317014862029	2589	321	81.2	blastp
1083	LYM137 H17	b juncea|gb164|EVGN01375409582897	2590	321	81.2	blastp
1084	LYM137 H223	b nigra|09v1|GT069407	2591	321	81.2	blastp
1085	LYM137 H18	b oleracea|gb161|AM392244	2592	321	81.2	blastp
1086	LYM137 H19	b oleracea|gb161|DY014383	2593	321	83.8	blastp
1087	LYM137 H20	b oleracea|gb161|DY023491	2594	321	83.8	blastp
1088	LYM137 H21	b oleracea|gb161|DY023494	2595	321	81.2	blastp
1089	LYM137 H22	b oleracea|gb161|DY027443	2596	321	81.2	blastp
1090	LYM137 H23	b oleracea|gb161|EE535717	2597	321	80.5	blastp
1091	LYM137 H24	b rapa|gb162|BG543640	2598	321	83.77	tblastn
1092	LYM137 H25	b rapa|gb162|BQ791808	2599	321	80.5	blastp
1093	LYM137 H26	b rapa|gb162|CA991997	2600	321	81.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1094	LYM137 H27	b rapa|gb162|CV432555	2601	321	81.2	blastp
1095	LYM137 H28	b rapa|gb162|CV432912	2602	321	81.2	blastp
1096	LYM137 H29	b rapa|gb162|CV432918	2603	321	83.8	blastp
1097	LYM137 H30	b rapa|gb162|CX267185	2604	321	81.2	blastp
1098	LYM137 H31	b rapa|gb162|CX271342	2605	321	81.2	blastp
1099	LYM137 H32	banana|gb167|DN239514	2606	321	85.7	blastp
1100	LYM137 H33	banana|gb167|ES431662	2607	321	86.4	blastp
1101	LYM137 H34	banana|gb167|FF558102	2608	321	85.7	blastp
1102	LYM137 H35	banana|gb167|FF558729	2609	321	86.4	blastp
1103	LYM137 H36	banana|gb167|FF560801	2610	321	85.7	blastp
1104	LYM137 H37	banana|gb167|FL657344	2611	321	85.8	blastp
1105	LYM137 H38	basilicum|gb157.3|DY342616	2612	321	80.5	blastp
1106	LYM137 H39	bean|gb167|CA897728	2613	321	85	blastp
1107	LYM137 H40	bean|gb167|CA897730	2614	321	83.1	blastp
1108	LYM137 H41	beet|gb162|BF011189	2615	321	82.5	blastp
1109	LYM137 H42	beet|gb162|BI096284	2616	321	84.4	blastp
1110	LYM137 H224	brachypodium|09v1|DV476457	2617	321	96.1	blastp
1111	LYM137 H225	brachypodium|09v1|DV489152	2618	321	96.1	blastp
1112	LYM137 H45	cacao|gb167|CA795798	2619	321	83.7	blastp
1113	LYM137 H46	cacao|gb167|CU476798	2620	321	83.8	blastp
1114	LYM137 H47	canola|gb161|CD811640	2621	321	83.8	blastp
1115	LYM137 H48	canola|gb161|CD812285	2622	321	81.2	blastp
1116	LYM137 H49	canola|gb161|CD812312	2623	321	81.2	blastp
1117	LYM137 H50	canola|gb161|CD812501	2624	321	81.2	blastp
1118	LYM137 H51	canola|gb161|CD815420	2625	321	81.2	blastp
1119	LYM137 H52	canola|gb161|CD816902	2626	321	81.2	blastp
1120	LYM137 H53	canola|gb161|CD817591	2627	321	81.2	blastp

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1121	LYM137 H54	canola|gb161|CD821663	2628	321	83.8	blastp
1122	LYM137 H55	canola|gb161|CN726029	2629	321	83.8	blastp
1123	LYM137 H56	canola|gb161|CN731028	2630	321	81.2	blastp
1124	LYM137 H57	canola|gb161|EE479368	2631	321	83.8	blastp
1125	LYM137 H58	canola|gb161|H07535	2632	321	83.8	blastp
1126	LYM137 H226	cassava|09v1|CK643771	2633	321	83.1	blastp
1127	LYM137 H227	cassava|09v1|CK647492	2634	321	83.8	blastp
1128	LYM137 H228	cassava|09v1|DV455355	2635	321	81.8	blastp
1129	LYM137 H229	castorbean|09v1|EG700188	2636	321	85	blastp
1130	LYM137 H230	castorbean|09v1|XM002531924	2637	321	84.9	blastp
1131	LYM137 H63	catharanthus|gb166|EG556131	2638	321	82.6	blastp
1132	LYM137 H64	catharanthus|gb166|EG557604	2639	321	82.6	blastp
1133	LYM137 H65	cenchrus|gb166|EB652612	2640	321	93.4	blastp
1134	LYM137 H66	centaurea|gb166|EH715158	2641	321	83	blastp
1135	LYM137 H67	centaurea|gb166|EH737696	2642	321	84.3	blastp
1136	LYM137 H68	centaurea|gb166|EH746709	2643	321	82.5	blastp
1137	LYM137 H231	chestnut|gb170|SRR006295S0004667	2644	321	83.8	blastp
1138	LYM137 H232	chestnut|gb170|SRR006295S0010167	2645	321	83.1	blastp
1139	LYM137 H233	chickpea|09v2|FE669244	2646	321	85.6	blastp
1140	LYM137 H234	chickpea|09v2|FE671615	2647	321	85.6	blastp
1141	LYM137 H235	cichorium|gb171|DT210912	2648	321	84.3	blastp
1142	LYM137 H236	cichorium|gb171|EH681883	2649	321	84.4	blastp
1143	LYM137 H237	cichorium|gb171|EH696050	2650	321	83.8	blastp
1144	LYM137 H72	citrus|gb166|CB610578	2651	321	83.7	blastp
1145	LYM137 H73	citrus|gb166|CN183415	2652	321	82.9	blastp
1146	LYM137 H74	coffea|gb157.2|DV663668	2653	321	85	blastp
1147	LYM137 H75	cotton|gb164|AI728522	2654	321	84.3	blastp

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1148	LYM137 H76	cotton|gb164|AI729531	2655	321	85	blastp
1149	LYM137 H77	cotton|gb164|BE055719	2656	321	83	blastp
1150	LYM137 H78	cotton|gb164|BF269641	2657	321	84.3	blastp
1151	LYM137 H79	cotton|gb164|BG441496	2658	321	81.8	blastp
1152	LYM137 H80	cowpea|gb166|BE336250	2659	321	83.9	blastp
1153	LYM137 H81	cowpea|gb166|FF382348	2660	321	85.1	blastp
1154	LYM137 H82	cowpea|gb166|FF391267	2661	321	86.9	blastp
1155	LYM137 H83	cryptomeria|gb166|BP176442	2662	321	80.5	blastp
1156	LYM137 H84	cryptomeria|gb166|BW996322	2663	321	81.2	blastp
1157	LYM137 H238	cucumber|09v1|BGI454H0165031	2664	321	81.6	blastp
1158	LYM137 H239	cucumber|09v1|CK085893	2665	321	83.7	blastp
1159	LYM137 H240	cucumber|09v1|DV632825	2666	321	85	blastp
1160	LYM137 H85	cynara|gb167|GE588138	2667	321	84.4	blastp
1161	LYM137 H86	dandelion|gb161|DY804086	2668	321	85.1	blastp
1162	LYM137 H87	dandelion|gb161|DY813115	2669	321	83.8	blastp
1163	LYM137 H88	eucalyptus|gb166|CT980143	2670	321	83.1	blastp
1164	LYM137 H89	eucalyptus|gb166|CT981000	2671	321	81.3	blastp
1165	LYM137 H90	fescue|gb161|DT686472	2672	321	80.9	blastp
1166	LYM137 H241	flax|09v1|EU829592	2673	321	81	blastp
1167	LYM137 H242	gerbera|09v1|AJ750707	2674	321	85.6	blastp
1168	LYM137 H243	gerbera|09v1|AJ753127	2675	321	84.31	tblastn
1169	LYM137 H244	gerbera|09v1|AJ755440	2676	321	81.7	blastp
1170	LYM137 H91	ginger|gb164|DY352000	2677	321	85.5	blastp
1171	LYM137 H92	ginger|gb164|DY356913	2678	321	83.7	blastp
1172	LYM137 H93	grape|gb160|CA816335	2679	321	80.6	blastp
1173	LYM137 H94	grape|gb160|CB348289	2680	321	81.3	blastp
1174	LYM137 H95	grape|gb160|CB979641	2681	321	84.5	blastp

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1175	LYM137 H96	iceplant|gb164|CA834927	2682	321	82.5	blastp
1176	LYM137 H97	ipomoea|gb157.2|BU690174	2683	321	82.2	blastp
1177	LYM137 H98	ipomoea|gb157.2|CJ738553	2684	321	82.9	blastp
1178	LYM137 H245	jatropha|09v1|GO247333	2685	321	85.6	blastp
1179	LYM137 H99	kiwi|gb166|FG413271	2686	321	83.1	blastp
1180	LYM137 H100	kiwi|gb166|FG421995	2687	321	84.2	blastp
1181	LYM137 H101	kiwi|gb166|FG429490	2688	321	83.9	blastp
1182	LYM137 H102	kiwi|gb166|FG461535	2689	321	84.2	blastp
1183	LYM137 H103	kiwi|gb166|FG501757	2690	321	83.6	blastp
1184	LYM137 H104	lettuce|gb157.2|CV700088	2691	321	83.8	blastp
1185	LYM137 H105	lettuce|gb157.2|DW046053	2692	321	83	blastp
1186	LYM137 H106	lettuce|gb157.2|DW049273	2693	321	83.8	blastp
1187	LYM137 H107	lettuce|gb157.2|DW077894	2694	321	83.8	blastp
1188	LYM137 H108	lettuce|gb157.2|DW080256	2695	321	83.7	blastp
1189	LYM137 H109	lettuce|gb157.2|DW080360	2696	321	83.1	blastp
1190	LYM137 H110	lettuce|gb157.2|DW112293	2697	321	83.8	blastp
1191	LYM137 H111	lettuce|gb157.2|DW145178	2698	321	83.8	blastp
1192	LYM137 H112	leymus|gb166|CD809209	2699	321	98.7	blastp
1193	LYM137 H246	liquorice|gb171|FS239986	2700	321	83.9	blastp
1194	LYM137 H113	liriodendron|gb166|CK743367	2701	321	85.3	blastp
1195	LYM137 H247	lolium|09v1|AU251012	2702	321	97.4	blastp
1196	LYM137 H248	lotus|09v1|LLBG662285	2703	321	85	blastp
1197	LYM137 H249	lotus|09v1|LLBI418687	2704	321	83.9	blastp
1198	LYM137 H250	lotus|09v1|LLGO006921	2705	321	83.7	blastp
1199	LYM137 H115	lovegrass|gb167|EH183574	2706	321	92.8	blastp
1200	LYM137 H116	lovegrass|gb167|EH185967	2707	321	90.1	blastp
1201	LYM137 H251	maize|gb170|AA979822	2708	321	93.4	blastp

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1202	LYM137 H252	maize|gb170|AI612349	2709	321	94.7	blastp
1203	LYM137 H253	maize|gb170|EY962027	2710	321	82.89	tblastn
1204	LYM137 H254	maize|gb170|LLBG320994	2711	321	94.1	blastp
1205	LYM137 H255	maize|gb170|LLDQ245209	2712	321	99.3	blastp
1206	LYM137 H256	maize|gb170|LLDQ245775	2713	321	81.2	blastp
1207	LYM137 H257	maize|gb170|T18742	2714	321	93.4	blastp
1208	LYM137 H258	medicago|09v1|AW208139	2715	321	85.1	blastp
1209	LYM137 H259	medicago|09v1|AW287975	2716	321	83.6	blastp
1210	LYM137 H260	medicago|09v1|LLAJ846422	2717	321	82.47	tblastn
1211	LYM137 H127	melon|gb165|DV632825	2718	321	85	blastp
1212	LYM137 H128	melon|gb165|DV632919	2719	321	83.7	blastp
1213	LYM137 H261	millet|09v1|CD725778	2720	321	94.7	blastp
1214	LYM137 H262	millet|09v1|EVO454PM001999	2721	321	91.4	blastp
1215	LYM137 H263	monkeyflower|09v1|DV211090	2722	321	81.3	blastp
1216	LYM137 H264	monkeyflower|09v1|GO948368	2723	321	81.3	blastp
1217	LYM137 H129	nicotiana benthamiana|gb162|ES885186	2724	321	85.7	blastp
1218	LYM137 H130	nuphar|gb166|FD386160	2725	321	85.8	blastp
1219	LYM137 H265	oak|gb170|CU656727	2726	321	83.1	blastp
1220	LYM137 H266	oak|gb170|SRR006307S0003551	2727	321	83.8	blastp
1221	LYM137 H131	oat|gb164|CN814837	2728	321	98	blastp
1222	LYM137 H132	oil palm|gb166|CN599457	2729	321	87.2	blastp
1223	LYM137 H133	oil palm|gb166|EL688664	2730	321	84.5	blastp
1224	LYM137 H134	onion|gb162|CF451442	2731	321	85.2	blastp
1225	LYM137 H135	papaya|gb165|EX238983	2732	321	83.1	blastp
1226	LYM137 H136	papaya|gb165|EX281727	2733	321	84.3	blastp
1227	LYM137 H267	peanut|gb171|CD038036	2734	321	84.4	blastp

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1228	LYM137 H268	peanut|gb171|CD038042	2735	321	83.2	blastp
1229	LYM137 H269	peanut|gb171|EH042912	2736	321	85.1	blastp
1230	LYM137 H270	pea|09v1|EX570565	2737	321	83.7	blastp
1231	LYM137 H271	pepper|gb171|BM063192	2738	321	83	blastp
1232	LYM137 H272	pepper|gb171|CA518436	2739	321	81.8	blastp
1233	LYM137 H273	petunia|gb171|CV298826	2740	321	83	blastp
1234	LYM137 H274	petunia|gb171|CV299096	2741	321	83.7	blastp
1235	LYM137 H275	petunia|gb171|FN007657	2742	321	83.1	blastp
1236	LYM137 H276	poplar|gb170|AI161822	2743	321	81.8	blastp
1237	LYM137 H277	poplar|gb170|AI164812	2744	321	80.4	blastp
1238	LYM137 H278	poplar|gb170|CN517615	2745	321	81.58	tblastn
1239	LYM137 H150	poppy|gb166|FE964482	2746	321	82.6	blastp
1240	LYM137 H151	poppy|gb166|FE968489	2747	321	83.9	blastp
1241	LYM137 H152	potato|gb157.2|BE923747	2748	321	83.7	blastp
1242	LYM137 H153	potato|gb157.2|BF459639	2749	321	83.7	blastp
1243	LYM137 H155	potato|gb157.2|BI407078	2750	321	82.5	blastp
1244	LYM137 H156	potato|gb157.2|BQ046658	2751	321	82.5	blastp
1245	LYM137 H157	prunus|gb167|BU048009	2752	321	83.8	blastp
1246	LYM137 H158	prunus|gb167|BU572674	2753	321	83.8	blastp
1247	LYM137 H159	pseudoroegneria|gb167|FF344271	2754	321	98.7	blastp
1248	LYM137 H160	radish|gb164|EV524412	2755	321	82.5	blastp
1249	LYM137 H161	radish|gb164|EV526732	2756	321	81.2	blastp
1250	LYM137 H162	radish|gb164|EV527806	2757	321	81.2	blastp
1251	LYM137 H163	radish|gb164|EV536949	2758	321	81.2	blastp
1252	LYM137 H164	radish|gb164|EV539087	2759	321	83.1	blastp
1253	LYM137 H165	radish|gb164|EV545248	2760	321	81.2	blastp
1254	LYM137 H166	radish|gb164|EV570492	2761	321	81.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1255	LYM137 H167	radish|gb164|EW7244 65	2762	321	81.2	blastp
1256	LYM137 H168	radish|gb164|EW7247 37	2763	321	83.1	blastp
1257	LYM137 H169	radish|gb164|EW7319 70	2764	321	81.2	blastp
1258	LYM137 H170	radish|gb164|EW7327 28	2765	321	81.2	blastp
1259	LYM137 H171	radish|gb164|EX75564 1	2766	321	80.4	blastp
1260	LYM137 H172	radish|gb164|EX75678 4	2767	321	83.8	blastp
1261	LYM137 H173	radish|gb164|EX75782 4	2768	321	81.2	blastp
1262	LYM137 H279	rice|gb170|OS01G246 90	2769	321	92.2	blastp
1263	LYM137 H280	rice|gb170|OS04G422 70	2770	321	94.1	blastp
1264	LYM137 H176	rye|gb164|BE493987	2771	321	100	blastp
1265	LYM137 H177	safflower|gb162|EL37 8228	2772	321	82.4	blastp
1266	LYM137 H178	safflower|gb162|EL39 9454	2773	321	83.8	blastp
1267	LYM137 H179	safflower|gb162|EL41 1711	2774	321	81.7	blastp
1268	LYM137 H281	senecio|gb170|DY666 439	2775	321	83.01	tblastn
1269	LYM137 H282	solanum phureja|09v1|SPHAA8 24956	2776	321	82.5	blastp
1270	LYM137 H283	solanum phureja|09v1|SPHBQ1 15070	2777	321	82.69	tblastn
1271	LYM137 H284	solanum phureja|09v1|SPHTO M289A	2778	321	83.7	blastp
1272	LYM137 H285	sorghum|09v1|SB06G 021660	2779	321	94.7	blastp
1273	LYM137 H286	sorghum|09v1|SB10G 005240	2780	321	94.1	blastp
1274	LYM137 H182	soybean|gb168|AL365 737	2781	321	85.6	blastp
1275	LYM137 H183	soybean|gb168|AW20 8139	2782	321	84.3	blastp
1276	LYM137 H184	soybean|gb168|AW28 7975	2783	321	85.6	blastp
1277	LYM137 H185	soybean|gb168|BE336 250	2784	321	81.9	blastp
1278	LYM137 H186	soybean|gb168|BE336 251	2785	321	84.5	blastp
1279	LYM137 H187	soybean|gb168|BI9675 38	2786	321	85	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1280	LYM137 H188	spurge|gb161|BI993574	2787	321	83.8	blastp
1281	LYM137 H189	strawberry|gb164|CO378565	2788	321	83.7	blastp
1282	LYM137 H190	strawberry|gb164|EX685316	2789	321	82.5	blastp
1283	LYM137 H287	sugarcane|gb157.3|AI216927	2790	321	94.7	blastp
1284	LYM137 H288	sugarcane|gb157.3|BQ535570	2791	321	92.8	blastp
1285	LYM137 H289	sugarcane|gb157.3|BQ535956	2792	321	94.1	blastp
1286	LYM137 H290	sugarcane|gb157.3|BQ537453	2793	321	93.4	blastp
1287	LYM137 H291	sugarcane|gb157.3|CA106878	2794	321	94.7	blastp
1288	LYM137 H292	sugarcane|gb157.3|CA111839	2795	321	93.4	blastp
1289	LYM137 H293	sugarcane|gb157.3|CA113465	2796	321	92.11	tblastn
1290	LYM137 H198	sunflower|gb162|CD846067	2797	321	84.3	blastp
1291	LYM137 H199	sunflower|gb162|CD848213	2798	321	84.3	blastp
1292	LYM137 H200	sunflower|gb162|CD851130	2799	321	85.6	blastp
1293	LYM137 H201	sunflower|gb162|CD853875	2800	321	83.8	blastp
1294	LYM137 H202	switchgrass|gb167|DN140751	2801	321	92.8	blastp
1295	LYM137 H203	switchgrass|gb167|DN143966	2802	321	90.8	blastp
1296	LYM137 H204	switchgrass|gb167|FE603312	2803	321	91.4	blastp
1297	LYM137 H205	switchgrass|gb167|FE645253	2804	321	92.8	blastp
1298	LYM137 H294	tea|gb171|GE652357	2805	321	84.52	tblastn
1299	LYM137 H295	tea|gb171|GH613259	2806	321	81.2	blastp
1300	LYM137 H206	thellungiella|gb167|DN773656	2807	321	81.2	blastp
1301	LYM137 H207	tobacco|gb162|DV157653	2808	321	82.5	blastp
1302	LYM137 H208	tobacco|gb162|EB444171	2809	321	85.1	blastp
1303	LYM137 H209	tobacco|gb162|EB445443	2810	321	85.6	blastp
1304	LYM137 H210	tobacco|gb162|EB679214	2811	321	83.8	blastp
1305	LYM137 H211	tobacco|gb162|TOBRPL25A	2812	321	85.7	blastp
1306	LYM137 H296	tomato|09v1|AA824956	2813	321	81.8	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1307	LYM137 H297	tomato|09v1|BQ115070	2814	321	83.8	blastp
1308	LYM137 H298	tomato|09v1|TOM289A	2815	321	83.7	blastp
1309	LYM137 H214	wheat|gb164|BE401860	2816	321	99.3	blastp
1310	LYM137 H215	wheat|gb164|BE403516	2817	321	99.3	blastp
1311	LYM137 H216	wheat|gb164|BE404488	2818	321	99.3	blastp
1312	LYM137 H217	wheat|gb164|CA612898	2819	321	82.89	tblastn
1313	LYM137 H299	zinnia|gb171|AU304473	2820	321	83	blastp
1314	LYM140 H18	apple|gb171|CN874007	2821	322	80.1	blastp
1315	LYM140 H1	banana|gb167|ES433790	2822	322	80	tblastn
1316	LYM140 H19	brachypodium|09v1|DV472528	2823	322	90.3	blastp
1317	LYM140 H20	cassava|09v1|BM259738	2824	322	80.3	blastp
1318	LYM140 H21	cassava|09v1|CK640886	2825	322	80.3	blastp
1319	LYM140 H22	castorbean|09v1|EG656528	2826	322	80.4	blastp
1320	LYM140 H23	chestnut|gb170|SRR006295S0060343	2827	322	80	blastp
1321	LYM140 H24	chestnut|gb170|SRR006296S0039724	2828	322	80.49	tblastn
1322	LYM140 H4	citrus|gb166|CB290479	2829	322	80.3	blastp
1323	LYM140 H5	cotton|gb164|BF271942	2830	322	81.4	blastp
1324	LYM140 H6	cotton|gb164|CA992695	2831	322	80.1	blastp
1325	LYM140 H7	cowpea|gb166|FC459791	2832	322	80.48	tblastn
1326	LYM140 H25	maize|gb170|AW331287	2833	322	89.2	blastp
1327	LYM140 H9	oil palm|gb166|ES414711	2834	322	80.8	blastp
1328	LYM140 H10	papaya|gb165|EX227799	2835	322	80	blastp
1329	LYM140 H11	radish|gb164|EV528272	2836	322	80.3	blastp
1330	LYM140 H26	rice|gb170|OS04G53210	2837	322	88.6	blastp
1331	LYM140 H27	sorghum|09v1|SB06G028990	2838	322	88.9	blastp
1332	LYM140 H13	soybean|gb168|AW126193	2839	322	80	blastp
1333	LYM140 H28	sugarcane|gb157.3|CA071893	2840	322	88.1	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1334	LYM140 H15	sunflower|gb162|BU671805	2841	322	80.1	blastp
1335	LYM140 H16	switchgrass|gb167|FE624047	2842	322	90.5	blastp
1336	LYM140 H17	wheat|gb164|BE415726	2843	322	98.1	blastp
1337	LYM140 H18	wheat|gb164|BF200613	2844	322	86.7	blastp
1338	LYM141 H0	rice|gb170|OS12G02910	2845	323	86.6	blastp
1339	LYM142 H7	barley|gb157SOLEXA|BQ761869	2846	324	86.6	blastp
1340	LYM142 H8	brachypodium|09v1|DV478753	2847	324	86.8	blastp
1341	LYM142 H3	leymus|gb166|EG401596	2848	324	97.7	blastp
1342	LYM142 H4	pseudoroegneria|gb167|FF362922	2849	324	97.7	blastp
1343	LYM142 H9	rice|gb170|OS02G33550	2850	324	83.9	blastp
1344	LYM142 H6	wheat|gb164|BE404843	2851	324	94.4	blastp
1345	LYM142 H7	wheat|gb164|CA631467	2852	324	83.9	blastp
1346	LYM144 H0	brachypodium|09v1|GT775853	2853	326	80.6	blastp
1347	LYM148 H10	brachypodium|09v1|DV478384	2854	328	91.1	blastp
1348	LYM148 H2	leymus|gb166|EG398961	2855	328	92.73	tblastn
1349	LYM148 H11	maize|gb170|AW060086	2856	328	84.5	blastp
1350	LYM148 H12	millet|09v1|EVO454PM023692	2857	328	82.9	blastp
1351	LYM148 H13	rice|gb170|OS06G45440	2858	328	82.4	blastp
1352	LYM148 H14	sorghum|09v1|SB10G026570	2859	328	83.3	blastp
1353	LYM148 H6	switchgrass|gb167|FE604043	2860	328	82.5	blastp
1354	LYM148 H7	switchgrass|gb167|FE641627	2861	328	81.1	blastp
1355	LYM148 H8	wheat|gb164|BE442896	2862	328	96.3	blastp
1356	LYM148 H9	wheat|gb164|BQ295259	2863	328	97	blastp
1357	LYM148 H10	wheat|gb164|BQ788641	2864	328	97	blastp
1358	LYM149 H5	brachypodium|09v1|DV488199	2865	329	83.2	blastp
1359	LYM149 H2	pseudoroegneria|gb167|FF346387	2866	329	87	blastp
1360	LYM149 H3	wheat|gb164|BE429052	2867	329	87.2	blastp

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1361	LYM149 H4	wheat|gb164|BQ620138	2868	329	87.5	blastp
1362	LYM149 H5	wheat|gb164|CA641424	2869	329	89.69	tblastn
1363	LYM152 H14	arabidopsis lyrata|09v1|BQ834051	2870	330	86.7	blastp
1364	LYM152 H15	arabidopsis lyrata|09v1|JGIAL030307	2871	330	96.7	blastp
1365	LYM152 H1	arabidopsis|gb165|AT4G25890	2872	330	82.5	tblastn
1366	LYM152 H2	b oleracea|gb161|DY027305	2873	330	95	blastp
1367	LYM152 H3	b oleracea|gb161|DY028937	2874	330	93.4	blastp
1368	LYM152 H4	b rapa|gb162|BG544013	2875	330	94.17	tblastn
1369	LYM152 H5	b rapa|gb162|L35776	2876	330	92.6	blastp
1370	LYM152 H6	b rapa|gb162|L35823	2877	330	95	blastp
1371	LYM152 H7	canola|gb161|CD812096	2878	330	94.2	blastp
1372	LYM152 H8	canola|gb161|CD812552	2879	330	95	blastp
1373	LYM152 H9	canola|gb161|CD817037	2880	330	95	blastp
1374	LYM152 H10	canola|gb161|CD830347	2881	330	92.6	blastp
1375	LYM152 H12	radish|gb164|EV548235	2882	330	92.5	blastp
1376	LYM152 H13	radish|gb164|EW718196	2883	330	92.5	blastp
1377	LYM152 H14	thellungiella|gb167|BM985697	2884	330	91.7	blastp
1378	LYM153 H6	barley|gb157SOLEXA|BF625242	2885	331	81.5	blastp
1379	LYM153 H7	brachypodium|09v1|SRR031796S0027091	2886	331	81.5	blastp
1380	LYM153 H2	cenchrus|gb166|EB654758	2887	331	80	blastp
1381	LYM153 H8	millet|09v1|EVO454PM017552	2888	331	83.1	blastp
1382	LYM153 H9	sorghum|09v1|SB10G003440	2889	331	81.5	blastp
1383	LYM153 H4	switchgrass|gb167|FE634744	2890	331	83.1	blastp
1384	LYM153 H5	wheat|gb164|CD490951	2891	331	94.03	tblastn
1385	LYM153 H6	wheat|gb164|CK215660	2892	331	80.3	tblastn

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1386	LYM156 H6	barley|gb157SOLEXA|AL506124	2893	332	96.1	blastp
1387	LYM156 H7	barley|gb157SOLEXA|BE195142	2894	332	93.1	blastp
1388	LYM156 H3	pseudoroegneria|gb167|FF346665	2895	332	92.8	blastp
1389	LYM156 H4	pseudoroegneria|gb167|FF354463	2896	332	86.3	blastp
1390	LYM156 H8	rice|gb170|OS07G46830	2897	332	80	blastp
1391	LYM156 H6	wheat|gb164|BE637888	2898	332	91.8	blastp
1392	LYM157 H1	barley|gb157SOLEXA|BG299283	2899	333	94.9	blastp
1393	LYM159 H1	wheat|gb164|CA598148	2900	334	81.01	tblastn
1394	LYM159 H2	wheat|gb164|CD866037	2901	334	87.7	blastp
1395	LYM159 H3	wheat|gb164|CD867356	2902	334	86.4	blastp
1396	LYM160 H1	wheat|gb164|BE399997	2903	335	87.6	tblastn
1397	LYM160 H2	wheat|gb164|BE500200	2904	335	80	blastp
1398	LYM161 H0	brachypodium|09v1|DV471902	2905	336	81.9	blastp
1398	LYM161 H0	brachypodium|09v1|DV471902	2905	444	81.02	tblastn
1399	LYM162 H5	maize|gb170|AW331105	2906	337	84.8	blastp
1400	LYM162 H6	millet|09v1|EVO454PM026751	2907	337	85.7	blastp
1401	LYM162 H7	sorghum|09v1|SB03G043995	2908	337	87.5	blastp
1402	LYM162 H8	sugarcane|gb157.3|BQ536349	2909	337	87.5	blastp
1403	LYM162 H4	switchgrass|gb167|FL738992	2910	337	83.9	blastp
1404	LYM162 H5	switchgrass|gb167|FL829126	2911	337	85.7	blastp
1405	LYM165 H5	maize|gb170|LLCO452769	2912	339	99.2	blastp
1406	LYM165 H6	sorghum|09v1|SB03G030690	2913	339	89.2	blastp
1407	LYM165 H7	sugarcane|gb157.3|BQ529806	2914	339	81.1	blastp
1408	LYM165 H8	sugarcane|gb157.3|CA084294	2915	339	90.4	blastp
1409	LYM165 H4	switchgrass|gb167|DN143471	2916	339	85.9	blastp
1410	LYM165 H5	switchgrass|gb167|DN144101	2917	339	85.7	blastp
1411	LYM166 H1	brachypodium|09v1|DV486893	2918	340	85.4	tblastn

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1411	LYM166 H1	brachypodium|09v1|DV486893	2918	445	85.36	tblastn
1412	LYM170 H7	barley|gb157SOLEXA|AV915706	2919	341	91.6	blastp
1413	LYM170 H8	brachypodium|09v1|SRR031797S0049196	2920	341	94.8	blastp
1414	LYM170 H9	maize|gb170|AI665902	2921	341	87.3	blastp
1415	LYM170 H10	maize|gb170|BE050628	2922	341	86.4	blastp
1416	LYM170 H11	sorghum|09v1|SB03G036440	2923	341	87.3	blastp
1417	LYM170 H12	sugarcane|gb157.3|CA067017	2924	341	88.3	blastp
1418	LYM170 H6	switchgrass|gb167|DN142710	2925	341	87.3	blastp
1419	LYM170 H7	wheat|gb164|BE415371	2926	341	93.5	blastp
1420	LYM172 H11	brachypodium|09v1|DV489358	2927	342	87.6	blastp
1421	LYM172 H12	maize|gb170|AA979770	2928	342	81.7	blastp
1422	LYM172 H13	maize|gb170|AI711966	2929	342	81.2	blastp
1423	LYM172 H14	maize|gb170|AI947521	2930	342	80.71	tblastn
1424	LYM172 H15	maize|gb170|AW120145	2931	342	82.9	blastp
1425	LYM172 H16	millet|09v1|EVO454PM002481	2932	342	85.6	tblastn
1426	LYM172 H17	rice|gb170|OS02G08364	2933	342	81.8	blastp
1427	LYM172 H18	sorghum|09v1|SB04G005430	2934	342	80.43	tblastn
1428	LYM172 H19	sorghum|09v1|SB10G025800	2935	342	83.9	blastp
1429	LYM172 H20	sugarcane|gb157.3|CA071007	2936	342	80.1	blastp
1430	LYM172 H9	switchgrass|gb167|FL692588	2937	342	80.7	blastp
1431	LYM172 H10	wheat|gb164|BE400761	2938	342	81.25	tblastn
1432	LYM172 H11	wheat|gb164|BE498868	2939	342	87.77	tblastn
1433	LYM213 H1	switchgrass|gb167|FE620008	2940	343	80.4	blastp
1433	LYM213 H1	switchgrass|gb167|FE620008	2940	386	88.7	blastp
1434	LYM174 H3	maize|gb170|AW144917	2941	344	89.4	blastp
1435	LYM174 H4	maize|gb170|AW267379	2942	344	86.6	blastp
1436	LYM174 H5	sugarcane|gb157.3|CA089309	2943	344	92.31	tblastn

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1437	LYM174 H3	switchgrass|gb167|DN150662	2944	344	80.9	blastp
1438	LYM175 H0	maize|gb170|AW498464	2945	345	81.2	blastp
1439	LYM175 H1	rice|gb170|OS01G69090	2946	345	95	blastp
1439	LYM175 H1	rice|gb170|OS01G69090	2946	446	100	blastp
1440	LYM215 H2	sorghum|09v1|SB03G043980	2947	345	81.2	blastp
1440	LYM215 H2	sorghum|09v1|SB03G043980	2947	387	94.6	blastp
1441	LYM176 H2	maize|gb170|CA452713	2948	346	82.2	blastp
1442	LYM176 H3	sorghum|09v1|SB03G036470	2949	346	83	blastp
1443	LYM176 H2	switchgrass|gb167|FE606366	2950	346	82	blastp
1444	LYM178 H9	brachypodium|09v1|DV472161	2951	347	84.9	blastp
1445	LYM178 H10	brachypodium|09v1|SRR031797S0177787	2952	347	84.6	blastp
1446	LYM178 H1	fescue|gb161|DT674427	2953	347	89.4	blastp
1447	LYM178 H2	leymus|gb166|EG394591	2954	347	84.08	tblastn
1448	LYM178 H11	maize|gb170|W21746	2955	347	83.4	blastp
1449	LYM178 H12	millet|09v1|EVO454PM001531	2956	347	83.1	blastp
1450	LYM178 H3	pseudoroegneria|gb167|FF358503	2957	347	93.6	blastp
1451	LYM178 H13	sorghum|09v1|SB03G008890	2958	347	83.1	blastp
1452	LYM178 H14	sorghum|09v1|SB07G001060	2959	347	81.9	blastp
1453	LYM178 H15	sugarcane|gb157.3|CA066169	2960	347	82.4	blastp
1454	LYM178 H16	sugarcane|gb157.3|CA079726	2961	347	83.1	blastp
1455	LYM178 H8	switchgrass|gb167|FE636508	2962	347	82.4	blastp
1456	LYM178 H9	wheat|gb164|BQ620752	2963	347	94.7	blastp
1457	LYM179 H0	sorghum|09v1|SB08G006470	2964	348	86.5	blastp
1458	LYM107 H2	brachypodium|09v1|GT808738	2965	349	86.9	blastp
1459	LYM107 H3	maize|gb170|CF075587	2966	349	95.2	blastp
1460	LYM107 H4	rice|gb170|OS05G26660	2967	349	86.4	blastp
1461	LYM107 H5	sorghum|09v1|SB03G036480	2968	349	95	blastp

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1462	LYM109 H1	maize|gb170|BG517163	2969	350	82.62	tblastn
1462	LYM109 H1	maize|gb170|BG517163	2969	447	82.6	tblastn
1463	LYM109 H2	sorghum|09v1|SB05G003660	2970	350	88.75	tblastn
1463	LYM109 H2	sorghum|09v1|SB05G003660	2970	447	88.87	tblastn
1464	LYM112 H1	maize|gb170|CF037322	2971	351	95.4	blastp
1464	LYM112 H1	maize|gb170|CF037322	2971	448	93.96	tblastn
1465	LYM112 H2	sorghum|09v1|SB02G039985	2972	351	92.43	tblastn
1465	LYM112 H2	sorghum|09v1|SB02G039985	2972	448	84.8	blastp
1466	LYM115 H0	sorghum|09v1|SB01G043900	2973	353	90.19	tblastn
1467	LYM116 H3	sorghum|09v1|SB06G031340	2974	354	88.2	blastp
1468	LYM116 H2	switchgrass|gb167|FE653493	2975	354	80.88	tblastn
1469	LYM116 H3	switchgrass|gb167|FL790906	2976	354	80.88	tblastn
1470	LYM117 H2	maize|gb170|GFXAF243041X1	2977	355	84.4	blastp
1470	LYM117 H2	maize|gb170|GFXAF243041X1	2977	449	84.5	blastp
1471	LYM117 H3	sorghum|09v1|SB07G027220	2978	355	82.3	blastp
1471	LYM117 H3	sorghum|09v1|SB07G027220	2978	449	82.3	blastp
1472	LYM121 H1	rice|gb170|OS12G02620	2979	357	90.6	blastp
1473	LYM123 H4	barley|gb157SOLEXA|AF268595	2980	358	85.5	blastp
1474	LYM123 H5	brachypodium|09v1|GT761722	2981	358	84	blastp
1475	LYM123 H6	maize|gb170|AI795558	2982	358	85.2	blastp
1476	LYM123 H7	sorghum|09v1|SB06G031680	2983	358	86.3	blastp
1477	LYM123 H4	wheat|gb164|BE401871	2984	358	85.6	blastp
1478	LYM135 H1	brachypodium|09v1|DV480514	2985	359	93.1	blastp
1479	LYM135 H2	maize|gb170|CB885667	2986	359	80.2	blastp
1480	LYM135 H3	sorghum|09v1|SB10G007850	2987	359	84.1	blastp
1481	LYM138 H2	brachypodium|09v1|GT810825	2988	360	84	blastp
1482	LYM138 H3	maize|gb170|AI612333	2989	360	86.17	tblastn

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1483	LYM138 H4	sorghum|09v1|SB06G031570	2990	360	86.33	tblastn
1484	LYM146 H2	brachypodium|09v1|SRR031798S0143459	2991	361	84.3	blastp
1485	LYM146 H3	rice|gb170|OS03G21730	2992	361	86.4	blastp
1486	LYM146 H4	sorghum|09v1|SB01G036160	2993	361	96	blastp
1487	LYM147 H0	sorghum|09v1|SB03G003200	2994	362	82	blastp
1488	LYM154 H0	wheat|gb164|BE500571	2995	363	82.5	blastp
1489	LYM155 H3	brachypodium|09v1|DV479969	2996	364	84.7	blastp
1489	LYM155 H3	brachypodium|09v1|DV479969	2996	451	83.5	blastp
1490	LYM155 H4	rice|gb170|OS03G58890	2997	364	81.3	blastp
1490	LYM155 H4	rice|gb170|OS03G58890	2997	451	80	blastp
1491	LYM155 H3	wheat|gb164|BQ801019	2998	364	92.3	blastp
1491	LYM155 H3	wheat|gb164|BQ801019	2998	451	91.6	blastp
1492	LYM180 H0	brachypodium|09v1|DV473436	2999	365	82.9	blastp
1492	LYM180 H0	brachypodium|09v1|DV473436	2999	452	83.54	tblastn
1493	LYM181 H3	brachypodium|09v1|DV485149	3000	366	85.3	blastp
1493	LYM181 H3	brachypodium|09v1|DV485149	3000	453	84.68	tblastn
1494	LYM181 H4	maize|gb170|DR452216	3001	366	80.8	blastp
1494	LYM181 H4	maize|gb170|DR452216	3001	453	81.25	tblastn
1495	LYM181 H5	rice|gb170|OS07G32010	3002	366	82.8	blastp
1496	LYM181 H6	sorghum|09v1|SB02G034110	3003	366	83.5	blastp
1497	LYM181 H2	wheat|gb164|BE425377	3004	453	87.16	tblastn
1498	LYM181 H3	wheat|gb164|BG905028	3005	453	93.58	tblastn
1499	LYM182 H8	brachypodium|09v1|GT780326	3006	367	87.64	tblastn
1500	LYM182 H9	maize|gb170|AI795737	3007	367	84.27	tblastn
1501	LYM182 H10	millet|09v1|EVO454PM084568	3008	367	82.02	tblastn
1502	LYM182 H11	rice|gb170|OS04G33300	3009	367	82.02	tblastn
1503	LYM182 H12	sorghum|09v1|SB06G015280	3010	367	83.15	tblastn

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1504	LYM182H13	sugarcane|gb157.3|CA066047	3011	367	83.15	tblastn
1505	LYM182H6	switchgrass|gb167|FE610729	3012	367	82.02	tblastn
1506	LYM182H7	switchgrass|gb167|FL699214	3013	367	83.15	tblastn
1507	LYM182H8	wheat|gb164|BF200136	3014	367	95.51	tblastn
1508	LYM184H5	brachypodium|09v1|DV476770	3015	454	82.68	tblastn
1509	LYM184H6	brachypodium|09v1|GT762544	3016	454	82.61	tblastn
1510	LYM184H7	brachypodium|09v1|SRR031799S0153720	3017	454	82.68	tblastn
1511	LYM184H3	leymus|gb166|EG385150	3018	454	84.8	blastp
1512	LYM184H8	maize|gb170|AI691210	3019	382	100	blastp
1512	LYM184H8	maize|gb170|AI691210	3019	454	80.87	tblastn
1513	LYM206H2	sorghum|09v1|SB07G021090	3020	382	84.5	blastp
1513	LYM206H2	sorghum|09v1|SB07G021090	3020	454	80.52	tblastn
1514	LYM184H4	switchgrass|gb167|FL704827	3021	454	80.5	blastp
1515	LYM184H5	wheat|gb164|AL821254	3022	368	82.66	tblastn
1515	LYM184H5	wheat|gb164|AL821254	3022	454	86.96	tblastn
1516	LYM185H1	pseudoroegneria|gb167|FF360278	3023	455	91.53	tblastn
1517	LYM185H2	wheat|gb164|BG906077	3024	455	85.31	tblastn
1518	LYM186H4	brachypodium|09v1|GT761126	3025	370	90.7	blastp
1519	LYM186H5	maize|gb170|BE552887	3026	370	82.5	tblastn
1520	LYM186H6	rice|gb170|OS10G39930	3027	370	86.3	blastp
1521	LYM186H7	sorghum|09v1|SB01G030050	3028	370	86.5	blastp
1522	LYM186H4	wheat|gb164|BE429425	3029	370	97.6	blastp
1523	LYM188H8	brachypodium|09v1|DV475481	3030	371	92.4	blastp
1523	LYM188H8	brachypodium|09v1|DV475481	3030	456	89.41	tblastn
1524	LYM188H9	maize|gb170|AI622726	3031	371	87.2	blastp
1524	LYM188H9	maize|gb170|AI622726	3031	456	83.47	tblastn
1525	LYM188H10	maize|gb170|AW424865	3032	371	86	blastp

Nucl. SEQ ID NO:	***Gene Name***	***cluster name***	***Polyp. SEQ ID NO:***	***Homolog. to SEQ ID NO:***	***% global identity***	***Algor.***
1525	LYM188H10	maize|gb170|AW424865	3032	456	83.9	tblastn
1526	LYM188H11	millet|09v1|EVO454PM011140	3033	456	85.17	tblastn
1527	LYM188H3	pseudoroegneria|gb167|FF341644	3034	456	80.5	blastp
1528	LYM188H12	rice|gb170|OS03G53960	3035	371	88.2	blastp
1528	LYM188H12	rice|gb170|OS03G53960	3035	456	84.75	tblastn
1529	LYM188H13	sorghum|09v1|SB01G007950	3036	371	87.4	blastp
1529	LYM188H13	sorghum|09v1|SB01G007950	3036	456	84.32	tblastn
1530	LYM188H14	sugarcane|gb157.3|BQ530106	3037	371	87.4	blastp
1530	LYM188H14	sugarcane|gb157.3|BQ530106	3037	456	84.32	tblastn
1531	LYM188H7	switchgrass|gb167|FL709807	3038	456	84.32	tblastn
1532	LYM188H8	wheat|gb164|CA742940	3039	456	81.78	tblastn
1533	LYM193H1	leymus|gb166|EG381914	3040	459	87.1	tblastn
1534	LYM193H2	wheat|gb164|BQ236678	3041	459	85.26	tblastn
1535	LYM194H0	brachypodium|09v1|SRR031796S0004815	3042	375	84.8	blastp
1536	LYM194H1	maize|gb170|BQ539102	3043	375	82.1	blastp
1537	LYM194H2	sorghum|09v1|SB06G015320	3044	375	84.9	blastp
1538	LYM194H3	switchgrass|gb167|FE645079	3045	375	82.9	blastp
1539	LYM194H4	wheat|gb164|BE518078	3046	375	96.3	blastp
1540	LYM197H2	sugarcane|gb157.3|BQ536804	3047	377	88.57	tblastn
1541	LYM198H1	sorghum|09v1|SB01G045460	3048	378	85.5	blastp
1542	LYM201H1	aquilegia|gb157.3|DR915888	3049	379	82.4	blastp
1543	LYM201H19	arabidopsis lyrata|09v1|JGIAL022871	3050	379	80.07	tblastn
1544	LYM201H2	artemisia|gb164|EY033288	3051	379	80.5	blastp
1545	LYM201H3	b rapa|gb162|CV433700	3052	379	80.3	blastp
1546	LYM201H20	brachypodium|09v1|DV471345	3053	379	93.8	blastp
1547	LYM201H21	brachypodium|09v1|GT759255	3054	379	81.2	blastp

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1548	LYM201 H22	cassava|09v1|DQ138370	3055	379	82.2	blastp
1549	LYM201 H23	cassava|09v1|FF380539	3056	379	81.3	blastp
1550	LYM201 H24	castorbean|09v1|EE256048	3057	379	81.4	blastp
1551	LYM201 H25	chestnut|gb170|SRR006295S0006313	3058	379	80.6	blastp
1552	LYM201 H7	cotton|gb164|AI728378	3059	379	81.7	blastp
1553	LYM201 H8	cotton|gb164|CO070970	3060	379	82	blastp
1554	LYM201 H26	cucumber|09v1|AM731598	3061	379	81.7	blastp
1555	LYM201 H27	lotus|09v1|BI419437	3062	379	80.5	blastp
1556	LYM201 H28	maize|gb170|AI978254	3063	379	98.2	blastp
1557	LYM201 H29	maize|gb170|DR971118	3064	379	80.1	blastp
1558	LYM201 H30	medicago|09v1|AW684099	3065	379	80.7	blastp
1559	LYM201 H31	oak|gb170|CU656181	3066	379	82.56	tblastn
1560	LYM201 H32	poplar|gb170|BI069637	3067	379	81.3	blastp
1561	LYM201 H33	poplar|gb170|BU887151	3068	379	80.7	blastp
1562	LYM201 H34	rice|gb170|OS02G34560	3069	379	95.2	blastp
1563	LYM201 H35	solanum phureja|09v1|SPHBG123984	3070	379	81.4	blastp
1564	LYM201 H36	solanum phureja|09v1|SPHBG129477	3071	379	81.2	blastp
1565	LYM201 H37	sorghum|09v1|SB04G022350	3072	379	98.4	blastp
1566	LYM201 H15	soybean|gb168|AL367670	3073	379	80.7	blastp
1567	LYM201 H16	soybean|gb168|AW684099	3074	379	80.5	blastp
1568	LYM201 H38	sugarcane|gb157.3|CA065291	3075	379	98.6	blastp
1569	LYM201 H18	switchgrass|gb167|FE641755	3076	379	98.2	blastp
1570	LYM201 H39	tomato|09v1|BG123984	3077	379	81.4	blastp
1571	LYM201 H40	tomato|09v1|BG129477	3078	379	81.2	blastp
1572	LYM201 H19	wheat|gb164|BE403168	3079	379	93.2	blastp
1573	LYM203 H9	barley|gb157SOLEXA|BI949918	3080	380	84.7	blastp

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1574	LYM203H10	lolium|09v1|AU247009	3081	380	85.2	blastp
1575	LYM203H11	maize|gb170|AI629675	3082	380	95.7	blastp
1576	LYM203H12	millet|09v1|EVO454PM058394	3083	380	81.7	blastp
1577	LYM203H13	rice|gb170|OS02G08380	3084	380	89.2	blastp
1578	LYM203H14	sorghum|09v1|SB04G005460	3085	380	96.8	blastp
1579	LYM203H15	sugarcane|gb157.3|CA119568	3086	380	94.1	blastp
1580	LYM203H6	switchgrass|gb167|DN142920	3087	380	95.2	blastp
1581	LYM203H7	switchgrass|gb167|FE617741	3088	380	95.7	blastp
1582	LYM203H8	wheat|gb164|BQ801966	3089	380	85.7	blastp
1583	LYM203H9	wheat|gb164|BQ903230	3090	380	86.2	blastp
1584	LYM206H3	maize|gb170|AW055997	3091	382	84.1	blastp
1585	LYM207H2	maize|gb170|BM340289	3092	383	86.5	blastp
1586	LYM207H3	sorghum|09v1|SB06G023870	3093	383	94.3	blastp
1587	LYM207H2	switchgrass|gb167|FE601320	3094	383	82.3	blastp
1588	LYM208H6	maize|gb170|AI691368	3095	384	94.4	blastp
1589	LYM208H7	rice|gb170|OS09G01690	3096	384	82	blastp
1590	LYM208H8	sorghum|09v1|SB01G032070	3097	384	92.1	blastp
1591	LYM208H9	sorghum|09v1|SB08G002510	3098	384	86.6	blastp
1592	LYM208H5	switchgrass|gb167|FE612629	3099	384	90.4	blastp
1593	LYM208H6	switchgrass|gb167|FL729765	3100	384	90.4	blastp
1594	LYM212H6	barley|gb157SOLEXA|BF623682	3101	385	80.3	blastp
1595	LYM212H7	maize|gb170|AI677474	3102	385	88.5	blastp
1596	LYM212H8	rice|gb170|OS03G07910	3103	385	80.11	tblastn
1597	LYM212H9	sorghum|09v1|SB01G045480	3104	385	92.5	blastp
1598	LYM212H10	sugarcane|gb157.3|CA088789	3105	385	92	blastp
1599	LYM212H6	wheat|gb164|BE402242	3106	385	80.38	tblastn
1600	LYM213H1	maize|gb170|AW282249	3107	386	90.9	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1601	LYM213 H2	sorghum|09v1|SB06G018770	3108	386	91.7	blastp
1602	LYM215 H2	switchgrass|gb167|FE618086	3109	387	90.42	tblastn
1603	LYM217 H3	sorghum|09v1|SB01G043910	3110	388	88.2	blastp
1604	LYM217 H4	sugarcane|gb157.3|CA136491	3111	388	87.7	blastp
1605	LYM217 H3	switchgrass|gb167|FE606442	3112	388	86.7	blastp
1606	LYM221 H1	brachypodium|09v1|GT792319	3113	391	83.8	blastp
1606	LYM221 H1	brachypodium|09v1|GT792319	3113	461	81.3	blastp
1607	LYM221 H2	rice|gb170|OS03G24870	3114	391	82.9	blastp
1607	LYM221 H2	rice|gb170|OS03G24870	3114	461	80.5	blastp
1608	LYM221 H3	sorghum|09v1|SB01G034610	3115	391	90.7	blastp
1608	LYM221 H3	sorghum|09v1|SB01G034610	3115	461	88.7	blastp
1609	LYM224 H2	brachypodium|09v1|GT762108	3116	393	82.4	blastp
1610	LYM224 H3	sorghum|09v1|SB02G040000	3117	393	92.9	blastp
1611	LYM224 H2	switchgrass|gb167|FE617506	3118	393	83.19	tblastn
1612	LYM227 H1	sorghum|09v1|SB01G043140	3119	394	88.3	blastp
1613	LYM228 H1	sorghum|09v1|SB09G006910	3120	395	85	blastp
1613	LYM228 H1	sorghum|09v1|SB09G006910	3120	462	83.7	blastp
1614	LYM232 H3	sorghum|09v1|SB02G000450	3121	396	80.4	blastp
1615	LYM232 H4	sugarcane|gb157.3|CA073189	3122	396	80.8	blastp
1616	LYM232 H3	switchgrass|gb167|FL849399	3123	396	80.7	blastp
1617	LYM233 H0	brachypodium|09v1|TMPLOS01G70020T1	3124	397	99.6	blastp
1618	LYM234 H0	rice|gb170|OS07G38290	3125	398	81.3	blastp
1619	LYM236 H99	apple|gb171|CN488568	3126	399	89.1	blastp
1620	LYM236 H100	apple|gb171|CN883100	3127	399	89.6	blastp
1621	LYM236 H3	aquilegia|gb157.3|DR919774	3128	399	87.4	blastp
1622	LYM236 H101	arabidopsis lyrata|09v1|JGIAL005113	3129	399	83.9	blastp

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1623	LYM236 H102	arabidopsis lyrata|09v1|JGIAL006646	3130	399	86.89	tblastn
1624	LYM236 H4	arabidopsis|gb165|AT1G54340	3131	399	83.5	blastp
1625	LYM236 H5	arabidopsis|gb165|AT1G65930	3132	399	87.1	blastp
1626	LYM236 H6	artemisia|gb164|EY034635	3133	399	87.9	blastp
1627	LYM236 H7	avocado|gb164|CO995120	3134	399	91.3	blastp
1628	LYM236 H8	b oleracea|gb161|DY028218	3135	399	87.2	blastp
1629	LYM236 H9	b rapa|gb162|CX269094	3136	399	87.2	blastp
1630	LYM236 H10	b rapa|gb162|GFXAF258246X1	3137	399	84.3	tblastn
1631	LYM236 H11	b rapa|gb162|L47856	3138	399	87.2	blastp
1632	LYM236 H103	barley|gb157SOLEXA|AL502504	3139	399	89.3	blastp
1633	LYM236 H13	basilicum|gb157.3|DY322368	3140	399	87.7	blastp
1634	LYM236 H14	bean|gb167|CA896841	3141	399	87.9	blastp
1635	LYM236 H104	brachypodium|09v1|DV478973	3142	399	85.3	blastp
1636	LYM236 H105	brachypodium|09v1|DV482439	3143	399	90.5	blastp
1637	LYM236 H17	cacao|gb167|DQ448875	3144	399	89.2	blastp
1638	LYM236 H18	canola|gb161|BQ704958	3145	399	87.2	blastp
1639	LYM236 H19	canola|gb161|CD817340	3146	399	87.2	blastp
1640	LYM236 H20	canola|gb161|CD833108	3147	399	83.9	blastp
1641	LYM236 H21	canola|gb161|CX189442	3148	399	86.5	blastp
1642	LYM236 H22	canola|gb161|DY011390	3149	399	87.2	blastp
1643	LYM236 H106	cassava|09v1|CK642610	3150	399	90.1	blastp
1644	LYM236 H107	cassava|09v1|DV457942	3151	399	87.5	blastp
1645	LYM236 H108	castorbean|09v1|EE256632	3152	399	86.1	blastp
1646	LYM236 H109	castorbean|09v1|EE259479	3153	399	90.6	blastp
1647	LYM236 H26	centaurea|gb166|EH731203	3154	399	81.2	blastp

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1648	LYM236 H27	centaurea|gb166|EL932337	3155	399	86.6	blastp
1649	LYM236 H110	chestnut|gb170|SRR006295S0002580	3156	399	82.27	tblastn
1650	LYM236 H111	chestnut|gb170|SRR006295S0002701	3157	399	89.6	blastp
1651	LYM236 H112	cichorium|gb171|EH675189	3158	399	87.3	blastp
1652	LYM236 H113	cichorium|gb171|EH683726	3159	399	89.1	blastp
1653	LYM236 H30	citrus|gb166|AF176669	3160	399	90.6	blastp
1654	LYM236 H31	citrus|gb166|CD573911	3161	399	85.1	blastp
1655	LYM236 H32	coffea|gb157.2|DV663279	3162	399	87.8	blastp
1656	LYM236 H33	cotton|gb164|AI727260	3163	399	87.2	blastp
1657	LYM236 H34	cotton|gb164|BF278588	3164	399	83.5	blastp
1658	LYM236 H35	cowpea|gb166|FC458136	3165	399	89.1	blastp
1659	LYM236 H36	cynara|gb167|GE577243	3166	399	86.47	tblastn
1660	LYM236 H37	cynara|gb167|GE579663	3167	399	88.6	blastp
1661	LYM236 H38	dandelion|gb161|DY804243	3168	399	86.96	tblastn
1662	LYM236 H39	eucalyptus|gb166|X97063	3169	399	88	blastp
1663	LYM236 H40	fescue|gb161|CK801045	3170	399	89.8	blastp
1664	LYM236 H41	fescue|gb161|DT674724	3171	399	90	blastp
1665	LYM236 H42	ginger|gb164|DY360289	3172	399	91.3	blastp
1666	LYM236 H43	grape|gb160|BM436755	3173	399	89.9	blastp
1667	LYM236 H44	kiwi|gb166|FG396670	3174	399	88.2	blastp
1668	LYM236 H45	kiwi|gb166|FG397107	3175	399	88.7	blastp
1669	LYM236 H46	kiwi|gb166|FG397291	3176	399	89.4	blastp
1670	LYM236 H47	lettuce|gb157.2|DW088948	3177	399	87.4	blastp
1671	LYM236 H48	leymus|gb166|CD809160	3178	399	89.6	blastp
1672	LYM236 H49	liriodendron|gb166|CK762229	3179	399	88.2	blastp
1673	LYM236 H114	lotus|09v1|AW428686	3180	399	89.4	blastp
1674	LYM236 H115	lotus|09v1|BP033879	3181	399	83.7	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1675	LYM236 H51	lovegrass|gb167|DN480596	3182	399	90.8	blastp
1676	LYM236 H116	maize|gb170|AI600815	3183	399	93.7	blastp
1677	LYM236 H117	maize|gb170|AW313297	3184	399	92.2	blastp
1678	LYM236 H118	maize|gb170|W21690	3185	399	91.3	blastp
1679	LYM236 H119	medicago|09v1|AW191201	3186	399	88.2	blastp
1680	LYM236 H120	medicago|09v1|AW689032	3187	399	84.9	blastp
1681	LYM236 H121	millet|09v1|CD725798	3188	399	92.5	blastp
1682	LYM236 H122	millet|09v1|EVO454PM002708	3189	399	94.2	blastp
1683	LYM236 H123	monkeyflower|09v1|DV206036	3190	399	87.4	blastp
1684	LYM236 H56	nicotiana benthamiana|gb162|CK291144	3191	399	86.5	blastp
1685	LYM236 H57	oil palm|gb166|EL684429	3192	399	87.3	blastp
1686	LYM236 H124	peanut|gb171|CD038682	3193	399	87.9	blastp
1687	LYM236 H125	pea|09v1|CD860585	3194	399	89.6	blastp
1688	LYM236 H126	pepper|gb171|BM061761	3195	399	88	blastp
1689	LYM236 H127	pepper|gb171|CA516582	3196	399	85.3	blastp
1690	LYM236 H128	petunia|gb171|DC240208	3197	399	88.2	blastp
1691	LYM236 H129	physcomitrella|10v1|AW497149	3198	399	82.2	blastp
1692	LYM236 H62	pine|gb157.2|AW010292	3199	399	85.6	blastp
1693	LYM236 H63	pine|gb157.2|BX249826	3200	399	85.6	blastp
1694	LYM236 H130	poplar|gb170|AI161956	3201	399	89.6	blastp
1695	LYM236 H131	poplar|gb170|BI127706	3202	399	86.6	blastp
1696	LYM236 H132	poplar|gb170|BI131610	3203	399	86.8	blastp
1697	LYM236 H133	poplar|gb170|BU821063	3204	399	90.4	blastp
1698	LYM236 H66	potato|gb157.2|BG591093	3205	399	88	blastp
1699	LYM236 H67	prunus|gb167|AF367443	3206	399	89.4	blastp
1700	LYM236 H68	radish|gb164|EV526847	3207	399	85.8	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1701	LYM236 H69	radish|gb164|EV531225	3208	399	86.9	blastp
1702	LYM236 H134	rice|gb170|OS01G14580	3209	399	84.8	blastp
1703	LYM236 H135	rice|gb170|OS01G46610	3210	399	93	blastp
1704	LYM236 H72	rye|gb164|BE494776	3211	399	86.17	tblastn
1705	LYM236 H73	safflower|gb162|EL372795	3212	399	87.3	blastp
1706	LYM236 H74	safflower|gb162|EL374725	3213	399	89.1	blastp
1707	LYM236 H136	solanum phureja|09v1|SPHBG131802	3214	399	86.3	blastp
1708	LYM236 H137	solanum phureja|09v1|SPHBG629432	3215	399	87.7	blastp
1709	LYM236 H138	sorghum|09v1|SB03G029840	3216	399	92	blastp
1710	LYM236 H139	sorghum|09v1|SB09G029110	3217	399	94.7	blastp
1711	LYM236 H77	soybean|gb168|AW257518	3218	399	88.7	blastp
1712	LYM236 H78	soybean|gb168|AW689032	3219	399	85.6	blastp
1713	LYM236 H79	soybean|gb168|FF554826	3220	399	84.7	blastp
1714	LYM236 H80	soybean|gb168|SOYIDH	3221	399	89.4	blastp
1715	LYM236 H81	spikemoss|gb165|FE441231	3222	399	84.2	blastp
1716	LYM236 H82	spikemoss|gb165|FE443181	3223	399	82.3	blastp
1717	LYM236 H83	spruce|gb162|CO225856	3224	399	85	blastp
1718	LYM236 H84	strawberry|gb164|DV438767	3225	399	82.6	blastp
1719	LYM236 H140	sugarcane|gb157.3|BU103347	3226	399	94.5	blastp
1720	LYM236 H141	sugarcane|gb157.3|CA070718	3227	399	92.5	blastp
1721	LYM236 H87	sunflower|gb162|CD846861	3228	399	86.6	blastp
1722	LYM236 H88	sunflower|gb162|CD854278	3229	399	87.9	blastp
1723	LYM236 H89	switchgrass|gb167|DN142415	3230	399	92	blastp
1724	LYM236 H90	switchgrass|gb167|DN143508	3231	399	95.4	blastp
1725	LYM236 H91	switchgrass|gb167|DN150237	3232	399	95.2	blastp
1726	LYM236 H92	switchgrass|gb167|DN151575	3233	399	92.2	blastp

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1727	LYM236 H93	thellungiella|gb167|DN774112	3234	399	87.14	tblastn
1728	LYM236 H94	tobacco|gb162|DV158343	3235	399	83.3	blastp
1729	LYM236 H95	tobacco|gb162|X77944	3236	399	88.5	blastp
1730	LYM236 H142	tomato|09v1|BG131802	3237	399	85.6	blastp
1731	LYM236 H143	tomato|09v1|BG629432	3238	399	87.3	blastp
1732	LYM236 H98	triphysaria|gb164|DR171747	3239	399	88.4	blastp
1733	LYM236 H99	wheat|gb164|BE442540	3240	399	84.1	blastp
1734	LYM238 H0	rice|gb170|OS05G45080	3241	400	95.4	blastp
1735	LYM240 H9	barley|gb157SOLEXA|AL508021	3242	402	91.9	blastp
1736	LYM240 H10	brachypodium|09v1|GT810642	3243	402	91.9	blastp
1737	LYM240 H11	maize|gb170|DR972790	3244	402	84.2	blastp
1738	LYM240 H12	sorghum|09v1|SB02G038240	3245	402	84.2	blastp
1739	LYM240 H13	sugarcane|gb157.3|CA075929	3246	402	82.3	blastp
1740	LYM240 H6	switchgrass|gb167|FE597498	3247	402	81.6	blastp
1741	LYM240 H7	switchgrass|gb167|FE610847	3248	402	80	blastp
1742	LYM240 H8	switchgrass|gb167|FL960804	3249	402	81.6	blastp
1743	LYM240 H9	wheat|gb164|CA674491	3250	402	89.93	tblastn
1744	LYM242 H7	barley|gb157SOLEXA|BE412570	3251	404	82.2	blastp
1745	LYM242 H8	brachypodium|09v1|GT764573	3252	404	86.1	blastp
1746	LYM242 H9	maize|gb170|AI746053	3253	404	83.4	blastp
1747	LYM242 H10	millet|09v1|EVO454PM008771	3254	404	85	blastp
1748	LYM242 H11	sorghum|09v1|SB03G003160	3255	404	82.6	blastp
1749	LYM242 H12	sugarcane|gb157.3|BQ534251	3256	404	83.8	blastp
1750	LYM242 H5	switchgrass|gb167|DN143169	3257	404	85.1	blastp
1751	LYM242 H6	switchgrass|gb167|FE654179	3258	404	85	blastp
1752	LYM242 H7	wheat|gb164|BE403285	3259	404	82.6	blastp
1753	LYM248 H3	brachypodium|09v1|GT773582	3260	407	84.5	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1754	LYM248 H4	maize|gb170|AI966957	3261	407	88.5	blastp
1755	LYM248 H5	sorghum|09v1|SB04G000645	3262	407	88.2	blastp
1756	LYM248 H2	switchgrass|gb167|DN149511	3263	407	81.1	blastp
1757	LYM248 H3	wheat|gb164|BE418033	3264	407	84.89	tblastn
1758	LYM250 H0	rice|gb170|OS09G38700	3265	409	100	tblastn
1758	LYM250 H0	rice|gb170|OS09G38700	3265	463	97.78	tblastn
1759	LYM251 H1	antirrhinum|gb166|AJ560114	3266	410	82	blastp
1760	LYM251 H76	apple|gb171|CN492643	3267	410	80.1	blastp
1761	LYM251 H77	arabidopsis lyrata|09v1|JGIAL012198	3268	410	81.4	blastp
1762	LYM251 H3	arabidopsis|gb165|AT2G17380	3269	410	80.7	blastp
1763	LYM251 H4	arabidopsis|gb165|AT4G35410	3270	410	80.12	tblastn
1764	LYM251 H5	b oleracea|gb161|AM385265	3271	410	81.4	blastp
1765	LYM251 H6	b rapa|gb162|L33527	3272	410	81.4	blastp
1766	LYM251 H7	banana|gb167|FF558300	3273	410	81.37	tblastn
1767	LYM251 H78	barley|gb157SOLEXA|BE421807	3274	410	81.4	blastp
1768	LYM251 H9	basilicum|gb157.3|DY343154	3275	410	80.12	tblastn
1769	LYM251 H11	bean|gb167|CV536707	3276	410	80.1	blastp
1770	LYM251 H79	brachypodium|09v1|DV469153	3277	410	82.6	blastp
1771	LYM251 H13	canola|gb161|CN726086	3278	410	81.4	blastp
1772	LYM251 H80	cassava|09v1|CK650427	3279	410	80.12	tblastn
1773	LYM251 H81	cassava|09v1|DV448885	3280	410	81.4	blastp
1774	LYM251 H82	castorbean|09v1|XM002514342	3281	410	81.4	blastp
1775	LYM251 H16	catharanthus|gb166|EG554670	3282	410	81.4	blastp
1776	LYM251 H17	centaurea|gb166|EH737707	3283	410	81.4	blastp
1777	LYM251 H18	centaurea|gb166|EH782010	3284	410	81.4	blastp
1778	LYM251 H83	chestnut|gb170|SRR006295S0001854	3285	410	80.1	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1779	LYM251 H84	chickpea|09v2|DY475463	3286	410	80.12	tblastn
1780	LYM251 H85	cichorium|gb171|EH677909	3287	410	81.4	blastp
1781	LYM251 H86	cichorium|gb171|EH681849	3288	410	80.7	blastp
1782	LYM251 H21	citrus|gb166|CF419015	3289	410	82	blastp
1783	LYM251 H22	clover|gb162|BB935136	3290	410	81.4	blastp
1784	LYM251 H23	cowpea|gb166|FF383763	3291	410	80.1	blastp
1785	LYM251 H87	cucumber|09v1|CK085508	3292	410	80.1	blastp
1786	LYM251 H24	dandelion|gb161|DY822878	3293	410	80.1	blastp
1787	LYM251 H25	eucalyptus|gb166|CT981708	3294	410	80.7	blastp
1788	LYM251 H88	fern|gb171|DK949355	3295	410	80.1	blastp
1789	LYM251 H26	fescue|gb161|DT702820	3296	410	82.6	blastp
1790	LYM251 H89	gerbera|09v1|AJ756319	3297	410	80.7	blastp
1791	LYM251 H27	grape|gb160|CB008191	3298	410	82	blastp
1792	LYM251 H28	grape|gb160|CD799819	3299	410	82	blastp
1793	LYM251 H29	ipomoea|gb157.2|CJ751066	3300	410	81.4	blastp
1794	LYM251 H90	jatropha|09v1|GO247140	3301	410	80.7	blastp
1795	LYM251 H30	lettuce|gb157.2|DW045452	3302	410	81.4	blastp
1796	LYM251 H31	liriodendron|gb166|CK762515	3303	410	83.2	blastp
1797	LYM251 H91	maize|gb170|AA979856	3304	410	83.23	tblastn
1798	LYM251 H92	maize|gb170|AI619342	3305	410	83.2	blastp
1799	LYM251 H93	maize|gb170|AW134457	3306	410	91.3	tblastn
1800	LYM251 H94	medicago|09v1|MSU93094	3307	410	82	blastp
1801	LYM251 H36	melon|gb165|DV633583	3308	410	80.1	blastp
1802	LYM251 H95	millet|09v1|EVO454PM010186	3309	410	83.2	blastp
1803	LYM251 H96	millet|09v1|EVO454PM104784	3310	410	91.93	tblastn
1804	LYM251 H97	monkeyflower|09v1|GR007448	3311	410	82.6	blastp
1805	LYM251 H37	nuphar|gb166|DT588573	3312	410	82	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1806	LYM251 H98	oak|gb170|DN949793	3313	410	80.1	blastp
1807	LYM251 H38	papaya|gb165|EX261560	3314	410	81.4	blastp
1808	LYM251 H99	peanut|gb171|EH046845	3315	410	82	blastp
1809	LYM251 H100	pepper|gb171|BM068291	3316	410	83.2	blastp
1810	LYM251 H101	petunia|gb171|FN005056	3317	410	82.6	blastp
1811	LYM251 H42	pine|gb157.2|AA556857	3318	410	81.4	blastp
1812	LYM251 H43	pine|gb157.2|AW289837	3319	410	81.4	blastp
1813	LYM251 H102	poplar|gb170|AI165130	3320	410	80.1	blastp
1814	LYM251 H45	poppy|gb166|FG613763	3321	410	80.1	blastp
1815	LYM251 H46	potato|gb157.2|BF054079	3322	410	82.6	blastp
1816	LYM251 H47	pseudoroegneria|gb167|FF342572	3323	410	80.7	blastp
1817	LYM251 H48	radish|gb164|EV525206	3324	410	80.7	blastp
1818	LYM251 H49	radish|gb164|EV528593	3325	410	80.7	blastp
1819	LYM251 H50	radish|gb164|EV534996	3326	410	81.4	blastp
1820	LYM251 H51	radish|gb164|EV565677	3327	410	81.4	blastp
1821	LYM251 H103	rice|gb170|OS03G57040	3328	410	82.6	blastp
1822	LYM251 H53	rye|gb164|BE637009	3329	410	80.7	blastp
1823	LYM251 H54	safflower|gb162|EL402398	3330	410	81.4	blastp
1824	LYM251 H104	solanum phureja|09v1|SPHBG126373	3331	410	82.6	blastp
1825	LYM251 H105	sorghum|09v1|SB01G003840	3332	410	91.3	tblastn
1826	LYM251 H106	sorghum|09v1|SB01G006180	3333	410	83.2	blastp
1827	LYM251 H57	soybean|gb168|AW685285	3334	410	81.4	blastp
1828	LYM251 H58	soybean|gb168|BQ154723	3335	410	80.1	blastp
1829	LYM251 H59	spruce|gb162|Z93754	3336	410	80.7	blastp
1830	LYM251 H107	sugarcane|gb157.3|BQ533200	3337	410	83.2	blastp
1831	LYM251 H108	sugarcane|gb157.3|BU103624	3338	410	83.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1832	LYM251 H62	sunflower|gb162|CD854801	3339	410	81.4	blastp
1833	LYM251 H63	sunflower|gb162|DY917387	3340	410	81.4	blastp
1834	LYM251 H64	sunflower|gb162|EL485634	3341	410	81.4	blastp
1835	LYM251 H65	switchgrass|gb167|DN152225	3342	410	83.2	blastp
1836	LYM251 H66	switchgrass|gb167|DN152580	3343	410	82	blastp
1837	LYM251 H67	switchgrass|gb167|FL827716	3344	410	92.5	blastp
1838	LYM251 H68	thellungiella|gb167|DN776639	3345	410	80.7	blastp
1839	LYM251 H69	tobacco|gb162|CV020782	3346	410	82	blastp
1840	LYM251 H109	tomato|09v1|BG126373	3347	410	83.2	blastp
1841	LYM251 H71	triphysaria|gb164|EY017996	3348	410	80.7	blastp
1842	LYM251 H72	walnuts|gb166|EL892983	3349	410	80.1	blastp
1843	LYM251 H73	walnuts|gb166|EL903496	3350	410	80.1	blastp
1844	LYM251 H74	wheat|gb164|BE444356	3351	410	81.4	blastp
1845	LYM251 H75	wheat|gb164|BE498579	3352	410	81.4	blastp
1846	LYM251 H76	wheat|gb164|BQ905308	3353	410	81.4	blastp
1847	LYM255 H3	brachypodium|09v1|DV486276	3354	413	83.9	blastp
1848	LYM255 H4	maize|gb170|AA072446	3355	413	80.8	blastp
1849	LYM255 H5	sorghum|09v1|SB04G034000	3356	413	82	blastp
1850	LYM255 H3	switchgrass|gb167|FE606184	3357	413	83.8	blastp
1851	LYM260 H0	rice|gb170|OS09G38800	3358	414	80.5	blastp
1852	LYM263 H0	maize|gb170|AI673859	3359	416	87.47	tblastn
1853	LYM183 H8	brachypodium|09v1|DV474476	3360	417	90.5	blastp
1853	LYM183 H8	brachypodium|09v1|DV474476	3360	464	90.5	blastp
1854	LYM183 H1	cenchrus|gb166|EB655853	3361	417	83.5	blastp
1854	LYM183 H1	cenchrus|gb166|EB655853	3361	464	83.5	blastp
1855	LYM183 H2	leymus|gb166|EG375719	3362	417	94.2	blastp
1855	LYM183 H2	leymus|gb166|EG375719	3362	464	94.2	blastp

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1856	LYM183 H9	maize|gb170|AI964673	3363	417	85.2	blastp
1856	LYM183 H9	maize|gb170|AI964673	3363	464	85.2	blastp
1857	LYM183 H10	rice|gb170|OS03G60780	3364	417	84.8	blastp
1857	LYM183 H10	rice|gb170|OS03G60780	3364	464	84.8	blastp
1858	LYM183 H11	sorghum|09v1|SB01G003070	3365	417	84.4	blastp
1858	LYM183 H11	sorghum|09v1|SB01G003070	3365	464	84.4	blastp
1859	LYM183 H12	sugarcane|gb157.3|CA111823	3366	417	83.6	blastp
1859	LYM183 H12	sugarcane|gb157.3|CA111823	3366	464	83.6	blastp
1860	LYM183 H6	switchgrass|gb167|DN151763	3367	417	83.4	blastp
1860	LYM183 H6	switchgrass|gb167|DN151763	3367	464	83.4	blastp
1861	LYM183 H7	wheat|gb164|BE515616	3368	417	93.9	tblastn
1861	LYM183 H7	wheat|gb164|BE515616	3368	464	93.63	tblastn
1862	LYM183 H8	wheat|gb164|BQ160803	3369	417	94.7	blastp
1862	LYM183 H8	wheat|gb164|BQ160803	3369	464	94.7	blastp
1863	LYM256 H2	rice|gb170|OS05G45110	3370	418	87.3	blastp
1864	LYM256 H3	rice|gb170|OS10G07970	3371	418	81.09	tblastn
1865	LYM200 H0	sorghum|09v1|SB04G005600	3372	419	86.5	blastp
1866	LYM267 H1	sorghum|09v1|SB01G044240	3373	420	88.3	blastp
1867	LYM268 H1	sugarcane|gb157.3|CA079076	3374	421	81.6	blastp
1868	LYM270 H0	sorghum|09v1|SB02G040045	3375	422	82.3	blastp
1869	LYM271 H7	barley|gb157SOLEXA|BG344953	3376	423	89.9	blastp
1870	LYM271 H8	brachypodium|09v1|GT838823	3377	423	89.9	blastp
1871	LYM271 H9	rice|gb170|OS07G43460	3378	423	91.1	blastp
1872	LYM271 H10	sorghum|09v1|SB02G040020	3379	423	96.5	blastp
1873	LYM271 H11	sugarcane|gb157.3|CA118167	3380	423	89.53	tblastn
1874	LYM271 H6	switchgrass|gb167|FL691032	3381	423	94.2	blastp
1875	LYM271 H7	wheat|gb164|CJ664209	3382	423	91.5	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1876	LYM273 H4	brachypodium|09v1|DV469687	3383	425	83.3	blastp
1877	LYM273 H5	maize|gb170|AW355978	3384	425	85.2	blastp
1878	LYM273 H6	sorghum|09v1|SB03G044410	3385	425	84	blastp
1879	LYM273 H4	wheat|gb164|BE518377	3386	425	85	blastp
1880	LYM274 H0	rice|gb170|OS01G70240	3387	426	100	blastp
1880	LYM274 H0	rice|gb170|OS01G70240	3387	466	89.2	blastp
1881	LYM278 H9	maize|gb170|LLDQ244681	3388	428	95.2	blastp
1882	LYM278 H2	rye|gb164|Z23257	3389	428	92.86	tblastn
1883	LYM278 H3	wheat|gb164|AL821264	3390	428	95.3	blastp
1884	LYM278 H4	wheat|gb164|BE516723	3391	428	94	blastp
1885	LYM278 H5	wheat|gb164|BF200402	3392	428	86.9	tblastn
1886	LYM278 H6	wheat|gb164|BF474423	3393	428	92.86	tblastn
1887	LYM278 H7	wheat|gb164|BG909462	3394	428	89.3	blastp
1888	LYM278 H8	wheat|gb164|BQ579097	3395	428	95.24	tblastn
1889	LYM278 H9	wheat|gb164|CA650349	3396	428	83.3	blastp
1890	LYM284 H16	barley|gb157SOLEXA|BE438857	3397	430	86.4	blastp
1891	LYM284 H17	brachypodium|09v1|DV474685	3398	430	84.3	blastp
1892	LYM284 H18	brachypodium|09v1|DV488161	3399	430	88.2	blastp
1893	LYM284 H3	fescue|gb161|DT674446	3400	430	86.91	tblastn
1894	LYM284 H19	maize|gb170|AI637256	3401	430	88.5	blastp
1895	LYM284 H20	maize|gb170|AI861131	3402	430	84.3	blastp
1896	LYM284 H21	maize|gb170|BM501276	3403	430	83.8	blastp
1897	LYM284 H22	rice|gb170|OS01G43020	3404	430	81.4	blastp
1898	LYM284 H23	rice|gb170|OS01G46570	3405	430	84.6	blastp
1899	LYM284 H24	sorghum|09v1|SB03G027960	3406	430	80.6	blastp
1900	LYM284 H25	sorghum|09v1|SB03G029790	3407	430	85.1	blastp
1901	LYM284 H26	sorghum|09v1|SB09G029130	3408	430	87.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1902	LYM284H27	sugarcane|gb157.3|BQ533889	3409	430	84.5	blastp
1903	LYM284H12	switchgrass|gb167|DN151636	3410	430	81	blastp
1904	LYM284H13	switchgrass|gb167|FE634580	3411	430	85.4	blastp
1905	LYM284H14	switchgrass|gb167|FL712120	3412	430	89.53	tblastn
1906	LYM284H15	wheat|gb164|BE400789	3413	430	88.1	blastp
1907	LYM284H16	wheat|gb164|BF200804	3414	430	80.4	blastp
1908	LYM285H3	brachypodium|09v1|DV476342	3415	431	89.2	blastp
1909	LYM285H4	maize|gb170|AI372298	3416	431	88.1	blastp
1910	LYM285H5	rice|gb170|OS01G69900	3417	431	99.82	tblastn
1911	LYM285H6	sorghum|09v1|SB03G044210	3418	431	89.3	blastp
1912	LYM285H3	switchgrass|gb167|DN142770	3419	431	89.75	tblastn
1913	LYM288H6	brachypodium|09v1|DV471350	3420	433	83.3	blastp
1914	LYM288H1	leymus|gb166|EG377996	3421	433	84.7	blastp
1915	LYM288H7	maize|gb170|AI977924	3422	433	84.5	blastp
1916	LYM288H8	sorghum|09v1|SB02G039240	3423	433	83.9	blastp
1917	LYM288H9	sugarcane|gb157.3|CA067537	3424	433	85.8	blastp
1918	LYM288H5	switchgrass|gb167|DN151710	3425	433	85.3	blastp
1919	LYM288H6	switchgrass|gb167|FE610990	3426	433	85.3	blastp
1920	LYM289H39	barley|gb157SOLEXA|AL500321	3427	434	91.1	blastp
1921	LYM289H40	barley|gb157SOLEXA|AV915627	3428	434	92.7	blastp
1922	LYM289H41	barley|gb157SOLEXA|BF624195	3429	434	98.2	blastp
1923	LYM289H42	barley|gb157SOLEXA|BF627133	3430	434	92.7	blastp
1924	LYM289H43	barley|gb157SOLEXA|BQ739963	3431	434	92.7	blastp
1925	LYM289H44	brachypodium|09v1|GFXEF059989X41	3432	434	81.8	blastp
1926	LYM289H7	cacao|gb167|CU568933	3433	434	85.5	blastp
1927	LYM289H8	fescue|gb161|CK801501	3434	434	90.9	blastp
1928	LYM289H9	fescue|gb161|DT683663	3435	434	90.9	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1929	LYM289 H10	leymus|gb166|EG376287	3436	434	96.4	blastp
1930	LYM289 H45	lolium|09v1|AU246683	3437	434	89.1	blastp
1931	LYM289 H11	lovegrass|gb167|DN480351	3438	434	87.3	blastp
1932	LYM289 H46	maize|gb170|AI637242	3439	434	81.8	blastp
1933	LYM289 H47	maize|gb170|LLEC865320	3440	434	81.8	blastp
1934	LYM289 H48	maize|gb170|T12715	3441	434	87.3	blastp
1935	LYM289 H49	millet|09v1|CD724594	3442	434	80	blastp
1936	LYM289 H50	millet|09v1|EB410971	3443	434	87.3	blastp
1937	LYM289 H15	oat|gb164|CN818354	3444	434	90.9	blastp
1938	LYM289 H16	pineapple|gb157.2|DT337702	3445	434	80	blastp
1939	LYM289 H51	rice|gb170|OS06G05120	3446	434	83.6	blastp
1940	LYM289 H52	sorghum|09v1|SB09G005410	3447	434	80	blastp
1941	LYM289 H53	sorghum|09v1|SB10G002980	3448	434	87.3	blastp
1942	LYM289 H54	sugarcane|gb157.3|CA117495	3449	434	87.3	blastp
1943	LYM289 H55	sugarcane|gb157.3|CA149658	3450	434	81.8	blastp
1944	LYM289 H56	sugarcane|gb157.3|CF575668	3451	434	87.3	blastp
1945	LYM289 H23	switchgrass|gb167|DN144776	3452	434	80	blastp
1946	LYM289 H24	switchgrass|gb167|DN144989	3453	434	89.1	blastp
1947	LYM289 H25	switchgrass|gb167|FE607508	3454	434	89.1	blastp
1948	LYM289 H26	switchgrass|gb167|FL736037	3455	434	81.8	blastp
1949	LYM289 H27	wheat|gb164|AL811119	3456	434	98.2	blastp
1950	LYM289 H28	wheat|gb164|BE443786	3457	434	96.4	blastp
1951	LYM289 H29	wheat|gb164|BG907098	3458	434	98.2	blastp
1952	LYM289 H30	wheat|gb164|BM136571	3459	434	96.4	blastp
1953	LYM289 H31	wheat|gb164|BQ804261	3460	434	96.4	blastp
1954	LYM289 H32	wheat|gb164|CA616586	3461	434	81.8	blastp
1955	LYM289 H33	wheat|gb164|CA640178	3462	434	98.2	blastp

Nucl. SEQ ID NO:	*Gene Name*	*cluster name*	*Polyp. SEQ ID NO:*	*Homolog. to SEQ ID NO:*	*% global identity*	*Algor.*
1956	LYM289 H34	wheat|gb164|CA643784	3463	434	98.2	blastp
1957	LYM289 H35	wheat|gb164|CA733972	3464	434	80.36	tblastn
1958	LYM289 H36	wheat|gb164|CD896873	3465	434	82.1	blastp
1959	LYM289 H37	wheat|gb164|CJ586709	3466	434	89.1	blastp
1960	LYM289 H38	wheat|gb164|CJ646970	3467	434	80	blastp
1961	LYM289 H39	wheat|gb164|CJ903378	3468	434	96.4	blastp
1962	LYM290 H10	barley|gb157SOLEXA|BE412989	3469	435	82.9	blastp
1963	LYM290 H11	brachypodium|09v1|GT759831	3470	435	81.9	blastp
1964	LYM290 H12	rice|gb170|OS04G20230	3471	435	82.9	blastp
1965	LYM290 H3	rye|gb164|BE495099	3472	435	81.9	blastp
1966	LYM290 H13	sorghum|09v1|SB01G009390	3473	435	95.2	blastp
1967	LYM290 H14	sorghum|09v1|SB06G004500	3474	435	94.8	blastp
1968	LYM290 H15	sugarcane|gb157.3|BQ535968	3475	435	95.7	blastp
1969	LYM290 H16	sugarcane|gb157.3|CA136629	3476	435	80.3	blastp
1970	LYM290 H8	switchgrass|gb167|FE622978	3477	435	91.4	blastp
1971	LYM290 H9	wheat|gb164|BE430090	3478	435	83.3	blastp
1972	LYM290 H10	wheat|gb164|BF199524	3479	435	82.4	blastp
1973	LYM293 H0	rice|gb170|OS09G38510	3480	437	91.8	blastp

Table 2: Provided are the homologous polypeptides and polynucleotides of the genes for increasing yield (e.g., oil yield, seed yield, fiber yield and/or quality), growth rate, vigor, biomass, abiotic stress tolerance, nitrogen use efficiency, water use efficiency and fertilizer use efficiency genes of a plant which are listed in Table 1 above. Homology was calculated as% of identity over the aligned sequences. The query sequences were polynucleotide sequences SEQ ID NOs:1-239 and polypeptide SEQ ID NOs:240-465 and the subject sequences are protein sequences identified in the database based on greater than 80% identity to the predicted translated sequences of the query nucleotide sequences or to the polypeptide sequences. "Nucl." = polynucleotide; "polyp." = polypeptide; "Algor." = algorithm (used for sequence alignment and determination of percent homology).

The following sequences were found to be 100% identical: SEQ ID NO: 4 is identical to SEQ ID NO: 478; SEQ ID NO: 24 is identical to SEQ ID NO: 914; SEQ ID

NO: 79 is identical to SEQ ID NO: 1050; SEQ ID NO: 132 is identical to SEQ ID NO: 3608; SEQ ID NO: 163 is identical to SEQ ID NO: 1734; SEQ ID NO: 249 is identical to SEQ ID NO: 2100, 2101, 2103, and 2108; SEQ ID NO: 321 is identical to SEQ ID NO: 2771; SEQ ID NO: 382 is identical to SEQ ID NO: 3019; SEQ ID NO: 387 is identical to SEQ ID NO: 2945; SEQ ID NO426 is identical to SEQ ID NO: 3387; SEQ ID NO: 446 is identical to SEQ ID NO: 2946; SEQ ID NO: 449 is identical to SEQ ID NO: 3705; SEQ ID NO: 2005 is identical to SEQ ID NO: 2011 and 2012; SEQ ID NO: 2007 is identical to SEQ ID NO: 2043 and 2045; SEQ ID NO: 2038 is identical to SEQ ID NO: 2039; SEQ ID NO: 2071 is identical to SEQ ID NO: 2072; SEQ ID NO: 2075 is identical to SEQ ID NO:2076, 2078, 2079, 2083, 2084, 2086, 2089, 2090, 2092, 2093, 2095, 2120, 2122, 2235, 2236, 2238, 2239, 2277, and 2278; SEQ ID NO: 2080 is identical to SEQ ID NO: 2155, 2176, 2179, 2248, and 2268; SEQ ID NO: 2102 is identical to SEQ ID NO: 2193; SEQ ID NO: 2105 is identical to SEQ ID NO: 2147, 2181, 2196, 2197, 2210, 2211, 2213, 2254, and 2256; SEQ ID NO: 2125 is identical to SEQ ID NO: 2126 and 2127; SEQ ID NO: 2130 is identical to SEQ ID NO: 2131, 2214, 2228, 2231, and 2251; SEQ ID NO: 2134 is identical to SEQ ID NO: 2247; SEQ ID NO: 2144 is identical to SEQ ID NO: 2153 and 2201; SEQ ID NO: 2188 is identical to SEQ ID NO: 2191, 2253, 2264, and 2271; SEQ ID NO: 2189 is identical to SEQ ID NO: 2202, 2252, 2265, 2266, 2270, and 2272; SEQ ID NO: 2215 is identical to SEQ ID NO: 2250 and 2284; SEQ ID NO: 2218 is identical to SEQ ID NO: 2219; SEQ ID NO: 2220 is identical to SEQ ID NO: 2221 and 2258; SEQ ID NO: 2356 is identical to SEQ ID NO: 2357 and 2359; SEQ ID NO: 2380 is identical to SEQ ID NO: 2402; SEQ ID NO: 2384 is identical to SEQ ID NO: 2387; SEQ ID NO: 2463 is identical to SEQ ID NO:2464; SEQ ID NO: 2481 is identical to SEQ ID NO: 2483; SEQ ID NO: 2485 is identical to SEQ ID NO: 2486; SEQ ID NO: 2533 is identical to SEQ ID NO: 2538; SEQ ID NO: 2582 is identical to SEQ ID NO: 2583; SEQ ID NO: 2588 is identical to SEQ ID NO: 2594, 2603, 2621, and 2629; SEQ ID NO: 2589 is identical to SEQ ID NO:2590, 2591, 2592, 2595, 2596, 2601, 2604, 2605, 2623, 2624, 2626, 2627, 2630, 2756, 2757, 2758, 2760, 2761, 2762, 2764, 2765, and 2807; SEQ ID NO:2593 is identical to SEQ ID NO:2632, and 2767; SEQ ID NO: 2600 is identical to SEQ ID NO: 2622; SEQ ID NO: 2606 is identical to SEQ ID NO: 2610; SEQ ID NO: 2607 is identical to SEQ ID NO: 2609; SEQ ID NO: 2625 is identical to SEQ ID NO: 2713;

SEQ ID NO: 2638 is identical to SEQ ID NO: 2639; SEQ ID NO: 2644 is identical to SEQ ID NO: 2727; SEQ ID NO: 2645 is identical to SEQ ID NO: 2726; SEQ ID NO: 2665 is identical to SEQ ID NO: 2719; SEQ ID NO: 2687 is identical to SEQ ID NO: 2689; SEQ ID NO: 2691 is identical to SEQ ID NO: 2693 and 2698; SEQ ID NO: 2694 is identical to SEQ ID NO: 2697; SEQ ID NO: 2712 is identical to SEQ ID NO: 2816, 2817 and 2818; SEQ ID NO: 2748 is identical to SEQ ID NO: 2749, 2778 and 2815; SEQ ID NO: 2750 is identical to SEQ ID NO: 2751 and 2776; SEQ ID NO: 2779 is identical to SEQ ID NO: 2790 and 2794; SEQ ID NO: 2801 is identical to SEQ ID NO: 2804; SEQ ID NO: 2873 is identical to SEQ ID NO: 2880; SEQ ID NO: 2876 is identical to SEQ ID NO: 2881; SEQ ID NO: 2877 is identical to SEQ ID NO: 2879; SEQ ID NO: 2908 is identical to SEQ ID NO: 2909; SEQ ID NO: 3135 is identical to SEQ ID NO: 3136; SEQ ID NO: 3138 is identical to SEQ ID NO: 3145; SEQ ID NO: 3268 is identical to SEQ ID NO: 3271, 3272, 3278, 3326, and 3327; SEQ ID NO: 3274 is identical to SEQ ID NO: 3351, 3352, and 3353; SEQ ID NO: 3277 is identical to SEQ ID NO: 3296; SEQ ID NO: 3285 is identical to SEQ ID NO: 3313; SEQ ID NO: 3287 is identical to SEQ ID NO: 3302; SEQ ID NO: 3309 is identical to SEQ ID NO: 3333, 3337, 3338, and 3342; SEQ ID NO: 3318 is identical to SEQ ID NO: 3319; SEQ ID NO: 3322 is identical to SEQ ID NO: 3331; SEQ ID NO: 3428 is identical to SEQ ID NO: 3430 3431; SEQ ID NO: 3434 is identical to SEQ ID NO: 3435; SEQ ID NO: 3439 is identical to SEQ ID NO: 3440 and 3461; SEQ ID NO: 3448 is identical to SEQ ID NO: 3449 and 3451; SEQ ID NO: 3453 is identical to SEQ ID NO: 3454; SEQ ID NO: 3456 is identical to SEQ ID NO: 3458, 3462 and 3463; SEQ ID NO: 3457 is identical to SEQ ID NO: 3459 and 3468;

The output of the functional genomics approach described herein is a set of genes highly predicted to improve yield and/or other agronomic important traits such as growth rate, vigor, oil content, fiber yield and/or quality, biomass, growth rate, abiotic stress tolerance, 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 3

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

In order to produce a high throughput correlation analysis, 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

RNA extraction – Five tissues at different developmental stages [meristem, flower, booting spike, stem, flag leaf], representing different plant characteristics, 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 a Set ID as summarized in Table 3 below.

Table 3
Barley transcriptom expression sets

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

Table 3

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 4, 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 4
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

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 4.

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 VI.

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

Table 5
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
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

Correlated parameter with (units)	*Correlation Id*
Harvest Index (ratio)	13

Table 5.

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 6 and 7 below. Subsequent correlation analysis between the various transcriptom sets (Table 3) and the average parameters, was conducted. Follow, results were integrated to the database.

Table 6
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 6. 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 7
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

Accession /Parameter	***8***	***9***	***4***	***11***	***12***	***13***
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 7. 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 8

Correlation between the expression level of the selected polynucleotides of the invention and their homologues in specific tissues or developmental stages and the phenotypic performance across Barley ecotypes

Gene Name	**Expression Set**	**Correlation Vector**	**R**	**P**
LYM26	A	12	0.87938	0.00178
LYM26	A	4	0.86421	0.00265
LYM26	A	12	0.85977	0.00069
LYM26	A	4	0.84991	0.00092
LYM26	A	9	0.83315	0.00145
LYM26	A	9	0.81930	0.00689
LYM26	A	5	0.81231	0.00238
LYM26	A	5	0.80624	0.00867
LYM26	C	1	0.74897	0.00799
LYM26	C	1	0.73316	0.02461
LYM26	A	10	0.72560	0.02691
LYM51	A	10	0.93629	0.00020
LYM51	A	12	0.92036	0.00043
LYM51	A	5	0.88679	0.00144
LYM51	A	9	0.87500	0.00201
LYM51	A	10	0.85681	0.00075
LYM51	A	4	0.82050	0.00674
LYM51	A	5	0.78204	0.00445
LYM51	A	9	0.77050	0.00552
LYM51	A	12	0.74603	0.00838
LYM51	A	4	0.71036	0.01430
LYM59	A	4	0.88939	0.00133
LYM59	A	3	0.80853	0.00834
LYM59	A	2	0.80307	0.00915
LYM59	A	12	0.79319	0.01075
LYM59	A	5	0.73433	0.02426
LYM59	A	10	0.72556	0.02693
LYM66	A	1	0.77697	0.01376
LYM66	A	1	0.75508	0.00722
LYM82	A	10	0.88760	0.00140

Gene Name	Expression Set	Correlation Vector	R	P
LYM82	A	12	0.86378	0.00061
LYM82	A	12	0.85529	0.00329
LYM82	A	10	0.84623	0.00102
LYM82	A	9	0.83000	0.00562
LYM82	A	9	0.82602	0.00173
LYM82	A	4	0.81534	0.00222
LYM82	A	4	0.79017	0.01127
LYM82	A	5	0.78467	0.00424
LYM82	A	5	0.76164	0.01709
LYM84	C	2	0.79418	0.01058
LYM84	B	2	0.79145	0.01928
LYM84	C	3	0.77694	0.01377
LYM84	B	3	0.75502	0.03033
LYM84	A	2	0.70823	0.01473
LYM99	C	7	0.75021	0.01989
LYM99	A	7	0.72294	0.02776
LYM95	B	2	0.81158	0.00436
LYM95	B	3	0.77615	0.00830
LYM95	B	10	0.73186	0.01612
LYM95	C	2	0.72471	0.02719
LYM95	B	5	0.71170	0.02097
LYM100	A	3	0.77258	0.01467
LYM100	A	4	0.76559	0.01619
LYM100	A	2	0.72628	0.02670
LYM105	A	4	0.80126	0.00943
LYM105	A	2	0.80060	0.00953
LYM105	A	3	0.78770	0.01171
LYM105	A	8	0.71795	0.02939
LYM105	B	1	0.71160	0.04775
LYM137	C	5	0.91789	0.00007
LYM137	C	4	0.87211	0.00046
LYM137	C	10	0.86290	0.00063
LYM137	C	12	0.85934	0.00070
LYM137	C	9	0.82372	0.00183
LYM137	C	3	0.73788	0.02323
LYM137	C	2	0.71562	0.03017
LYM140	C	6	0.83623	0.00968
LYM142	B	6	0.85850	0.01338
LYM142	A	4	0.80126	0.00943
LYM142	A	2	0.80060	0.00953
LYM142	A	3	0.78770	0.01171
LYM142	A	8	0.73208	0.01042
LYM142	A	8	0.71795	0.02939
LYM142	B	1	0.71160	0.04775
LYM148	A	4	0.79887	0.00318
LYM148	A	12	0.76743	0.00583
LYM148	A	4	0.76342	0.01668
LYM148	A	9	0.74349	0.00873
LYM148	A	5	0.70612	0.01516
LYM149	B	7	0.75092	0.03177
LYM156	C	2	0.79406	0.00352
LYM156	C	2	0.77724	0.01371
LYM156	A	2	0.76712	0.00586

Gene Name	Expression Set	Correlation Vector	R	P
LYM156	A	3	0.73707	0.00965
LYM156	C	3	0.71152	0.01407
LYM156	B	3	0.70014	0.05315
LYM157	A	4	0.78681	0.01187
LYM157	A	3	0.73234	0.02485
LYM157	A	12	0.72729	0.02639
LYM160	A	12	0.87825	0.00184
LYM160	A	10	0.82699	0.00596
LYM160	A	12	0.82567	0.00174
LYM160	A	9	0.80855	0.00834
LYM160	A	9	0.80222	0.00297
LYM160	A	10	0.74770	0.00815
LYM160	A	5	0.72266	0.02785
LYM160	A	5	0.71752	0.01292
LYM154	C	2	0.92810	0.00004
LYM154	C	3	0.90313	0.00014
LYM154	C	4	0.85169	0.00088
LYM154	C	5	0.73538	0.00991
LYM154	C	10	0.71818	0.01280
LYM154	C	12	0.70985	0.01440
LYM155	C	6	0.72312	0.04266
LYM155	C	1	0.70598	0.01519
LYM180	C	1	0.76320	0.00628
LYM180	B	6	0.75133	0.05153
LYM181	C	6	0.78450	0.02115
LYM184	B	6	0.82395	0.02266
LYM184	B	6	0.73704	0.01501
LYM189	A	10	0.81585	0.00733
LYM189	A	12	0.81256	0.00777
LYM189	A	9	0.72388	0.02746
LYM189	A	5	0.71589	0.03008
LYM192	A	2	0.86386	0.00061
LYM192	A	3	0.80919	0.00255
LYM192	A	3	0.77612	0.01393
LYM278	A	4	0.90217	0.00088
LYM278	A	4	0.87108	0.00048
LYM278	A	12	0.81518	0.00742
LYM278	A	3	0.79925	0.00975
LYM278	A	3	0.78102	0.00454
LYM278	A	12	0.76569	0.00601
LYM278	A	2	0.73983	0.00925
LYM38	A	4	0.97624	0.00001
LYM38	A	12	0.82191	0.00191
LYM38	A	8	0.82190	0.00656
LYM38	A	3	0.82153	0.00193
LYM38	A	5	0.81079	0.00246
LYM52	B	8	0.88462	0.00352
LYM52	A	2	0.80812	0.00261
LYM52	A	4	0.80802	0.00841
LYM52	A	3	0.78340	0.01251
LYM52	A	12	0.77364	0.01444
LYM52	A	9	0.75221	0.01938
LYM52	A	5	0.74914	0.02016

Gene Name	Expression Set	Correlation Vector	R	P
LYM52	A	8	0.71086	0.03181
LYM56	A	3	0.85797	0.00073
LYM56	A	4	0.85130	0.00089
LYM56	A	2	0.82071	0.00196
LYM56	A	8	0.76236	0.01692
LYM56	A	12	0.72510	0.01157
LYM83	A	9	0.87556	0.00198
LYM83	A	5	0.87005	0.00050
LYM83	A	12	0.82187	0.00191
LYM90	C	4	0.86848	0.00238
LYM90	C	3	0.81261	0.00777
LYM90	C	12	0.77921	0.01332
LYM90	C	2	0.76512	0.01629
LYM93	A	9	0.86630	0.00056
LYM93	A	12	0.78696	0.00405
LYM93	A	5	0.76542	0.00604
LYM106	A	3	0.79483	0.01047
LYM106	A	2	0.75674	0.01825
LYM106	C	6	0.73962	0.03596
LYM159	C	1	0.82807	0.00584
LYM159	B	8	0.79356	0.01873
LYM161	C	3	0.89287	0.00119
LYM161	C	2	0.88206	0.00165
LYM161	A	6	0.85373	0.00699
LYM161	C	4	0.74623	0.02093
LYM178	C	6	0.83756	0.00945
LYM182	A	6	0.93567	0.00063
LYM185	C	4	0.76455	0.01642
LYM185	A	1	0.75952	0.01759
LYM185	A	6	0.70292	0.01584
LYM186	A	6	0.86003	0.00616
LYM188	A	6	0.82774	0.00166
LYM188	C	2	0.73602	0.02377
LYM188	C	3	0.71072	0.03186
LYM194	A	2	0.89053	0.00024
LYM194	A	3	0.82982	0.00157
LYM289	A	9	0.77609	0.01394
LYM289	A	5	0.77182	0.01483

Table 8. Provided are the correlations (R) and p-values (P) between the expression levels of selected genes of some embodiments of the invention in various tissues or developmental stages (Expression sets) and the phenotypic performance in various yield (seed yield, oil yield, oil content), biomass, growth rate and/or vigor components [Correlation (Corr.) vector (Vec.)] Corr. Vec. = correlation vector specified in Tables 5, 6 and 7; Exp. Set = expression set specified in Table 3.

EXAMPLE 4

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, 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

RNA extraction – 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 in Example 3 above. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table 9 below.

Table 9

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 9: 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 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 is freely available on the internet.

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 VII.

Formula VII:

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

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

Formula VIII

Relative vegetative growth rate area = Regression coefficient of vegetative area along time course.

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 IX.

Formula IX:

Seed Oil yield = Seed yield per plant (gr) * Oil% in seed

Harvest Index (seed) **-** The harvest index was calculated using Formula IV (described above): Harvest Index = Average seed yield per plant/ Average dry weight.

Experimental Results

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

Table 10
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

Correlated parameter with	*Correlation ID*
Blade circularity	7
Lamina width (cm)	8
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 10. 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 11 and 12 below.

Table 11
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 11. 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 12
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

Ecotype	6	3	2	1	4	9	8	18	7
Shakdara	0.471	0.782	1.251	7.041	3.710	4.149	1.668	0.307	0.409

Table 12. 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.

Table 13, below, provides selected genes of some embodiments of the invention, the characterized parameters (which are used as x axis for correlation) and the correlated tissue transcriptom along with the correlation value (R, calculated using Pearson correlation). When the correlation coefficient (R) between the levels of a gene's expression in a certain tissue and a phenotypic performance across ecotypes is high in absolute value (between 0.5-1), there is an association between the gene (specifically the expression level of this gene) and the phenotypic character.

Table 13

Correlation between the expression level of selected genes in specific tissues or developmental stages and the phenotypic performance across Arabidopsis ecotypes

Gene Name	Expression Set	Correlation Vector	R	P
LYM88	E	13	0.75035	0.03198
LYM89	D	10	0.88062	0.00886
LYM89	D	4	0.84712	0.01614
LYM89	A	6	0.84690	0.00797
LYM89	D	5	0.83715	0.01879
LYM89	D	6	0.70174	0.07884
LYM152	E	14	0.85500	0.00682

Table 13. Provided are the correlations between the expression level of yield improving genes and their homologs in specific tissues or developmental stages (expression sets) and the phenotypic performance (correlation vector) across Arabidopsis ecotypes. The phenotypic characters [correlation (Corr.) vector (Vec.)] include yield (seed yield, oil yield, oil content), biomass, growth rate and/or vigor components as described in Tables 10-12. Exp. Set = expression set according to Table 9 hereinabove.

EXAMPLE 5

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

In order to produce a high throughput correlation analysis, 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

RNA extraction – 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 in Examples 3 above. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table14 below.

Table 14
Tissues used for Arabidopsis transcriptom expression 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 14: Provided are the identification (ID) letters of each of the Arabidopsis expression sets.

Assessment of Arabidopsis yield components and vigor related parameters under different nitrogen fertilization levels – 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 (Normal Nitrogen 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 15, hereinbelow.

Table 15
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

Correlated parameter with	*Correlation Id*
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
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 15. Provided are the Arabidopsis correlated parameters (vectors). "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; "FW" = Plant Fresh 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; Rosette Area (measured using digital analysis); Plot Coverage at the indicated day [%] (calculated by the dividing the total plant area with the total plot area); Leaf Blade Area at the indicated day [cm^2] (measured using digital analysis); RGR (relative growth rate) of Rosette Area at the indicated day [cm^2/day]; t50 Flowering [day] (the day in which 50% of plant flower); seed yield/ rosette area at day 10 [gr/cm^2] (calculated); seed yield/leaf blade [gr/cm^2] (calculated); seed yield/ N level [gr/ SPAD unit] (calculated).

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.

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, plot coverage, Rosette diameter and Rosette area.

Relative growth rate area: The relative growth rate of the rosette and the leaves was calculated according to Formulas XIV and XVII , respectively.

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 (seed) - The harvest index was calculated using Formula IV as described above [Harvest Index = Average seed yield per plant/ Average dry weight].

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. Subsequent correlation analysis between the various transcriptom sets (Table 14) was conducted. Following are the results integrated to the database.

Table 16

Correlation between the expression level of selected genes of the invention and their homologs in tissues under limiting or normal nitrogen fertilization and the phenotypic performance across Arabidopsis ecotypes

Gene Name	Expression Set	Correlation Vector	R	P
LYM88	C	17	0.93533	0.01955
LYM88 LYM8_H1	D D	16 31	0.79502 0.745282	0.01044 0.021184
LYM10_H7	C	24	0.895562	0.000458
LYM10_H7	C	5	0.77817	0.008026
LYM10_H7	C	21	0.725922	0.017459
LYM10_H7	C	2	0.717752	0.019423
LYM10_H8	C	8	0.850748	0.001806
LYM10_H8	C	27	0.7752	0.008432
LYM10_H8	C	15	0.77175	0.008921
LYM10_H9	A	1	0.844351	0.002119

Gene Name	Expression Set	Correlation Vector	R	P
LYM10_H9	A	2	0.755723	0.01146
LYM10_H9	A	20	0.733447	0.015776
LYM10_H9	A	21	0.722114	0.018356
LYM14_H2	B	27	0.892136	0.000519
LYM14_H2	B	8	0.830273	0.002942
LYM14_H2	C	8	0.816286	0.003967
LYM14_H2	C	8	0.794197	0.006071
LYM14_H2	C	27	0.767463	0.009557
LYM14_H2	C	27	0.733255	0.015818
LYM14_H2	D	1	0.725116	0.027066
LYM14_H3	B	15	0.855842	0.001582
LYM14_H3	C	8	0.802977	0.005158
LYM14_H3	B	8	0.79811	0.005651
LYM14_H3	B	12	0.792747	0.006233
LYM14_H3	B	27	0.785721	0.007057
LYM14_H3	C	27	0.734206	0.015613
LYM14_H3	A	9	0.720081	0.018848
LYM137_H11	C	20	0.815207	0.004055
LYM137_H11	C	21	0.79814	0.005648
LYM137_H11	D	5	0.754601	0.018779
LYM137_H11	C	24	0.701843	0.023676
LYM152_H1	D	5	0.714383	0.030592
LYM152_H1	D	5	0.713442	0.030914
LYM236_H4	B	27	0.937557	6.17E-05
LYM236_H4	B	8	0.921247	0.000153
LYM236_H4	B	15	0.865782	0.001204
LYM236_H4	B	28	0.709595	0.02153
LYM236_H5	A	10	0.737484	0.014922
LYM236_H5	B	10	0.71158	0.021004

Table 16. Provided are the correlations (R) between the expression levels of yield improving genes and their homologs in tissues (leaves or stems) under limiting (1.5 mM Nitrogen) or normal (6 mM Nitrogen) conditions (Expression sets) and the phenotypic performance in various yield (seed yield, oil yield, oil content), biomass, growth rate and/or vigor components [Correlation (Corr.) vector (Vec.)] under limiting or normal Nitrogen conditions. Corr. Vec. = correlation vector according to Table 15 hereinabove; Exp. Set = expression set according to Table 14 hereinabove.

EXAMPLE 6

PRODUCTION OF SORGHUM TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS WITH ABST RELATED PARAMETRERS USING 44K 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, Flower meristem and Flower] growing under severe drought stress and plants grown under Normal conditions were sampled and RNA was extracted as described in Examples 3 above. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table 17 below.

Table 17
Sorghum transcriptom expression sets

Expression Set	*Set ID*
Sorghum field/Normal/flower meristem	1
Sorghum field/Normal/flower	2
Sorghum field/Normal/flag leaf	3

Drought Stress: Flag leaf	4

Table 17: Provided are the sorghum transcriptom expression sets 1, 2, 3 and 4. Flag leaf = the leaf below the flower; Flower meristem = Apical meristem following panicle initiation; Flower = the flower at the anthesis day. Expression sets 1, 2 and 3 are from plants grown under normal conditions. Expression set 4 derived from plants grown under drought conditions.

The following parameters were collected using digital imaging system:

Average Grain Area (cm^2) - At the end of the growing period the grains were separated from the Plant 'Head'. 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.

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

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

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

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 5 plants per plot or by measuring the parameter across all the plants within the plot.

Total Seed Weight/Head (gr.) - At the end of the experiment (plant 'Heads') heads from plots within blocks A-C were collected. 5 heads were separately threshed and grains were weighted, all additional heads were threshed together and weighted as well. The average grain weight per head was calculated by dividing the total grain weight by number of total heads per plot (based on plot). In case of 5 heads, the total grains weight of 5 heads was divided by 5.

FW Head/Plant gr - At the end of the experiment (when heads were harvested) total and 5 selected heads per plots within blocks A-C were collected separetaly. The heads (total and 5) were weighted (gr.) separately and the average fresh weight per plant was calculated for total (FW Head/Plant gr based on plot) and for 5 (FW Head/Plant gr based on 5 plants).

Plant height – Plants were characterized for height during growing period at 5 time points. In each measure, plants were measured for their height using a measuring tape. Height was measured from ground level to top of the longest leaf.

Plant leaf number - 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 Formulas X and XI.

Formula X

Relative growth rate of plant height = Regression coefficient of plant height along time course.

Formula XI

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

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.

Vegetative dry weight and Heads - 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 Heads weight of each plot was separated, measured and divided by the number of Heads.

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) (Sorghum)- The harvest index was calculated using Formula XII.

Formula XII:

Harvest Index = Average grain dry weight per Head / (Average vegetative dry weight per Head + Average Head dry weight)

FW Heads/(FW Heads + FW Plants) - The total fresh weight of heads and their respective plant biomass were measured at the harvest day. The heads weight was divided by the sum of weights of heads and plants.

Experimental Results

16 different sorghum varieties were grown and characterized for different parameters: The average for each of the measured parameter was calculated using the JMP software (Tables 19-20) and a subsequent correlation analysis between the various transcriptom sets (Table 17) and the average parameters, was conducted (Tables 21). Results were then integrated to the database.

Table 18

Sorghum correlated parameters (vectors)

Correlation Vector	*Correlation Id*
Average Seed Area cm2-normal	A
Average Seed Length cm-normal	B
FW/Plant gr based on plot-normal	C
FW Head/Plant gr based on 5 plants-normal	D
FW Head/Plant gr based on plot-normal	E
FW Heads/(FW Heads + FW Plants) based on plot-normal	F
Head Average Area cm2-normal	G
Head Average Length cm-normal	H
HI-normal	J
Leaf SPAD 64 Days Post Sowing-normal	K
Relative Growth Rate of Leaf Num-normal	L
Relative Growth Rate of Plant Height-normal	M
Total Seed Weight/Head gr based on plot-normal	N
Total Seed Weight /Head gr based on 5 heads-normal	O

Table 18. Provided are the Sorghum correlated parameters (vectors). “gr.” = grams; “SPAD” = chlorophyll levels; "FW" = Plant Fresh weight;”normal” = standard growth conditions.

Table 19
Measured parameters in Sorghum accessions

Seed Id	*A*	*B*	*C*	*D*	*E*	*F*	*G*	*H*	*J*
20	0.1047	0.3856	162.6	406.5	175.2	0.51	120.1	25.58	200.7
21	0.1124	0.4017	212.6	518	223.5	0.5101	167.6	26.84	127
22	0.1313	0.4446	334.8	148	56.4	0.1154	85.14	21.02	51.8
24	0.1293	0.4496	313.5	423	111.6	0.2626	157.3	26.84	122.4
25						0.1204			54.53
26						0.177			93.92
27	0.1098	0.3999	151.1	423.5	126.2	0.4591	168.5	31.33	327.3
28	0.1134	0.4054	137.6	386.5	107.7	0.4316	109.3	23.18	231.5
29	0.1022	0.3837	168	409.5	123.9	0.4249	135.1	25.7	241.4
30	0.118	0.4186	129	328.9	102.8	0.4416	169	28.82	304.1
31	0.1205	0.4302	97.62	391	82.33	0.4581	156.1	28.13	335.6
32	0.1106	0.4003	99.32	435.8	77.59	0.4473	112.1	22.97	349.6
33	0.1165	0.4094	112.2	429.5	91.17	0.4474	154.7	28.09	293.2
34	0.108	0.4008	157.4	441	150.4	0.5134	171.7	30	410.9
35	0.1048	0.3947	130.5	415.8	109.1	0.4595	168.5	30.54	285.1
36	0.1097	0.3953	135.7	429.5	107.6	0.4425	162.5	27.17	282.7
37	0.1053	0.3924	209.2	428.5	130.9	0.3856	170.5	29.26	204

Table 19: Provided are the values of each of the parameters (as described above) measured in Sorghum accessions (Seed ID) under normal and drought conditions. Growth conditions are specified in the experimental procedure section.

Table 20
Additional measured parameters in Sorghum accessions

Seed Id	*L*	*M*	*N*	*O*
20	0.1032	1.891	31.12	47.4
21		1.622	26.35	46.3
22	0.2128	3.418	18.72	28.37
24	0.1862	2.425	38.38	70.4
25	0.1898	3.118		
26	0.1599	3.323		
27	0.1957	2.178	47.67	63.45
28	0.1694	2.188	31	44.45
29	0.1821	2.572	39.99	56.65
30		2.046	38.36	60
31		2.069	32.1	45.45
32	0.1754	2.547	32.69	58.19
33	0.117	2.327	32.79	70.6
34	0.207	3.039	51.53	70.1
35	0.1859	2.335	35.71	53.95
36	0.151	2.516	38.31	59.87
37	0.24	2.81	42.44	52.65

Table 20: Provided are the values of each of the parameters (as described above) measured in Sorghum accessions (Seed ID) under normal and drought conditions. Growth conditions are specified in the experimental procedure section.

Table 21

Correlation between the expression level of selected genes of some embodiments of the invention in various tissues and the phenotypic performance under normal or abiotic stress conditions across Sorghum accessions

Gene Name	Cluster Name	Exp. Set	Corr. Vec.	R	P
LYM174	sorghum|gb161.crp|AW284303	1	J	0.746	0.013251
LYM263	sorghum|gb161.crp|AI622410	2	O	0.860	0.00292
LYM263	sorghum|gb161.crp|AI622410	2	J	0.847	0.00196
LYM5 H21	sorghum|09v1|SB04G031180	1	B	0.898	0.00101
LYM5 H21	sorghum|09v1|SB04G031180	1	A	0.896	0.00107
LYM8 H23	sorghum|09v1|SB01G000490	1	O	0.755	0.018718
LYM8 H23	sorghum|09v1|SB01G000490	2	O	0.714	0.030884
LYM10 H272	sorghum|09v1|SB04G005280	3	L	0.756	0.029952
LYM14 H44	sorghum|09v1|SB02G044050	2	E	0.769	0.015504
LYM24 H10	sorghum|09v1|SB03G044280	2	C	0.774	0.014343
LYM24 H10	sorghum|09v1|SB03G044280	3	B	0.743	0.021898
LYM24 H10	sorghum|09v1|SB03G044280	3	A	0.728	0.026226
LYM35 H7	sorghum|09v1|SB06G031730	2	E	0.823	0.006385
LYM73 H8	sorghum|09v1|SB07G004300	1	E	0.748	0.02039
LYM82 H16	sorghum|09v1|SB10G002420	3	J	0.783	0.007439
LYM82 H16	sorghum|09v1|SB10G002420	3	N	0.780	0.013111
LYM82 H16	sorghum|09v1|SB10G002420	3	O	0.726	0.02673
LYM82 H16	sorghum|09v1|SB10G002420	3	G	0.723	0.027818
LYM111 H10	sorghum|09v1|SB03G036350	3	C	0.892	0.00122
LYM111 H10	sorghum|09v1|SB03G036350	3	A	0.753	0.019062
LYM111 H10	sorghum|09v1|SB03G036350	3	B	0.702	0.035192
LYM119 H1	sorghum|09v1|SB05G003680	2	C	0.759	0.017691
LYM131 H19	sorghum|09v1|SB06G027970	1	E	0.841	0.004488
LYM131 H19	sorghum|09v1|SB06G027970	3	B	0.787	0.011775
LYM131 H19	sorghum|09v1|SB06G027970	3	A	0.762	0.017013
LYM131 H19	sorghum|09v1|SB06G027970	1	F	0.700	0.024184
LYM131 H20	sorghum|09v1|SB07G006320	1	E	0.854	0.003353
LYM137 H285	sorghum|09v1|SB06G021660	2	F	0.747	0.013056
LYM137 H285	sorghum|09v1|SB06G021660	1	E	0.716	0.030132
LYM137 H286	sorghum|09v1|SB10G005240	1	E	0.786	0.012037
LYM140 H27	sorghum|09v1|SB06G028990	1	C	0.772	0.014832
LYM148 H14	sorghum|09v1|SB10G026570	1	B	0.812	0.007885
LYM148 H14	sorghum|09v1|SB10G026570	1	A	0.770	0.015311
LYM148 H14	sorghum|09v1|SB10G026570	1	C	0.768	0.015705
LYM162 H7	sorghum|09v1|SB03G043995	1	N	0.837	0.004911
LYM215 H2	sorghum|09v1|SB03G043980	1	N	0.718	0.029262
LYM178 H13	sorghum|09v1|SB03G008890	3	B	0.862	0.002833
LYM178 H13	sorghum|09v1|SB03G008890	3	A	0.792	0.010892
LYM178 H14	sorghum|09v1|SB07G001060	2	A	0.768	0.01572
LYM179 H0	sorghum|09v1|SB08G006470	1	O	0.818	0.006992
LYM109 H2	sorghum|09v1|SB05G003660	1	B	0.762	0.017077
LYM109 H2	sorghum|09v1|SB05G003660	3	A	0.751	0.019579
LYM109 H2	sorghum|09v1|SB05G003660	1	A	0.732	0.025074
LYM112 H2	sorghum|09v1|SB02G039985	1	B	0.827	0.005944
LYM112 H2	sorghum|09v1|SB02G039985	3	B	0.790	0.011246
LYM112 H2	sorghum|09v1|SB02G039985	1	A	0.789	0.011426
LYM112 H2	sorghum|09v1|SB02G039985	3	A	0.701	0.035452
LYM123 H7	sorghum|09v1|SB06G031680	1	B	0.769	0.015524

Gene Name	Cluster Name	Exp. Set	Corr. Vec.	R	P
LYM181 H6	sorghum|09v1|SB02G034110	1	B	0.740	0.022556
LYM181 H6	sorghum|09v1|SB02G034110	3	N	0.724	0.027264
LYM181 H6	sorghum|09v1|SB02G034110	3	O	0.702	0.035114
LYM182 H12	sorghum|09v1|SB06G015280	1	E	0.767	0.015834
LYM206 H2	sorghum|09v1|SB07G021090	3	N	0.795	0.010488
LYM188 H13	sorghum|09v1|SB01G007950	1	E	0.788	0.011658
LYM198 H1	sorghum|09v1|SB01G045460	1	E	0.829	0.005689
LYM201 H37	sorghum|09v1|SB04G022350	2	N	0.741	0.022246
LYM201 H37	sorghum|09v1|SB04G022350	2	D	0.709	0.032326
LYM201 H37	sorghum|09v1|SB04G022350	2	H	0.701	0.035468
LYM207 H3	sorghum|09v1|SB06G023870	3	K	0.781	0.007669
LYM207 H3	sorghum|09v1|SB06G023870	1	E	0.768	0.015595
LYM207 H3	sorghum|09v1|SB06G023870	3	O	0.718	0.029344
LYM207 H3	sorghum|09v1|SB06G023870	1	N	0.716	0.02988
LYM208 H8	sorghum|09v1|SB01G032070	1	N	0.734	0.024302
LYM208 H8	sorghum|09v1|SB01G032070	1	E	0.701	0.03525
LYM212 H9	sorghum|09v1|SB01G045480	1	E	0.841	0.004537
LYM221 H3	sorghum|09v1|SB01G034610	2	A	0.728	0.02604
LYM221 H3	sorghum|09v1|SB01G034610	2	C	0.721	0.028264
LYM224 H3	sorghum|09v1|SB02G040000	3	C	0.835	0.005096
LYM224 H3	sorghum|09v1|SB02G040000	3	L	0.827	0.011397
LYM224 H3	sorghum|09v1|SB02G040000	3	M	0.708	0.021888
LYM232 H3	sorghum|09v1|SB02G000450	1	O	0.808	0.00839
LYM232 H3	sorghum|09v1|SB02G000450	1	N	0.759	0.017814
LYM236 H139	sorghum|09v1|SB09G029110	1	A	0.859	0.00303
LYM236 H139	sorghum|09v1|SB09G029110	1	B	0.836	0.004971
LYM248 H5	sorghum|09v1|SB04G000645	3	L	0.878	0.004118
LYM248 H5	sorghum|09v1|SB04G000645	1	N	0.868	0.002424
LYM183 H11	sorghum|09v1|SB01G003070	1	E	0.832	0.005437
LYM183 H11	sorghum|09v1|SB01G003070	1	N	0.749	0.020124
LYM267 H1	sorghum|09v1|SB01G044240	2	A	0.797	0.010102
LYM267 H1	sorghum|09v1|SB01G044240	2	B	0.753	0.019206
LYM267 H1	sorghum|09v1|SB01G044240	1	H	0.707	0.033248
LYM267 H1	sorghum|09v1|SB01G044240	1	O	0.705	0.033872
LYM267 H1	sorghum|09v1|SB01G044240	1	N	0.705	0.033976
LYM270 H0	sorghum|09v1|SB02G040045	1	E	0.820	0.006742
LYM271 H10	sorghum|09v1|SB02G040020	1	N	0.780	0.013152
LYM273 H6	sorghum|09v1|SB03G044410	3	B	0.955	5.91E-05
LYM273 H6	sorghum|09v1|SB03G044410	3	A	0.950	8.6E-05
LYM284 H24	sorghum|09v1|SB03G027960	1	E	0.867	0.00247
LYM289 H52	sorghum|09v1|SB09G005410	3	O	0.928	0.000307
LYM289 H52	sorghum|09v1|SB09G005410	3	N	0.830	0.005588
LYM289 H52	sorghum|09v1|SB09G005410	3	H	0.781	0.012924
LYM289 H52	sorghum|09v1|SB09G005410	3	G	0.714	0.03066
LYM289 H52	sorghum|09v1|SB09G005410	3	D	0.704	0.03412
LYM290 H13	sorghum|09v1|SB01G009390	1	E	0.766	0.01617

Table 21. Provided are the correlations (R) between the expression levels of yield improving genes and their homologs in tissues (Flag leaf, Flower meristem and Flower; Expression (Exp.) sets) and the phenotypic performance in various yield, biomass, growth rate and/or vigor components [Correlation (Corr.) vector (Vec.)] under stress conditions or normal conditions across Sorghum accessions.

Sorghum vigor related parameters under 100 mM NaCl and low temperature

*(*10 ± 2 °C*)* – 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 in addition to the Full Hogland solution), low temperature (10 ± 2 °C in the presence of Full Hogland solution) or at Normal growth solution [Full Hogland solution at 28 ± 2 °C].

Full Hogland solution consists of: KNO_3 - 0.808 grams/liter, $MgSO_4$ - 0.12 grams/liter, KH_2PO_4 - 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 sampled per each treatment. Two tissues [leaves and roots] growing at 100 mM NaCl, low temperature (10 ± 2 °C) or under Normal conditions (full Hogland at a temperature between 28 ± 2 °C) were sampled and RNA was extracted as described in Example 3 above.

Table 22
Sorghum transcriptom expression sets

Expression Set	*Set ID*
Sorghum roots under cold	1
Sorghum vegetative meristem NaCl	2
Sorghum vegetative meristem under low nitrogen	3
Sorghum vegetative meristem under cold conditions	4
Sorghum roots under NaCl	5
Sorghum vegetative meristem under normal conditions	6
Sorghum roots under low nitrogen	7
Sorghum roots under normal	8

Table 22: Provided are the Sorghum transcriptom expression sets. Cold conditions = 10 ± 2 °C; NaCl = 100 mM NaCl; low nitrogen =1.2 mM Nitrogen; Normal conditions = 16 mM Nitrogen.

Experimental Results

10 different Sorghum varieties were grown and characterized for the following parameters: "Leaf number Normal" = leaf number per plant under normal conditions (average of five plants); "Plant Height Normal" = plant height under normal conditions (average of five plants); "Root DW 100 mM NaCl" – root dry weight per plant under

salinity conditions (average of five plants); The average for each of the measured parameter was calculated using the JMP software and values are summarized in Table 24 below. Subsequent correlation analysis between the various transcriptom sets and the average parameters were conducted (Table 25). Results were then integrated to the database.

Table 23
Sorghum correlated parameters (vectors)

Correlation Vector	Corr. Id
DW Root/Plant - Cold	A
DW Root/Plant - 100 mM NaCl	B
DW Shoot/Plant - Low Nitrogen	C
DW Root/Plant - Low Nitrogen	D
Leaf number TP-3* - Cold	E
Leaf number TP-3*- 100 mM NaCl	F
Plant Height TP-3*- 100 mM NaCl	G
DW Shoot/Plant - Cold	H
DW Shoot/Plant - Normal	I
Plant Height TP-3* - Low Nitrogen	J
Leaf number TP-3* - Low Nitrogen	K
DW Shoot/Plant - 100 mM NaCl	L
Leaf number TP-3* - Normal	M

Table 23: Provided are the Sorghum correlated parameters. Cold conditions = 10 ± 2 °C; NaCl = 100 mM NaCl; low nitrogen = 1.2 mM Nitrogen; Normal conditions = 16 mM Nitrogen * TP-3 refers to time point 3.

Table 24
Sorghum accessions, measured parameters

Seed ID	*F*	*B*	*L*	*G*	*E*	*A*	*H*	*M*	*I*
20	3.67	0.35	0.66	14.63	3.88	0.83	1.03	4.17	0.81
22	3.88	1.45	2.43	16.31	4.16	0.95	1.34	4.48	1.89
26	4.28	1.49	2.40	20.56	4.52	1.47	1.71	4.93	2.51
27	4.03	0.81	1.61	14.70	4.28	1.06	1.28	4.53	1.26
28	3.97	1.03	1.77	16.43	4.33	0.71	1.12	4.52	1.55
29	3.98	0.95	1.66	16.12	4.17	1.38	1.69	4.64	1.50
30	3.90	2.00	2.23	15.61	3.94	2.04	2.24	4.49	1.93
31	4.18	1.39	2.76	18.71	4.26	1.03	1.26	4.79	1.95
34	3.70	1.29	1.29	13.65	4.20	1.01	1.08	4.37	1.48
37	3.82	1.76	1.55	15.72	4.04	1.01	1.02	4.54	1.85

Table 24: 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 23 above) as follows: F [100 mM NaCl: leaf Number]; B [100 mM NaCl: Root DW]; L [100 mM NaCl: Shoot DW]; G [100 mM NaCl: Plant height]; E [low temperature: leaf Number]; A [low temperature: Root DW]; H [low temperature: Shoot DW];; M [Normal: leaf Number]; I [Normal: Shoot DW].

Table 25
Correlation between the expression level of selected genes of some embodiments of the invention in roots and the phenotypic performance under normal or abiotic stress conditions across Sorghum accessions

Gene Name	*Cluster Id*	*Exp. Set*	*Corr. Vec.*	*R*	*P*
LYM263	sorghum|gb161.crp|AI622410	5	G	0.705635	0.183016
LYM263	sorghum|gb161.crp|AI622410	5	F	0.908761	0.032626
LYM263	sorghum|gb161.crp|AI622410	8	I	0.836212	0.004969
LYM2 H8	sorghum|09v1|SB07G004285	1	A	0.73969	0.01447
LYM4 H11	sorghum|09v1|SB03G000920	2	B	0.83675	0.00491
LYM4 H11	sorghum|09v1|SB03G000920	2	B	0.73187	0.02499
LYM4 H11	sorghum|09v1|SB03G000920	4	E	0.70634	0.03342
LYM14 H43	sorghum|09v1|SB01G038730	1	A	0.71433	0.02029
LYM19 H12	sorghum|09v1|SB05G009990	5	F	0.97628	0.00437
LYM19 H12	sorghum|09v1|SB05G009990	5	G	0.88580	0.04552
LYM24 H10	sorghum|09v1|SB03G044280	4	H	0.75256	0.01929
LYM24 H10	sorghum|09v1|SB03G044280	4	H	0.74948	0.02008
LYM73 H8	sorghum|09v1|SB07G004300	5	F	0.97233	0.00550
LYM73 H8	sorghum|09v1|SB07G004300	5	F	0.92449	0.02462
LYM73 H8	sorghum|09v1|SB07G004300	4	E	0.73646	0.02364
LYM83 H12	sorghum|09v1|SB09G026370	2	F	0.70736	0.03305
LYM129 H4	sorghum|09v1|SB03G044510	1	E	0.72429	0.01784
LYM129 H4	sorghum|09v1|SB03G044510	2	F	0.72339	0.02761
LYM129 H4	sorghum|09v1|SB03G044510	6	I	0.71891	0.02907
LYM129 H4	sorghum|09v1|SB03G044510	6	I	0.71123	0.03168
LYM129 H4	sorghum|09v1|SB03G044510	2	F	0.70792	0.03285
LYM140 H27	sorghum|09v1|SB06G028990	2	G	0.80589	0.00873
LYM140 H27	sorghum|09v1|SB06G028990	2	F	0.78965	0.01136
LYM140 H27	sorghum|09v1|SB06G028990	6	I	0.71625	0.02996

Gene Name	***Cluster Id***	***Exp. Set***	***Corr. Vec.***	***R***	***P***
LYM153 H9	sorghum|09v1|SB10G003440	4	H	0.78966	0.01136
LYM153 H9	sorghum|09v1|SB10G003440	4	H	0.73143	0.02512
LYM153 H9	sorghum|09v1|SB10G003440	4	A	0.71026	0.03202
LYM115 H0	sorghum|09v1|SB01G043900	2	F	0.74903	0.02019
LYM188 H13	sorghum|09v1|SB01G007950	5	F	0.87882	0.04971
LYM203 H14	sorghum|09v1|SB04G005460	2	B	0.78001	0.01316
LYM217 H3	sorghum|09v1|SB01G043910	5	B	0.94269	0.01633
LYM217 H3	sorghum|09v1|SB01G043910	5	B	0.93691	0.01884
LYM228 H1	sorghum|09v1|SB09G006910	1	A	0.72334	0.01806
LYM232 H3	sorghum|09v1|SB02G000450	2	L	0.77653	0.01385
LYM232 H3	sorghum|09v1|SB02G000450	2	F	0.72326	0.02766
LYM240 H12	sorghum|09v1|SB02G038240	4	H	0.76382	0.01659
LYM240 H12	sorghum|09v1|SB02G038240	2	L	0.73895	0.02293
LYM251 H106	sorghum|09v1|SB01G006180	5	F	0.95275	0.01224
LYM284 H24	sorghum|09v1|SB03G027960	6	M	0.76300	0.01677
LYM289 H53	sorghum|09v1|SB10G002980	5	G	0.91500	0.02936

Table 25. Provided are the correlations (R) between the expression levels yield improving genes and their homologs in various tissues [Expression (Exp.) sets] and the phenotypic performance [yield, biomass, growth rate and/or vigor components (Correlation vector)] under abiotic stress conditions (salinity) or normal conditions across Sorghum accessions. Corr. Vec. = correlation vector as described hereinabove (Table 23).

EXAMPLE 7

GENE CLONING AND GENERATION OF BINARY VECTORS FOR PLANT EXPRESSION

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

Cloning strategy

Genes listed in Examples 1-6 hereinabove were cloned into binary vectors for the generation of transgenic plants. For cloning, the full-length open reading frame (ORF) was first identified. In case of ORF-EST clusters and in some cases already published 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. To clone the full-length cDNAs, reverse transcription (RT) followed by polymerase chain reaction (PCR; RT-PCR) was performed on total RNA extracted from leaves, flowers, siliques or other plant tissues, growing under normal conditions. Total RNA was extracted as described in Example 3 above. Production of cDNA and PCR amplification was 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 were purified using PCR purification kit (Qiagen). In case where the entire coding sequence was not found, RACE kit from Invitrogen (RACE = R apid A ccess to cDNA E nds) was used to access the full cDNA transcript of the gene from the RNA samples described above.

In case genomic DNA was cloned, as in the case of LYM122 (SEQ ID NO:3739) and LYM273 (SEQ ID NO:3738), the genes were amplified by direct PCR on genomic DNA extracted from leaf tissue using the DNAeasy kit (Qiagen Cat. No. 69104).

Usually, 2 sets of primers were synthesized for the amplification of each gene from a cDNA or a genomic sequence; an external set of primers and an internal set (nested PCR primers). When needed (e.g., when the first PCR reaction did not result in a satisfactory product for sequencing), an additional primer (or two) of the nested PCR primers were used. Table 26 below provides primers used for cloning of selected genes.

Table 26
The PCR primers used for cloning the genes of some embodiments of the invention into high copy vectors

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
LYM1	SalI,XbaI	LYM1_NF_SalI (SEQ ID NO: 3740) AAAGTCGACAGTAGGCAATCATGTGTGAGG
		LYM1_NR_XbaI (SEQ ID NO: 3741) AATTCTAGACTAAGCTAGAGAGCTCGACTAATGC
LYM10	XhoI,KpnI	LYM10 NF XhoI (SEQ ID NO: 3742) ATACTCGAGTCTCCAACCTTGCGAAGG
		LYM10 EF XhoI (SEQ ID NO: 3743) ATACTCGAGAACCCGATCTCTCCAACC
		LYM10 NR KpnI (SEQ ID NO: 3744) TATGGTACCCCTGCGAATTCTTGCCTTAG
		LYM10 ER KpnI (SEQ ID NO: 3745) TATGGTACCTGACGCCACCCTCAACTC
LYM100	SalI,XbaI	LYM100_NF_SalI (SEQ ID NO: 3746) AAAGTCGACAGGAAACCCTAACGAAGATACC
		LYM100_EF_SalI (SEQ ID NO: 3747) AAAGTCGACGGAAACATACAGGTCGATTGAG
		LYM100_NR_XbaI (SEQ ID NO: 3748) AAATCTAGAGGGAAAGTTTAGTAGCACCAAC
		LYM100_ER_XbaI (SEQ ID NO: 3749) AAATCTAGAATATAACGTTAGAGCGGAGTGG
LYM102	BamHI,XhoI	LYM102_NF_BamHI (SEQ ID NO: 3750) AAAGGATCCGAGCTGCTGATTGTGAGTCAAG

Gene Name	***Restriction Enzymes used for cloning***	***Primers used for amplification***
		LYM102_NR_XhoI (SEQ ID NO: 3751) AAACTCGAGCTAGGACAGCACTTCAGATAAGACC
LYM103	BamHI,XhoI	LYM103_NF_BamHI (SEQ ID NO: 3752) AAAGGATCCCGACCGAGTCAATCAATCC
		LYM103_NR_XhoI (SEQ ID NO: 3753) AAACTCGAGAACAAGTATGACAGGCCAACTC
LYM105	BamHI,XhoI	LYM105_NF_BamHI (SEQ ID NO: 3754) AAAGGATCCTAGCTAGCTTACTCCACAGTGC
		LYM105_EF_BamHI (SEQ ID NO: 3755) AAAGGATCCAGCCACACGCTTAGCTTAGC
		LYM105_NR_XhoI (SEQ ID NO: 3756) AAACTCGAGCGAGCAGAAATTAACAGCTAAC
		LYM105_ER_XhoI (SEQ ID NO: 3757) AAACTCGAGACTACAGATCCAAAGCACGAAC
LYM106	SalI,XbaI	LYM106_NF_SalI (SEQ ID NO: 3758) AAAGTCGACACTCAACGTAGTTCCTCACCTG
		LYM106_NR_XbaI (SEQ ID NO: 3759) AAATCTAGAAAGCTTTAGTTCTAGCACACGAC
LYM107	BamHI,XhoI	LYM107_NF_BamHI (SEQ ID NO: 3760) AAAGGATCCGTACTCCTATATTAGGCTCGCTC
		LYM107_EF_BamHI (SEQ ID NO: 3761) AAAGGATCCCTGCGTACTCCTATATTAGGCTC
		LYM107_NR_XhoI (SEQ ID NO: 3762) AAACTCGAGAATTTGGTATCAGAAACCTTGC
		LYM107_ER_XhoI (SEQ ID NO: 3763) AATCTCGAGTGAATCACTCAGTGTGCATGAC
LYM109	XhoI,StuI	LYM109_F2_XhoI (SEQ ID NO: 3764) AAACTCGAGCCCAGCGGACTCCTACTCTG
		LYM109_F2_XhoI (SEQ ID NO: 3764) AAACTCGAGCCCAGCGGACTCCTACTCTG
		LYM109_R2_StuI (SEQ ID NO: 3765) TTTAGGCCTTCACAGTCTTACAAGTCCGATTGCC
		LYM109_R2_StuI (SEQ ID NO: 3765) TTTAGGCCTTCACAGTCTTACAAGTCCGATTGCC
LYM110	BamHI,XhoI	LYM110_NF_BamHI (SEQ ID NO: 3766) AAAGGATCCGAACCAAACCTCGGAGAAAC
		LYM110_NR_XhoI (SEQ ID NO: 3767) AAACTCGAGACCATCACCTGTAATACAACTACC
LYM111	XhoI,SacI	LYM111_NF_XhoI (SEQ ID NO: 3768) AAACTCGAGGAATCTGGTTGCTCATCTCATC
		LYM111_EF_XhoI (SEQ ID NO: 3769) AAACTCGAGCTTCACAACGGACGAGAGG
		LYM111_NR_SacI (SEQ ID NO: 3770) AAAGAGCTCATAATCGTTGGAACTTGGAATC
		LYM111_ER_SacI (SEQ ID NO: 3771) AAAGAGCTCACAGCTTATCCCTACATGCTTC
LYM112	BamHI,XhoI	LYM112_NF_BamHI (SEQ ID NO: 3772) AAAGGATCCTCAATTGAATCAGATGCTCCAC
		LYM112_EF_BamHI (SEQ ID NO: 3773) AAAGGATCCATTCCTTTGACCGATTTCTTG

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM112_NR_XhoI (SEQ ID NO: 3774) AAACTCGAGCTAATTAAGACAAATCAGTGGCACC
		LYM112_ER_XhoI (SEQ ID NO: 3775) AAACTCGAGACAGAAGGTCGATGTTGATCTG
LYM113	SalI,XbaI	LYM113_NF_SalI (SEQ ID NO: 3776) AAAGTCGACTTCTTGATCTAAATTTGGGTGG
		LYM113_EF_SalI (SEQ ID NO: 3777) AAAGTCGACACTAGCTCTGCACTTTCCCTG
		LYM113_NR_XbaI (SEQ ID NO: 3778) AAATCTAGAGATTCAAGTGCGTTGTCTGTC
		LYM113_ER_XbaI (SEQ ID NO: 3779) AAATCTAGACTTGGTATTTACAGGACAATCG
LYM115	BamHI,XhoI	LYM115_F_BamHI (SEQ ID NO: 3780) AAAGGATCCTCGCCGCAGATGGAAGTCT
		LYM115_ER_XhoI (SEQ ID NO: 3781) TTTCTCGAGCAAACTCGTCTGGAGATGGG
LYM116	SalI,XbaI	LYM116_EF_SalI (SEQ ID NO: 3782) AAAGTCGACTTGGCTCCGGATATCGCA
		LYM116_ER_XbaI (SEQ ID NO: 3783) AAATCTAGAAGGCAGATGTTCATAACCACAC
LYM117		LYM117_F2_BamHI (SEQ ID NO: 3784) AAAGGATCCCGTCGTCAAGTGCTGGC
		LYM117_R2_EcoRV (SEQ ID NO: 3785) AGTGATATCTCAATGTTTAGGGTCTCGGCATG
LYM119	SalI,XbaI	LYM119_NF_SalI (SEQ ID NO: 3786) AAAGTCGACATCGAGTTGTTCGTCCGTC
		LYM119_NR_XbaI (SEQ ID NO: 3787) AAATCTAGAACACCAAGCGTACATCTCAGAC
LYM12	XhoI,KpnI	LYM12 EF XhoI (SEQ ID NO: 3788) TTACTCGAGTGCTTCTCTTCTTTCCTCTCTG
		LYM12 ER KpnI (SEQ ID NO: 3789) ATAGGTACCTCACAGCAAACTAACATGAACCG
LYM120	BamHI,XhoI	LYM120_NF_BamHI (SEQ ID NO: 3790) AAAGGATCCGGAAGTCCGGAGTTGGAAG
		LYM120_NR_XhoI (SEQ ID NO: 3791) AAACTCGAGCAGTCACTCACACGCTACTACG
LYM121	BamHI,XhoI	LYM121_NF_BamHI (SEQ ID NO: 3792) AAAGGATCCACTGCTGACCAACTTCAGTGTC
		LYM121_EF_BamHI (SEQ ID NO: 3793) AAAGGATCCGACAAGGCTATCACATCCAATC
		LYM121_NR_XhoI (SEQ ID NO: 3794) AAACTCGAGTTCTAAAGAAACAATCACGCAC
		LYM121_ER_XhoI (SEQ ID NO: 3795) AAACTCGAGAGCAGAAGAAACTAGGCATGTG
LYM122_G		LYM122_EF_BamHI (SEQ ID NO: 3796) AAAGGATCCTGCAGCCCTGACACACAAC
		LYM122_ER_XhoI (SEQ ID NO: 3797) AAACTCGAGACCATCATGTAATACCCACCTC
LYM125		LYM125_EF_BamHI (SEQ ID NO: 3798) AAAGGATCCCTGTGCTTGGAGTAGACACGAG

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM125_ER_KpnI (SEQ ID NO: 3799) AAAGGTACCGGAGAATTTGGATCAGTGCAG
LYM127		LYM127_F2_BamHI (SEQ ID NO: 3800) TTTGGATCCCTTCTTGCTGTCGAACACCAG
		LYM127_R2_XhoI (SEQ ID NO: 3801) TTTCTCGAGGTCATGGGATTCTTGTCAGATACTAG
LYM128	BamHI,XhoI	LYM128_NF_BamHI (SEQ ID NO: 3802) TTTGGATCCTTCACACCTCACCGAGCG
		LYM128_EF_BamHI (SEQ ID NO: 3803) AAAGGATCCAACCCGTTCACACCTCACC
		LYM128_NR_XhoI (SEQ ID NO: 3804) AAACTCGAGGATCACTTGACAATTACCGTGC
		LYM128_ER_XhoI (SEQ ID NO: 3805) AAACTCGAGTATGCTGATATGCCAGGTTTAC
LYM129	SalI,XbaI	LYM129_NF_SalI (SEQ ID NO: 3806) AAAGTCGACATTCAGTCTTGTCGGCTACATC
		LYM129_EF_SalI (SEQ ID NO: 3807) AAAGTCGACTAGATCAGCCTCGATTCATCTC
		LYM129_NR_XbaI (SEQ ID NO: 3808) AAATCTAGAGCTTAATCAGAAGAAACGAACC
		LYM129_ER_XbaI (SEQ ID NO: 3809) AAATCTAGAAATTGCACAATACATGAACACG
LYM13	SalI,BamHI	LYM13_NF_SalI (SEQ ID NO: 3810) AAAGTCGACCAAGCGGTAGGAGATGAGG
		LYM13_NR_BamHI (SEQ ID NO: 3811) AAAGGATCCTTATAACAACTATTCCCGGTAAGC
LYM130	SalI,XbaI	LYM130_NF_SalI (SEQ ID NO: 3812) AAAGTCGACAGAAATTAAGTTGCCGGAGAG
		LYM130_NR_XbaI (SEQ ID NO: 3813) AAATCTAGAATGCAGATGAGAGCTCAAGATG
LYM131	SalI,XhoI	LYM131_NF_SalI (SEQ ID NO: 3814) AAAGTCGACTCCCTACCCTAGTCGATCTCC
		LYM131_EF_SalI (SEQ ID NO: 3815) AAAGTCGACGACTCGTCTCCTCGTTGCTC
		LYM131_NF_SalI (SEQ ID NO: 3814) AAAGTCGACTCCCTACCCTAGTCGATCTCC
		LYM131_ER_XhoI (SEQ ID NO: 3816) AAACTCGAGTATAACACAGGCATAAAGCAGC
LYM132	BamHI,XhoI	LYM132_EF_BamHI (SEQ ID NO: 3817) AAAGGATCCATATTGGAATGCTTCTGTCGTC
		LYM132_ER_XhoI (SEQ ID NO: 3818) AAACTCGAGTACACGATAATCACAAACCACG
LYM134	BamHI,XhoI	LYM134_NF_BamHI (SEQ ID NO: 3819) AAAGGATCCATGGTGATTCGGTTGTTGTTAG
		LYM134_EF_BamHI (SEQ ID NO: 3820) AAAGGATCCATCGTTGAATTGATGGTGATTC
		LYM134_NR_XhoI (SEQ ID NO: 3821) AAACTCGAGTCATACGTCGAAGAACCAGAAC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM134_ER_XhoI (SEQ ID NO: 3822) AAACTCGAGTGAAACTTTCGCCAACTACAC
LYM135		LYM135_NF_SalI (SEQ ID NO: 3823) AAAGTCGACTTCTGATCTGCTCAGCTAAAGG
		LYM135_NR_SacI (SEQ ID NO: 3824) AAAGAGCTCCTGATGCACAAATATGGTAACG
LYM136	BamHI,KpnI	LYM136_NF_BamHI (SEQ ID NO: 3825) AAAGGATCCCCGGTTCTATGTGTAGGAAGAG
		LYM136_EF_BamHI (SEQ ID NO: 3826) AAAGGATCCCAGGATGAGTGTTGATCCATTC
		LYM136_NR_KpnI (SEQ ID NO: 3827) AAAGGTACCGTCACAAACGCCTCAACATATC
		LYM136_ER_KpnI (SEQ ID NO: 3828) AAAGGTACCTTCACCATATTGCTACGAAATC
LYM137	SalI,XbaI	LYM137_NF_SalI (SEQ ID NO: 3829) AAAGTCGACAGTTCAAGAGGCTGTCCTGAG
		LYM137_NR_XbaI (SEQ ID NO: 3830) AAATCTAGATCCAATAACATAAGAAACCACG
LYM138	SalI,SacI	LYM138_EF_SalI (SEQ ID NO: 3831) AAAGTCGACAACGAACCACTCTTCTGCATC
		LYM138_ER_SacI (SEQ ID NO: 3832) AAAGAGCTCGAAGCAACCTGGAAATAAACTC
LYM14	EcoRV,PstI	LYM14_NF_EcoRV (SEQ ID NO: 3833) AAAGATATCCTCCTCAGATCCACCACCAC
		LYM14_NR_PstI (SEQ ID NO: 3834) AATCTGCAGCTAAAATATTCAGGGCTTGTTG
LYM140	XhoI,SacI	LYM140_F_XhoI (SEQ ID NO: 3835) AAACTCGAGCTCCAGCACACGGACGAG
		LYM140_ER_SacI (SEQ ID NO: 3836) AAAGAGCTCTACGAGTACGAATTATTGCCAG
LYM141		LYM141_NF_BamHI (SEQ ID NO: 3837) AAAGGATCCACAAGCGTCTTCTTCGTCTTC
		LYM141_NR_KpnI (SEQ ID NO: 3838) AAAGGTACCCCATGCCACCCTTACTATACTC
LYM142	SalI,SacI	LYM142_NF_SalB (SEQ ID NO: 3839) TAAGTCGACCACACAGAGCACAGCACAGAG
		LYM142_NR_SacB (SEQ ID NO: 3840) TGAGCTCTGAACATGCGACCGTATGC
LYM143	SalI,XbaI	LYM143_NF_SalI (SEQ ID NO: 3841) AAAGTCGACCACTAGCGCACAGATCTCCTAC
		LYM143_NR_XbaI (SEQ ID NO: 3842) AAATCTAGAAATAGTGTCCATGAGACGAACG
LYM144	SalI,EcoRV	LYM144_NF_SalI (SEQ ID NO: 3843) AAAGTCGACACGACGAGGAGGAGGATG
		LYM144_NR_EcoRV (SEQ ID NO: 3844) AATGATATCACGCATGGATTTCTTTAAGTTG
LYM145	BamHI,XhoI	LYM145_F2_BamHI (SEQ ID NO: 3845) ATCGGATCCTAGCTTTGCCCAGTTTTGCT

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM145_F2_BamHI (SEQ ID NO: 3845) ATCGGATCCTAGCTTTGCCCAGTTTTGCT
		LYM145_R2_XhoI (SEQ ID NO: 3846) TTTCTCGAGCTATGCAGTTTTAGCCTAAGGCAAG
		LYM145_R2_XhoI (SEQ ID NO: 3846) TTTCTCGAGCTATGCAGTTTTAGCCTAAGGCAAG
LYM146		LYM146_F2_KpnI (SEQ ID NO: 3847) AAAGGTACCCGAGGTCGTCACGCACAG
		LYM146_R2_KpnI (SEQ ID NO: 3848) AATGGTACCTGGGTGGTTAGACAGCAAGG
LYM147	SalI,XbaI	LYM147_NF_SalI (SEQ ID NO: 3849) AAAGTCGACCTCTGGCGCTCTCCTATACTC
		LYM147_EF_SalI (SEQ ID NO: 3850) AAAGTCGACAGTACGTGTACGTTTCAGGGAG
		LYM147_NR_XbaI (SEQ ID NO: 3851) AAATCTAGAAGTACCACTAGCAGAAAGGCAG
		LYM147_ER_XbaI (SEQ ID NO: 3852) AAATCTAGATGGCACCCAATACTAGTACCAC
LYM148	BamHI,XhoI	LYM148_NF_BamHI (SEQ ID NO: 3853) AAAGGATCCCTTACCCTTCCCTGAGATCC
		LYM148_NR_XhoI (SEQ ID NO: 3854) AAACTCGAGCTAACTACCAAAGTTCAAGCAGCTC
LYM149	SalI,XbaI	LYM149_NF_SalI (SEQ ID NO: 3855) AAAGTCGACACCATGAGTTCATAACAAGAAGG
		LYM149_NR_XbaI (SEQ ID NO: 3856) AAATCTAGACTAATACATGGAAGTGCAGACATGC
LYM15	SalI,XbaI	LYM15_NF_SalI (SEQ ID NO: 3857) AAAGTCGACAGGTACAGTATAGTATGACACCGAC
		LYM15_NR_XbaI (SEQ ID NO: 3858) AATTCTAGACTACTGTTAACCGCTGATTATATCC
LYM152	SalI,XbaI	LYM152_NF_SalI (SEQ ID NO: 3859) TTTGTCGACGAAGAAGAGATGGGAGTTTTCTC
		LYM152_NR_XbaI (SEQ ID NO: 3860) AAATCTAGAATTTCTGACATTACATTATAGTCTCG
LYM153	SalI,XbaI	LYM153_NF_SalI (SEQ ID NO: 3861) AAAGTCGACTTCTCCTCCTACGTTCTACTGG
		LYM153_NR_XbaI (SEQ ID NO: 3862) AAATCTAGACTAACAGGGTTTCTCCACTAAGTAAG
LYM155	SalI,XbaI	LYM155_NF_SalI (SEQ ID NO: 3863) AAAGTCGACTCCACTATAAGCAACGCACC
		LYM155_EF_SalI (SEQ ID NO: 3864) AAAGTCGACGAAGGAAACTCGGTGACACG
		LYM155_NR_XbaI (SEQ ID NO: 3865) AAATCTAGAATGCCATGCTACTAAGAACCTAC
		LYM155_ER_XbaI (SEQ ID NO: 3866) AAATCTAGATAAACATCTCATGCCATGCTAC
LYM156	StuI,StuI	LYM156_NF_StuI (SEQ ID NO: 3867) TTTAGGCCTCAAGATCCGCAGAGATGATC
		LYM156 NR StuI_2 (SEQ ID NO: 3868) AAAAGGCCTTTAAGTGCTTGCGTCGTTTTACAG

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
LYM157_G	XbaI,SacI	LYM157_EF_Xba_B (SEQ ID NO: 3869) AATCTAGACCTCGAGCCACCCACTTTC
		LYM157_ER_Sac_B (SEQ ID NO: 3870) TGAGCTCTCACCTTCATCTTGTCTTCACTGGT
LYM159	SalI,XbaI	LYM159_NF_SalI (SEQ ID NO: 3871) AAAGTCGACCTCTACCTTCTTCTTCGGTCAG
		LYM159_NR_XbaI (SEQ ID NO: 3872) AAATCTAGAAGCTTAGCTAGGCCAACAATAC
LYM16	SalI,XbaI	LYM16 NF SalI (SEQ ID NO: 3873) CTAGTCGACAAGAAATTGGCACAGAAATGG
		LYM16 NR XbaI (SEQ ID NO: 3874) TATTCTAGATCAAAGAGCCTAGTGAGCGTCTTC
LYM160	SalI,XbaI	LYM160_F2_SalI (SEQ ID NO: 3875) AAAGTCGACAGGCCAGACCAAAACCATG
		LYM160_F2_SalI (SEQ ID NO: 3875) AAAGTCGACAGGCCAGACCAAAACCATG
		LYM160_NR_XbaI (SEQ ID NO: 3876) AAATCTAGAAGAGTAACATGGACACACGACC
		LYM160_R2_XbaI (SEQ ID NO: 3877) AATTCTAGATCAGTACAAGAGCCAGATGTCTGA
LYM161	BamHI,XhoI	LYM161_EF_BamHI (SEQ ID NO: 3878) AAAGGATCCGAGAGAGGAGCAAAGATTCACC
		LYM161_ER_XhoI (SEQ ID NO: 3879) AAACTCGAGTACAGGATGGTTGGTCTTCTTC
LYM162	BamHI,XhoI	LYM162_NF_BamHI (SEQ ID NO: 3880) TTTGGATCCGCATCTAAGCCGAATTGAAG
		LYM162_NR_XhoI (SEQ ID NO: 3881) AAACTCGAGCTATTTCATGCTCAGTACCTGCAC
LYM164	SalI,XbaI	LYM164_NF_SalI (SEQ ID NO: 3882) AAAGTCGACATCCAGATGCTTCACATTCTTG
		LYM164_NR_XbaI (SEQ ID NO: 3883) AAATCTAGATCGAGTTTGACACGAACTTATG
LYM165		LYM165_F2_XhoI (SEQ ID NO: 3884) AAACTCGAGCTACTCCGATCGGATCCTGAC
		LYM165_R2_SacI (SEQ ID NO: 3885) AAAGAGCTCAAACGACGCACGGTCTCAC
LYM17	SmaI,KpnI	LYM17 NF X/SmaI (SEQ ID NO: 3886) ATACCCGGGTCTCTCAAGATGGTGGTGCTG
		LYM17 NR KpnI (SEQ ID NO: 3887) TATGGTACCAAGGGCTTAGCAAATTCTTTC
LYM170	SalI,XbaI	LYM170_NF_SalI (SEQ ID NO: 3888) AAAGTCGACATTCTTCGACCTCCTAAACTCC
		LYM170_EF_SalI (SEQ ID NO: 3889) AAAGTCGACAGTCTCACACAGATCGCTTCAC
		LYM170_NR_XbaI (SEQ ID NO: 3890) AAATCTAGACTACCAACTCAGAACCAGGATGAG
		LYM170_ER_XbaI (SEQ ID NO: 3891) AAATCTAGACATACCTATAAGGCTATAACACTGC
LYM172	BamHI,XhoI	LYM172_NF_BamHI (SEQ ID NO: 3892) AAAGGATCCCTCGTCTTCGTCTACTCCACC

Gene Name	***Restriction Enzymes used for cloning***	***Primers used for amplification***
		LYM172_EF_BamHI (SEQ ID NO: 3893) AAAGGATCCCCTCACTCGTAGTCTCGTCTTC
		LYM172_NR_XhoI (SEQ ID NO: 3894) AAACTCGAGGGAGCTTTGGAGAATAACAAAC
		LYM172_ER_XhoI (SEQ ID NO: 3895) AAACTCGAGCAACAGGTAACTCATTTCCACC
LYM173	BamHI,XhoI	LYM173_NF_BamHI (SEQ ID NO: 3896) AAAGGATCCTCATCAGTTCCCTGTTCTTCAG
		LYM173_NR_XhoI (SEQ ID NO: 3897) AAACTCGAGATGACTGGACTAAAGCAACCAC
LYM174	BamHI,KpnI	LYM174_NF_BamHI (SEQ ID NO: 3898) AAAGGATCCCTCTTGCTAGGAGTAGCCTGC
		LYM174_NR_KpnI (SEQ ID NO: 3899) AAAGGTACCTATTATCCTACATGCCACATGC
LYM175	SalI,XbaI	LYM175_NF_SalI (SEQ ID NO: 3900) AAAGTCGACCACTCCCTCTTATAGCCCACC
		LYM175_NR_XbaI (SEQ ID NO: 3901) AAATCTAGACTAAGTGTACAGTTCACGGCACG
LYM176	SalI,XbaI	LYM176_NF_SalI (SEQ ID NO: 3902) AAAGTCGACTCTCGTTTCTCCTACCCTACAG
		LYM176_NR_XbaI (SEQ ID NO: 3903) AAATCTAGACTAACAGTTTCCAGTCAAAGCTACAG
LYM178	SalI,XbaI	LYM178_NF_SalI (SEQ ID NO: 3904) AAAGTCGACCTATCCATCCGCCACAAGAC
		LYM178_NR_XbaI (SEQ ID NO: 3905) AAATCTAGAACACAAGACACCATTTCTGGAG
LYM179	SalI,XhoI	LYM179_NF_SalI (SEQ ID NO: 3906) AAAGTCGACAGGATTTCTCTAGGATAGCAGC
		LYM179_EF_SalI (SEQ ID NO: 3907) AAAGTCGACCTCAGTCGAGCGAGGATTTC
		LYM179_NR_XhoI (SEQ ID NO: 3908) AAACTCGAGAAACAGAGCCTAACAGACATGG
		LYM179_ER_XhoI (SEQ ID NO: 3909) AAACTCGAGGGGATGTTTAGACTGCTACAGG
LYM180	BamHI,XhoI	LYM180_NF_BamHI (SEQ ID NO: 3910) TATGGATCCCGACCTTTGATACCAAGCAAG
		LYM180_NR_XhoI (SEQ ID NO: 3911) TTACTCGAGCACGGATTAGTTTGTAGTAGCATGG
LYM181		LYM181_F2_BamHI (SEQ ID NO: 3912) AATGGATCCTAAAAATGGCGGCTGCTACTC
		LYM181_R2_EcoRV (SEQ ID NO: 3913) TTTGATATCTCATACACGGTTTCATATGGTCGG
LYM183		LYM183_EF_SalI (SEQ ID NO: 3914) AAAGTCGACATCAAACCAACGAGAGCACTAC
		LYM183_ER_XbaI (SEQ ID NO: 3915) AAATCTAGAACTTCAGTGTACTTTCCCTTGC
LYM184		LYM184_NF_BamHI (SEQ ID NO: 3916) AAAGGATCCAACACGACTTGTGAGTGAGAGC
		LYM184_EF_BamHI (SEQ ID NO: 3917) AAAGGATCCATATGAGTAACGCCATCAGGAG

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM184_NR_XhoI (SEQ ID NO: 3918) AAACTCGAGTGCCTCATTTAATCTTGGGTC
		LYM184_ER_XhoI (SEQ ID NO: 3919) AAACTCGAGGAAATTGCCTCATTTAATCTTG
LYM185	BamHI,KpnI	LYM185_NF_BamHI (SEQ ID NO: 3920) AAAGGATCCAATTCGAGATATTTGGCTGTTC
		LYM185_EF_BamHI (SEQ ID NO: 3921) AAAGGATCCAGATAGCAAGATAGTCCGGTTG
		LYM185_NR_KpnI (SEQ ID NO: 3922) AAAGGTACCGGTCTATCACAAGCATCCTCAC
		LYM185_ER_KpnI (SEQ ID NO: 3923) AAAGGTACCACCACCTTTGTGATTGTTTCTC
LYM186	SalI,XbaI	LYM186_NF_SalI (SEQ ID NO: 3924) AAAGTCGACCGACCCAAATTGACATAACTC
		LYM186_NR_XbaI (SEQ ID NO: 3925) AAATCTAGAATAGCTGGAACCTGGTATTGAC
LYM188	BamHI,XhoI	LYM188_EF_BamHI (SEQ ID NO: 3926) AAAGGATCCCGAGCTAGGGTTAGGGTTTC
		LYM188_ER_XhoI (SEQ ID NO: 3927) AAACTCGAGCAACAACTCACGCTACACATTC
LYM189	SalI,XbaI	LYM189_NF_SalI (SEQ ID NO: 3928) AAAGTCGACCCACGTCCTAGAATGAAAGAG
		LYM189_EF_SalI (SEQ ID NO: 3929) AAAGTCGACTTCCTCTGCTTCCCACAGC
		LYM189_NR_XbaI (SEQ ID NO: 3930) AAATCTAGACTGTTCATTCACGGTTGCAC
		LYM189_ER_XbaI (SEQ ID NO: 3931) AAATCTAGAGCAAATCTGTCGCTTTATTAGG
LYM19	SalI,XbaI	LYM19_NF_SalI (SEQ ID NO: 3932) AAAGTCGACGAGAGAAGAGAGATGGTCCTCC
		LYM19_NR_XbaI (SEQ ID NO: 3933) AAATCTAGATTATCATGCTGACTTCTTGCCAC
LYM192	XhoI,EcoRV	LYM192_EF_XhoI (SEQ ID NO: 3934) AAACTCGAGTGAGCAGCGAGCCCTAAC
		LYM192_R_EcoRV (SEQ ID NO: 3935) TTTGATATCTCACACTACTAGGGAGTGGAGTAGTAACTTGA
LYM193	BamHI,XhoI	LYM193_NF_BamHI (SEQ ID NO: 3936) AAAGGATCCCTAGTAGTGTTCTTCCCATTCG
		LYM193_EF_BamHI (SEQ ID NO: 3937) AAAGGATCCAACAATCCGTCCTTTCATTTG
		LYM193_NR_XhoI (SEQ ID NO: 3938) AAACTCGAGTAAACGACAGCGGTACACATAC
		LYM193_ER_XhoI (SEQ ID NO: 3939) AAACTCGAGTACATCTCTAGGCAGCAAACAG
LYM196		LYM196_NF_BamHI (SEQ ID NO: 3940) AAAGGATCCGAGGACACCGCTTGCTTTC
		LYM196_NR_XhoI (SEQ ID NO: 3941) AAACTCGAGAACCTTGGATATGACCAATCAG
LYM197	BamHI,XhoI	LYM197_EF_BamHI (SEQ ID NO: 3942) AAAGGATCCCTGTTGCCACATCTAGTGGTTC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM197_ER_XhoI (SEQ ID NO: 3943) AAACTCGAGCACAATTCAGCGATTATTTCAG
LYM198	BamHI,XhoI	LYM198_F2_BamHI (SEQ ID NO: 3944) ATTGGATCCTTCATTTCCGCCATCCGT
		LYM198_R2_XhoI (SEQ ID NO: 3945) AAACTCGAGCACCATCTCTTGCAGAAGGC
LYM2	EcoRV,KpnI	LYM2_NF_EcoRV (SEQ ID NO: 3946) AAAGATATCCGGTAGGTAGATGAAATTAAGG
		LYM2_NR_KpnI (SEQ ID NO: 3947) CGAGGTACCCTAATATGCAGGTCAGCACACAAG
LYM20	EcoRV,KpnI	LYM20 NF EcoRV (SEQ ID NO: 3948) ATAGATATCACTCCGAATCCGACGCAC
		LYM20 EF EcoRV (SEQ ID NO: 3949) ATAGATATCGAGATCCCAACTCCGAATCC
		LYM20 NR KpnI (SEQ ID NO: 3950) TATGGTACCCTACGTAAATCTCAGCACATGC
		LYM20 ER KpnI (SEQ ID NO: 3951) TATGGTACCCTTCTGCAACGTTATTTGAGG
LYM200	BamHI,XhoI	LYM200_NF_BamHI (SEQ ID NO: 3952) AAAGGATCCACTTTACCGGGCTACCATTC
		LYM200_EF_BamHI (SEQ ID NO: 3953) AAAGGATCCTTACAAGAGCCTGTGAGCTGAG
		LYM200_NR_XhoI (SEQ ID NO: 3954) AAACTCGAGCTTATCTGGACCACACTTGGAC
		LYM200_ER_XhoI (SEQ ID NO: 3955) AAACTCGAGAAGAAATACATAGCCCTCCTCC
LYM201	BamHI,XhoI	LYM201_NF_BamHI (SEQ ID NO: 3956) AAAGGATCCGCCTCATCTCGGTTTACTATAAG
		LYM201_NR_XhoI (SEQ ID NO: 3957) AAACTCGAGAAGTAGACACAAACCATCCTGG
LYM203	BamHI,XhoI	LYM203_EF_BamHI (SEQ ID NO: 3958) AAAGGATCCTCTATCAAATCAGCCACCTGTC
		LYM203_ER_XhoI (SEQ ID NO: 3959) AAACTCGAGCTAGCAACTTTGTAGACCAGACGTG
LYM204		LYM204_NF_BamHI (SEQ ID NO: 3960) AAAGGATCCCTACTACCAGACAGAGAGGACAGG
		LYM204_EF_BamHI (SEQ ID NO: 3961) TTTGGATCCGCTTTCTGGCATCGCTACTAC
		LYM204_NR_XhoI (SEQ ID NO: 3962) TGTCTCGAGTCAGTAGGAGTTTATGAGATGAACC
		LYM204_ER_Xho (SEQ ID NO: 3963) AAACTCGAGTCAACTCATCATCCGGAACATGGTAC
LYM206	XhoI,EcoRV	LYM206_EF_XhoI (SEQ ID NO: 3964) AAACTCGAGAATTCTAGCAAGGCAGCTCAG
		LYM206_ER_EcoRV (SEQ ID NO: 4199) AAAGATATCTAAAGGAGTCGTAGCCCTCTC
LYM207		LYM207_EF_BamHI (SEQ ID NO: 3966) AAAGGATCCACTCTTCCAACCGCTCCTC
		LYM207_ER_KpnI (SEQ ID NO: 4200) AAAGGTACCCTAGTCTTGCGAAGTGCGAG
LYM208	BamHI,XhoI	LYM208_F2_BamHI (SEQ ID NO: 3968) AAAGGATCCTGCGGCTGAGTACAGACGAC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM208_R2_KpnI (SEQ ID NO: 3969) AAAGGTACCCATCAATCCATGCTAATGTAGAGC
LYM21	EcoRV,KpnI	LYM21_NF_EcoRV (SEQ ID NO: 3970) AAAGATATCTCTCGCAGCACAAAGATGG
		LYM21 NR KpnI (SEQ ID NO: 3971) ATAGGTACCTCACCCTTAGTTCTTCACAGTGGTG
LYM212	SalI,XbaI	LYM212_NF_SalI (SEQ ID NO: 3972) AAAGTCGACCTGATACCCATCCATCCACC
		LYM212_EF_SalI (SEQ ID NO: 3973) AAAGTCGACACTGACAAACCGGACCCAC
		LYM212_NR_XbaI (SEQ ID NO: 3974) AAATCTAGACTAGCAGAGCCGAAGTAGTACGAG
		LYM212_ER_XbaI (SEQ ID NO: 3975) AAATCTAGACTAGAACGAAGTAGTACGAGCAAGC
LYM213	BamHI,XhoI	LYM213_EF_BamHI (SEQ ID NO: 3976) AAAGGATCCCAGCTCATCAGAACACAGAAGG
		LYM213_ER_XhoI (SEQ ID NO: 3977) AAACTCGAGTTCGACAATTTGCAATAGAAAG
LYM215	BamHI,XhoI	LYM215_F2_BamHI (SEQ ID NO: 3978) AATGGATCCTTCCCTCCCACCGAAATG
		LYM215_F2_BamHI (SEQ ID NO: 3978) AATGGATCCTTCCCTCCCACCGAAATG
		LYM215_R2_XhoI (SEQ ID NO: 3979) AAACTCGAGGAGCATGCAAAATGGACTAGACT
		LYM215_R2_XhoI (SEQ ID NO: 3979) AAACTCGAGGAGCATGCAAAATGGACTAGACT
LYM217	SalI,XbaI	LYM217_F2_SalI (SEQ ID NO:4201) AAAGTCGACCGACCGATCCAAGTAGTGAGC
		LYM217_R2_XbaI (SEQ ID NO:4202) AAATCTAGAAGCTGATAGGCCAGTCAATCC
LYM219	BamHI,KpnI	LYM219_F_BamHI (SEQ ID NO: 3980) AAAGGATCCTAGCAGTCTCGATGGCCG
		LYM219_F_BamHI (SEQ ID NO: 3980) AAAGGATCCTAGCAGTCTCGATGGCCG
		LYM219_R_KpnI (SEQ ID NO: 3981) TTTGGTACCCGAGTCAGCTTTTGTAATGATAG
		LYM219_R_KpnI (SEQ ID NO: 3981) TTTGGTACCCGAGTCAGCTTTTGTAATGATAG
LYM22	SalI,XbaI	LYM22_NF_SalI (SEQ ID NO: 3982) AAAGTCGACTTAGCACACATGGCGTCTTC
		LYM22_EF_SalI (SEQ ID NO: 3983) AAAGTCGACCATCGGCATCTTCCTAACTG
		LYM22_NR_XbaI (SEQ ID NO: 3984) AATTCTAGATAATCTGTAGATGGCTGCCG
		LYM22_ER_SmaI (SEQ ID NO: 3985) AATCCCGGGTAACAACGTACATGCAAGTCATC
LYM220	BamHI,EcoRV	LYM220_NF_BamHI (SEQ ID NO: 3986) AAAGGATCCCGACTTCAAGCATCAGACTACC

Gene Name	***Restriction Enzymes used for cloning***	***Primers used for amplification***
		LYM220_EF_BamHI (SEQ ID NO: 3987) AAAGGATCCAGCACACACATCCTCTAAGTGC
		LYM220_NR_EcoRV (SEQ ID NO: 3988) AAAGATATCAACAGCAGTCACTTCACTCGTC
		LYM220_ER_EcoRV (SEQ ID NO: 3989) AAAGATATCAAGTGGTACGGCTGAGTGTAAC
LYM221	BamHI,XhoI	LYM221_NF_BamHI (SEQ ID NO: 3990) AAAGGATCCACTGTCCACTGCGTCTGTCTC
		LYM221_EF_BamHI (SEQ ID NO: 3991) AAAGGATCCATCGTTAGAGGCTCAGAGTCAG
		LYM221_NR_XhoI (SEQ ID NO: 3992) AAACTCGAGACTACGTATTACACGGAGGTGG
		LYM221_ER_XhoI (SEQ ID NO: 3993) AAACTCGAGTCTGCAGCATTCCTTAACCTAC
LYM223	XhoI,SacI	LYM223_NF_XhoI (SEQ ID NO: 3994) AAACTCGAGACCTGCCTGCCACTATACTATC
		LYM223_EF_XhoI (SEQ ID NO: 3995) AAACTCGAGAGACCCGTCTTAACTCTACCTG
		LYM223_NR_SacI (SEQ ID NO: 3996) AAAGAGCTCAGCACCGGTTGATCTAGAATAC
		LYM223_ER_SacI (SEQ ID NO: 3997) AAAGAGCTCATTTATCCACGAACCCATATTC
LYM224	BamHI,XhoI	LYM224_EF_BamHI (SEQ ID NO: 3998) AAAGGATCCCAGGCCTCACGTGTCATTC
		LYM224_EF_BamHI (SEQ ID NO: 3998) AAAGGATCCCAGGCCTCACGTGTCATTC
		LYM224_R2_XhoI (SEQ ID NO: 3999) AAACTCGAGGTTTCCAGCCAACCAGAACAC
		LYM224_ER_XhoI (SEQ ID NO: 4000) AAACTCGAGGATCCAAATTGGTAATGCTTTG
LYM228		LYM228_NF_BamHI (SEQ ID NO: 4001) AAAGGATCCGCAAGCACTCCACTTCAAGC
		LYM228_F2_BamHI (SEQ ID NO: 4002) AAAGGATCCCTCGAAGTGTCCAAGAAGAACACA
		LYM228_R2_KpnI (SEQ ID NO: 4003) TAAGGTACCGAGCTGCAAACATAACGTCGAG
		LYM228_R2_KpnI (SEQ ID NO: 4003) TAAGGTACCGAGCTGCAAACATAACGTCGAG
LYM23	BamHI,KpnI	LYM23_NF_BamHI (SEQ ID NO: 4004) AAAGGATCCTCATCTCTCTCCCTCTCATCG
		LYM23_NR_KpnI (SEQ ID NO: 4005) AAAGGTACCGTGCTGCTTCAACTATCCTCTC
LYM232		LYM232_EF_BamHI (SEQ ID NO: 4006) AAAGGATCCAAATTCCCAATTTCTTCGGTC
		LYM232_ER_XhoI (SEQ ID NO: 4007) AAACTCGAGAGCACACACAGGTTCCTAAGAG
LYM236	SalI,XbaI	LYM236_F_SalI (SEQ ID NO: 4008) AAAGTCGACGACTACCAATCCAATCTCCTCC
		LYM236_ER_XbaI (SEQ ID NO: 4009) AAATCTAGAAGAAATGTATAATCGAAGTGCATC
LYM238		LYM238_EF_SmaI (SEQ ID NO: 4010) AAACCCGGGTAGTGGTGGAGAGACGAAACAC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM238_ER_SacI (SEQ ID NO: 4011) AAAGAGCTCCTACAAGTGCTGACTGCTGAAG
LYM239	BamHI,XhoI	LYM239_EF_BamHI (SEQ ID NO: 4012) AAAGGATCCCTTGGTCCGTCTCCACTCTC
		LYM239_R_XhoI (SEQ ID NO: 4013) AAACTCGAGCTAGGATTGGTACTCATTTCTTTGTG
LYM24	SalI,XbaI	LYM24_NF_SalI (SEQ ID NO: 4014) AACGTCGACTCTTCTCTTTCTCTTCTCCTCG
		LYM24_NR_XbaI (SEQ ID NO: 4015) ATATCTAGACATTCCAAACATTGTTATCAAAC
LYM240	BamHI,KpnI	LYM240_NF_BamHI (SEQ ID NO: 4016) AAAGGATCCTACTGTAAGCAGTTTCCCACC
		LYM240_EF_BamHI (SEQ ID NO: 4017) AAAGGATCCAACAACGCTCGTACTGTAAGC
		LYM240_NR_KpnI (SEQ ID NO: 4018) AAAGGTACCACAAGTCATTCTACCAAGCACC
		LYM240_ER_KpnI (SEQ ID NO: 4019) AAAGGTACCATACTTTCCTTGCTCTGCTGTC
LYM241	,	LYM241_NF_BamHI (SEQ ID NO: 4020) AAAGGATCCAAACGGTTGGGAGGTTAGC
		LYM241_NR_XhoI (SEQ ID NO: 4021) AAACTCGAGACTGGATCAGATTGTGAAGGTG
LYM242	BamHI,XhoI	LYM242_NF_BamHI (SEQ ID NO: 4022) AAAGGATCCACGACTCCGACGAGCGAC
		LYM242_NR_XhoI (SEQ ID NO: 4023) AAACTCGAGAACTCAAGTGGACAAATGTTGC
LYM243	BamHI,XhoI	LYM243_EF_BamHI (SEQ ID NO: 4024) AAAGGATCCAGAAGCGTAGAGCGGTCAAG
		LYM243_ER_XhoI (SEQ ID NO: 4025) AAACTCGAGCATTAAGCGAATTAACCATGTG
LYM245	BamHI,KpnI	LYM245_F_BamHI (SEQ ID NO: 4026) AAAGGATCCGCTAGCTACTAGCAAATTGAAGC
		LYM245_F_BamHI (SEQ ID NO: 4026) AAAGGATCCGCTAGCTACTAGCAAATTGAAGC
		LYM245_NR_KpnI (SEQ ID NO: 4027) AAAGGTACCGGTCACCCGTTAGACTTATGC
		LYM245_ER_KpnI (SEQ ID NO: 4028) AAAGGTACCTGGTAAATTATGGGTATTCAGC
LYM248	BamHI,EcoRV	LYM248_F_BamHI (SEQ ID NO: 4029) AAAGGATCCACCACCGCTCGTCTCCAC
		LYM248_NR_EcoRV (SEQ ID NO: 4030) AAAGATATCACAAGAGAGATGGTGTGTCAGC
LYM249		LYM249_EF_BamHI (SEQ ID NO: 4031) AAAGGATCCGGGTGTCATCAAACGGACTAC
		LYM249_ER_KpnI (SEQ ID NO: 4032) AAAGGTACCCTAAACGAGGTTACGGAATGTGTC
LYM250	SalI,XbaI	LYM250_EF_SalI (SEQ ID NO: 4033) AAAGTCGACGGAATTGGTGAGGTGATGC
		LYM250_ER_XbaI (SEQ ID NO: 4034) AAATCTAGACAGATAAACCTCAATCAAAGTCG
LYM251		LYM251_NF_SalI (SEQ ID NO: 4035) AAAGTCGACCTGTCCTCTACTACGCATCTCTC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM251_NR_XbaI (SEQ ID NO: 4036) AAATCTAGATAATCATCATTGTAGCAGGCAC
LYM252	BamHI,KpnI	LYM252_NF_BamHI (SEQ ID NO: 4037) AAAGGATCCTAGGAAGGATGGTACTGGCTG
		LYM252_EF_BamHI (SEQ ID NO: 4038) AAAGGATCCGCGATAGGAAGGATGGTACTG
		LYM252_NR_KpnI (SEQ ID NO: 4039) AAAGGTACCAGGCAAACACAATGATTTCAAC
		LYM252_ER_KpnI (SEQ ID NO: 4040) AAAGGTACCTGTAACATAAGTACCGGGCAG
LYM254		LYM254_EF_SalI (SEQ ID NO: 4041) AAAGTCGACAATCTCCCACGCTCCAAAG
		LYM254_ER_XbaI (SEQ ID NO: 4042) AAATCTAGAAGTTACATTCTTGACCAGCAGC
LYM255	BamHI,XhoI	LYM255_NF_BamHI (SEQ ID NO: 4043) AAAGGATCCCTTCTAGTAGCACAGTAGTAGCAGC
		LYM255_NR_XhoI (SEQ ID NO: 4044) AAACTCGAGAACGAGGAAGAATCGGTATATG
LYM256	BamHI,XhoI	LYM256_NF_BamHI (SEQ ID NO: 4045) AAAGGATCCGGAACAACTCGTAGCCATGAC
		LYM256_EF_BamHI (SEQ ID NO: 4046) TATGGATCCCAATTTGAGAGCATTTGCTACG
		LYM256_NR_XhoI (SEQ ID NO: 4047) TAACTCGAGCTGAACTTAATAGCAATTCCGTAGC
		LYM256_ER_XhoI (SEQ ID NO: 4048) AAACTCGAGCGCACTACTGTGCTTCTGAAC
LYM26	SalI,XbaI	LYM26_EF_SalI (SEQ ID NO: 4049) AAAGTCGACTTGCTCCCTCTCTCTCTCTTG
		LYM26_ER_XbaI (SEQ ID NO: 4050) AAATCTAGATGTATTCACGAGGTAAACAACG
LYM260		LYM260_NF_BamHI (SEQ ID NO: 4051) AAAGGATCCGAGAGATTAATTAAGTGGCAGG
		LYM260_EF_BamHI (SEQ ID NO: 4052) AAAGGATCCAGAAGAGAGATTAATTAAGTGGCAG
		LYM260_NR_KpnI (SEQ ID NO: 4053) AAAGGTACCCTAATATCGATCCAAACTCACACAAG
		LYM260_ER_KpnI (SEQ ID NO: 3965) AAAGGTACCTACGTGCGTATCATACATGGAG
LYM261		LYM261_EF_SmaI (SEQ ID NO: 4054) AATCCCGGGTCGAGAGGTTTCATTCAGTGC
		LYM261_ER_KpnI (SEQ ID NO: 4055) TTTGGTACCTTATTACATTTGGATGGGCTGT
LYM267	SalI,EcoRV	LYM267_F_SalI (SEQ ID NO: 4056) AAAGTCGACGAGCACAGGTAGGGTTTCG
		LYM267_ER_EcoRV (SEQ ID NO: 4057) AAAGATATCCACTACCGAAGACTCACACGAC
LYM268		LYM268_EF_XhoI (SEQ ID NO: 4058) AAACTCGAGAACCCTCGCGAATCTGAG
		LYM268_ER_EcoRV (SEQ ID NO: 4059) AAAGATATCTAGTTCTCCATTCAGCATCTCC
LYM270	BamHI,XhoI	LYM270_NF_BamHI (SEQ ID NO: 4060) AAAGGATCCAAAGCAGTTCCAGCCTTCC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM270_EF_BamHI (SEQ ID NO: 4061) AAAGGATCCACCAATGGCTGCCTGAGAC
		LYM270_NF_BamHI (SEQ ID NO: 4060) AAAGGATCCAAAGCAGTTCCAGCCTTCC
		LYM270_ER_XhoI (SEQ ID NO: 4062) AAACTCGAGGATTGGATATGCCACTTGATTG
LYM271	BamHI,XhoI	LYM271_EF_BamHI (SEQ ID NO: 4063) AAAGGATCCCACCTTCTTCCCAGATCAATAG
		LYM271_ER_XhoI (SEQ ID NO: 4064) AAACTCGAGGAAACAAAGCACAGTCAGTAGTAG
LYM273_S	BamHI,XhoI	LYM273_EF_BamHI (SEQ ID NO: 4065) AAAGGATCCTACTAACAAACAGATAATCTCCACG
		LYM273_R2_XhoI (SEQ ID NO: 4066) ATACTCGAGAACATGTTGGAGATCTTTGATGC
LYM274	BamHI,XhoI	LYM274_EF_BamHI (SEQ ID NO: 4067) AAAGGATCCGAGAAGCTCCACTCTTCTCCAC
		LYM274_ER_XhoI (SEQ ID NO: 4068) AAACTCGAGTATAATGCACAGTTATGGGCAG
LYM277		LYM277_NF_SalI (SEQ ID NO: 4069) AAAGTCGACTCAACGCCCAAGCTAGATTAC
		LYM277_NR_SacI (SEQ ID NO: 4070) AAAGAGCTCCTCAACATTGCAACAACTATGG
LYM278	SalI,SacI	LYM278_EF_SalI (SEQ ID NO: 4071) AAAGTCGACGCAGCCACACAACACTATCTC
		LYM278_ER_SacI (SEQ ID NO: 4072) AAAGAGCTCTTGACGATACATAGCACATAAGG
LYM283		LYM283_NF_SmaI (SEQ ID NO: 4073) TTTCCCGGGTGCCACTTGTGCGAGGAG
		LYM283_R_KpnI (SEQ ID NO: 4074) AACGGTACCTCACCAATCAAAATGTACAATCATGT
LYM284	BamHI,KpnI	LYM284_EF_BamHI (SEQ ID NO: 4075) AAAGGATCCGAGCAACCACCCGTAGTCAG
		LYM284_ER_KpnI (SEQ ID NO: 4076) AAAGGTACCACAGCTCAAGTGCTCATTTCTC
LYM285	XhoI,EcoRV	LYM285_NF_XhoI (SEQ ID NO: 4077) AAACTCGAGCCGCCATCTACTCGGAGC
		LYM285_EF_XhoI (SEQ ID NO: 4078) AAACTCGAGCCTCCTCCGCCATCTACTC
		LYM285_NR_EcoRV (SEQ ID NO: 4079) AAAGATATCAGAATTCACACTGTCCCAACAC
		LYM285_ER_EcoRV (SEQ ID NO: 4080) AAAGATATCCAGTTATTATAGGCCTCGTTCC
LYM287	XhoI,EcoRV	LYM287_EF_XhoI (SEQ ID NO: 4081) AAACTCGAGTGATTGCGTTTCCTTAAATATG
		LYM287_ER_EcoRV (SEQ ID NO: 4082) AAAGATATCCAATCAATCCTACAAACACAGC
LYM288	XhoI,SacI	LYM288_EF_XhoI (SEQ ID NO: 4083) AAACTCGAGTGTTAGGAAGTGAGGACTGAGC
		LYM288_ER_SacI (SEQ ID NO: 4084) AAAGAGCTCGCTCAATTATTCACCATTTCATC
LYM289	SalI,XbaI	LYM289_EF_SalI (SEQ ID NO: 4085) AAAGTCGACGCACAACCCTTGGAGACTTC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM289_ER_XbaI (SEQ ID NO: 4086) AAATCTAGATCCTCTCATCGAGCTAAGACAC
LYM290	BamHI,KpnI	LYM290_EF_BamHI (SEQ ID NO: 4087) AAAGGATCCATCCGGATCTCCACATTCC
		LYM290_ER_KpnI (SEQ ID NO: 4088) AAAGGTACCGAAACAATCTCATGGTCTCTGC
LYM291	SalI,BamHI	LYM291_EF_SalI (SEQ ID NO: 4089) AAAGTCGACACTGAGCTCTCTGCTAAGTTGG
		LYM291_ER_BamHI (SEQ ID NO: 4090) AAAGGATCCTCCTAGCAACAGAAGATCCAAG
LYM293	XhoI,SacI	LYM293_NF_XhoI (SEQ ID NO: 4091) AAACTCGAGAGCTTCCTCCCTAGCTGTCC
		LYM293_EF_XhoI (SEQ ID NO: 4092) AAACTCGAGGTGTAGCTTCCTCCCTAGCTG
		LYM293_NR_SacI (SEQ ID NO: 4093) AAAGAGCTCCTATTCCAGGAGAAGAACAATAAGAG
		LYM293_ER_SacI (SEQ ID NO: 4094) AAAGAGCTCCTATTCATGTTCCAGGAGAAGAAC
LYM3	XhoI,KpnI	LYM3_EF_XhoI (SEQ ID NO: 4095) AATCTCGAGATTTATCTGCTTCAATGGCAAC
		LYM3_ER_KpnI (SEQ ID NO: 4096) ATAGGTACCCTAAGCATCATTCTGCCTACC
LYM30	SalI,XhoI	LYM30_NF_SalI (SEQ ID NO: 4097) AAAGTCGACCCTCCATCCTTCAGTAATTGG
		LYM30_NR_XhoI (SEQ ID NO: 4098) TTTCTCGAGTCAGTCTCCTTGGATGTTTGAGTTG
LYM31	SalI,XhoI	LYM31_NF_SalI (SEQ ID NO: 4099) AAGGTCGACACTCCCAACGTCTACTCTTCC
		LYM31_EF_SalI (SEQ ID NO: 4100) AATGTCGACCTCACCACTCCCAACGTCTAC
		LYM31_NR_XhoI (SEQ ID NO: 4101) AAACTCGAGATGTAAGAATGAAATCTTGTAGCTC
		LYM31_ER_XhoI (SEQ ID NO: 4102) AATCTCGAGTGCAAGGATGTAAGAATGAAATC
LYM34	BamHI,KpnI	LYM34_NF_BamHI (SEQ ID NO: 4103) AAAGGATCCGAGATAATTAGCTCACTCCATGG
		LYM34_NR_KpnI (SEQ ID NO: 4104) TATGGTACCGAATTGGGCCTATGAGACG
LYM35	SalI,XbaI	LYM35_NF_SalI (SEQ ID NO: 4105) AAAGTCGACAACACCTCTCTGGCTCTCTCC
		LYM35_NR_SacI (SEQ ID NO: 4106) AAAGAGCTCTCCTAAGACTTTCTCAGCCATC
LYM37	SalI,XbaI	LYM37_NF_SalI (SEQ ID NO: 4203) AAAGTCGACAAAGTTAGCGACCAAGAAACC
		LYM37_NR_XbaI (SEQ ID NO: 4204) AAATCTAGACATTTCTTTTGGATGGATGAAC
LYM4	EcoRV,KpnI	LYM4_NF_EcoRV (SEQ ID NO: 4107) AAAGATATCACCTCGAAACCCTAGATCG
		LYM4_EF_EcoRV (SEQ ID NO: 4108) AAAGATATCATTCCTCGACCAGCTCACG
		LYM4_NR_Kpn (SEQ ID NO: 4109) TTAGGTACCACTCAAAGGAGAGCTTCAGCC

Gene Name	***Restriction Enzymes used for cloning***	***Primers used for amplification***
		LYM4 ER KpnI (SEQ ID NO: 4110) TAAGGTACCGTTGGCATTCTTCAAACCAG
LYM40		LYM40_NF_SalI (SEQ ID NO: 4111) AAAGTCGACCTCGAGAGCTCAATGATTCG
		LYM40_NR_XbaI (SEQ ID NO: 4112) AAATCTAGAACCAACCAATTAAAGGCTAATG
LYM41	SalI,XbaI	LYM41_NF_SalI (SEQ ID NO: 4113) AAAGTCGACGATTGGTTGCTTGGGTTTG
		LYM41_NR_XbaI (SEQ ID NO: 4114) AAATCTAGATGCTTTCTTTCAGAACATCTCC
LYM42	SalI,XbaI	LYM42_NF_SalI (SEQ ID NO: 4115) AAAGTCGACAACCTCTCCTCCTCGTCACAC
		LYM42_EF_SalI (SEQ ID NO: 4116) AAAGTCGACATCAAACCTCTCCTCCTCGTC
		LYM42_NR_XbaI (SEQ ID NO: 4117) AATTCTAGATCACAGGAAGGAGGGGTAGTAACAG
		LYM42_ER_XbaI (SEQ ID NO: 4118) AAATCTAGAATTTCCTGCTGTTCATTCAAAG
LYM43	SalI,XbaI	LYM43_NF_SalI (SEQ ID NO: 4119) AAAGTCGACTCAGTGTTCTTCCATTCTTTCC
		LYM43_NR_XbaI (SEQ ID NO: 4120) AAATCTAGATTGAATTAGCAGCAGCAAGAG
LYM44	SalI,XbaI	LYM44_NF_SalI (SEQ ID NO: 4121) AAAGTCGACCGAACTAACTAACCATCTCATCC
		LYM44_NR_XbaI (SEQ ID NO: 4122) AAATCTAGAATCGTTCGATTATTATTGCTCC
LYM5	EcoRV,PstI	LYM5_EF_EcoRV (SEQ ID NO: 4123) AAAGATATCTCCTCTTCTCAAACTCCATCTC
		LYM5_ER_PstI (SEQ ID NO: 4124) AATCTGCAGGGTCCTGTCATGCTGTGTAGTC
LYM51	SalI,XbaI	LYM51_EF_SalI (SEQ ID NO: 4125) AAAGTCGACAATTCACCTCCCAAGCAGAG
		LYM51_ER_XbaI (SEQ ID NO: 4126) AAATCTAGAATACAAGGCCTGCACTACCTAC
LYM52	EcoRV,XhoI	LYM52_F_XhoI (SEQ ID NO: 4127) AAACTCGAGAAACCCGATAAGAAAATGGC
		LYM52_ER_EcoRV (SEQ ID NO: 4128) TTTGATATCCTAGTGCCATACGTGCCTAACCT
LYM53	SalI,XbaI	LYM53_NF_SalI (SEQ ID NO: 4129) AAAGTCGACATCCTCTCTTTCCACTCCTAGC
		LYM53_NR_XbaI (SEQ ID NO: 4130) AAATCTAGATAGCACTCAGCTTAATTGGATG
LYM56	SalI,XbaI	LYM56_F_SalI (SEQ ID NO: 4131) AAAGTCGACCTCGCTTGCCCACTCCTT
		LYM56_F_SalI (SEQ ID NO: 4131) AAAGTCGACCTCGCTTGCCCACTCCTT
		LYM56_NR_XbaI (SEQ ID NO: 4132) AAATCTAGACTAGCATGATCCTGGATGTTTACTC
		LYM56_ER_XbaI (SEQ ID NO: 4133) AAATCTAGAAGCAGAGATAGGCATAAGTCCA
LYM57	EcoRV,XhoI	LYM57_NF_EcoRV (SEQ ID NO: 4134) AAAGATATCACCACTAGGACTCAACGAGAAG

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM57_NR_XhoI (SEQ ID NO: 4135) AACCTCGAGAGTAACATCCGAACGTATACACC
LYM6	SmaI,KpnI	LYM6_NF_X/SmaI (SEQ ID NO: 4136) ATACCCGGGAACCACGCGAAGACATGG
		LYM6_NR_KpnI (SEQ ID NO: 4137) TATGGTACCGGATCAGGTTATACTTCTTATTGAC
LYM61	BamHI,XhoI	LYM61_NF_BamHI (SEQ ID NO: 4138) AAAGGATCCAAGCCTGTTCTCTGTCGATTG
		LYM61_NR_XhoI (SEQ ID NO: 4139) AAACTCGAGAATGCATGTCCTAGTCTTTACG
LYM62	BamHI,KpnI	LYM62_NF_BamHI (SEQ ID NO: 4140) TTAGGATCCAACATTTACGCGATCCATTG
		LYM62_EF_BamHI (SEQ ID NO: 4141) TTAGGATCCATCATCTGCTTTGTCTACCTCG
		LYM62_NR_KpnI (SEQ ID NO: 4142) ATCGGTACCTCAACTGAATTCGCTGAAACTTGTC
		LYM62_ER_KpnI (SEQ ID NO: 4143) AAAGGTACCGAAAACAAATGGAAGCAATCTG
LYM66	EcoRV,XhoI	LYM66_NF_EcoRV (SEQ ID NO: 4144) AAAGATATCGAGACGCAAGAAACATAGCTC
		LYM66_NR_XhoI (SEQ ID NO: 4145) AAACTCGAGCAATCACTGCTACAAATCCGT
LYM67	SalI,XbaI	LYM67_NF_SalI (SEQ ID NO: 4146) TATGTCGACTCTTCTTCACTGAGGCAAGTTC
		LYM67_NR_XbaI (SEQ ID NO: 4147) AAGTCTAGATCAAAGATCCATAACATTCCATGC
LYM68	SalI,XhoI	LYM68_NF_SalI (SEQ ID NO: 4148) ATTGTCGACTTGAGATAAAGGCAAAATTACG
		LYM68_EF_SalI (SEQ ID NO: 4149) TTTGTCGACGTCTCGTTTCAGATTCTTCTGC
		LYM68_NR_XhoI (SEQ ID NO: 4150) TTCCTCGAGTCTCTAGAGTTGCATTCCTTCC
		LYM68_ER_XhoI (SEQ ID NO: 4151) TGACTCGAGCATCGTTTACACTGAACCACTG
LYM69	SalI,XbaI	LYM69_NF_SalI (SEQ ID NO: 4152) AAAGTCGACACCCAGGAACACATCATCATC
		LYM69_NR_XbaI (SEQ ID NO: 4153) AAATCTAGAAGGACACGTCAAATGAGAAAAC
LYM7	SalI,XbaI	LYM7_NF_SalI (SEQ ID NO: 4154) AAAGTCGACAGTCAGATCCATTCCTCCTCC
		LYM7_NR_XbaI (SEQ ID NO: 4155) AATTCTAGAAAAAGTAGCAGCCGGTCATC
LYM73		LYM73_EF_SalI (SEQ ID NO: 4156) AACGTCGACAATCTTGACACCATCTCGCTC
		LYM73_ER_StuI (SEQ ID NO: 4157) TTTAGGCCTCTCGCACATTATTTTGTACAGC
LYM79	SalI,XbaI	LYM79_F_SalI (SEQ ID NO: 4158) AAAGTCGACGCGACAGAGAATCCATGGC
		LYM79_F_SalI (SEQ ID NO: 4158) AAAGTCGACGCGACAGAGAATCCATGGC
		LYM79_NR_XbaI (SEQ ID NO: 4159) AATTCTAGATCAAACTCCTCTTATATGCACCTGC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM79_ER_XbaI (SEQ ID NO: 4160) AAATCTAGATCAGAAACTAACTCCTCTTATATGCACC
LYM8	XhoI,KpnI	LYM8 NF XhoI (SEQ ID NO: 4161) ATACTCGAGCTTCCCCGATAGAAATCCATC
		LYM8 NR KpnI (SEQ ID NO: 4162) TAGGGTACCACCAAACAGCACATATGCGG
LYM82	SalI,XbaI	LYM82_EF_SalI (SEQ ID NO: 4163) AAAGTCGACCGCAACCGGAGAGAAATC
		LYM82_ER_XbaI (SEQ ID NO: 4164) AAATCTAGATCGACAATCTTCATACACAACG
LYM83		LYM83_NF_BamHI (SEQ ID NO: 4165) AAAGGATCCCGACAGTCACCACTCACCAAC
		LYM83_F2_BamHI (SEQ ID NO: 4166) AAAGGATCCTCCGCACGCAACTCAGTG
		LYM83_R2_XhoI (SEQ ID NO: 4167) AAACTCGAGCAACGGTAACACACAAGCATTC
		LYM83_R2_XhoI (SEQ ID NO: 4167) AAACTCGAGCAACGGTAACACACAAGCATTC
LYM84	BamHI,XhoI	LYM84_NF_BamHI (SEQ ID NO: 4168) AAAGGATCCACCCAGAACCCGAAGAATG
		LYM84_F2_BamHI (SEQ ID NO: 4169) AATGGATCCTAAACCCAGAACCCGAAGAATG
		LYM84_R2_XhoI (SEQ ID NO: 4170) AAACTCGAGCAAACTGGAGCATAGCAACTAGG
		LYM84_R2_XhoI (SEQ ID NO: 4170) AAACTCGAGCAAACTGGAGCATAGCAACTAGG
LYM86	BamHI,XhoI	LYM86_EF_BamHI (SEQ ID NO: 4171) AAAGGATCCCACACACCACAGTCGCAATC
		LYM86_ER_XhoI (SEQ ID NO: 4172) AAACTCGAGAGAATCGATGCAGGTAACTACG
LYM88	BamHI,XhoI	LYM88_F_BamHI (SEQ ID NO: 4173) AAAGGATCCACAATAAACAAGATAAATGGAGG
		LYM88_F_BamHI (SEQ ID NO: 4173) AAAGGATCCACAATAAACAAGATAAATGGAGG
		LYM88_NR_XhoI (SEQ ID NO: 4174) AAACTCGAGTCACACGCAACTTCAGGTTC
		LYM88_ER_XhoI (SEQ ID NO: 4175) AAACTCGAGCAAACCGAATTATTACATCAGG
LYM89	SalI,SacI	LYM89_NF_SalI (SEQ ID NO: 4176) AAAGTCGACGGCCGACACATCTGATCTAAC
		LYM89_NR_SacI (SEQ ID NO: 4177) AAAGAGCTCTCCCAGAAATATATAAGAACAAGC
LYM9	SalI,XbaI	LYM9_NF_SalI (SEQ ID NO: 4178) AAAGTCGACAACTCCCCAACCAAGCAG
		LYM9_NR_XbaI (SEQ ID NO: 4179) AAATCTAGATTAGTACTAAGAGTCGGCTTTGGC
LYM90	SalI,XbaI	LYM90_NF_SalI (SEQ ID NO: 4180) AAAGTCGACCTAAACCCTAACCCTAGATTGG
		LYM90_NR_XbaI (SEQ ID NO: 4181) AAATCTAGAAGACTTGGCTAATGCTAACCTG
LYM91	SalI,XbaI	LYM91_F2_SalI (SEQ ID NO: 4182) TAAGTCGACCGTCTCTCAAGCTCGCAGC

Gene Name	*Restriction Enzymes used for cloning*	*Primers used for amplification*
		LYM91_F2_SalI (SEQ ID NO: 4182) TAAGTCGACCGTCTCTCAAGCTCGCAGC
		LYM91_R2_XbaI (SEQ ID NO: 4183) ATTTCTAGACGAGAGCCTCTAATGGATCACAG
		LYM91_R2_XbaI (SEQ ID NO: 4183) ATTTCTAGACGAGAGCCTCTAATGGATCACAG
LYM93		LYM93_EF_SalI (SEQ ID NO: 4184) AAAGTCGACATTGCACTGCATAGGGCTG
		LYM93_ER_XbaI (SEQ ID NO: 4185) AAATCTAGACTAAGAGTTGAGCATGATAAATACGAC
LYM95	SalI,XbaI	LYM95_NF_SalI (SEQ ID NO: 4186) ATAGTCGACGAGAAAGTGGAAGAGAACATGG
		LYM95_EF_SalI (SEQ ID NO: 4187) AAAGTCGACCCGCTGGAGAAAGTGGAAG
		LYM95_NR_XbaI (SEQ ID NO: 4188) AAATCTAGAGTCCACAGATCCATGTCAAATC
		LYM95_ER_XbaI (SEQ ID NO: 4189) AAATCTAGAGTGAATTTGATTTATTGCCAAC
LYM99	BamHI,KpnI	LYM99_NF_BamHI (SEQ ID NO: 4190) AAAGGATCCCCGACCACGGATTGATTC
		LYM99_EF_BamHI (SEQ ID NO: 4191) AAAGGATCCTTGACTTGGGTGTCTGGTCC
		LYM99_NR_KpnI (SEQ ID NO: 4192) AAAGGTACCGTGCCTATGTCTTCCTAGCATC
		LYM99_ER_KpnI (SEQ ID NO: 4193) AAAGGTACCATATTTAGGCGCCAGTAAAGAC

Table 26. Provided are the PCR primers used for cloning the genes of some embodiments of the invention. Fwd = forward primer; Rev = reverse primer; Nested = nested primer for PCR (internal primer); External = external primer for PCR.

To facilitate cloning of the cDNAs/ genomic sequences, a 8-12 bp extension was added to the 5' of each primer. The primer extension includes an endonuclease restriction site. The restriction sites were selected using two parameters: (a). The site did not exist in the cDNA sequence; and (b). The restriction sites in the forward and reverse primers were designed such that the digested cDNA is inserted in the sense formation into the binary vector utilized for transformation.

Each digested PCR product was inserted into a high copy vector pBlue-script KS plasmid vector or into plasmids originating from this vector. In cases where the pGXN/ pGXNa high copy vector (originated from pBlue-script KS) was used, the PCR product was inserted upstream to the NOS terminator (SEQ ID NO: 4194) originated from pBI 101.3 binary vector (GenBank Accession No. U12640, nucleotides 4356 to 4693) and downstream to the 35S promoter. The digested products and the linearized plasmid vector were ligated using T4 DNA ligase enzyme (Roche, Switzerland). In some cases PCR products were cloned without digestion into pCR-Blunt II-TOPO vector (Invitrogen).

Sequencing of the amplified PCR products was performed, using ABI 377 sequencer (Amersham Biosciences Inc). In all cases, after confirmation of the sequence of the cloned genes, the cloned cDNA accompanied or not with the NOS terminator was introduced into the modified pGI binary vector containing the 6669 promoter [pQFN or pQYN_6669] according to Table 27, via digestion with appropriate restriction endonucleases. In any case the insert was followed by single copy of the NOS terminator (SEQ ID NO:4194).

High copy plasmids containing the cloned genes were digested with restriction endonucleases (New England BioLabs Inc) and cloned into binary vectors according to Table 27, below.

Binary vectors used for cloning:

Evolution of binary vectors construction: The plasmid pPI was constructed by inserting a synthetic poly-(A) signal sequence, originating from pGL3 basic plasmid vector (Promega, Acc No U47295; bp 4658-4811) into the *Hind*III restriction site of the binary vector pBI101.3 (Clontech, Acc. No. U12640). pGI (pBXYN) is similar to pPI, but the original gene in the backbone, the GUS gene, was replaced by the GUS-Intron gene followed by the NOS terminator (SEQ ID NO:4194) (Vancanneyt. G, *et al* MGG 220, 245-50, 1990). The modified pGI vector (pQXYN) 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.

Vectors used for cloning the polynucleotides of some embodiments of the invention: Cloned genes were digested from the high copy vectors and cloned into one of the following binary vectors: pQFN or pQYN_6669.

pQFN (see Figure 2) and pQYN_6669 (see Figure 1) are modified pGI vectors in which the 35S promoter was replaced by the new At6669 promoter (SEQ ID NO:4198). pQYN_6669 contains the GUSintron sequence, while pQFN lacks the GUSintron sequence

Table 27
Restriction enzyme sites used to clone identified genes according to some embodiments of the invention into binary vectors

Gene name	*Binary vector*	*Restriction enzymes used for cloning into binary vector-FORWARD*	*Restriction enzymes used for cloning into binary vector-REVERSE*	*Restriction enzymes used for digesting the binary vector*
LYM1	pQFN	SalI	EcoRI	SalI, EcoRI
LYM10	pQFN	XhoI	KpnI	XhoI, KpnI
LYM100	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM102	pQFN	BamHI	XhoI	BamHI, XhoI
LYM103	pQFN	BamHI	XhoI	BamHI, XhoI
LYM105	pQFN	BamHI	XhoI	BamHI, XhoI
LYM106	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM107	pQFN	BamHI	XhoI	BamHI, XhoI
LYM109	pQFN	XhoI	StuI	XhoI, StuI
LYM110	pQFN	BamHI	XhoI	BamHI, XhoI
LYM111	pQFN	XhoI	EcoRI	XhoI, EcoRI
LYM112	pQFN	BamHI	XhoI	BamHI, XhoI
LYM113	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM115	pQFN	BamHI	XhoI	BamHI, XhoI
LYM116	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM117	pQFN	BamHI	EcoRV	BamHI, StuI
LYM118	pQFN	BamHI	XhoI	BamHI, XhoI
LYM119	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM12	pQFN	XhoI	KpnI	XhoI, KpnI
LYM120	pQFN	BamHI	XhoI	BamHI, XhoI
LYM121	pQFN	BamHI	XhoI	BamHI, XhoI
LYM122_G	pQFN	BamHI	XhoI	BamHI, XhoI
LYM122_S	pQFN	BamHI	XhoI	BamHI, XhoI
LYM123	pQFN	BamHI	XhoI	BamHI, XhoI
LYM125	pQFN	BamHI	KpnI	BamHI, KpnI
LYM126	pQFN	BamHI	KpnI	BamHI, KpnI
LYM127	pQFN	BamHI	XhoI	BamHI, XhoI
LYM128	pQFN	BamHI	XhoI	BamHI, XhoI
LYM129	pQFN	SalI	EcoRI	SalI, EcoRI
LYM13	pQFN	SalI	BamHI	SalI, BamHI
LYM130	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM131	pQFN	SalI	XhoI	SalI, XhoI
LYM132	pQFN	BamHI	XhoI	BamHI, XhoI
LYM134	pQFN	BamHI	XhoI	BamHI, XhoI
LYM135	pQFN	SalI	KpnI	SalI, KpnI
LYM136	pQFN	BamHI	KpnI	BamHI, KpnI
LYM137	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM138	pQFN	SalI	Ecl136II	SalI, StuI
LYM14	pQFN	SalI	BamHI	SalI, BamHI
LYM140	pQFN	XhoI	EcoRI	XhoI, EcoRI
LYM141	pQFN	BamHI	KpnI	BamHI, KpnI
LYM142	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM143	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM144	pQFN	SalI	EcoRV	SalI, StuI
LYM145	pQFN	BamHI	XhoI	BamHI, XhoI

Gene name	***Binary vector***	***Restriction enzymes used for cloning into binary vector-FORWARD***	***Restriction enzymes used for cloning into binary vector-REVERSE***	***Restriction enzymes used for digesting the binary vector***
LYM146	pQFN	KpnI	KpnI	KpnI, KpnI
LYM147	pQFN	SalI	EcoRI	SalI, EcoRI
LYM148	pQFN	BamHI	XbaI	BamHI, XhoI
LYM149	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM15	pQFN	SalI	EcoRI	SalI, EcoRI
LYM152	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM153	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM154	pQFN	XhoI	StuI	XhoI, StuI
LYM155	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM156	pQFN	StuI	StuI	SmaI, SmaI
LYM157_G	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM157_S	pQFN	SalI	StuI	SalI, StuI
LYM159	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM16	pQFN	SalI	EcoRI	SalI, EcoRI
LYM160	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM161	pQFN	BamHI	XhoI	BamHI, XhoI
LYM162	pQFN	BamHI	XhoI	BamHI, XhoI
LYM164	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM165	pQFN	XhoI	Ecl136II	XhoI, StuI
LYM17	pQFN	SmaI	KpnI	SmaI, KpnI
LYM170	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM172	pQFN	BamHI	XhoI	BamHI, XhoI
LYM173	pQFN	BamHI	XhoI	BamHI, XhoI
LYM174	pQFN	BamHI	KpnI	BamHI, KpnI
LYM175	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM176	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM178	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM179	pQFN	SalI	StuI	SalI, StuI
LYM180	pQFN	BamHI	XhoI	BamHI, XhoI
LYM181	pQFN	BamHI	EcoRV	BamHI, StuI
LYM183	pQFN	SalI	XbaI	SalI, StuI
LYM184	pQFN	BamHI	XhoI	BamHI, XhoI
LYM185	pQFN	BamHI	KpnI	BamHI, KpnI
LYM186	pQFN	SalI	Ecl136II	SalI, StuI
LYM188	pQFN	BamHI	XhoI	BamHI, XhoI
LYM189	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM19	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM192	pQFN	XhoI	EcoRV	XhoI, StuI
LYM193	pQFN	BamHI	XhoI	BamHI, XhoI
LYM194	pQFN	SalI	XhoI	SalI, SalI
LYM196	pQFN	BamHI	XhoI	BamHI, XhoI
LYM197	pQFN	BamHI	XhoI	BamHI, XhoI
LYM198	pQFN	BamHI	XhoI	BamHI, XhoI
LYM2	pQFN	EcoRV	KpnI	SmaI, KpnI
LYM20	pQFN	EcoRV	KpnI	SmaI, KpnI
LYM200	pQFN	BamHI	XhoI	BamHI, XhoI
LYM201	pQFN	BamHI	XhoI	BamHI, XhoI
LYM203	pQFN	BamHI	XhoI	BamHI, XhoI
LYM204	pQFN	BamHI	XhoI	BamHI, XhoI
LYM206	pQFN	XhoI	EcoRV	XhoI, StuI

Gene name	***Binary vector***	***Restriction enzymes used for cloning into binary vector-FORWARD***	***Restriction enzymes used for cloning into binary vector-REVERSE***	***Restriction enzymes used for digesting the binary vector***
LYM207	pQFN	BamHI	KpnI	BamHI, KpnI
LYM208	pQFN	BamHI	KpnI	BamHI, KpnI
LYM21	pQFN	EcoRV	KpnI	SmaI, KpnI
LYM212	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM213	pQFN	BamHI	XhoI	BamHI, XhoI
LYM215	pQFN	BamHI	XhoI	BamHI, XhoI
LYM217	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM219	pQFN	BamHI	KpnI	BamHI, KpnI
LYM22	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM220	pQFN	BamHI	EcoRV	BamHI, StuI
LYM221	pQFN	BamHI	XhoI	BamHI, XhoI
LYM223	pQFN	XhoI	EcoRI	XhoI, EcoRI
LYM224	pQFN	BamHI	XhoI	BamHI, XhoI
LYM227	pQFN	BamHI	KpnI	BamHI, KpnI
LYM228	pQFN	StuI	KpnI	KpnI, EcoRV
LYM23	pQFN	BamHI	KpnI	BamHI, KpnI
LYM232	pQFN	BamHI	XhoI	BamHI, XhoI
LYM233	pQFN	BamHI	XhoI	BamHI, XhoI
LYM234	pQFN	BamHI	XhoI	BamHI, XhoI
LYM236	pQFN	SalI	EcoRI	SalI, EcoRI
LYM238	pQFN	SmaI	KpnI	SmaI, KpnI
LYM239	pQFN	BamHI	XhoI	BamHI, XhoI
LYM24	pQFN	SalI	EcoRI	SalI, EcoRI
LYM240	pQFN	BamHI	KpnI	BamHI, KpnI
LYM241	pQFN	BamHI	XhoI	BamHI, XhoI
LYM242	pQFN	BamHI	XhoI	BamHI, XhoI
LYM243	pQFN	BamHI	XhoI	BamHI, XhoI
LYM245	pQFN	BamHI	KpnI	BamHI, KpnI
LYM248	pQFN	BamHI	EcoRV	BamHI, StuI
LYM249	pQFN	BamHI	KpnI	BamHI, KpnI
LYM250	pQFN	SalI	XbaI	SalI, StuI
LYM251	pQFN	SalI	Ecl136II	SalI, StuI
LYM252	pQFN	BamHI	KpnI	BamHI, KpnI
LYM254	pQFN	SalI	BamHI	SalI, BamHI
LYM255	pQFN	BamHI	XhoI	BamHI, XhoI
LYM256	pQFN	BamHI	XhoI	BamHI, XhoI
LYM26	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM260	pQFN	BamHI	KpnI	BamHI, KpnI
LYM261	pQFN	SmaI	KpnI	SmaI, KpnI
LYM267	pQFN	SalI	EcoRV	SalI, StuI
LYM268	pQFN	XhoI	EcoRV	XhoI, StuI
LYM270	pQFN	BamHI	XhoI	BamHI, XhoI
LYM271	pQFN	BamHI	XhoI	BamHI, XhoI
LYM273_G	pQFN	BamHI	XhoI	BamHI, XhoI
LYM273_S	pQFN	BamHI	XhoI	BamHI, XhoI
LYM274	pQFN	BamHI	XhoI	BamHI, XhoI
LYM277	pQFN	SalI	Ecl136II	SalI, StuI
LYM278	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM283	pQFN	SmaI	KpnI	SmaI, KpnI
LYM284	pQFN	BamHI	KpnI	BamHI, KpnI

Gene name	***Binary vector***	***Restriction enzymes used for cloning into binary vector-FORWARD***	***Restriction enzymes used for cloning into binary vector-REVERSE***	***Restriction enzymes used for digesting the binary vector***
LYM285	pQFN	XhoI	EcoRV	XhoI, StuI
LYM287	pQFN	XhoI	EcoRV	XhoI, StuI
LYM288	pQFN	XhoI	EcoRI	XhoI, EcoRI
LYM289	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM290	pQFN	BamHI	KpnI	BamHI, KpnI
LYM291	pQFN	SalI	BamHI	SalI, BamHI
LYM293	pQFN	XhoI	EcoRI	XhoI, EcoRI
LYM3	pQFN	XhoI	KpnI	XhoI, KpnI
LYM30	pQFN	SalI	XhoI	SalI, XhoI
LYM31	pQFN	SalI	XhoI	SalI, XhoI
LYM32	pQFN	BamHI	KpnI	BamHI, KpnI
LYM34	pQFN	BamHI	KpnI	BamHI, KpnI
LYM35	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM36	pQFN	StuI	StuI	StuI, StuI
LYM37	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM38	pQFN	SalI	BamHI	SalI, BamHI
LYM4	pQFN	EcoRV	KpnI	SmaI, KpnI
LYM40	pQFN	SalI	EcoRV	SalI, StuI
LYM41	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM42	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM43	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM44	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM5	pQFN	SalI	BamHI	SalI, BamHI
LYM51	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM52	pQFN	XhoI	EcoRV	XhoI, StuI
LYM53	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM56	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM57	pQFN	EcoRV	XhoI	SmaI, XhoI
LYM6	pQFN	SmaI	KpnI	SmaI, KpnI
LYM61	pQFN	BamHI	XhoI	BamHI, XhoI
LYM62	pQFN	BamHI	KpnI	BamHI, KpnI
LYM66	pQFN	EcoRV	XhoI	SmaI, XhoI
LYM67	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM68	pQFN	SalI	XhoI	SalI, XhoI
LYM69	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM7	pQFN	SalI	EcoRI	SalI, EcoRI
LYM73	pQFN	SalI	StuI	SalI, StuI
LYM74	pQFN	SalI	Ecl136II	SalI, StuI
LYM79	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM8	pQFN	XhoI	KpnI	XhoI, KpnI
LYM82	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM83	pQFN	BamHI	XhoI	BamHI, XhoI
LYM84	pQFN	BamHI	XhoI	BamHI, XhoI
LYM86	pQFN	BamHI	XhoI	BamHI, XhoI
LYM88	pQFN	BamHI	XhoI	BamHI, XhoI
LYM89	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM9	pQFN	SalI	EcoRI	SalI, EcoRI
LYM90	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM91	pQYN_6669	SalI	EcoRI	SalI, EcoRI
LYM93	pQFN	SalI	XhoI	SalI, XhoI
LYM95	pQYN_6669	SalI	EcoRI	SalI, EcoRI

Gene name	***Binary vector***	***Restriction enzymes used for cloning into binary vector-FORWARD***	***Restriction enzymes used for cloning into binary vector-REVERSE***	***Restriction enzymes used for digesting the binary vector***
LYM99	pQFN	BamHI	KpnI	BamHI, KpnI

Table 27.

Table 28
Genes cloned from cDNA libraries or genomic DNA in a High copy number plasmid

Gene Name	***High copy plasmid***	***Amplified from***		***Polynucleotide SEQ ID NO:***	***Polypeptide SEQ ID NO:***
		Organism	***Origin***		
LYM1	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3481	240
LYM10	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3490	249
LYM100	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3542	301
LYM102	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3543	302
LYM103	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3544	3689
LYM105	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3545	3690
LYM106	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3546	305
LYM107	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3589	349
LYM109	pGXNa	MAIZE Zea mays L. ND	cDNA	3590	3702
LYM110	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3547	3691
LYM111	pGXNa	MAIZE Zea mays L. Pioneer 30G54	cDNA	3548	307
LYM112	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3591	3703
LYM113	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3592	352
LYM115	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3593	3704
LYM116	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. ND	cDNA	3594	354
LYM117	Topo B	MAIZE Zea mays L. ND	cDNA	3595	3705

Gene Name	*High copy plasmid*	*Amplified from*		*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
		Organism	*Origin*		
LYM118			GeneArt	3596	356
LYM119	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. ND	cDNA	3549	3692
LYM12	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3491	250
LYM120	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3550	309
LYM121	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3597	357
LYM122_G	Topo B	RICE Oryza sativa L. Japonica ND	Genomic	3739	310
LYM122_S			GeneArt	3551	310
LYM123			GeneArt	3598	358
LYM125	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3552	311
LYM126			GeneArt	3553	312
LYM127	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3554	313
LYM128	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3555	314
LYM129	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Indica ND+ RICE Oryza sativa L. Japonica ND	cDNA	3556	315
LYM13	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3492	251
LYM130	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Indica ND	cDNA	3557	316
LYM131	pGXNa	RICE Oryza sativa L. Japonica ND	cDNA	3558	3693
LYM132	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3559	318
LYM134	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3560	319
LYM135	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3599	359
LYM136	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3561	3694

Gene Name	High copy plasmid	Amplified from		Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:
		Organism	Origin		
LYM137	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3562	321
LYM138	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3600	360
LYM14	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3493	252
LYM140	pGXNa	BARLEY Hordeum vulgare L. Manit	cDNA	3563	322
LYM141	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3564	323
LYM142	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3565	324
LYM143	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3566	325
LYM144	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3567	3695
LYM145	pKS(Pks_J)	RICE Oryza sativa L. ND	cDNA	3568	327
LYM146	Topo B	MAIZE Zea mays L. ND	Genomic	3601	3706
LYM147	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. ND	cDNA	3602	3707
LYM148	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3569	3696
LYM149	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3570	329
LYM15	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3494	253
LYM152	pGXN (pKG+Nos+35S)	ARABIDOPSIS Arabidopsis thaliana Transgenic Columbia	cDNA	3571	330
LYM153	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3572	331
LYM154			GeneArt	3603	363
LYM155	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3604	3708
LYM156	pGXNa	BARLEY Hordeum vulgare L. Manit	cDNA	3573	332

Gene Name	*High copy plasmid*	*Amplified from*		*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
		Organism	*Origin*		
LYM157_G	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3574	333
LYM157_S			GeneArt	3574	333
LYM159	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3575	3697
LYM16	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3495	254
LYM160	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3576	3698
LYM161	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3577	3699
LYM162	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3578	337
LYM164	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3579	3700
LYM165	Topo B	MAIZE Zea mays L. Pioneer 30G54	cDNA	3580	339
LYM17	pKS(Pks_J)	RICE Oryza sativa L. ND	cDNA	3496	255
LYM170	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3581	341
LYM172	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3582	342
LYM173	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3583	343
LYM174	pKS(Pks_J)	SORGHUM Sorghum bicolor Monsanto S5	cDNA	3584	344
LYM175	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3585	345
LYM176	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3586	346
LYM178	pGXN (pKG+Nos+35S)	ARABIDOPSIS Arabidopsis thaliana ND	cDNA	3587	347
LYM179	pGXNa	MAIZE Zea mays L. Pioneer 30G54	cDNA	3588	3701
LYM180	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3605	365
LYM181	Topo B	BARLEY Hordeum vulgare L. Manit	cDNA	3606	366
LYM183	Topo B	BARLEY Hordeum vulgare L. Manit	cDNA	3655	3733

Gene Name	*High copy plasmid*	*Amplified from*		*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
		Organism	*Origin*		
LYM184	Topo B	BARLEY Hordeum vulgare L. Manit	cDNA	3607	3709
LYM185	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3608	369
LYM186	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3609	3710
LYM188	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3610	371
LYM189	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3611	3711
LYM19	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3497	256
LYM192	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3612	3712
LYM193	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3613	374
LYM194			GeneArt	3614	3713
LYM196	Topo B	MAIZE Zea mays L. ND	cDNA	3615	376
LYM197	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3616	3714
LYM198	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3617	378
LYM2	pKS(Pks_J)	RICE Oryza sativa L. ND	cDNA	3482	241
LYM20	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3498	257
LYM200	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3657	419
LYM201	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3618	379
LYM203	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3619	380
LYM204	Topo B	MAIZE Zea mays L. Pioneer 30G54	cDNA	3620	381
LYM206	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3621	3715
LYM207	Topo B	MAIZE Zea mays L. Pioneer 30G54	cDNA	3622	3716
LYM208	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3623	384

Gene Name	High copy plasmid	Amplified from Organism	Origin	Polynucleotide SEQ ID NO:	Polypeptide SEQ ID NO:
LYM21	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3499	258
LYM212	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. ND	cDNA	3624	3717
LYM213	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3625	386
LYM215	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3626	3718
LYM217	pGXN	MAIZE Zea mays L. ND	cDNA	3627	3719
LYM219	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3628	3720
LYM22	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3500	259
LYM220	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3629	3721
LYM221	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3630	3722
LYM223	pGXNa	MAIZE Zea mays L. Pioneer 30G54	cDNA	3631	392
LYM224	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3632	3723
LYM227			GeneArt	3633	394
LYM228	Topo B	MAIZE Zea mays L. Pioneer 30G54	cDNA	3634	3724
LYM23	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3501	260
LYM232	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3635	3725
LYM233			GeneArt	3636	397
LYM234			GeneArt	3637	398
LYM236	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3638	3726
LYM238	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3639	400
LYM239	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3640	3727
LYM24	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3502	261

Gene Name	*High copy plasmid*	*Amplified from*		*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
		Organism	*Origin*		
LYM240	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3641	402
LYM241	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3642	3728
LYM242	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3643	404
LYM243	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3644	405
LYM245	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3645	406
LYM248	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3646	3729
LYM249	Topo B	RICE Oryza sativa L. Japonica ND+ RICE Oryza sativa L. ND	cDNA	3647	3730
LYM250	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3648	409
LYM251	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3649	410
LYM252	pKS(Pks_J)	RICE Oryza sativa L. Indica ND+ RICE Oryza sativa L. Japonica ND	cDNA	3650	411
LYM254	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3651	3731
LYM255	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3652	3732
LYM256	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3656	418
LYM26	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3503	262
LYM260	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3653	414
LYM261	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3654	415
LYM267	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3658	420

Gene Name	***High copy plasmid***	***Amplified from***		***Polynucleotide SEQ ID NO:***	***Polypeptide SEQ ID NO:***
		Organism	***Origin***		
LYM268	Topo B	RICE Oryza sativa L. Indica ND+ RICE Oryza sativa L. Japonica ND	cDNA	3659	421
LYM270	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3660	422
LYM271	pKS(Pks_J)	MAIZE Zea mays L. Pioneer 30G54	cDNA	3661	423
LYM273_G	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	Genomic	3738	425
LYM273_S			GeneArt	3662	425
LYM274	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3663	3734
LYM277	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3664	3735
LYM278	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3665	3736
LYM283	Topo B	RICE Oryza sativa L. ND	cDNA	3666	429
LYM284	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3667	430
LYM285	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3668	431
LYM287	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3669	432
LYM288	pGXNa	RICE Oryza sativa L. Indica ND+ RICE Oryza sativa L. Japonica ND	cDNA	3670	3737
LYM289	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3671	434
LYM290	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3672	435
LYM291	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3673	436
LYM293	pGXNa	RICE Oryza sativa L. Indica ND	cDNA	3674	437
LYM3	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3483	3675
LYM30	pGXNa	RICE Oryza sativa L. ND	cDNA	3504	3677

Gene Name	***High copy plasmid***	***Amplified from***		***Polynucleotide SEQ ID NO:***	***Polypeptide SEQ ID NO:***
		Organism	***Origin***		
LYM31	pGXNa	RICE Oryza sativa L. ND	cDNA	3505	264
LYM32			GeneArt	3506	265
LYM34	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3507	3678
LYM35	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3508	267
LYM36			GeneArt	3509	268
LYM37	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3510	269
LYM38			GeneArt	3511	270
LYM4	pKS(Pks_J)	RICE Oryza sativa L. ND	cDNA	3484	243
LYM40	Topo B	RICE Oryza sativa L. Japonica ND	cDNA	3512	271
LYM41	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3513	272
LYM42	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3514	273
LYM43	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3515	274
LYM44	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. Japonica ND	cDNA	3516	275
LYM5	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3485	244
LYM51	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3517	3679
LYM52	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3518	277
LYM53	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. ND	cDNA	3519	3680
LYM56	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3520	3681
LYM57	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3521	3682
LYM6	pKS(Pks_J)	RICE Oryza sativa L. ND	cDNA	3486	3676
LYM61	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3522	3683
LYM62	pKS(Pks_J)	MAIZE Zea mays L. ND	cDNA	3523	3684
LYM66	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3524	3685

Gene Name	*High copy plasmid*	*Amplified from*		*Polynucleotide SEQ ID NO:*	*Polypeptide SEQ ID NO:*
		Organism	*Origin*		
LYM67	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3525	284
LYM68	pGXNa	RICE Oryza sativa L. ND	cDNA	3526	3686
LYM69	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3527	286
LYM7	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3487	246
LYM73	Topo B	RICE Oryza sativa L. ND	cDNA	3528	287
LYM74			GeneArt	3529	288
LYM79	pGXN (pKG+Nos+35S)	MAIZE Zea mays L. ND	cDNA	3530	3687
LYM8	pKS(Pks_J)	RICE Oryza sativa L. Japonica ND	cDNA	3488	247
LYM82	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3531	290
LYM83	Topo B	BARLEY Hordeum vulgare L. Manit	cDNA	3532	3688
LYM84	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3533	292
LYM86	pKS(Pks_J)	RICE Oryza sativa L. Indica ND	cDNA	3534	293
LYM88	pKS(Pks_J)	ARABIDOPSIS Arabidopsis thaliana Transgenic Columbia	cDNA	3535	294
LYM89	pGXN (pKG+Nos+35S)	ARABIDOPSIS Arabidopsis thaliana Transgenic Columbia	cDNA	3536	295
LYM9	pGXN (pKG+Nos+35S)	RICE Oryza sativa L. ND	cDNA	3489	248
LYM90	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3537	296
LYM91	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3538	297
LYM93	Topo B	BARLEY Hordeum vulgare L. Manit	cDNA	3539	298
LYM95	pGXN (pKG+Nos+35S)	BARLEY Hordeum vulgare L. Manit	cDNA	3541	300
LYM99	pKS(Pks_J)	BARLEY Hordeum vulgare L. Manit	cDNA	3540	299

Table 28: Cloned and synthetic genes are provided along with the sequence identifiers of their polynucleotides and polypeptides. Also provided are the source organism, tissue and the cloning vectors. ND = not a determined ecotype.

Selected DNA sequences were synthesized by a commercial supplier GeneArt, GmbH. Synthetic DNA is designed in silico. Suitable restriction enzymes sites were added to the cloned sequences at the 5' end and at the 3' end to enabled later cloning into the pQFN/ pQYN_6669 binary vectors downstream of the 6669 promoter (SEQ ID NO:4198).

EXAMPLE 8

TRANSFORMING AGROBACTERIUM TUMEFACIENS CELLS WITH BINARY VECTORS HARBORING PUTATIVE GENES

Each of the binary vectors described in Example 7 above are used to transform *Agrobacterium* cells. Two additional binary constructs, having a GUS/Luciferase reporter gene replacing the selected gene (positioned downstream of the At6669 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 developed on the selective media are analyzed by PCR using the primers which are designed to span the inserted sequence in the pPI plasmid. The resulting PCR products are isolated and sequenced as described in Example 3 above, to verify that the correct yield sequences are properly introduced to the *Agrobacterium* cells.

EXAMPLE 9

PRODUCING TRANSGENIC ARABIDOPSIS PLANTS EXPRESSING SELECTED GENES ACCORDING TO SOME EMBODIMENTS OF THE INVENTION

Materials and Experimental Methods

Plant transformation - The *Arabidopsis thaliana* var Columbia (T_0 plants) were transformed according to the Floral Dip procedure [Clough SJ, Bent AF. (1998) Floral dip: a simplified method for Agrobacterium-mediated transformation of *Arabidopsis thaliana*. Plant J. 16(6): 735-43; and Desfeux C, Clough SJ, Bent AF. (2000) Female reproductive tissues are the primary targets of Agrobacterium-mediated transformation by the *Arabidopsis* floral-dip method. Plant Physiol. 123(3): 895-904] with minor modifications. Briefly, *Arabidopsis thaliana* Columbia (Col0) T_0 plants were sown in 250 ml pots filled with wet peat-based growth mix. The pots were covered with aluminum foil and a plastic dome, kept at 4 °C for 3–4 days, then uncovered and incubated in a growth chamber at 18–24 °C under 16/8 hours light/dark cycles. The T_0 plants were ready for transformation six days before anthesis.

Single colonies of *Agrobacterium* carrying the binary vectors harboring the yield genes were cultured in LB medium supplemented with kanamycin (50 mg/L) and gentamycin (50 mg/L). The cultures were incubated at 28 °C for 48 hours under vigorous shaking and centrifuged at 4000 rpm for 5 minutes. The pellets comprising *Agrobacterium* cells were resuspended in a transformation medium which contained half-strength (2.15 g/L) Murashige-Skoog (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 was performed by inverting each plant into an *Agrobacterium* suspension such that the above ground plant tissue was submerged for 3-5 seconds. Each inoculated T_0 plant was immediately placed in a plastic tray, then covered with clear plastic dome to maintain humidity and was kept in the dark at room temperature for 18 hours to facilitate infection and transformation. Transformed (transgenic) plants were then uncovered and transferred to a greenhouse for recovery and maturation. The transgenic T_0 plants were grown in the greenhouse for 3-5 weeks until siliques were brown and dry, then seeds were 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 were surface-sterilized by soaking in 70% ethanol for 1 minute, followed by soaking in 5% sodium hypochlorite and 0.05% Triton® for 5 minutes. The surface-sterilized seeds were thoroughly washed in sterile distilled water then placed on culture plates containing half-strength Murashig-Skoog (Duchefa); 2% sucrose; 0.8% plant agar; 50 mM kanamycin; and 200 mM carbenicylin (Duchefa). The culture plates were 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 were transferred to a fresh culture plates for another week of incubation. Following incubation the T_1 plants were removed from culture plates and planted in growth mix contained in 250 ml pots. The transgenic plants were allowed to grow in a greenhouse to maturity. Seeds harvested from T_1 plants were cultured and grown to maturity as T_2 plants under the same conditions as used for culturing and growing the T_1 plants.

EXAMPLE 10

IMPROVED TRANSGENIC PLANT PERFORMANCE – GREENHOUSE ASSAYS

To analyze the effect of expression of the isolated polynucleotides in plants, plants performance was tested under greenhouse conditions.

Greenhouse assays - The plants were analyzed for their overall size, growth rate, flowering, seed yield, weight of 1,000 seeds, dry matter and harvest index (HI- seed yield/dry matter). Transgenic plants performance was compared to control plants grown in parallel under the same conditions. Mock- transgenic plants expressing the uidA reporter gene (GUS-Intron) or with no gene at all, under the same promoter were used as control.

The experiment was planned in nested randomized plot distribution. For each gene of the invention three to five independent transformation events were analyzed from each construct. In cases where a certain event appears more than once, the event was tested in several independent experiments.

Tables 29 and 31 specify the parameters measured in plants in the greenhouse assays (till seed maturation and bolting assay, respectively).

Digital imaging - A laboratory image acquisition system, which consists of a digital reflex camera (Canon EOS 300D) attached with a 55 mm focal length lens

(Canon EF-S series), mounted on a reproduction device (Kaiser RS), which included 4 light units (4 x 150 Watts light bulb) is used for capturing images of plant samples.

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

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

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

Leaf growth analysis - Using the digital analysis leaves data was calculated, including leaf number, rosette area, rosette diameter, leaf blade area, plot coverage, leaf petiole length.

The vegetative growth rate of the plant was defined by formulas XIII, XIV, XV and XVI.

Formula XIII:

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

Formula XIV:

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

Formula XV

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

Formula XVI

Relative growth rate of plot coverage = Regression coefficient of plot coverage along time course.

Seeds average weight (Seed weight or 1000 seed weight) - At the end of the experiment all seeds were collected. The seeds were scattered on a glass tray and a picture was taken. Using the digital analysis, the number of seeds in each sample was calculated.

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

Seed yield per plant = total seed weight per plant (gr.).

1000 seed weight (the weight of 1000 seeds) (gr.).

The harvest index was calculated using Formula IV (Harvest Index = Average seed yield per plant/ Average dry weight) as described above.

Oil percentage in seeds - At the end of the experiment all seeds from plots 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.

Oil yield - The oil yield was calculated using Formula IX (described above).

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.

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

Experimental Results

Plants expressing the polynucleotides of the some embodiments of the invention were assayed for a number of commercially desired traits. In cases where a certain event appears more than once, the event was tested in several independent experiments.

Table 29
Measured parameters at the greenhouse till seed maturation assay (T2 experiment) for transformed agriculture improving trait genes

Tested Parameters	***Id***
Dry Weight (gr)	A
Harvest Index	B
Leaf Blade Area TP4 (cm^2)	C
Leaf Number TP4	D
Leaf Petiole Length TP4 (cm)	E
Petiole Relative Area TP4	F
Plot Coverage TP4 (cm^2)	G
RGR Of Leaf Blade Area	H
RGR Of Plot Coverage	I
RGR Of Rosette Area	J
RGR Of Rosette Diameter	K
Rosette Area TP4 (cm^2)	L
Rosette Diameter TP4 (cm)	M
Seed Yield (gr)	N
Seeds Weight (gr)	O
Blade Relative Area TP4	P
Oil Content	Q
RGR Of Leaf Number	R

Table 29: Provided are the identification (ID) letters of each of the Tested Parameters. RGR-Relative Growth Rate; TP4- time point 4.

Table 30
Results obtained in a Greenhouse till seed maturation assay

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM16	11623.2	A	0.739	2.97E-02	10.4	LYM9	11633.7	P	93.115	4.23E-03	3.2
LYM57	12012.6	A	0.841	4.23E-02	25.7	LYM15	11611.3	P	93.131	5.66E-03	3.2
LYM17	11681.4	A	0.728	5.16E-02	8.8	LYM4	11702.1	P	93.167	7.54E-03	3.2
LYM10	11744.1	A	0.723	8.27E-02	8	LYM17	11682.3	P	92.747	8.70E-03	2.8
LYM95	12121.3	A	0.779	9.81E-02	16.5	LYM17	11684.5	P	92.554	1.28E-02	2.6
CONTROL	—	A	0.669	—	0	LYM2	11691.2	P	92.875	1.35E-02	2.9
LYM16	11623.5	B	0.543	6.50E-05	45.1	LYM7	11594.3	P	92.513	1.79E-02	2.5
LYM24	12063.3	B	0.515	2.78E-04	37.6	LYM67	11782.5	P	94.037	1.83E-02	4.2
LYM10	11741.4	B	0.499	3.74E-04	33.4	LYM44	11884.3	P	92.306	2.09E-02	2.3
LYM7	11594.2	B	0.498	1.10E-03	33.1	LYM62	12022.4	P	92.296	2.21E-02	2.3
LYM44	11885.3	B	0.473	1.50E-03	26.6	LYM19	11751.4	P	92.244	2.38E-02	2.2
LYM15	11611.3	B	0.477	3.91E-03	27.7	LYM17	11684.4	P	92.438	3.04E-02	2.4
LYM2	11695.1	B	0.457	4.23E-03	22.2	LYM31	11923.1	P	92.399	3.32E-02	2.4
LYM30	11913.3	B	0.462	4.25E-03	23.6	LYM34	11903.3	P	92.07	3.49E-02	2
LYM8	11984.1	B	0.472	4.44E-03	26.3	LYM12	11871.3	P	91.999	3.94E-02	2
LYM31	11923.1	B	0.471	4.64E-03	26	LYM15	11614.3	P	91.996	5.05E-02	1.9
LYM14	12051.1	B	0.454	5.37E-03	21.5	LYM15	11614.4	P	91.877	5.09E-02	1.8
LYM2	11692.3	B	0.546	5.62E-03	46	LYM10	11741.4	P	91.979	5.99E-02	1.9
LYM16	11624.6	B	0.468	8.76E-03	25.1	LYM57	12012.4	P	91.752	6.64E-02	1.7
LYM66	11954.4	B	0.455	9.16E-03	21.7	LYM24	12063.3	P	92.883	6.73E-02	2.9
LYM34	11904.3	B	0.442	1.11E-02	18.3	LYM16	11624.6	P	91.723	7.65E-02	1.6
LYM53	11843.2	B	0.506	1.24E-02	35.4	LYM26	11824.3	P	91.672	7.95E-02	1.6
LYM35	11812.4	B	0.446	1.49E-02	19.2	LYM66	11955.2	P	91.693	8.09E-02	1.6
LYM4	11706.5	B	0.456	1.57E-02	21.9	LYM62	12023.7	P	92.17	8.37E-02	2.1

Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM15	11612.2	B	0.437	1.59E-02	16.9	LYM30	11913.3	P	91.637	8.66E-02	1.5
LYM19	11754.1	B	0.448	1.60E-02	19.8	LYM12	11873.4	P	91.84	9.17E-02	1.8
LYM9	11634.6	B	0.466	1.61E-02	24.6	LYM51	11891.1	P	92.63	9.56E-02	2.6
LYM1	11601.1	B	0.465	1.63E-02	24.3	CONTROL	—	P	90.239	—	0
LYM57	12013.1	B	0.429	3.09E-02	14.8	LYM17	11684.5	Q	31.925	1.22E-04	13.3
LYM17	11684.5	B	0.501	3.38E-02	34.1	LYM66	11952.1	Q	31.76	1.43E-04	12.7
LYM30	11912.6	B	0.506	3.67E-02	35.3	LYM34	11904.3	Q	31.585	2.06E-04	12.1
LYM24	12061.2	B	0.481	4.69E-02	28.5	LYM17	11682.3	Q	32.16	2.39E-04	14.1
LYM82	12203.2	B	0.53	4.78E-02	41.7	LYM82	12203.2	Q	31.185	4.56E-04	10.7
LYM31	11924.4	B	0.437	4.78E-02	16.7	LYM2	11692.3	Q	31.17	7.38E-04	10.6
LYM6	11735.1	B	0.42	5.60E-02	12.3	LYM14	12051.1	Q	30.425	2.85E-03	8
LYM8	11983.1	B	0.47	6.47E-02	25.8	LYM43	11791.2	Q	31.015	3.17E-03	10.1
LYM6	11734.3	B	0.418	6.56E-02	11.9	LYM43	11793.2	Q	31.92	4.77E-03	13.3
LYM30	11912.7	B	0.512	6.75E-02	36.9	LYM26	11824.3	Q	30.13	5.77E-03	6.9
LYM26	11824.3	B	0.483	6.80E-02	29.2	LYM51	11893.4	Q	30.12	7.02E-03	6.9
LYM8	11982.4	B	0.475	7.82E-02	27.1	LYM10	11741.4	Q	30.01	8.17E-03	6.5
LYM12	11871.1	B	0.457	8.07E-02	22.2	LYM22	11761.3	Q	30.895	8.20E-03	9.6
LYM67	11782.6	B	0.49	8.15E-02	31.1	LYM15	11611.3	Q	30.05	8.49E-03	6.6
LYM22	11764.1	B	0.474	8.22E-02	26.8	LYM24	12063.3	Q	30.215	1.03E-02	7.2
LYM51	11893.4	B	0.476	8.62E-02	27.4	LYM43	11792.2	Q	29.985	1.19E-02	6.4
LYM21	11674.5	B	0.516	8.83E-02	38	LYM62	12023.2	Q	29.855	1.23E-02	5.9
LYM7	11594.3	B	0.464	8.85E-02	24	LYM7	11591.5	Q	29.845	1.27E-02	5.9
LYM24	12064.1	B	0.491	8.92E-02	31.2	LYM66	11955.2	Q	30.365	1.58E-02	7.7
LYM2	11691.2	B	0.454	9.14E-02	21.4	LYM24	12061.2	Q	29.76	1.61E-02	5.6
LYM13	11772.2	B	0.474	9.21E-02	26.9	LYM69	11852.2	Q	29.82	1.91E-02	5.8
LYM68	11942.3	B	0.426	9.22E-02	13.9	LYM62	12023.7	Q	29.69	2.03E-02	5.3

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM 44	11884.3	B	0.414	9.80E-02	10.6	LYM 17	11684.4	Q	29.68	2.16E-02	5.3
CONTROL	—	B	0.374	—	0	LYM 7	11592.1	Q	31.66	3.45E-02	12.3
LYM 95	12121.3	C	0.73	2.06E-04	46.2	LYM 31	11923.1	Q	29.53	3.69E-02	4.8
LYM 10	11741.2	C	0.655	3.02E-03	31.2	LYM 53	11841.2	Q	30.06	3.89E-02	6.7
LYM 21	11671.2	C	0.619	4.67E-03	23.9	LYM 57	12012.6	Q	29.38	4.78E-02	4.2
LYM 62	12024.2	C	0.626	7.02E-03	25.3	LYM 66	11954.4	Q	31.52	5.68E-02	11.8
LYM 66	11953.1	C	0.602	1.02E-02	20.5	LYM 14	12052.4	Q	29.42	5.94E-02	4.4
LYM 10	11744.1	C	0.602	1.02E-02	20.5	LYM 51	11894.2	Q	30.185	6.04E-02	7.1
LYM 4	11706.5	C	0.575	3.74E-02	15.2	LYM 68	11941.3	Q	30.515	6.20E-02	8.3
LYM 44	11882.1	C	0.569	5.06E-02	13.9	LYM 8	11984.1	Q	29.395	6.25E-02	4.3
LYM 66	11955.2	C	0.586	5.09E-02	17.4	LYM 30	11912.6	Q	31.815	6.57E-02	12.9
LYM 82	12201.1	C	0.567	6.28E-02	13.6	LYM 13	11772.1	Q	29.53	8.65E-02	4.8
LYM 68	11941.4	C	0.564	6.49E-02	13.1	LYM 24	12064.1	Q	30.505	9.05E-02	8.2
LYM 95	12121.2	C	0.557	9.41E-02	11.6	LYM 44	11885.4	Q	29.57	9.26E-02	4.9
CONTROL	—	C	0.499	—	0	LYM 1	11601.1	Q	29.685	9.43E-02	5.3
LYM 31	11923.1	D	9.125	4.78E-04	8.8	CONTROL	—	Q	28.183	—	0
LYM 26	11824.6	D	8.938	4.23E-03	6.5	LYM 175	12651.6	A	1.514	2.92E-03	50.2
LYM 4	11705.2	D	8.938	4.23E-03	6.5	LYM 256	13321.2	A	1.169	5.61E-02	16
LYM 9	11632.1	D	8.938	4.23E-03	6.5	LYM 147	12581.4	A	1.154	6.79E-02	14.5
LYM 44	11882.1	D	8.875	4.88E-03	5.8	CONTROL	—	A	1.008	—	0
LYM 8	11984.1	D	8.875	4.88E-03	5.8	LYM 207	13251.4	B	0.356	7.41E-02	8.2
LYM 4	11702.1	D	9.5	5.72E-03	13.3	LYM 73	12624.1	B	0.362	9.94E-02	9.9
LYM 10	11744.5	D	8.813	1.53E-02	5.1	CONTROL	—	B	0.329	—	0
LYM 24	12061.1	D	8.813	1.53E-02	5.1	LYM 206	12601.3	C	0.313	3.92E-03	31.8

Gene name	**Event**	**ID**	**Mean**	**P value**	*% incr. vs. cont.*	**Gene name**	**Event**	**ID**	**Mean**	**P value**	**% incr. vs. cont.**
LYM 66	11952.1	D	8.75	1.97E-02	4.3	LYM 207	13251.4	C	0.281	2.47E-02	18.2
LYM 69	11851.2	D	8.75	1.97E-02	4.3	LYM 241	13271.2	C	0.291	3.27E-02	22.5
LYM 95	12121.3	D	8.75	1.97E-02	4.3	LYM 159	13354.5	C	0.272	4.39E-02	14.8
LYM 53	11842.4	D	9	3.32E-02	7.3	LYM 91	13283.1	C	0.268	7.20E-02	13
LYM 16	11623.2	D	8.875	6.05E-02	5.8	CONTROL	—	C	0.237	—	0
LYM 37	11803.2	D	8.875	6.05E-02	5.8	LYM 175	12653.3	D	9	1.81E-02	3
LYM 57	12012.6	D	8.875	6.05E-02	5.8	LYM 206	12603.1	D	9	1.81E-02	3
LYM 15	11614.4	D	8.688	6.06E-02	3.6	LYM 147	12581.4	D	9.25	7.10E-02	5.9
LYM 43	11791.5	D	8.688	6.06E-02	3.6	LYM 147	12584.4	D	9.25	7.10E-02	5.9
LYM 44	11885.3	D	8.625	8.97E-02	2.8	CONTROL	—	D	8.734	—	0
LYM 53	11844.2	D	8.625	8.97E-02	2.8	LYM 207	13251.4	E	0.494	2.25E-03	29
LYM 7	11594.3	D	8.625	8.97E-02	2.8	LYM 206	12601.3	E	0.49	3.51E-03	27.9
CONTROL	—	D	8.388	—	0	LYM 91	13283.1	E	0.451	2.44E-02	17.8
LYM 95	12121.3	E	0.871	6.40E-05	20.5	CONTROL	—	E	0.383	—	0
LYM 10	11741.2	E	0.854	1.68E-04	18	LYM 175	12651.6	F	8.457	9.98E-03	14.9
LYM 51	11893.4	E	0.814	1.64E-03	12.5	LYM 241	13271.2	F	7.999	8.84E-02	8.7
LYM 26	11824.1	E	0.864	3.71E-03	19.4	CONTROL	—	F	7.36	—	0
LYM 16	11623.2	E	0.793	8.69E-03	9.6	LYM 241	13271.2	G	13.924	3.22E-02	20.3
LYM 12	11871.1	E	0.79	8.71E-03	9.2	LYM 256	13322.3	G	13.012	5.32E-02	12.5
LYM 41	11834.3	E	0.788	9.62E-03	9	LYM 91	13283.1	G	12.996	5.81E-02	12.3
LYM 44	11885.4	E	0.791	2.21E-02	9.3	CONTROL	—	G	11.57	—	0
LYM 17	11681.4	E	0.788	2.38E-02	8.9	LYM 206	12601.3	H	0.038	9.68E-03	39.1
LYM 21	11673.1	E	0.822	2.48E-02	13.7	LYM 206	12602.1	H	0.037	3.48E-02	35.7

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	**% incr. vs. cont.**
LYM20	11711.1	E	0.786	4.67E-02	8.7	LYM147	12584.4	H	0.036	4.44E-02	30.6
LYM4	11706.5	E	0.818	5.29E-02	13.1	LYM147	12583.3	H	0.035	4.93E-02	29.1
LYM68	11942.3	E	0.786	6.52E-02	8.7	LYM203	12664.1	H	0.035	7.71E-02	27.4
LYM53	11841.1	E	0.823	9.25E-02	13.8	LYM159	13354.6	H	0.035	8.34E-02	28.1
CONTROL	—	E	0.723	—	0	LYM241	13271.2	H	0.034	9.00E-02	24.6
LYM34	11902.2	F	13.363	5.21E-03	33.8	CONTROL	—	H	0.027	—	0
LYM17	11681.4	F	11.764	3.07E-02	17.8	LYM206	12601.3	I	1.904	2.91E-02	34.1
LYM37	11802.2	F	11.839	5.95E-02	18.5	LYM147	12583.3	I	1.834	5.96E-02	29.1
CONTROL	—	F	9.989	—	0	LYM147	12584.4	I	1.823	6.86E-02	28.3
LYM21	11671.2	G	29.318	2.73E-03	29	CONTROL	—	I	1.421	—	0
LYM95	12121.3	G	35.398	5.12E-03	55.7	LYM206	12601.3	J	0.238	2.91E-02	34.1
LYM44	11882.1	G	28.419	6.04E-03	25	LYM147	12583.3	J	0.229	5.96E-02	29.1
LYM10	11741.2	G	31.636	7.14E-03	39.1	LYM147	12584.4	J	0.228	6.86E-02	28.3
LYM66	11953.1	G	28.02	8.78E-03	23.2	CONTROL	—	J	0.178	—	0
LYM4	11706.5	G	28.515	1.11E-02	25.4	LYM206	12601.3	K	0.227	3.54E-02	26.3
LYM62	12024.2	G	30.017	1.16E-02	32	LYM203	12664.1	K	0.225	6.18E-02	25.1
LYM66	11955.2	G	27.277	1.76E-02	20	LYM159	13354.6	K	0.22	8.46E-02	22.6
LYM68	11941.4	G	26.646	3.40E-02	17.2	LYM206	12602.1	K	0.223	8.54E-02	24
LYM82	12201.1	G	26.548	4.02E-02	16.8	LYM241	13271.2	K	0.217	9.49E-02	21.1
LYM9	11632.1	G	26.845	4.65E-02	18.1	CONTROL	—	K	0.179	—	0
LYM53	11841.1	G	28.482	7.52E-02	25.3	LYM241	13271.2	L	1.74	3.22E-02	20.3
LYM95	12121.2	G	26.986	9.98E-02	18.7	LYM256	13322.3	L	1.627	5.32E-02	12.5
CONTROL	—	G	22.735	—	0	LYM91	13283.1	L	1.625	5.81E-02	12.3

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM95	12121.3	H	0.094	1.34E-02	47.3	CONTROL	—	L	1.446	—	0
LYM10	11741.2	H	0.084	7.76E-02	31.9	LYM206	12601.3	M	2.453	2.09E-03	18
CONTROL	—	H	0.064	—	0	LYM241	13271.2	M	2.397	1.28E-02	15.3
LYM95	12121.3	I	4.691	6.13E-03	54.8	LYM207	13251.4	M	2.296	3.04E-02	10.4
LYM10	11741.2	I	4.228	3.51E-02	39.5	LYM147	12584.4	M	2.386	8.91E-02	14.8
LYM62	12024.2	I	3.957	8.88E-02	30.6	LYM256	13322.3	M	2.239	9.17E-02	7.7
LYM10	11744.5	I	3.988	9.32E-02	31.6	CONTROL	—	M	2.079	—	0
CONTROL	—	I	3.03	—	0	LYM236	12594.3	O	0.026	6.00E-02	15.3
LYM95	12121.3	J	0.586	8.07E-03	52.2	LYM147	12584.4	O	0.028	6.46E-02	22.5
LYM10	11741.2	J	0.529	4.45E-02	37.2	CONTROL	—	O	0.023	—	0
CONTROL	—	J	0.385	—	0	LYM157	13341.3	P	93.977	3.21E-02	2.1
LYM95	12121.3	K	0.411	5.44E-03	28.5	LYM256	13324.2	P	93.954	3.46E-02	2.1
LYM10	11741.2	K	0.392	2.01E-02	22.4	LYM159	13354.5	P	93.983	7.24E-02	2.1
LYM10	11744.5	K	0.383	4.42E-02	19.7	LYM223	12671.2	P	93.587	8.19E-02	1.7
LYM10	11744.1	K	0.378	5.54E-02	18.2	LYM157	13341.7	P	93.616	9.88E-02	1.7
LYM26	11824.1	K	0.377	6.36E-02	17.6	CONTROL	—	P	92.018	—	0
LYM21	11671.2	K	0.377	6.69E-02	17.8	LYM250	12613.4	Q	30.535	3.32E-03	7.9
LYM68	11941.4	K	0.373	7.72E-02	16.6	LYM206	12601.2	Q	29.685	1.79E-02	4.9
CONTROL	—	K	0.32	—	0	LYM147	12582.3	Q	29.84	3.32E-02	5.5
LYM21	11671.2	L	3.665	3.75E-03	26.8	LYM203	12662.3	Q	31.715	3.46E-02	12.1
LYM95	12121.3	L	4.425	5.70E-03	53.1	LYM157	13341.3	Q	29.42	4.35E-02	4
LYM10	11741.2	L	3.954	8.47E-03	36.9	LYM206	12603.2	Q	29.34	6.50E-02	3.7

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	**% incr. vs. cont.**
LYM 44	11882.1	L	3.552	8.51E-03	22.9	LYM 91	13283.1	Q	29.245	7.37E-02	3.3
LYM 66	11953.1	L	3.502	1.25E-02	21.2	CONTROL	—	Q	28.298	—	0
LYM 10	11744.1	L	3.498	1.28E-02	21.1	LYM 206	12603.1	R	0.682	1.24E-02	27.2
LYM 62	12024.2	L	3.752	1.43E-02	29.9	CONTROL	—	R	0.536	—	0
LYM 4	11706.5	L	3.564	1.51E-02	23.4	LYM 113	12443.1	B	0.532	9.57E-03	25.9
LYM 66	11955.2	L	3.41	2.53E-02	18	LYM 267	13604.5	B	0.48	2.91E-02	13.6
LYM 68	11941.4	L	3.331	4.96E-02	15.3	LYM 285	12734.7	B	0.477	3.69E-02	12.8
LYM 82	12201.1	L	3.319	5.85E-02	14.8	LYM 113	12444.4	B	0.464	9.15E-02	9.7
LYM 9	11632.1	L	3.356	6.43E-02	16.1	CONTROL	—	B	0.423	—	0
LYM 53	11841.1	L	3.56	8.80E-02	23.2	CONTROL	—	E	0.515	—	0
CONTROL	—	L	2.889	—	0	LYM 255	13081.5	F	8.406	9.80E-05	18.5
LYM 95	12121.3	M	3.993	1.50E-05	26.6	LYM 116	13204.6	F	7.893	5.11E-04	11.2
LYM 10	11741.2	M	3.71	3.24E-04	17.6	LYM 287	12771.6	F	7.885	5.55E-04	11.1
LYM 62	12024.2	M	3.594	1.18E-03	14	LYM 284	12884.6	F	7.834	7.75E-04	10.4
LYM 10	11744.1	M	3.58	1.97E-03	13.5	LYM 239	13041.7	F	7.666	3.45E-03	8
LYM 82	12201.1	M	3.499	8.49E-03	10.9	LYM 113	12444.5	F	8.133	6.77E-03	14.6
LYM 44	11885.4	M	3.407	2.47E-02	8	LYM 287	12771.7	F	7.628	7.48E-03	7.5
LYM 9	11632.1	M	3.475	2.70E-02	10.2	LYM 110	12923.5	F	8.115	1.19E-02	14.4
LYM 20	11711.1	M	3.387	2.94E-02	7.4	LYM 52	12895.7	F	7.749	1.33E-02	9.2
LYM 66	11953.1	M	3.494	3.07E-02	10.8	LYM 238	12764.8	F	8.587	4.56E-02	21
LYM 21	11673.1	M	3.421	3.23E-02	8.5	LYM 112	13374.4	F	7.715	6.97E-02	8.7
LYM 51	11893.4	M	3.481	3.65E-02	10.4	LYM 56	13112.5	F	7.798	9.00E-02	9.9
LYM 43	11792.2	M	3.43	5.63E-02	8.7	CONTROL	—	F	7.096	—	0

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM 26	11824.1	M	3.537	6.22E-02	12.1	LYM 56	13111.7	N	0.554	7.80E-02	10.8
LYM 17	11682.3	M	3.353	6.60E-02	6.3	CONTROL	—	N	0.5	—	0
LYM 16	11623.2	M	3.512	6.70E-02	11.3	LYM 255	13082.9	O	0.025	3.34E-02	7.8
LYM 66	11955.2	M	3.419	8.25E-02	8.4	LYM 141	12402.4	O	0.027	3.92E-02	19.5
LYM 17	11681.4	M	3.326	8.35E-02	5.5	LYM 113	12442.1	O	0.025	4.02E-02	7.8
LYM 41	11834.3	M	3.318	9.59E-02	5.2	CONTROL	—	O	0.023	—	0
LYM 21	11671.2	M	3.649	9.83E-02	15.7	LYM 181	13572.2	P	95.247	4.17E-02	1.9
CONTROL	—	M	3.154	—	0	LYM 239	13044.9	P	95.317	9.21E-02	2
LYM 66	11954.4	N	0.311	2.80E-03	25.1	LYM 232	13023.6	P	93.976	9.43E-02	0.6
LYM 31	11923.1	N	0.302	5.66E-03	21.3	LYM 156	12963.5	P	94.452	9.56E-02	1.1
LYM 8	11982.4	N	0.301	5.78E-03	21.2	CONTROL	—	P	93.441	—	0
LYM 17	11683.1	N	0.296	1.02E-02	18.9	LYM 255	13082.9	Q	34.415	9.06E-03	8.2
LYM 7	11594.3	N	0.284	4.39E-02	14	LYM 112	13372.3	Q	34.23	1.03E-02	7.6
LYM 57	12012.6	N	0.285	5.22E-02	14.6	LYM 196	13613.1	Q	33.735	3.50E-02	6.1
LYM 17	11684.5	N	0.277	8.28E-02	11.1	LYM 121	13211.8	Q	33.46	7.26E-02	5.2
LYM 13	11772.2	N	0.311	9.17E-02	25.1	LYM 287	12771.7	Q	33.23	7.99E-02	4.5
CONTROL	—	N	0.249	—	0	LYM 56	13111.7	Q	33.21	8.34E-02	4.4
LYM 12	11872.1	O	0.024	1.60E-05	19.6	LYM 156	12963.3	Q	33.4	9.09E-02	5
LYM 22	11762.1	O	0.022	4.50E-05	13.3	LYM 238	12761.6	Q	34.2	9.81E-02	7.5
LYM 43	11792.2	O	0.026	4.80E-05	33.1	CONTROL	—	Q	31.809	—	0
LYM 31	11923.4	O	0.022	1.05E-04	12.1						
LYM 43	11791.2	O	0.022	1.77E-04	11.2						
LYM 53	11841.1	O	0.022	3.43E-04	10						

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM 95	12121.3	O	0.026	3.71E-04	33.1						
LYM 95	12121.2	O	0.023	3.96E-04	14.5						
LYM 10	11744.1	O	0.023	2.55E-03	15.8						
LYM 4	11702.1	O	0.021	3.43E-03	8.2						
LYM 82	12204.6	O	0.021	4.85E-03	6.4						
LYM 82	12204.2	O	0.021	6.10E-03	6.4						
LYM 34	11904.3	O	0.021	6.18E-03	6.7						
LYM 14	12054.2	O	0.021	1.02E-02	5.5						
LYM 66	11954.4	O	0.023	3.15E-02	14.6						
LYM 6	11734.3	O	0.024	6.98E-02	22.1						
LYM 16	11623.2	O	0.023	7.55E-02	15.8						
LYM 82	12201.1	O	0.024	9.20E-02	21.9						
CONTROL	—	O	0.02	—	0						

Table 30. Results of the greenhouse experiments. Provided are the measured values of each tested parameter [parameters (ID.) A-P according to the parameters described in Table 29 above] in plants expressing the indicated polynucleotides. "Ev" = event; "P" = P-value; "Mean " = the average of measured parameter across replicates.% incr. vs. cont. = percentage of increase versus control (as compared to control).

Table 31
Measured parameters at the greenhouse till bolting assay (T2 experiment) for transformed agriculture improving trait genes

Tested Parameters	*ID*
Blade Relative Area TP4	A
Dry Weight (gr)	B
Fresh Weight (gr)	C
Leaf Blade Area TP4 (cm^2)	D
Leaf Number TP4	E
Leaf Petiole Length TP4 (cm)	F
Petiole Relative Area TP4	G
Plot Coverage TP4 (cm^2)	H
RGR Of Leaf Blade Area	J
RGR Of Leaf Number	K

Tested Parameters	***ID***
RGR Of Plot Coverage	L
RGR Of Rosette Area	M
RGR Of Rosette Diameter	N
Rosette Area TP4 (cm^2)	O
Rosette Diameter TP4 (cm)	P

Table 31: Provided are the identification (ID) letters of each of the Tested Parameters. TP4-time Point 4; RGR – Relative Growth Rate.

Table 32

Results obtained in a T2 experiment at the bolting assay

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM14	12052.5	A	92.405	3.09E-03	2.5	LYM31	11923.4	F	0.489	1.69E-04	26.4
LYM62	12022.4	A	92.349	4.28E-03	2.5	LYM116	13202.12	F	0.479	5.48E-04	23.8
LYM20	11712.2	A	92.893	5.39E-03	3.1	LYM238	12764.8	F	0.459	1.64E-03	18.6
LYM24	12064.1	A	92.339	6.75E-03	2.5	LYM20	11711.2	F	0.458	1.80E-03	18.5
LYM57	12012.2	A	92.251	6.81E-03	2.4	LYM67	11782.6	F	0.455	2.14E-03	17.7
LYM2	11695.1	A	92.121	7.11E-03	2.2	LYM88	12193.1	F	0.494	2.43E-03	27.7
LYM15	11612.2	A	94.348	1.01E-02	4.7	LYM99	12244.2	F	0.45	3.75E-03	16.4
LYM21	11672.4	A	92.404	1.14E-02	2.5	LYM239	13044.8	F	0.441	9.74E-03	13.9
LYM19	11751.4	A	91.836	1.32E-02	1.9	LYM24	12061.4	F	0.435	1.27E-02	12.5
LYM53	11844.2	A	91.822	1.53E-02	1.9	LYM53	11841.1	F	0.434	1.43E-02	12.2
LYM12	11871.1	A	92.949	1.90E-02	3.2	LYM82	12201.1	F	0.454	1.47E-02	17.4
LYM17	11683.1	A	92.267	2.24E-02	2.4	LYM26	11824.1	F	0.46	3.65E-02	18.9
LYM57	12012.4	A	91.637	2.27E-02	1.7	LYM30	11912.6	F	0.433	4.15E-02	12
LYM51	11891.1	A	91.813	2.38E-02	1.9	LYM26	11824.3	F	0.436	4.37E-02	12.7
LYM41	11832.2	A	91.578	2.83E-02	1.6	LYM285	12733.9	F	0.518	4.87E-02	34
LYM19	11753.1	A	91.958	3.26E-02	2.1	LYM62	12023.2	F	0.445	6.80E-02	15.1
LYM51	11893.4	A	91.504	3.29E-02	1.5	LYM99	12243.2	F	0.418	7.28E-02	7.9
LYM35	11812.3	A	91.489	3.40E-02	1.5	LYM128	12641.5	F	0.546	8.57E-02	41
LYM2	11695.3	A	91.533	5.57E-02	1.6	LYM95	12121.2	F	0.512	1.12E-01	32.3
LYM34	11903.2	A	91.766	6.00E-02	1.8	LYM66	11953.6	F	0.427	1.18E-01	10.3

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM37	11802.2	A	92.49	7.93E-02	2.6	LYM239	13042.9	F	0.431	1.30E-01	11.4
LYM10	11742.2	A	91.536	7.98E-02	1.6	LYM12	11872.1	F	0.548	1.47E-01	41.7
LYM31	11923.4	A	91.474	8.92E-02	1.5	LYM128	12641.3	F	0.409	1.66E-01	5.8
LYM30	11912.7	A	91.122	9.52E-02	1.1	LYM99	12243.1	F	0.554	1.68E-01	43.1
LYM9	11632.1	A	91.352	1.07E-01	1.4	LYM66	11954.4	F	0.483	1.83E-01	24.8
LYM26	11824.6	A	91.076	1.19E-01	1.1	LYM232	13024.6	F	0.42	1.96E-01	8.6
LYM57	12012.6	A	91.044	1.24E-01	1	LYM26	11824.6	F	0.429	2.22E-01	10.8
LYM16	11623.2	A	92.118	1.47E-01	2.2	LYM43	11791.4	F	0.41	2.43E-01	5.9
LYM69	11854.2	A	92.115	1.61E-01	2.2	LYM12	11873.4	F	0.462	2.56E-01	19.5
LYM57	12013.1	A	91.886	1.66E-01	2	LYM103	12713.5	F	0.444	3.55E-01	14.8
LYM15	11613.3	A	91.904	1.68E-01	2	LYM53	11842.4	F	0.411	3.55E-01	6.3
LYM20	11711.3	A	91.669	1.89E-01	1.7	LYM285	12734.9	F	0.456	4.57E-01	18
LYM41	11833.1	A	91.384	1.92E-01	1.4	LYM12	11871.1	F	0.448	4.60E-01	15.7
LYM67	11783.5	A	91.023	1.94E-01	1	LYM128	12641.1	F	0.407	5.45E-01	5.2
LYM22	11764.1	A	90.853	2.00E-01	0.8	LYM30	11913.4	F	0.397	5.70E-01	2.6
LYM69	11851.2	A	91.74	2.05E-01	1.8	LYM69	11852.2	F	0.411	5.90E-01	6.2
LYM66	11953.1	A	92.257	2.06E-01	2.4	LYM95	12124.4	F	0.425	6.13E-01	9.9
LYM26	11822.5	A	91.028	2.12E-01	1	LYM43	11793.2	F	0.421	6.52E-01	8.9
LYM30	11912.6	A	90.841	2.14E-01	0.8	LYM14	12051.4	F	0.408	6.57E-01	5.6
LYM31	11924.4	A	91.921	2.30E-01	2	LYM232	13024.7	F	0.435	6.69E-01	12.5
LYM4	11701.1	A	91.754	2.39E-01	1.8	LYM24	12064.1	F	0.416	7.26E-01	7.6
LYM14	12051.4	A	90.83	2.43E-01	0.8	LYM67	11782.4	F	0.416	7.28E-01	7.6
LYM67	11782.6	A	91.469	2.52E-01	1.5	LYM30	11913.5	F	0.403	7.37E-01	4.3
LYM62	12023.2	A	91.752	2.52E-01	1.8	LYM43	11791.5	F	0.397	7.38E-01	2.6
LYM57	12013.5	A	91.699	2.60E-01	1.8	LYM145	12951.9	F	0.394	7.61E-01	1.9
LYM68	11942.2	A	90.959	2.62E-01	0.9	LYM30	11912.7	F	0.4	7.69E-01	3.4

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM19	11752.2	A	91.08	2.63E-01	1.1	LYM31	11924.4	F	0.407	7.75E-01	5.2
LYM44	11884.1	A	91.109	2.88E-01	1.1	LYM99	12244.1	F	0.402	7.94E-01	3.8
LYM53	11841.1	A	92.28	2.88E-01	2.4	LYM26	11824.5	F	0.406	8.37E-01	5
LYM69	11852.2	A	91.959	2.91E-01	2.1	LYM20	11716.5	F	0.395	8.66E-01	2.1
LYM31	11923.1	A	90.876	2.91E-01	0.9	LYM66	11955.2	F	0.392	8.71E-01	1.4
LYM66	11955.2	A	92.703	2.94E-01	2.9	LYM53	11843.2	F	0.394	8.94E-01	1.8
LYM1	11603.2	A	92.051	3.02E-01	2.2	LYM232	13024.4	F	0.397	9.29E-01	2.6
LYM41	11831.5	A	91.826	3.07E-01	1.9	LYM156	12963.1	F	0.389	9.65E-01	0.6
LYM20	11711.2	A	90.881	3.47E-01	0.9	LYM88	12194.2	F	0.387	9.95E-01	0.1
LYM13	11771.6	A	90.65	3.62E-01	0.6	CONTROL	—	F	0.387	—	0
LYM67	11781.5	A	90.995	3.69E-01	1	LYM88	12193.1	G	8.066	2.50E-05	25.2
LYM2	11691.2	A	91.385	3.77E-01	1.4	LYM232	13024.4	G	7.589	2.58E-04	17.8
LYM30	11913.4	A	90.853	3.81E-01	0.8	LYM99	12244.2	G	7.549	3.29E-04	17.2
LYM1	11601.1	A	90.859	3.94E-01	0.8	LYM88	12191.2	G	7.736	2.37E-03	20.1
LYM10	11741.2	A	91.019	3.97E-01	1	LYM62	12023.2	G	7.932	2.88E-03	23.1
LYM24	12061.1	A	91.643	3.97E-01	1.7	LYM30	11912.6	G	7.215	4.09E-03	12
LYM13	11772.1	A	91.742	4.02E-01	1.8	LYM128	12641.5	G	7.228	5.32E-03	12.2
LYM14	12051.1	A	90.781	4.03E-01	0.7	LYM116	13204.4	G	7.075	8.47E-03	9.8
LYM4	11705.2	A	92.132	4.20E-01	2.2	LYM82	12201.1	G	7.084	8.81E-03	9.9
LYM17	11682.1	A	92.467	4.22E-01	2.6	LYM69	11852.2	G	7.055	9.96E-03	9.5
LYM1	11604.4	A	91.803	4.50E-01	1.9	LYM66	11953.1	G	7.118	1.07E-02	10.5
LYM8	11982.4	A	91.723	4.54E-01	1.8	LYM53	11844.2	G	7.005	1.48E-02	8.7
LYM34	11902.2	A	91.334	4.56E-01	1.4	LYM57	12012.6	G	7.014	1.54E-02	8.9
LYM43	11793.2	A	91.534	4.59E-01	1.6	LYM238	12764.8	G	7.251	2.21E-02	12.5
LYM51	11894.2	A	91.583	4.61E-01	1.6	LYM31	11921.3	G	6.955	2.21E-02	7.9
LYM21	11674.5	A	90.703	4.62E-01	0.7	LYM30	11913.5	G	7.742	2.81E-02	20.2

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM69	11853.4	A	91.048	5.05E-01	1	LYM43	11791.5	G	7.093	2.87E-02	10.1
LYM12	11874.1	A	90.863	5.30E-01	0.8	LYM53	11842.4	G	7.517	3.17E-02	16.7
LYM44	11885.3	A	91.411	5.42E-01	1.4	LYM99	12244.1	G	6.952	3.21E-02	7.9
LYM12	11872.1	A	91.494	5.47E-01	1.5	LYM156	12963.1	G	6.886	3.95E-02	6.9
LYM9	11633.7	A	90.819	5.50E-01	0.8	LYM41	11831.1	G	7	4.82E-02	8.6
LYM13	11772.2	A	91.548	5.65E-01	1.6	LYM31	11923.4	G	7.551	4.93E-02	17.2
LYM34	11903.3	A	91.319	5.74E-01	1.3	LYM271	12724.9	G	6.864	5.02E-02	6.5
LYM67	11782.5	A	90.978	5.82E-01	1	LYM95	12124.4	G	6.873	5.19E-02	6.7
LYM51	11893.2	A	90.82	5.94E-01	0.8	LYM82	12204.2	G	7.052	1.10E-01	9.4
LYM15	11611.3	A	90.387	6.12E-01	0.3	LYM125	12932.6	G	6.752	1.22E-01	4.8
LYM12	11874.3	A	90.471	6.22E-01	0.4	LYM12	11872.1	G	7.499	1.25E-01	16.4
LYM13	11771.9	A	90.421	6.27E-01	0.3	LYM121	13214.5	G	6.737	1.37E-01	4.6
LYM62	12022.2	A	90.902	6.52E-01	0.9	LYM239	13042.9	G	6.75	1.43E-01	4.8
LYM41	11834.2	A	90.979	6.83E-01	1	LYM66	11954.4	G	6.902	1.52E-01	7.1
LYM19	11751.5	A	91.121	6.90E-01	1.1	LYM51	11894.2	G	7.54	1.56E-01	17
LYM35	11813.5	A	90.606	7.22E-01	0.6	LYM285	12734.9	G	8.179	1.81E-01	26.9
LYM22	11762.2	A	90.475	7.23E-01	0.4	LYM128	12641.4	G	6.702	1.87E-01	4
LYM16	11622.4	A	90.591	7.35E-01	0.5	LYM57	12012.4	G	6.725	1.88E-01	4.4
LYM67	11783.4	A	90.578	7.36E-01	0.5	LYM14	12052.5	G	7.472	1.90E-01	16
LYM17	11684.4	A	90.539	7.37E-01	0.5	LYM239	13044.8	G	7.087	1.96E-01	10
LYM41	11831.1	A	90.519	7.60E-01	0.5	LYM43	11791.4	G	8.567	2.01E-01	33
LYM9	11633.2	A	90.343	7.61E-01	0.3	LYM121	13212.6	G	7.746	2.15E-01	20.2
LYM14	12052.4	A	90.586	7.64E-01	0.5	LYM99	12243.1	G	7.935	2.19E-01	23.1
LYM43	11792.2	A	90.67	7.75E-01	0.6	LYM62	12022.4	G	7.209	2.28E-01	11.9
LYM66	11953.6	A	90.649	7.76E-01	0.6	LYM56	13112.6	G	7.567	2.56E-01	17.4
LYM20	11716.5	A	90.596	7.79E-01	0.5	LYM14	12054.2	G	7.747	2.74E-01	20.2

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM37	11803.1	A	90.346	8.10E-01	0.3	LYM69	11853.4	G	7.201	3.46E-01	11.8
LYM30	11913.5	A	90.539	8.10E-01	0.5	LYM12	11873.4	G	8.016	3.55E-01	24.4
LYM21	11673.1	A	90.585	8.23E-01	0.5	LYM51	11891.1	G	7.386	3.60E-01	14.6
LYM17	11684.5	A	90.747	8.33E-01	0.7	LYM95	12121.2	G	6.912	3.61E-01	7.3
LYM34	11904.3	A	90.407	8.52E-01	0.3	LYM145	12952.9	G	7.17	3.74E-01	11.3
LYM24	12063.3	A	90.682	8.56E-01	0.6	LYM284	12884.7	G	6.91	3.81E-01	7.2
LYM2	11692.3	A	90.203	8.71E-01	0.1	LYM53	11841.2	G	7.39	3.85E-01	14.7
LYM24	12062.3	A	90.6	8.81E-01	0.5	LYM238	12762.8	G	7.075	3.94E-01	9.8
LYM22	11762.1	A	90.201	8.83E-01	0.1	LYM62	12022.1	G	7.525	3.95E-01	16.8
LYM37	11803.2	A	90.244	9.04E-01	0.2	LYM43	11791.2	G	7.703	4.20E-01	19.5
LYM62	12022.1	A	90.233	9.15E-01	0.1	LYM51	11893.4	G	7.272	4.52E-01	12.9
LYM51	11892.1	A	90.154	9.39E-01	0.1	LYM156	12961.9	G	6.677	4.65E-01	3.6
LYM10	11744.1	A	90.187	9.50E-01	0.1	LYM31	11922.3	G	6.661	4.71E-01	3.4
LYM68	11941.4	A	90.163	9.56E-01	0.1	LYM43	11793.2	G	7.393	4.87E-01	14.7
LYM17	11683.3	A	90.195	9.65E-01	0.1	LYM232	13024.6	G	6.596	4.89E-01	2.4
LYM9	11632.2	A	90.128	9.71E-01	0	LYM232	13024.5	G	6.732	4.92E-01	4.5
LYM19	11754.1	A	90.118	9.95E-01	0	LYM145	12954.7	G	6.58	4.97E-01	2.1
CONTROL	—	A	90.108	—	0	LYM41	11833.1	G	6.865	5.04E-01	6.5
LYM14	12051.4	B	0.211	5.89E-03	26.4	LYM128	12641.1	G	6.796	5.07E-01	5.5
LYM10	11744.1	B	0.2	1.92E-02	20	LYM14	12051.1	G	6.808	5.14E-01	5.7
LYM34	11902.2	B	0.192	6.57E-02	15.1	LYM53	11841.1	G	6.947	5.15E-01	7.8
LYM9	11632.1	B	0.191	7.00E-02	14.4	LYM88	12194.2	G	6.864	5.26E-01	6.5
LYM2	11695.1	B	0.188	1.04E-01	12.5	LYM24	12061.4	G	6.842	5.31E-01	6.2
LYM57	12013.1	B	0.188	1.04E-01	12.5	LYM62	12023.4	G	7.308	5.31E-01	13.4
LYM66	11954.4	B	0.191	1.36E-01	14.4	LYM51	11893.2	G	6.689	5.34E-01	3.8
LYM57	12012.4	B	0.191	1.42E-01	14.7	LYM57	12012.2	G	6.686	5.42E-01	3.8

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM66	11953.6	B	0.186	1.65E-01	11.7	LYM30	11912.7	G	6.949	5.55E-01	7.8
LYM37	11803.1	B	0.183	1.75E-01	10.1	LYM66	11953.6	G	6.632	5.60E-01	2.9
LYM53	11844.2	B	0.184	1.80E-01	10.2	LYM53	11843.2	G	6.959	5.75E-01	8
LYM9	11632.2	B	0.186	1.90E-01	11.4	LYM56	13111.7	G	7.268	5.80E-01	12.8
LYM35	11812.3	B	0.189	2.46E-01	13.2	LYM67	11783.5	G	6.724	5.88E-01	4.4
LYM4	11701.1	B	0.184	2.47E-01	10.2	LYM95	12124.5	G	6.849	6.12E-01	6.3
LYM31	11924.4	B	0.181	2.72E-01	8.4	LYM31	11924.4	G	6.597	6.17E-01	2.4
LYM35	11813.5	B	0.219	2.93E-01	31.2	LYM41	11832.2	G	6.533	6.27E-01	1.4
LYM57	12012.6	B	0.187	2.98E-01	12.1	LYM51	11892.1	G	6.978	6.31E-01	8.3
LYM1	11604.4	B	0.184	3.17E-01	10.6	LYM43	11792.2	G	6.782	6.47E-01	5.2
LYM14	12051.1	B	0.18	3.27E-01	8	LYM285	12734.7	G	7.284	6.55E-01	13
LYM30	11912.6	B	0.191	3.85E-01	14.3	LYM271	12721.8	G	6.637	6.59E-01	3
LYM13	11771.6	B	0.208	4.16E-01	24.9	LYM30	11913.4	G	7.07	6.73E-01	9.7
LYM13	11771.9	B	0.192	4.37E-01	15.1	LYM31	11923.1	G	6.854	6.88E-01	6.4
LYM31	11923.1	B	0.176	4.57E-01	5.4	LYM82	12203.2	G	6.635	7.11E-01	3
LYM67	11783.5	B	0.178	4.69E-01	6.9	LYM20	11716.3	G	6.74	7.14E-01	4.6
LYM10	11741.2	B	0.177	5.16E-01	6.1	LYM239	13041.7	G	6.709	7.58E-01	4.1
LYM21	11673.1	B	0.176	5.27E-01	5.7	LYM24	12064.1	G	6.573	7.64E-01	2
LYM69	11851.2	B	0.178	5.36E-01	6.5	LYM239	13044.7	G	6.629	7.70E-01	2.9
LYM69	11852.2	B	0.179	5.45E-01	7.6	LYM88	12193.5	G	6.595	7.72E-01	2.4
LYM1	11603.2	B	0.173	6.15E-01	3.5	LYM20	11712.2	G	6.616	7.87E-01	2.7
LYM7	11594.2	B	0.184	6.18E-01	10.2	LYM62	12022.2	G	6.612	7.91E-01	2.6
LYM34	11903.2	B	0.188	6.33E-01	12.9	LYM67	11782.6	G	6.509	7.99E-01	1
LYM21	11674.5	B	0.172	6.73E-01	3.1	LYM20	11716.5	G	6.541	8.15E-01	1.5
LYM68	11942.3	B	0.176	6.91E-01	5.7	LYM232	13024.7	G	6.663	8.27E-01	3.4
LYM14	12054.2	B	0.176	7.18E-01	5.4	LYM26	11824.1	G	6.558	8.57E-01	1.8

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM30	11913.4	B	0.176	7.18E-01	5.4	LYM99	12243.2	G	6.512	8.64E-01	1.1
LYM51	11893.2	B	0.171	7.40E-01	2.4	LYM121	13211.8	G	6.511	8.82E-01	1
LYM53	11842.4	B	0.182	7.45E-01	9.1	LYM99	12241.1	G	6.503	8.85E-01	0.9
LYM44	11884.3	B	0.171	8.45E-01	2.4	LYM14	12051.4	G	6.468	8.96E-01	0.4
LYM17	11683.3	B	0.169	8.75E-01	1.2	LYM67	11782.4	G	6.536	9.09E-01	1.4
LYM15	11611.3	B	0.168	9.01E-01	0.9	LYM26	11824.5	G	6.469	9.55E-01	0.4
LYM8	11982.7	B	0.169	9.10E-01	1.2	LYM26	11824.3	G	6.475	9.58E-01	0.5
LYM12	11872.1	B	0.169	9.21E-01	1.6	LYM95	12121.4	G	6.458	9.88E-01	0.2
LYM51	11893.4	B	0.169	9.25E-01	1.6	LYM24	12062.3	G	6.457	9.90E-01	0.2
LYM34	11903.3	B	0.168	9.59E-01	0.5	LYM239	13041.1	G	6.448	9.93E-01	0.1
LYM7	11592.1	B	0.168	9.67E-01	0.5	LYM12	11871.1	G	6.445	9.94E-01	0
CONTROL	—	B	0.167	—	0	CONTROL	—	G	6.444	—	0
LYM10	11744.1	C	2.881	4.60E-03	21	LYM116	13202.12	H	18.312	4.00E-06	47.5
LYM35	11813.5	C	2.85	6.51E-03	19.7	LYM88	12193.1	H	15.681	1.86E-04	26.3
LYM9	11632.1	C	2.85	6.67E-03	19.7	LYM31	11923.4	H	14.837	1.11E-03	19.5
LYM57	12013.1	C	2.738	2.45E-02	15	LYM20	11711.2	H	17.126	1.79E-03	38
LYM9	11633.7	C	2.713	3.07E-02	13.9	LYM53	11841.1	H	15.641	2.39E-03	26
LYM35	11812.3	C	2.681	6.94E-02	12.6	LYM67	11782.6	H	16.773	4.00E-03	35.1
LYM66	11953.6	C	2.606	1.11E-01	9.5	LYM82	12201.1	H	14.907	1.38E-02	20.1
LYM14	12051.4	C	2.788	2.12E-01	17.1	LYM12	11871.3	H	14.033	1.64E-02	13.1
LYM57	12012.4	C	2.55	2.56E-01	7.1	LYM26	11824.3	H	15.354	2.22E-02	23.7
LYM13	11771.9	C	2.694	2.59E-01	13.2	LYM238	12764.8	H	15.539	2.58E-02	25.2
LYM1	11603.2	C	2.55	2.80E-01	7.1	LYM88	12194.2	H	13.639	3.29E-02	9.9
LYM66	11954.4	C	2.525	3.28E-01	6.1	LYM99	12244.2	H	14.055	4.42E-02	13.2
LYM68	11942.2	C	2.494	4.00E-01	4.8	LYM53	11843.2	H	13.752	6.09E-02	10.8
LYM30	11912.6	C	2.662	4.05E-01	11.8	LYM128	12641.5	H	19.01	6.58E-02	53.2

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LYM57	12012.6	C	2.813	4.19E-01	18.1	LYM99	12243.1	H	18.3	8.16E-02	47.4
LYM34	11902.2	C	2.681	4.48E-01	12.6	LYM26	11824.1	H	16.706	8.96E-02	34.6
LYM51	11893.4	C	2.556	4.54E-01	7.4	LYM128	12641.3	H	16.77	9.41E-02	35.1
LYM2	11695.1	C	2.538	5.35E-01	6.6	LYM239	13042.9	H	15.316	1.28E-01	23.4
LYM69	11851.2	C	2.65	5.41E-01	11.3	LYM26	11824.6	H	15.643	1.64E-01	26
LYM13	11771.6	C	2.525	5.65E-01	6.1	LYM285	12733.9	H	18.928	1.66E-01	52.5
LYM53	11844.2	C	2.619	5.75E-01	10	LYM20	11716.5	H	13.667	1.68E-01	10.1
LYM16	11623.2	C	2.456	6.08E-01	3.2	LYM24	12061.4	H	15.875	1.72E-01	27.9
LYM24	12061.2	C	2.45	6.15E-01	2.9	LYM30	11912.7	H	13.113	1.73E-01	5.7
LYM1	11604.4	C	2.506	6.22E-01	5.3	LYM116	13202.7	H	14.52	1.78E-01	17
LYM14	12051.1	C	2.475	6.44E-01	4	LYM103	12713.5	H	16.234	1.81E-01	30.8
LYM31	11924.4	C	2.456	6.45E-01	3.2	LYM66	11954.4	H	16.504	1.98E-01	33
LYM7	11594.2	C	2.519	6.45E-01	5.8	LYM66	11953.6	H	13.082	2.10E-01	5.4
LYM34	11903.2	C	2.525	6.69E-01	6.1	LYM12	11872.1	H	19.153	2.18E-01	54.3
LYM67	11783.5	C	2.563	7.21E-01	7.6	LYM95	12124.4	H	14.508	2.21E-01	16.9
LYM68	11942.3	C	2.569	7.32E-01	7.9	LYM66	11955.2	H	14.124	2.35E-01	13.8
LYM53	11842.4	C	2.581	7.49E-01	8.4	LYM31	11924.4	H	14.278	2.42E-01	15
LYM17	11683.3	C	2.406	8.49E-01	1.1	LYM95	12121.2	H	17.135	3.06E-01	38.1
LYM30	11913.4	C	2.456	8.69E-01	3.2	LYM69	11852.2	H	14.517	3.11E-01	17
LYM69	11852.2	C	2.425	8.75E-01	1.9	LYM14	12051.4	H	14.254	3.15E-01	14.8
LYM51	11891.1	C	2.438	8.88E-01	2.4	LYM12	11871.1	H	16.236	3.18E-01	30.8
LYM44	11884.3	C	2.413	9.00E-01	1.3	LYM43	11791.4	H	13.352	3.60E-01	7.6
LYM1	11602.6	C	2.388	9.61E-01	0.3	LYM103	12712.8	H	14.075	4.03E-01	13.4
LYM8	11982.7	C	2.394	9.68E-01	0.6	LYM239	13044.8	H	13.881	4.35E-01	11.8
LYM14	12054.2	C	2.388	9.72E-01	0.3	LYM62	12023.2	H	13.479	4.46E-01	8.6
LYM10	11741.2	C	2.388	9.76E-01	0.3	LYM232	13024.6	H	13.49	4.54E-01	8.7

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LYM9	11632.2	C	2.381	9.97E-01	0	LYM67	11782.4	H	14.203	4.80E-01	14.4
CONTROL	—	C	2.381	—	0	LYM30	11912.6	H	13.885	4.95E-01	11.9
LYM9	11632.1	D	0.63	7.73E-04	26.2	LYM156	12963.1	H	13.692	5.55E-01	10.3
LYM57	12013.1	D	0.604	2.91E-03	21.1	LYM232	13024.7	H	15.409	5.68E-01	24.1
LYM30	11912.6	D	0.59	6.70E-03	18.3	LYM43	11791.5	H	12.738	5.74E-01	2.6
LYM35	11812.3	D	0.574	1.51E-02	15.1	LYM99	12243.2	H	13.041	5.75E-01	5.1
LYM9	11633.7	D	0.564	7.87E-02	13	LYM128	12641.1	H	13.474	6.12E-01	8.6
LYM10	11744.1	D	0.58	9.91E-02	16.2	LYM12	11873.4	H	12.838	6.27E-01	3.4
LYM10	11741.2	D	0.544	9.99E-02	9.1	LYM26	11824.5	H	14.928	6.29E-01	20.3
LYM57	12012.4	D	0.541	1.20E-01	8.5	LYM103	12711.8	H	12.75	6.58E-01	2.7
LYM31	11924.4	D	0.567	1.79E-01	13.5	LYM24	12064.1	H	13.685	6.61E-01	10.3
LYM1	11602.6	D	0.541	1.97E-01	8.5	LYM26	11821.2	H	13.651	6.78E-01	10
LYM1	11603.2	D	0.581	2.09E-01	16.4	LYM116	13204.4	H	14.229	7.49E-01	14.6
LYM51	11891.1	D	0.543	2.39E-01	8.7	LYM43	11793.2	H	13.044	8.21E-01	5.1
LYM13	11771.9	D	0.538	2.66E-01	7.8	LYM145	12951.9	H	12.489	8.72E-01	0.6
LYM53	11842.4	D	0.586	3.05E-01	17.5	LYM30	11913.5	H	12.846	8.73E-01	3.5
LYM35	11813.5	D	0.558	3.13E-01	11.8	LYM30	11913.4	H	12.658	8.85E-01	2
LYM13	11771.6	D	0.524	3.24E-01	5	LYM62	12023.5	H	12.488	8.95E-01	0.6
LYM14	12051.4	D	0.565	3.33E-01	13.3	LYM285	12734.9	H	12.563	9.45E-01	1.2
LYM69	11852.2	D	0.533	3.41E-01	6.8	LYM103	12712.5	H	12.458	9.73E-01	0.4
LYM66	11953.6	D	0.536	3.86E-01	7.4	CONTROL	—	H	12.412	—	0
LYM57	12012.6	D	0.601	3.94E-01	20.5	LYM12	11872.1	J	0.05	1.96E-04	59.7
LYM1	11604.4	D	0.591	4.48E-01	18.5	LYM116	13202.12	J	0.046	3.31E-04	47.1
LYM14	12051.1	D	0.54	4.53E-01	8.3	LYM20	11711.2	J	0.045	6.36E-04	44.3
LYM34	11902.2	D	0.562	4.60E-01	12.6	LYM128	12641.5	J	0.044	7.56E-04	40.5
LYM2	11695.1	D	0.542	4.83E-01	8.6	LYM285	12733.9	J	0.045	1.31E-03	43.5

Gene name	**Event**	**ID**	**Mean**	**P value**	*% incr. vs. cont.*	**Gene name**	**Event**	**ID**	**Mean**	**P value**	*% incr. vs. cont.*
LYM31	11923.4	D	0.546	5.90E-01	9.3	LYM238	12764.8	J	0.042	4.59E-03	34.9
LYM69	11851.2	D	0.516	6.13E-01	3.3	LYM26	11824.1	J	0.042	7.07E-03	33.7
LYM12	11872.1	D	0.53	6.82E-01	6.2	LYM239	13042.9	J	0.041	8.56E-03	31.8
LYM7	11594.2	D	0.53	6.83E-01	6.2	LYM103	12713.5	J	0.042	9.55E-03	34
LYM21	11674.5	D	0.51	6.94E-01	2.3	LYM99	12243.1	J	0.039	1.57E-02	26.4
LYM68	11942.3	D	0.538	7.30E-01	7.7	LYM12	11871.1	J	0.041	1.61E-02	31
LYM53	11844.2	D	0.508	7.44E-01	1.7	LYM67	11782.6	J	0.04	1.77E-02	28.2
LYM35	11811.3	D	0.529	7.70E-01	6.1	LYM116	13202.7	J	0.04	2.12E-02	28.6
LYM24	12061.2	D	0.508	7.91E-01	1.9	LYM24	12061.4	J	0.04	2.32E-02	28.1
LYM51	11893.4	D	0.513	8.07E-01	2.9	LYM26	11824.6	J	0.039	2.72E-02	25.9
LYM34	11903.2	D	0.535	8.16E-01	7.1	LYM128	12641.3	J	0.039	3.65E-02	25.4
LYM1	11601.1	D	0.515	8.25E-01	3.2	LYM26	11824.3	J	0.039	4.30E-02	23.4
LYM30	11913.4	D	0.507	9.38E-01	1.6	LYM66	11954.4	J	0.038	4.56E-02	22.5
LYM43	11791.4	D	0.5	9.64E-01	0.2	LYM103	12712.8	J	0.038	5.16E-02	22.9
CONTROL	—	D	0.499	—	0	LYM95	12121.2	J	0.039	5.69E-02	23.8
LYM35	11811.3	E	10	1.23E-02	7.1	LYM24	12064.1	J	0.039	6.86E-02	23.9
LYM10	11744.1	E	10.313	2.53E-02	10.4	LYM232	13024.7	J	0.04	8.05E-02	28.4
LYM30	11912.6	E	9.857	8.06E-02	5.6	LYM232	13024.6	J	0.038	8.34E-02	20.4
LYM34	11902.2	E	9.75	1.25E-01	4.4	LYM14	12051.4	J	0.037	9.99E-02	19.7
LYM69	11851.2	E	9.688	1.30E-01	3.8	LYM12	11871.3	J	0.037	1.14E-01	18.1
LYM69	11852.2	E	10.188	1.53E-01	9.1	LYM30	11912.6	J	0.037	1.23E-01	18.6
LYM9	11632.1	E	10.125	2.33E-01	8.4	LYM239	13044.8	J	0.037	1.34E-01	17.6
LYM1	11604.4	E	9.625	2.62E-01	3.1	LYM31	11924.4	J	0.036	1.64E-01	15.9
LYM13	11772.1	E	9.563	3.10E-01	2.4	LYM156	12963.1	J	0.036	1.70E-01	15.9
LYM12	11872.1	E	9.5	4.38E-01	1.7	LYM238	12763.7	J	0.036	1.78E-01	14.5
LYM26	11824.6	E	9.625	4.45E-01	3.1	LYM53	11841.1	J	0.036	1.78E-01	14.9

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM13	11771.9	E	9.688	4.47E-01	3.8	LYM116	13204.4	J	0.038	1.81E-01	22.8
LYM14	12051.4	E	9.75	4.53E-01	4.4	LYM20	11716.5	J	0.036	1.95E-01	14.5
LYM37	11801.1	E	9.563	4.57E-01	2.4	LYM26	11821.2	J	0.036	2.34E-01	14.6
LYM9	11633.7	E	9.563	4.57E-01	2.4	LYM26	11824.5	J	0.037	2.36E-01	17.1
LYM35	11812.3	E	9.813	4.59E-01	5.1	LYM128	12641.1	J	0.035	3.24E-01	11.7
LYM14	12054.2	E	9.5	5.11E-01	1.7	LYM31	11923.4	J	0.035	3.32E-01	10.6
LYM53	11842.4	E	9.813	5.48E-01	5.1	LYM53	11843.2	J	0.034	3.70E-01	9.8
LYM21	11674.5	E	9.75	6.27E-01	4.4	LYM69	11852.2	J	0.034	3.93E-01	9.1
LYM1	11601.1	E	9.438	6.42E-01	1.1	LYM67	11782.4	J	0.034	4.05E-01	9
LYM14	12051.1	E	9.438	6.42E-01	1.1	LYM103	12712.5	J	0.034	4.13E-01	9.1
LYM15	11611.3	E	9.438	6.42E-01	1.1	LYM30	11913.5	J	0.034	4.32E-01	9.6
LYM53	11844.2	E	9.438	6.42E-01	1.1	LYM88	12193.1	J	0.034	4.41E-01	8.1
LYM35	11811.2	E	9.5	6.51E-01	1.7	LYM103	12711.8	J	0.034	4.68E-01	7.8
LYM37	11803.2	E	9.5	6.51E-01	1.7	LYM99	12244.2	J	0.034	4.71E-01	7.7
LYM30	11913.4	E	9.75	6.79E-01	4.4	LYM95	12124.4	J	0.034	4.71E-01	7.6
LYM34	11903.2	E	9.438	7.32E-01	1.1	LYM31	11921.3	J	0.033	5.04E-01	7.3
LYM19	11751.4	E	9.5	7.45E-01	1.7	LYM66	11955.2	J	0.033	5.27E-01	6.6
LYM1	11602.6	E	9.375	8.76E-01	0.4	LYM30	11912.7	J	0.033	5.60E-01	6.4
LYM57	12012.6	E	9.438	8.89E-01	1.1	LYM62	12023.2	J	0.033	5.61E-01	6.2
LYM51	11891.1	E	9.375	9.39E-01	0.4	LYM20	11716.3	J	0.033	5.84E-01	6.4
CONTROL	—	E	9.337	—	0	LYM30	11913.4	J	0.033	6.20E-01	5.8
LYM57	12012.4	F	0.806	7.51E-02	8.8	LYM238	12762.8	J	0.033	6.21E-01	5.6
LYM35	11811.3	F	0.83	2.97E-01	12.1	LYM238	12763.5	J	0.033	6.27E-01	5.3
LYM53	11842.4	F	0.787	3.26E-01	6.2	LYM156	12961.9	J	0.033	6.33E-01	5.1
LYM14	12051.4	F	0.846	3.32E-01	14.3	LYM57	12012.2	J	0.033	6.41E-01	5.1
LYM35	11813.5	F	0.777	3.52E-01	4.9	LYM145	12951.9	J	0.033	6.87E-01	4.4

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM68	11942.3	F	0.786	3.74E-01	6.2	LYM12	11873.4	J	0.032	7.45E-01	3.6
LYM30	11912.6	F	0.805	4.37E-01	8.6	LYM20	11712.2	J	0.032	7.62E-01	3.5
LYM51	11891.1	F	0.764	4.68E-01	3.1	LYM41	11831.5	J	0.032	7.96E-01	2.8
LYM9	11632.1	F	0.769	5.87E-01	3.8	LYM103	12714.6	J	0.032	8.74E-01	1.9
LYM9	11633.7	F	0.76	5.93E-01	2.6	LYM285	12734.9	J	0.032	8.76E-01	1.8
LYM13	11771.6	F	0.761	6.04E-01	2.7	LYM239	13044.7	J	0.032	9.02E-01	1.4
LYM13	11771.9	F	0.76	6.32E-01	2.7	LYM82	12201.1	J	0.032	9.28E-01	0.9
LYM37	11801.1	F	0.758	6.33E-01	2.3	LYM66	11953.6	J	0.031	9.36E-01	0.8
LYM7	11594.2	F	0.759	6.93E-01	2.5	LYM238	12761.6	J	0.031	9.94E-01	0.1
LYM57	12012.6	F	0.761	7.81E-01	2.8	LYM24	12062.3	J	0.031	9.97E-01	0
LYM57	12013.1	F	0.759	8.06E-01	2.5	CONTROL	—	J	0.031	—	0
LYM35	11811.2	F	0.75	8.65E-01	1.2	LYM26	11824.3	K	0.686	7.37E-03	43.8
LYM14	12051.1	F	0.748	8.75E-01	0.9	LYM69	11852.2	K	0.659	2.22E-02	38.2
LYM10	11744.1	F	0.747	8.99E-01	0.9	LYM128	12641.1	K	0.641	3.49E-02	34.5
LYM34	11903.2	F	0.757	9.24E-01	2.2	LYM95	12121.2	K	0.641	3.71E-02	34.4
LYM1	11604.4	F	0.745	9.30E-01	0.5	LYM24	12061.4	K	0.633	4.62E-02	32.8
CONTROL	—	F	0.741	—	0	LYM14	12051.4	K	0.627	5.47E-02	31.5
LYM37	11801.1	G	11.978	9.54E-04	26.2	LYM128	12642.1	K	0.635	5.90E-02	33.2
LYM19	11754.1	G	10.53	1.26E-01	11	LYM128	12641.5	K	0.623	7.60E-02	30.6
LYM35	11813.5	G	10.283	1.29E-01	8.4	LYM116	13202.12	K	0.603	8.80E-02	26.5
LYM9	11633.2	G	10.294	1.30E-01	8.5	LYM238	12764.8	K	0.608	8.89E-02	27.5
LYM68	11942.3	G	10.196	1.75E-01	7.4	LYM30	11912.6	K	0.605	9.08E-02	26.8
LYM4	11706.5	G	10.33	2.38E-01	8.8	LYM277	13103.1	K	0.602	9.87E-02	26.1
LYM35	11811.3	G	10.931	2.53E-01	15.2	LYM26	11824.1	K	0.595	1.15E-01	24.7
LYM19	11752.2	G	10.007	3.09E-01	5.5	LYM285	12733.9	K	0.597	1.19E-01	25.2
LYM22	11761.3	G	10.119	3.11E-01	6.6	LYM43	11791.4	K	0.596	1.21E-01	25

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM37	11801.2	G	10.859	3.30E-01	14.4	LYM62	12023.5	K	0.593	1.29E-01	24.3
LYM43	11791.4	G	10.473	3.51E-01	10.4	LYM12	11873.4	K	0.592	1.35E-01	24.2
LYM43	11791.5	G	10.532	3.81E-01	11	LYM116	13204.4	K	0.607	1.36E-01	27.4
LYM7	11594.2	G	10.052	4.96E-01	5.9	LYM30	11913.4	K	0.593	1.53E-01	24.3
LYM20	11716.5	G	10.104	5.90E-01	6.5	LYM121	13212.6	K	0.584	1.56E-01	22.4
LYM8	11983.1	G	9.748	5.93E-01	2.7	LYM285	12734.7	K	0.6	1.70E-01	25.9
LYM7	11591.2	G	9.771	6.16E-01	3	LYM53	11842.4	K	0.581	1.70E-01	21.9
LYM67	11781.5	G	9.718	6.39E-01	2.4	LYM95	12124.4	K	0.574	1.84E-01	20.4
LYM62	12023.4	G	9.723	6.48E-01	2.5	LYM20	11711.2	K	0.581	1.90E-01	21.7
LYM16	11624.4	G	9.761	6.89E-01	2.9	LYM128	12641.3	K	0.569	2.06E-01	19.3
LYM9	11634.5	G	9.753	7.05E-01	2.8	LYM62	12023.2	K	0.577	2.14E-01	21
LYM53	11842.4	G	9.673	7.13E-01	1.9	LYM145	12953.5	K	0.571	2.18E-01	19.7
LYM12	11874.1	G	9.655	7.33E-01	1.7	LYM53	11841.2	K	0.568	2.21E-01	19
LYM37	11803.2	G	9.663	7.61E-01	1.8	LYM285	12734.9	K	0.576	2.21E-01	20.8
LYM43	11791.2	G	9.676	8.13E-01	2	LYM232	13024.4	K	0.578	2.36E-01	21.2
LYM35	11811.2	G	9.598	8.21E-01	1.1	LYM103	12712.5	K	0.571	2.39E-01	19.7
LYM62	12023.7	G	9.592	8.31E-01	1.1	LYM232	13024.6	K	0.566	2.45E-01	18.6
LYM68	11943.2	G	9.652	8.34E-01	1.7	LYM53	11841.1	K	0.568	2.50E-01	19.2
LYM15	11612.3	G	9.59	8.47E-01	1.1	LYM99	12243.1	K	0.576	2.57E-01	20.8
LYM19	11753.4	G	9.661	8.70E-01	1.8	LYM24	12064.1	K	0.568	2.60E-01	19
LYM67	11782.5	G	9.594	9.27E-01	1.1	LYM110	12923.8	K	0.559	2.60E-01	17.2
LYM2	11693.3	G	9.593	9.33E-01	1.1	LYM66	11954.4	K	0.565	2.60E-01	18.4
LYM43	11793.2	G	9.569	9.71E-01	0.8	LYM103	12713.5	K	0.565	2.61E-01	18.6
LYM44	11882.1	G	9.529	9.82E-01	0.4	LYM12	11871.1	K	0.57	2.69E-01	19.5
LYM14	12051.4	G	9.501	9.83E-01	0.1	LYM99	12241.1	K	0.558	2.70E-01	17.1
LYM13	11773.2	G	9.501	9.83E-01	0.1	LYM82	12201.1	K	0.56	2.74E-01	17.5

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM15	11614.4	G	9.493	9.97E-01	0	LYM31	11923.4	K	0.564	2.76E-01	18.2
CONTROL	—	G	9.49	—	0	LYM99	12243.2	K	0.559	2.99E-01	17.2
LYM9	11632.1	H	33.914	2.21E-04	36.9	LYM145	12954.8	K	0.554	3.06E-01	16.1
LYM57	12013.1	H	29.579	9.76E-03	19.4	LYM66	11955.2	K	0.557	3.10E-01	16.7
LYM35	11812.3	H	29.204	1.31E-02	17.9	LYM284	12884.6	K	0.554	3.10E-01	16.1
LYM57	12012.4	H	27.626	1.08E-01	11.5	LYM232	13024.7	K	0.554	3.11E-01	16.1
LYM10	11744.1	H	31.643	1.14E-01	27.7	LYM239	13044.8	K	0.555	3.13E-01	16.4
LYM35	11813.5	H	27.993	1.18E-01	13	LYM43	11793.2	K	0.563	3.17E-01	18.1
LYM10	11741.2	H	26.964	1.50E-01	8.8	LYM14	12051.1	K	0.553	3.22E-01	15.9
LYM69	11852.2	H	27.516	1.79E-01	11	LYM116	13202.7	K	0.552	3.34E-01	15.7
LYM9	11633.7	H	27.959	1.85E-01	12.8	LYM95	12124.5	K	0.548	3.45E-01	14.9
LYM1	11602.6	H	27.965	1.95E-01	12.9	LYM121	13211.8	K	0.546	3.49E-01	14.4
LYM1	11603.2	H	28.246	2.79E-01	14	LYM24	12062.3	K	0.547	3.50E-01	14.8
LYM30	11912.6	H	28.163	2.82E-01	13.6	LYM67	11782.5	K	0.546	3.51E-01	14.5
LYM14	12051.4	H	29.876	3.41E-01	20.6	LYM53	11843.2	K	0.545	3.52E-01	14.3
LYM51	11891.1	H	27.805	3.42E-01	12.2	LYM110	12924.5	K	0.548	3.55E-01	15
LYM1	11604.4	H	30.541	3.49E-01	23.2	LYM99	12244.2	K	0.549	3.59E-01	15.1
LYM53	11842.4	H	30.36	3.95E-01	22.5	LYM12	11871.3	K	0.547	3.66E-01	14.6
LYM31	11924.4	H	28.244	4.58E-01	14	LYM99	12244.1	K	0.549	3.66E-01	15.1
LYM57	12012.6	H	29.977	4.61E-01	21	LYM271	12724.7	K	0.549	3.69E-01	15.1
LYM13	11771.9	H	26.732	4.87E-01	7.9	LYM26	11824.5	K	0.557	3.69E-01	16.8
LYM34	11902.2	H	27.88	5.04E-01	12.5	LYM30	11913.5	K	0.544	3.88E-01	14.1
LYM14	12051.1	H	26.648	5.19E-01	7.5	LYM67	11781.5	K	0.54	3.88E-01	13.3
LYM21	11674.5	H	25.858	5.35E-01	4.3	LYM238	12762.8	K	0.544	3.90E-01	14.1
LYM35	11811.3	H	28.152	5.73E-01	13.6	LYM62	12023.4	K	0.544	3.93E-01	14.1
LYM2	11695.1	H	25.97	6.93E-01	4.8	LYM14	12052.5	K	0.547	3.97E-01	14.8

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM69	11851.2	H	25.499	6.95E-01	2.9	LYM31	11921.3	K	0.544	4.06E-01	14
LYM7	11594.2	H	26.064	7.54E-01	5.2	LYM26	11821.2	K	0.54	4.06E-01	13.3
LYM13	11771.6	H	25.204	7.64E-01	1.7	LYM43	11792.2	K	0.54	4.06E-01	13.3
LYM12	11872.1	H	26.31	7.68E-01	6.2	LYM62	12022.4	K	0.54	4.18E-01	13.3
LYM31	11923.4	H	26.115	7.78E-01	5.4	LYM271	12721.8	K	0.536	4.26E-01	12.3
LYM34	11903.2	H	27.351	7.84E-01	10.4	LYM56	13112.6	K	0.536	4.32E-01	12.4
LYM51	11893.4	H	25.767	7.97E-01	4	LYM145	12951.9	K	0.535	4.47E-01	12.2
LYM66	11953.6	H	25.492	8.09E-01	2.9	LYM110	12923.5	K	0.534	4.49E-01	12.1
LYM68	11942.3	H	26.014	8.37E-01	5	LYM110	12921.7	K	0.537	4.51E-01	12.6
LYM30	11913.4	H	26.041	8.38E-01	5.1	LYM12	11872.1	K	0.536	4.52E-01	12.3
LYM1	11601.1	H	25.377	8.67E-01	2.4	LYM20	11711.3	K	0.533	4.57E-01	11.8
LYM24	12061.2	H	25.011	9.20E-01	0.9	LYM57	12012.2	K	0.534	4.71E-01	11.9
LYM1	11602.1	H	24.992	9.73E-01	0.9	LYM88	12193.1	K	0.529	4.85E-01	11
LYM53	11844.2	H	24.831	9.74E-01	0.2	LYM66	11953.6	K	0.53	4.94E-01	11.1
CONTROL	—	H	24.78	—	0	LYM31	11924.4	K	0.53	5.07E-01	11.1
LYM9	11632.1	J	0.079	1.51E-01	24.8	LYM67	11782.4	K	0.532	5.13E-01	11.5
LYM57	12013.1	J	0.078	1.83E-01	23	LYM285	12731.4	K	0.525	5.18E-01	10
LYM57	12012.6	J	0.077	2.25E-01	21.2	LYM239	13041.1	K	0.523	5.35E-01	9.7
LYM30	11912.6	J	0.076	2.26E-01	20.6	LYM24	12063.3	K	0.521	5.41E-01	9.2
LYM53	11842.4	J	0.076	2.65E-01	19.4	LYM156	12963.1	K	0.522	5.54E-01	9.4
LYM1	11604.4	J	0.075	2.97E-01	18.6	LYM12	11874.1	K	0.521	5.55E-01	9.2
LYM1	11603.2	J	0.074	3.28E-01	16.8	LYM271	12724.9	K	0.522	5.59E-01	9.5
LYM10	11744.1	J	0.073	3.53E-01	15.7	LYM103	12713.7	K	0.52	5.64E-01	9.1
LYM31	11924.4	J	0.072	3.90E-01	14.6	LYM14	12054.2	K	0.518	5.72E-01	8.6
LYM14	12051.4	J	0.072	4.24E-01	13.6	LYM57	12013.3	K	0.519	5.89E-01	8.9
LYM35	11812.3	J	0.072	4.25E-01	13.3	LYM31	11923.1	K	0.515	6.17E-01	7.9

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM9	11633.7	J	0.071	4.52E-01	12.5	LYM238	12761.6	K	0.518	6.24E-01	8.5
LYM34	11902.2	J	0.071	4.57E-01	12.9	LYM232	13024.5	K	0.515	6.30E-01	7.9
LYM35	11813.5	J	0.071	4.85E-01	11.8	LYM56	13112.7	K	0.512	6.37E-01	7.3
LYM57	12012.4	J	0.07	5.22E-01	10.3	LYM26	11824.6	K	0.51	6.47E-01	6.9
LYM51	11891.1	J	0.069	5.53E-01	9.8	LYM103	12712.8	K	0.511	6.48E-01	7.2
LYM2	11695.1	J	0.069	5.59E-01	9.8	LYM41	11831.1	K	0.509	6.63E-01	6.8
LYM31	11923.4	J	0.069	5.64E-01	9.9	LYM277	13101.1	K	0.508	6.88E-01	6.6
LYM13	11771.9	J	0.069	5.93E-01	9	LYM56	13111.7	K	0.509	6.88E-01	6.7
LYM68	11942.3	J	0.069	5.94E-01	9.5	LYM284	12884.7	K	0.506	6.90E-01	6.2
LYM7	11594.2	J	0.069	5.99E-01	8.8	LYM62	12022.1	K	0.504	7.05E-01	5.7
LYM66	11953.6	J	0.069	6.12E-01	8.5	LYM30	11912.7	K	0.507	7.06E-01	6.3
LYM14	12051.1	J	0.069	6.16E-01	8.5	LYM41	11833.1	K	0.501	7.36E-01	5.1
LYM10	11741.2	J	0.068	6.23E-01	8.2	LYM103	12714.6	K	0.502	7.61E-01	5.3
LYM1	11602.6	J	0.068	6.34E-01	7.8	LYM51	11891.1	K	0.5	7.77E-01	4.8
LYM12	11872.1	J	0.068	6.36E-01	8	LYM239	13042.9	K	0.498	7.78E-01	4.5
LYM69	11852.2	J	0.068	6.55E-01	7.3	LYM24	12061.2	K	0.498	7.80E-01	4.5
LYM35	11811.3	J	0.068	6.90E-01	6.8	LYM116	13201.8	K	0.495	8.03E-01	3.9
LYM34	11903.2	J	0.068	7.08E-01	6.9	LYM66	11953.1	K	0.496	8.07E-01	3.9
LYM13	11771.6	J	0.067	7.11E-01	6.2	LYM271	12723.2	K	0.497	8.18E-01	4.3
LYM69	11851.2	J	0.066	7.59E-01	5.1	LYM277	13101.8	K	0.495	8.23E-01	3.9
LYM1	11601.1	J	0.065	8.32E-01	3.5	LYM125	12934.7	K	0.494	8.28E-01	3.6
LYM51	11893.4	J	0.065	8.37E-01	3.4	LYM121	13214.3	K	0.493	8.30E-01	3.4
LYM43	11791.4	J	0.065	8.52E-01	3.1	LYM88	12194.2	K	0.492	8.37E-01	3.2
LYM24	12061.2	J	0.065	8.93E-01	2.2	LYM20	11716.5	K	0.49	8.59E-01	2.8
LYM53	11844.2	J	0.064	9.21E-01	1.6	LYM57	12013.5	K	0.488	8.85E-01	2.3
LYM30	11913.4	J	0.064	9.24E-01	1.6	LYM66	11952.2	K	0.488	8.89E-01	2.4

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM15	11612.2	J	0.064	9.40E-01	1.3	LYM156	12961.9	K	0.487	8.92E-01	2.1
LYM21	11674.5	J	0.064	9.43E-01	1.2	LYM67	11783.5	K	0.485	9.13E-01	1.7
CONTROL	—	J	0.063	—	0	LYM232	13022.1	K	0.485	9.18E-01	1.8
LYM57	12012.4	K	0.724	2.06E-01	19.4	LYM67	11782.6	K	0.483	9.35E-01	1.3
LYM37	11803.2	K	0.711	2.92E-01	17.3	LYM145	12954.7	K	0.482	9.41E-01	1.2
LYM26	11824.6	K	0.699	3.16E-01	15.3	LYM125	12932.6	K	0.483	9.42E-01	1.4
LYM31	11921.3	K	0.696	3.36E-01	14.9	LYM125	12933.8	K	0.481	9.60E-01	0.8
LYM41	11831.1	K	0.695	3.63E-01	14.6	LYM285	12732.5	K	0.48	9.74E-01	0.6
LYM62	12023.7	K	0.684	4.19E-01	12.8	LYM156	12961.7	K	0.478	9.91E-01	0.2
LYM62	12023.2	K	0.699	4.20E-01	15.4	CONTROL	—	K	0.477	—	0
LYM37	11801.1	K	0.681	4.37E-01	12.4	LYM128	12641.5	L	2.449	2.11E-04	59.2
LYM35	11811.3	K	0.68	4.38E-01	12.2	LYM116	13202.12	L	2.375	4.83E-04	54.4
LYM69	11852.2	K	0.676	4.46E-01	11.6	LYM12	11872.1	L	2.465	7.52E-04	60.2
LYM16	11622.4	K	0.683	4.47E-01	12.6	LYM285	12733.9	L	2.38	9.95E-04	54.7
LYM21	11671.2	K	0.674	4.59E-01	11.1	LYM99	12243.1	L	2.246	1.78E-03	46
LYM53	11841.2	K	0.674	4.66E-01	11.1	LYM20	11711.2	L	2.203	4.00E-03	43.2
LYM24	12062.3	K	0.668	5.01E-01	10.2	LYM26	11824.1	L	2.171	5.72E-03	41.1
LYM51	11892.1	K	0.669	5.09E-01	10.3	LYM128	12641.3	L	2.156	5.90E-03	40.1
LYM10	11744.1	K	0.668	5.14E-01	10.1	LYM95	12121.2	L	2.155	1.11E-02	40.1
LYM34	11902.2	K	0.666	5.18E-01	9.9	LYM67	11782.6	L	2.107	1.18E-02	36.9
LYM14	12054.2	K	0.665	5.20E-01	9.7	LYM66	11954.4	L	2.091	1.19E-02	35.9
LYM67	11782.6	K	0.66	5.62E-01	8.9	LYM12	11871.1	L	2.088	2.29E-02	35.7
LYM9	11632.1	K	0.66	5.63E-01	8.9	LYM24	12061.4	L	2.044	2.38E-02	32.9
LYM15	11611.3	K	0.659	6.00E-01	8.7	LYM238	12764.8	L	2.035	2.46E-02	32.3
LYM4	11706.5	K	0.655	6.01E-01	8	LYM103	12713.5	L	2.065	2.84E-02	34.2
LYM12	11872.1	K	0.656	6.03E-01	8.3	LYM26	11824.3	L	2.01	2.91E-02	30.7

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM35	11812.3	K	0.655	6.07E-01	8	LYM26	11824.6	L	1.98	3.86E-02	28.7
LYM62	12022.4	K	0.651	6.30E-01	7.4	LYM239	13042.9	L	1.977	4.34E-02	28.5
LYM30	11912.6	K	0.649	6.64E-01	7	LYM53	11841.1	L	1.971	4.77E-02	28.1
LYM20	11716.5	K	0.646	6.74E-01	6.6	LYM88	12193.1	L	1.936	5.80E-02	25.8
LYM67	11781.5	K	0.643	6.97E-01	6	LYM116	13202.7	L	1.907	8.77E-02	24
LYM4	11702.3	K	0.64	7.22E-01	5.6	LYM232	13024.7	L	1.971	1.00E-01	28.1
LYM69	11851.2	K	0.639	7.23E-01	5.4	LYM69	11852.2	L	1.875	1.06E-01	21.9
LYM68	11942.2	K	0.64	7.29E-01	5.6	LYM31	11923.4	L	1.872	1.15E-01	21.7
LYM35	11812.4	K	0.643	7.31E-01	6	LYM82	12201.1	L	1.843	1.30E-01	19.8
LYM7	11592.1	K	0.64	7.32E-01	5.6	LYM95	12124.4	L	1.829	1.51E-01	18.9
LYM30	11913.4	K	0.641	7.33E-01	5.8	LYM103	12712.8	L	1.841	1.53E-01	19.6
LYM30	11913.3	K	0.638	7.35E-01	5.2	LYM30	11912.6	L	1.842	1.64E-01	19.7
LYM8	11982.6	K	0.638	7.37E-01	5.2	LYM14	12051.4	L	1.83	1.66E-01	18.9
LYM2	11692.3	K	0.641	7.40E-01	5.8	LYM26	11824.5	L	1.909	1.69E-01	24.1
LYM4	11702.1	K	0.634	7.62E-01	4.5	LYM31	11924.4	L	1.818	1.86E-01	18.2
LYM41	11832.2	K	0.631	7.80E-01	4.1	LYM12	11871.3	L	1.814	1.86E-01	17.9
LYM9	11633.2	K	0.634	7.80E-01	4.5	LYM24	12064.1	L	1.814	2.15E-01	17.9
LYM9	11634.5	K	0.63	8.00E-01	3.9	LYM156	12963.1	L	1.792	2.30E-01	16.4
LYM9	11632.2	K	0.63	8.04E-01	3.9	LYM232	13024.6	L	1.789	2.39E-01	16.2
LYM53	11842.4	K	0.631	8.07E-01	4.1	LYM67	11782.4	L	1.786	2.40E-01	16.1
LYM68	11941.3	K	0.629	8.08E-01	3.7	LYM116	13204.4	L	1.859	2.45E-01	20.8
LYM13	11771.9	K	0.629	8.13E-01	3.7	LYM99	12244.2	L	1.772	2.57E-01	15.2
LYM57	12012.2	K	0.626	8.34E-01	3.3	LYM239	13044.8	L	1.776	2.66E-01	15.4
LYM21	11674.1	K	0.624	8.48E-01	2.9	LYM26	11821.2	L	1.773	2.99E-01	15.3
LYM34	11902.4	K	0.624	8.48E-01	2.9	LYM20	11716.5	L	1.749	3.04E-01	13.7
LYM41	11833.1	K	0.624	8.52E-01	2.9	LYM128	12641.1	L	1.763	3.04E-01	14.6

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM1	11604.4	K	0.62	8.86E-01	2.3	LYM53	11843.2	L	1.746	3.06E-01	13.5
LYM9	11633.7	K	0.62	8.87E-01	2.3	LYM66	11955.2	L	1.74	3.08E-01	13.1
LYM17	11683.1	K	0.619	8.89E-01	2.1	LYM62	12023.2	L	1.735	3.31E-01	12.7
LYM15	11614.4	K	0.618	9.03E-01	1.9	LYM88	12194.2	L	1.681	4.65E-01	9.3
LYM20	11716.3	K	0.618	9.05E-01	1.9	LYM43	11791.4	L	1.687	4.68E-01	9.6
LYM62	12022.2	K	0.616	9.13E-01	1.7	LYM12	11873.4	L	1.658	5.55E-01	7.8
LYM4	11705.2	K	0.616	9.15E-01	1.7	LYM30	11913.5	L	1.667	5.55E-01	8.3
LYM21	11674.5	K	0.615	9.26E-01	1.5	LYM30	11912.7	L	1.652	5.73E-01	7.4
LYM26	11824.3	K	0.615	9.27E-01	1.5	LYM30	11913.4	L	1.644	6.15E-01	6.8
LYM69	11854.2	K	0.615	9.30E-01	1.5	LYM103	12711.8	L	1.637	6.20E-01	6.4
LYM67	11783.4	K	0.611	9.57E-01	0.8	LYM43	11793.2	L	1.645	6.21E-01	6.9
LYM37	11801.2	K	0.611	9.57E-01	0.8	LYM99	12243.2	L	1.628	6.46E-01	5.8
LYM67	11782.5	K	0.61	9.67E-01	0.6	LYM66	11953.6	L	1.627	6.52E-01	5.7
LYM62	12023.4	K	0.61	9.70E-01	0.6	LYM103	12712.5	L	1.629	6.58E-01	5.9
LYM7	11594.2	K	0.61	9.70E-01	0.6	LYM285	12734.9	L	1.608	7.44E-01	4.5
LYM16	11624.4	K	0.609	9.77E-01	0.4	LYM145	12951.9	L	1.593	7.83E-01	3.5
LYM7	11591.5	K	0.609	9.79E-01	0.4	LYM103	12714.6	L	1.595	8.01E-01	3.7
LYM31	11922.3	K	0.608	9.89E-01	0.2	LYM62	12023.5	L	1.586	8.08E-01	3.1
LYM8	11984.1	K	0.606	1.00E+00	0	LYM238	12762.8	L	1.587	8.13E-01	3.1
CONTROL	—	K	0.606	—	0	LYM43	11791.5	L	1.576	8.47E-01	2.4
LYM9	11632.1	L	4.464	4.79E-02	36.6	LYM156	12961.9	L	1.57	8.76E-01	2
LYM10	11744.1	L	4.166	1.32E-01	27.5	LYM57	12012.2	L	1.551	9.48E-01	0.8
LYM53	11842.4	L	4.036	2.03E-01	23.5	LYM20	11716.3	L	1.551	9.50E-01	0.8
LYM1	11604.4	L	4.026	2.08E-01	23.2	LYM24	12062.3	L	1.546	9.69E-01	0.5
LYM57	12012.6	L	3.962	2.47E-01	21.3	CONTROL	—	L	1.539	—	0
LYM14	12051.4	L	3.941	2.56E-01	20.6	LYM128	12641.5	M	0.306	5.45E-04	53.9

Gene name	**Event**	**ID**	**Mean**	**P value**	**%** ***incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	**%** ***incr. vs. cont.***
LYM57	12013.1	L	3.929	2.56E-01	20.2	LYM116	13202.12	M	0.297	1.21E-03	49.2
LYM35	11812.3	L	3.814	3.35E-01	16.7	LYM12	11872.1	M	0.308	1.61E-03	54.8
LYM30	11912.6	L	3.736	4.19E-01	14.3	LYM285	12733.9	M	0.298	2.23E-03	49.5
LYM31	11924.4	L	3.738	4.20E-01	14.4	LYM99	12243.1	M	0.281	4.33E-03	41.1
LYM57	12012.4	L	3.713	4.26E-01	13.6	LYM20	11711.2	M	0.275	8.94E-03	38.4
LYM35	11811.3	L	3.73	4.30E-01	14.2	LYM26	11824.1	M	0.271	1.25E-02	36.4
LYM1	11603.2	L	3.705	4.48E-01	13.4	LYM128	12641.3	M	0.269	1.31E-02	35.4
LYM9	11633.7	L	3.674	4.69E-01	12.4	LYM95	12121.2	M	0.269	2.19E-02	35.4
LYM51	11891.1	L	3.68	4.70E-01	12.6	LYM67	11782.6	M	0.263	2.45E-02	32.3
LYM35	11813.5	L	3.677	4.70E-01	12.5	LYM66	11954.4	M	0.261	2.53E-02	31.3
LYM34	11902.2	L	3.687	4.71E-01	12.8	LYM12	11871.1	M	0.261	4.25E-02	31.2
LYM1	11602.6	L	3.671	4.75E-01	12.3	LYM24	12061.4	M	0.256	4.64E-02	28.4
LYM69	11852.2	L	3.634	5.13E-01	11.2	LYM238	12764.8	M	0.254	4.83E-02	27.8
LYM34	11903.2	L	3.605	5.97E-01	10.3	LYM103	12713.5	M	0.258	5.18E-02	29.7
LYM13	11771.9	L	3.541	6.32E-01	8.4	LYM26	11824.3	M	0.251	5.70E-02	26.3
LYM10	11741.2	L	3.518	6.56E-01	7.7	LYM26	11824.6	M	0.248	7.39E-02	24.4
LYM12	11872.1	L	3.507	6.78E-01	7.3	LYM239	13042.9	M	0.247	8.11E-02	24.2
LYM14	12051.1	L	3.504	6.80E-01	7.2	LYM53	11841.1	M	0.246	8.78E-02	23.8
LYM7	11594.2	L	3.493	6.89E-01	6.9	LYM88	12193.1	M	0.242	1.07E-01	21.6
LYM31	11923.4	L	3.441	7.61E-01	5.3	LYM116	13202.7	M	0.238	1.51E-01	19.8
LYM2	11695.1	L	3.433	7.69E-01	5.1	LYM232	13024.7	M	0.246	1.54E-01	23.8
LYM68	11942.3	L	3.44	7.72E-01	5.3	LYM69	11852.2	M	0.234	1.83E-01	17.8
LYM30	11913.4	L	3.435	7.78E-01	5.1	LYM31	11923.4	M	0.234	1.95E-01	17.6
LYM51	11893.4	L	3.402	8.13E-01	4.1	LYM82	12201.1	M	0.23	2.22E-01	15.8
LYM69	11851.2	L	3.391	8.26E-01	3.8	LYM26	11824.5	M	0.239	2.44E-01	19.9
LYM21	11674.5	L	3.385	8.32E-01	3.6	LYM103	12712.8	M	0.23	2.49E-01	15.6

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM66	11953.6	L	3.366	8.62E-01	3	LYM95	12124.4	M	0.229	2.51E-01	14.9
LYM1	11601.1	L	3.336	9.04E-01	2.1	LYM30	11912.6	M	0.23	2.60E-01	15.7
LYM13	11771.6	L	3.324	9.20E-01	1.7	LYM14	12051.4	M	0.229	2.67E-01	14.9
LYM24	12061.2	L	3.304	9.49E-01	1.1	LYM31	11924.4	M	0.227	2.94E-01	14.2
LYM1	11602.1	L	3.288	9.72E-01	0.6	LYM12	11871.3	M	0.227	2.96E-01	14
LYM7	11592.1	L	3.269	9.97E-01	0.1	LYM24	12064.1	M	0.227	3.27E-01	14
CONTROL	—	L	3.268	—	0	LYM116	13204.4	M	0.232	3.38E-01	16.8
LYM9	11632.1	M	0.558	5.61E-02	34.5	LYM156	12963.1	M	0.224	3.54E-01	12.6
LYM10	11744.1	M	0.521	1.52E-01	25.5	LYM232	13024.6	M	0.224	3.65E-01	12.4
LYM53	11842.4	M	0.505	2.31E-01	21.6	LYM67	11782.4	M	0.223	3.66E-01	12.2
LYM1	11604.4	M	0.503	2.37E-01	21.3	LYM99	12244.2	M	0.222	3.92E-01	11.3
LYM30	11912.6	M	0.498	2.52E-01	20.1	LYM239	13044.8	M	0.222	3.98E-01	11.6
LYM57	12012.6	M	0.495	2.79E-01	19.4	LYM26	11821.2	M	0.222	4.31E-01	11.4
LYM14	12051.4	M	0.493	2.90E-01	18.8	LYM128	12641.1	M	0.22	4.42E-01	10.8
LYM57	12013.1	M	0.491	2.91E-01	18.4	LYM20	11716.5	M	0.219	4.53E-01	9.9
LYM35	11812.3	M	0.477	3.79E-01	14.9	LYM53	11843.2	M	0.218	4.57E-01	9.7
LYM31	11924.4	M	0.467	4.69E-01	12.6	LYM66	11955.2	M	0.218	4.64E-01	9.3
LYM57	12012.4	M	0.464	4.78E-01	11.9	LYM62	12023.2	M	0.217	4.90E-01	9
LYM35	11811.3	M	0.466	4.79E-01	12.4	LYM43	11791.4	M	0.211	6.50E-01	6
LYM1	11603.2	M	0.463	5.00E-01	11.7	LYM88	12194.2	M	0.21	6.56E-01	5.6
LYM51	11891.1	M	0.46	5.23E-01	10.9	LYM30	11913.5	M	0.208	7.36E-01	4.7
LYM9	11633.7	M	0.459	5.24E-01	10.7	LYM12	11873.4	M	0.207	7.49E-01	4.2
LYM34	11902.2	M	0.461	5.24E-01	11.1	LYM30	11912.7	M	0.207	7.70E-01	3.8
LYM35	11813.5	M	0.46	5.24E-01	10.8	LYM43	11793.2	M	0.206	8.08E-01	3.4
LYM1	11602.6	M	0.459	5.29E-01	10.6	LYM30	11913.4	M	0.205	8.09E-01	3.3
LYM69	11852.2	M	0.454	5.70E-01	9.5	LYM103	12711.8	M	0.205	8.25E-01	2.8

Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*
LYM34	11903.2	M	0.451	6.52E-01	8.6	LYM238	12763.7	M	0.204	8.41E-01	2.5
LYM13	11771.9	M	0.443	6.95E-01	6.7	LYM99	12243.2	M	0.204	8.56E-01	2.3
LYM10	11741.2	M	0.44	7.21E-01	6	LYM103	12712.5	M	0.204	8.60E-01	2.3
LYM12	11872.1	M	0.438	7.42E-01	5.7	LYM66	11953.6	M	0.203	8.63E-01	2.2
LYM14	12051.1	M	0.438	7.44E-01	5.6	LYM285	12734.9	M	0.201	9.42E-01	1
LYM7	11594.2	M	0.437	7.55E-01	5.3	LYM31	11921.3	M	0.2	9.69E-01	0.5
LYM31	11923.4	M	0.43	8.29E-01	3.7	LYM103	12714.6	M	0.199	9.90E-01	0.2
LYM68	11942.3	M	0.43	8.37E-01	3.7	LYM145	12951.9	M	0.199	9.95E-01	0.1
LYM2	11695.1	M	0.429	8.38E-01	3.5	CONTROL	—	M	0.199	—	0
LYM30	11913.4	M	0.429	8.44E-01	3.5	LYM116	13202.12	N	0.255	2.10E-05	39.1
LYM51	11893.4	M	0.425	8.82E-01	2.5	LYM12	11872.1	N	0.263	2.76E-04	43.6
LYM69	11851.2	M	0.424	8.97E-01	2.2	LYM128	12641.5	N	0.241	3.00E-04	31.6
LYM21	11674.5	M	0.423	9.04E-01	2	LYM20	11711.2	N	0.234	6.41E-04	28
LYM66	11953.6	M	0.421	9.33E-01	1.4	LYM238	12764.8	N	0.236	7.16E-04	29.2
LYM1	11601.1	M	0.417	9.76E-01	0.5	LYM26	11824.1	N	0.234	1.33E-03	28
LYM13	11771.6	M	0.415	9.93E-01	0.2	LYM128	12641.3	N	0.232	1.75E-03	26.7
CONTROL	—	M	0.415	—	0	LYM103	12713.5	N	0.231	2.00E-03	26.5
LYM9	11632.1	N	0.364	3.31E-01	10.1	LYM24	12061.4	N	0.227	3.42E-03	24.1
LYM30	11912.6	N	0.363	3.56E-01	9.8	LYM232	13024.6	N	0.228	3.85E-03	24.4
LYM53	11842.4	N	0.363	3.57E-01	10.1	LYM285	12733.9	N	0.229	4.57E-03	25
LYM57	12012.4	N	0.357	4.27E-01	8.1	LYM26	11824.3	N	0.226	4.79E-03	23.5
LYM35	11813.5	N	0.356	4.55E-01	7.8	LYM66	11954.4	N	0.224	5.52E-03	22.5
LYM35	11811.3	N	0.357	4.59E-01	8.1	LYM239	13042.9	N	0.226	5.90E-03	23.3
LYM57	12013.1	N	0.355	4.83E-01	7.5	LYM30	11912.6	N	0.227	6.07E-03	24
LYM14	12051.4	N	0.352	5.51E-01	6.5	LYM128	12641.1	N	0.225	9.15E-03	23.1
LYM9	11633.7	N	0.349	5.80E-01	5.6	LYM116	13202.7	N	0.221	1.09E-02	20.9

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM57	12012.6	N	0.349	5.90E-01	5.8	LYM31	11924.4	N	0.221	1.24E-02	21
LYM43	11791.4	N	0.347	6.19E-01	5.2	LYM12	11871.1	N	0.226	1.29E-02	23.3
LYM68	11942.3	N	0.348	6.27E-01	5.5	LYM14	12051.4	N	0.22	1.51E-02	20.4
LYM31	11924.4	N	0.346	6.55E-01	4.8	LYM24	12064.1	N	0.226	1.54E-02	23.5
LYM34	11902.2	N	0.345	6.78E-01	4.4	LYM103	12712.8	N	0.219	1.66E-02	19.4
LYM51	11891.1	N	0.344	6.78E-01	4.2	LYM53	11841.1	N	0.219	1.67E-02	19.7
LYM10	11744.1	N	0.344	6.92E-01	4.2	LYM95	12121.2	N	0.22	1.74E-02	20.4
LYM66	11953.6	N	0.341	7.64E-01	3.2	LYM30	11913.5	N	0.224	1.83E-02	22.5
LYM1	11604.4	N	0.34	7.75E-01	3.1	LYM31	11923.4	N	0.217	2.07E-02	18.9
LYM37	11801.1	N	0.339	8.01E-01	2.5	LYM232	13024.7	N	0.235	2.12E-02	28.2
LYM13	11771.9	N	0.338	8.16E-01	2.5	LYM99	12243.1	N	0.22	2.16E-02	20.1
LYM7	11594.2	N	0.337	8.44E-01	2.1	LYM239	13044.8	N	0.217	2.68E-02	18.4
LYM1	11603.2	N	0.337	8.51E-01	2	LYM26	11824.6	N	0.217	2.69E-02	18.4
LYM13	11771.6	N	0.336	8.71E-01	1.7	LYM116	13204.4	N	0.233	2.78E-02	27.6
LYM35	11812.3	N	0.336	8.72E-01	1.7	LYM12	11871.3	N	0.218	3.06E-02	18.9
LYM9	11633.2	N	0.335	8.86E-01	1.5	LYM67	11782.6	N	0.215	3.30E-02	17.4
LYM69	11852.2	N	0.333	9.38E-01	0.8	LYM53	11843.2	N	0.212	4.67E-02	15.7
LYM12	11872.1	N	0.333	9.45E-01	0.8	LYM103	12712.5	N	0.212	5.01E-02	16.1
LYM35	11811.2	N	0.331	9.70E-01	0.4	LYM30	11913.4	N	0.213	5.21E-02	16.1
LYM34	11903.2	N	0.331	9.79E-01	0.3	LYM88	12193.1	N	0.211	5.46E-02	15.1
CONTROL	—	N	0.33	—	0	LYM238	12762.8	N	0.211	5.60E-02	15.4
LYM9	11632.1	O	4.239	1.94E-04	34.8	LYM12	11873.4	N	0.211	5.78E-02	15.1
LYM30	11912.6	O	3.754	6.17E-03	19.4	LYM26	11821.2	N	0.215	6.72E-02	17.8
LYM57	12013.1	O	3.697	1.13E-02	17.5	LYM69	11852.2	N	0.21	6.75E-02	14.7
LYM35	11812.3	O	3.65	1.50E-02	16	LYM285	12734.9	N	0.212	7.54E-02	16.1
LYM10	11744.1	O	3.955	1.30E-01	25.7	LYM26	11824.5	N	0.222	7.68E-02	21.1

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM57	12012.4	O	3.453	1.41E-01	9.8	LYM156	12961.9	N	0.208	7.99E-02	13.9
LYM35	11813.5	O	3.499	1.51E-01	11.2	LYM43	11791.4	N	0.208	8.13E-02	13.6
LYM10	11741.2	O	3.37	2.00E-01	7.1	LYM99	12244.2	N	0.207	8.64E-02	13.3
LYM9	11633.7	O	3.495	2.27E-01	11.1	LYM238	12763.7	N	0.205	1.20E-01	12
LYM69	11852.2	O	3.439	2.27E-01	9.3	LYM156	12963.1	N	0.208	1.24E-01	13.5
LYM1	11602.6	O	3.496	2.38E-01	11.1	LYM82	12201.1	N	0.204	1.29E-01	11.7
LYM1	11603.2	O	3.531	3.22E-01	12.2	LYM95	12124.4	N	0.204	1.34E-01	11.7
LYM14	12051.4	O	3.735	3.69E-01	18.7	LYM20	11716.5	N	0.204	1.46E-01	11.3
LYM1	11604.4	O	3.818	3.73E-01	21.4	LYM31	11921.3	N	0.203	1.70E-01	10.9
LYM51	11891.1	O	3.476	3.93E-01	10.5	LYM145	12951.9	N	0.202	1.80E-01	10.4
LYM53	11842.4	O	3.795	4.20E-01	20.6	LYM30	11912.7	N	0.202	1.85E-01	10.1
LYM57	12012.6	O	3.747	4.88E-01	19.1	LYM67	11782.4	N	0.203	2.23E-01	11.2
LYM31	11924.4	O	3.531	5.00E-01	12.2	LYM20	11712.2	N	0.203	2.24E-01	10.7
LYM34	11902.2	O	3.485	5.50E-01	10.8	LYM285	12734.7	N	0.2	2.27E-01	9.4
LYM13	11771.9	O	3.342	5.66E-01	6.2	LYM103	12714.6	N	0.204	2.42E-01	11.7
LYM14	12051.1	O	3.331	5.99E-01	5.9	LYM20	11716.3	N	0.2	2.43E-01	9.3
LYM35	11811.3	O	3.519	6.11E-01	11.9	LYM62	12023.2	N	0.2	2.46E-01	9.3
LYM21	11674.5	O	3.232	6.76E-01	2.8	LYM66	11953.6	N	0.197	3.17E-01	7.7
LYM2	11695.1	O	3.246	7.85E-01	3.2	LYM238	12763.5	N	0.197	3.17E-01	7.7
LYM34	11903.2	O	3.419	8.15E-01	8.7	LYM232	13024.5	N	0.197	3.18E-01	7.7
LYM12	11872.1	O	3.289	8.23E-01	4.5	LYM24	12062.3	N	0.197	3.20E-01	7.7
LYM7	11594.2	O	3.258	8.24E-01	3.6	LYM239	13044.7	N	0.197	3.34E-01	7.9
LYM31	11923.4	O	3.264	8.39E-01	3.8	LYM57	12012.2	N	0.196	3.40E-01	7.3
LYM69	11851.2	O	3.187	8.50E-01	1.3	LYM103	12711.8	N	0.195	4.17E-01	6.4
LYM51	11893.4	O	3.221	8.73E-01	2.4	LYM53	11842.4	N	0.194	4.55E-01	5.8
LYM30	11913.4	O	3.255	8.86E-01	3.5	LYM88	12194.2	N	0.193	4.99E-01	5.2

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM68	11942.3	O	3.252	8.86E-01	3.4	LYM145	12954.8	N	0.194	5.03E-01	6.2
LYM66	11953.6	O	3.186	9.10E-01	1.3	LYM121	13212.6	N	0.193	5.34E-01	5.4
LYM1	11601.1	O	3.172	9.52E-01	0.8	LYM232	13024.4	N	0.194	5.39E-01	6.1
LYM13	11771.6	O	3.151	9.76E-01	0.2	LYM67	11782.5	N	0.19	5.94E-01	4.1
CONTROL	—	O	3.146	—	0	LYM43	11793.2	N	0.192	5.99E-01	4.7
LYM9	11632.1	P	3.799	3.19E-03	12.7	LYM145	12954.7	N	0.192	6.07E-01	4.8
LYM10	11744.1	P	3.642	4.04E-02	8	LYM277	13103.1	N	0.19	6.17E-01	3.9
LYM57	12012.4	P	3.618	9.72E-02	7.3	LYM121	13211.8	N	0.19	6.20E-01	3.8
LYM30	11912.6	P	3.638	1.05E-01	7.9	LYM53	11844.2	N	0.189	6.49E-01	3.5
LYM9	11633.7	P	3.554	1.21E-01	5.4	LYM128	12642.1	N	0.19	6.64E-01	3.8
LYM35	11813.5	P	3.611	1.25E-01	7.1	LYM20	11711.3	N	0.189	6.73E-01	3.3
LYM35	11812.3	P	3.533	1.68E-01	4.8	LYM238	12761.6	N	0.19	6.91E-01	3.7
LYM57	12013.1	P	3.581	1.87E-01	6.2	LYM66	11955.2	N	0.188	7.07E-01	2.9
LYM53	11842.4	P	3.713	3.40E-01	10.1	LYM41	11831.5	N	0.188	7.21E-01	2.7
LYM14	12051.4	P	3.67	3.72E-01	8.9	LYM239	13041.7	N	0.188	7.27E-01	2.8
LYM1	11603.2	P	3.508	4.36E-01	4.1	LYM145	12952.9	N	0.189	7.54E-01	3.5
LYM35	11811.3	P	3.641	4.94E-01	8	LYM41	11834.2	N	0.188	7.59E-01	2.7
LYM51	11891.1	P	3.47	5.07E-01	2.9	LYM277	13101.1	N	0.186	8.04E-01	1.9
LYM13	11771.9	P	3.469	5.23E-01	2.9	LYM24	12063.3	N	0.186	8.26E-01	1.8
LYM57	12012.6	P	3.6	5.25E-01	6.8	LYM99	12243.2	N	0.185	8.58E-01	1.4
LYM1	11604.4	P	3.57	5.61E-01	5.9	LYM239	13041.1	N	0.186	8.59E-01	1.6
LYM31	11924.4	P	3.505	5.77E-01	4	LYM43	11791.5	N	0.185	8.70E-01	1.2
LYM34	11902.2	P	3.484	6.13E-01	3.3	LYM156	12961.7	N	0.185	9.12E-01	0.9
LYM37	11801.1	P	3.43	6.41E-01	1.7	LYM31	11923.1	N	0.185	9.12E-01	0.9
LYM1	11602.6	P	3.472	6.46E-01	3	LYM62	12023.5	N	0.184	9.24E-01	0.7
LYM13	11771.6	P	3.42	6.49E-01	1.4	LYM156	12963.4	N	0.185	9.26E-01	1

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM7	11594.2	P	3.454	7.12E-01	2.4	LYM116	13201.8	N	0.184	9.37E-01	0.6
LYM68	11942.3	P	3.496	7.55E-01	3.7	LYM41	11832.2	N	0.184	9.65E-01	0.4
LYM14	12051.1	P	3.422	7.70E-01	1.5	LYM110	12924.5	N	0.183	9.85E-01	0.2
LYM12	11872.1	P	3.447	8.61E-01	2.2	CONTROL	—	N	0.183	—	0
LYM43	11791.4	P	3.388	8.73E-01	0.5	LYM116	13202.12	O	2.289	9.00E-06	42.6
LYM34	11903.2	P	3.431	9.24E-01	1.8	LYM88	12193.1	O	1.96	6.36E-04	22.1
LYM35	11811.2	P	3.39	9.29E-01	0.5	LYM20	11711.2	O	2.141	2.08E-03	33.4
LYM69	11852.2	P	3.381	9.42E-01	0.3	LYM53	11841.1	O	1.955	4.31E-03	21.8
LYM30	11913.4	P	3.387	9.73E-01	0.4	LYM67	11782.6	O	2.097	4.70E-03	30.6
CONTROL	—	P	3.372	—	0	LYM31	11923.4	O	1.855	4.75E-03	15.6
LYM128	12641.3	A	93.331	6.75E-03	3.8	LYM82	12201.1	O	1.863	2.54E-02	16.1
LYM90	12393.2	A	93.321	6.94E-03	3.8	LYM26	11824.3	O	1.919	3.12E-02	19.6
LYM86	12183.1	A	93.089	9.82E-03	3.5	LYM238	12764.8	O	1.942	3.40E-02	21
LYM89	12211.4	A	92.845	1.42E-02	3.2	LYM12	11871.3	O	1.754	6.30E-02	9.3
LYM149	12343.1	A	92.942	1.62E-02	3.4	LYM128	12641.5	O	2.376	6.82E-02	48.1
LYM157	13341.7	A	94.877	1.64E-02	5.5	LYM99	12243.1	O	2.287	8.62E-02	42.5
LYM178	12163.4	A	92.918	1.64E-02	3.3	LYM26	11824.1	O	2.088	9.91E-02	30.1
LYM90	12393.1	A	92.555	2.23E-02	2.9	LYM128	12641.3	O	2.096	1.04E-01	30.6
LYM128	12642.3	A	92.517	2.39E-02	2.9	LYM99	12244.2	O	1.757	1.07E-01	9.5
LYM99	12243.2	A	92.543	2.43E-02	2.9	LYM88	12194.2	O	1.705	1.51E-01	6.2
LYM206	12601.3	A	93.451	2.44E-02	3.9	LYM239	13042.9	O	1.915	1.56E-01	19.3
LYM129	12573.5	A	92.522	2.60E-02	2.9	LYM53	11843.2	O	1.719	1.75E-01	7.1
LYM107	12631.4	A	92.899	2.65E-02	3.3	LYM285	12733.9	O	2.366	1.77E-01	47.4
LYM86	12182.3	A	93.033	2.93E-02	3.5	LYM26	11824.6	O	1.955	1.91E-01	21.8
LYM128	12641.1	A	92.897	2.99E-02	3.3	LYM24	12061.4	O	1.984	1.96E-01	23.6
LYM178	12163.3	A	92.504	3.08E-02	2.9	LYM103	12713.5	O	2.029	2.03E-01	26.4

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM149	12344.2	A	92.323	3.24E-02	2.7	LYM66	11954.4	O	2.063	2.20E-01	28.5
LYM73	12623.2	A	92.762	3.28E-02	3.2	LYM12	11872.1	O	2.394	2.31E-01	49.2
LYM6	11735.1	A	92.326	3.43E-02	2.7	LYM116	13202.7	O	1.815	2.36E-01	13.1
LYM86	12181.3	A	93.242	4.14E-02	3.7	LYM95	12124.4	O	1.814	2.85E-01	13
LYM250	12613.2	A	92.215	4.16E-02	2.5	LYM31	11924.4	O	1.785	3.22E-01	11.2
LYM250	12613.4	A	92.165	4.20E-02	2.5	LYM20	11716.5	O	1.708	3.22E-01	6.4
LYM89	12214.2	A	92.355	4.43E-02	2.7	LYM66	11955.2	O	1.765	3.26E-01	10
LYM90	12395.3	A	92.938	4.47E-02	3.4	LYM95	12121.2	O	2.142	3.32E-01	33.5
LYM86	12183.3	A	92.937	4.54E-02	3.4	LYM12	11871.1	O	2.03	3.52E-01	26.5
LYM157	13341.4	A	92.35	4.58E-02	2.7	LYM69	11852.2	O	1.815	3.82E-01	13.1
LYM129	12573.3	A	92.84	4.79E-02	3.2	LYM14	12051.4	O	1.782	4.01E-01	11
LYM6	11734.3	A	92.288	5.09E-02	2.6	LYM103	12712.8	O	1.759	5.04E-01	9.6
LYM256	13322.3	A	92.641	6.65E-02	3	LYM239	13044.8	O	1.735	5.52E-01	8.1
LYM157	13342.4	A	94.106	7.45E-02	4.7	LYM67	11782.4	O	1.775	5.69E-01	10.6
LYM88	12191.2	A	91.953	7.61E-02	2.3	LYM43	11791.4	O	1.669	5.91E-01	4
LYM99	12244.1	A	93.509	7.70E-02	4	LYM30	11912.7	O	1.639	5.96E-01	2.1
LYM178	12164.3	A	91.816	8.24E-02	2.1	LYM30	11912.6	O	1.736	6.07E-01	8.1
LYM250	12614.1	A	91.729	8.76E-02	2	LYM232	13024.7	O	1.926	6.15E-01	20
LYM90	12395.1	A	93.165	8.97E-02	3.6	LYM62	12023.2	O	1.685	6.23E-01	5
LYM91	13283.4	A	91.631	1.00E-01	1.9	LYM232	13024.6	O	1.686	6.28E-01	5.1
LYM178	12161.2	A	92.239	1.02E-01	2.6	LYM66	11953.6	O	1.635	6.53E-01	1.9
LYM129	12571.3	A	91.667	1.10E-01	1.9	LYM156	12963.1	O	1.711	6.79E-01	6.6
LYM256	13323.3	A	93.178	1.29E-01	3.6	LYM26	11824.5	O	1.866	6.82E-01	16.3
LYM107	12633.4	A	91.472	1.31E-01	1.7	LYM128	12641.1	O	1.684	7.51E-01	4.9
LYM91	13283.1	A	93.948	1.50E-01	4.5	LYM24	12064.1	O	1.711	7.64E-01	6.6
LYM88	12193.1	A	91.377	1.54E-01	1.6	LYM26	11821.2	O	1.706	7.79E-01	6.3

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM157	13341.1	A	93.647	1.57E-01	4.1	LYM116	13204.4	O	1.779	8.04E-01	10.8
LYM90	12392.1	A	92.786	1.71E-01	3.2	LYM99	12243.2	O	1.63	8.51E-01	1.6
LYM147	12583.3	A	91.846	1.98E-01	2.1	LYM43	11793.2	O	1.63	9.41E-01	1.6
LYM6	11735.2	A	92.319	2.06E-01	2.7	LYM30	11913.5	O	1.606	9.98E-01	0.1
LYM107	12631.2	A	92.349	2.08E-01	2.7	CONTROL	—	O	1.605	—	0
LYM250	12614.2	A	91.184	2.30E-01	1.4	LYM20	11711.2	P	2.438	2.52E-04	17.1
LYM283	13304.4	A	91.862	2.32E-01	2.2	LYM238	12764.8	P	2.357	1.15E-03	13.2
LYM147	12584.4	A	91.139	2.56E-01	1.4	LYM116	13202.12	P	2.552	3.04E-03	22.6
LYM99	12243.1	A	91.086	2.57E-01	1.3	LYM53	11841.1	P	2.338	3.08E-03	12.3
LYM88	12192.1	A	91.579	2.62E-01	1.8	LYM82	12201.1	P	2.294	5.04E-03	10.2
LYM283	13304.5	A	91.337	2.62E-01	1.6	LYM31	11923.4	P	2.284	6.11E-03	9.7
LYM73	12623.1	A	92.42	2.83E-01	2.8	LYM88	12193.1	P	2.393	7.93E-03	14.9
LYM147	12581.4	A	91.997	2.92E-01	2.3	LYM67	11782.6	P	2.393	1.64E-02	14.9
LYM89	12214.3	A	91.734	2.94E-01	2	LYM128	12641.5	P	2.579	3.82E-02	23.9
LYM283	13302.2	A	90.934	2.99E-01	1.1	LYM99	12244.2	P	2.243	4.31E-02	7.7
LYM256	13321.2	A	92.248	3.12E-01	2.6	LYM12	11871.3	P	2.21	4.39E-02	6.1
LYM159	13354.6	A	91.458	3.15E-01	1.7	LYM285	12733.9	P	2.538	4.87E-02	21.9
LYM129	12572.2	A	91.727	3.32E-01	2	LYM26	11824.3	P	2.31	5.40E-02	10.9
LYM178	12164.2	A	92.077	3.32E-01	2.4	LYM24	12061.4	P	2.344	5.96E-02	12.5
LYM88	12191.1	A	93.357	3.33E-01	3.8	LYM128	12641.3	P	2.412	6.15E-02	15.8
LYM250	12611.3	A	91.245	3.42E-01	1.5	LYM53	11843.2	P	2.23	6.53E-02	7.1
LYM283	13302.1	A	90.834	3.50E-01	1	LYM66	11954.4	P	2.443	6.54E-02	17.3
LYM91	13284.3	A	90.961	3.56E-01	1.2	LYM43	11791.4	P	2.211	6.54E-02	6.2
LYM147	12584.5	A	93.996	4.12E-01	4.5	LYM99	12243.1	P	2.582	9.80E-02	24
LYM159	13352.4	A	91.01	4.60E-01	1.2	LYM31	11924.4	P	2.269	1.13E-01	9
LYM283	13303.2	A	91.406	4.71E-01	1.6	LYM103	12713.5	P	2.421	1.17E-01	16.3

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM107	12632.1	A	91.645	4.88E-01	1.9	LYM88	12194.2	P	2.185	1.24E-01	4.9
LYM129	12572.4	A	90.878	5.03E-01	1.1	LYM26	11824.6	P	2.334	1.30E-01	12.1
LYM89	12214.4	A	93.157	5.04E-01	3.6	LYM66	11955.2	P	2.2	1.41E-01	5.6
LYM128	12642.2	A	91.558	5.33E-01	1.8	LYM12	11872.1	P	2.739	1.65E-01	31.5
LYM256	13321.3	A	91.538	5.33E-01	1.8	LYM116	13202.7	P	2.163	1.71E-01	3.9
LYM206	12603.3	A	91.15	5.58E-01	1.4	LYM95	12121.2	P	2.456	1.79E-01	17.9
LYM236	12592.3	A	91.439	5.75E-01	1.7	LYM26	11824.1	P	2.389	2.02E-01	14.7
LYM236	12594.3	A	91.377	6.02E-01	1.6	LYM12	11873.4	P	2.153	2.17E-01	3.4
LYM236	12592.4	A	90.999	6.25E-01	1.2	LYM239	13044.8	P	2.223	2.38E-01	6.7
LYM147	12583.1	A	90.912	6.62E-01	1.1	LYM66	11953.6	P	2.169	2.58E-01	4.2
LYM149	12341.1	A	91.327	6.71E-01	1.6	LYM239	13042.9	P	2.33	2.67E-01	11.9
LYM73	12622.2	A	91.911	6.73E-01	2.2	LYM232	13024.6	P	2.221	2.68E-01	6.6
LYM206	12601.2	A	90.459	7.06E-01	0.6	LYM12	11871.1	P	2.378	3.29E-01	14.2
LYM206	12603.1	A	90.27	7.13E-01	0.4	LYM95	12124.4	P	2.245	3.30E-01	7.8
LYM6	11733.2	A	90.249	7.32E-01	0.4	LYM14	12051.4	P	2.234	3.46E-01	7.3
LYM256	13324.2	A	90.178	7.88E-01	0.3	LYM30	11912.7	P	2.134	3.65E-01	2.5
LYM149	12341.3	A	90.221	7.91E-01	0.3	LYM62	12023.2	P	2.202	3.71E-01	5.7
LYM91	13284.4	A	90.429	8.53E-01	0.6	LYM103	12712.8	P	2.201	3.96E-01	5.7
LYM6	11736.1	A	90.297	9.04E-01	0.4	LYM20	11716.5	P	2.155	4.05E-01	3.5
LYM236	12593.4	A	90.02	9.77E-01	0.1	LYM69	11852.2	P	2.188	4.52E-01	5.1
LYM89	12211.2	A	89.955	9.84E-01	0	LYM30	11912.6	P	2.202	5.00E-01	5.7
CONTROL	—	A	89.923	—	0	LYM145	12951.9	P	2.117	5.23E-01	1.7
LYM99	12243.1	B	0.444	1.98E-03	23	LYM128	12641.1	P	2.19	5.43E-01	5.2
LYM178	12163.3	B	0.408	2.91E-02	13.1	LYM67	11782.4	P	2.221	5.46E-01	6.7
LYM283	13302.1	B	0.491	3.45E-02	36	LYM232	13024.7	P	2.366	5.92E-01	13.6
LYM159	13354.6	B	0.406	1.13E-01	12.6	LYM30	11913.5	P	2.21	6.02E-01	6.1

Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*
LYM129	12573.5	B	0.409	1.16E-01	13.3	LYM26	11824.5	P	2.268	6.14E-01	8.9
LYM250	12613.4	B	0.403	1.57E-01	11.6	LYM116	13204.4	P	2.292	6.62E-01	10.1
LYM178	12164.2	B	0.399	2.93E-01	10.5	LYM156	12961.9	P	2.106	6.63E-01	1.1
LYM236	12594.3	B	0.391	2.93E-01	8.4	LYM285	12734.9	P	2.189	6.81E-01	5.1
LYM89	12214.4	B	0.379	3.31E-01	5	LYM24	12064.1	P	2.182	6.92E-01	4.8
LYM6	11736.1	B	0.395	3.53E-01	9.5	LYM156	12963.1	P	2.138	7.88E-01	2.7
LYM91	13284.3	B	0.486	3.66E-01	34.6	LYM30	11913.4	P	2.119	8.02E-01	1.8
LYM88	12193.1	B	0.378	3.74E-01	4.6	LYM26	11821.2	P	2.139	8.11E-01	2.7
LYM283	13302.2	B	0.382	3.95E-01	5.8	LYM43	11793.2	P	2.119	8.47E-01	1.8
LYM206	12601.2	B	0.447	4.11E-01	23.9	LYM43	11791.5	P	2.096	8.52E-01	0.6
LYM91	13284.5	B	0.389	4.14E-01	7.9	LYM103	12712.5	P	2.085	9.78E-01	0.1
LYM236	12592.3	B	0.403	4.39E-01	11.7	CONTROL	—	P	2.082	—	0
LYM283	13304.4	B	0.491	4.67E-01	36	LYM289	12492.2	A	92.947	1.86E-01	1.4
LYM206	12603.1	B	0.39	4.67E-01	8.1	LYM255	13082.5	A	92.825	2.17E-01	1.3
LYM175	12651.2	B	0.442	4.72E-01	22.5	LYM173	12981.6	A	93.646	2.22E-01	2.2
LYM73	12623.2	B	0.425	4.91E-01	17.8	LYM106	12144.4	A	92.705	3.20E-01	1.2
LYM250	12611.3	B	0.429	4.98E-01	19	LYM212	13032.8	A	92.513	3.49E-01	1
LYM206	12603.3	B	0.39	4.98E-01	8.1	LYM102	12222.1	A	92.53	3.64E-01	1
LYM159	13352.4	B	0.396	5.08E-01	9.7	LYM61	13171.8	A	96.667	3.77E-01	5.5
LYM157	13342.4	B	0.374	5.11E-01	3.6	LYM220	12851.12	A	92.99	4.10E-01	1.5
LYM159	13354.5	B	0.412	5.21E-01	14.3	LYM111	12254.3	A	92.606	4.40E-01	1.1
LYM99	12243.2	B	0.451	5.34E-01	25.1	LYM287	12771.6	A	93.304	4.59E-01	1.8
LYM89	12211.2	B	0.454	5.40E-01	25.9	LYM212	13031.5	A	93.614	4.80E-01	2.2
LYM178	12163.4	B	0.388	5.58E-01	7.4	LYM106	12142.2	A	92.275	4.86E-01	0.7
LYM129	12573.3	B	0.393	5.67E-01	9	LYM138	12562.2	A	92.321	4.89E-01	0.8
LYM178	12164.3	B	0.448	5.70E-01	24.2	LYM119	12461.1	A	92.376	4.93E-01	0.8

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM107	12631.4	B	0.436	5.95E-01	20.9	LYM288	12743.8	A	92.288	5.05E-01	0.7
LYM250	12613.2	B	0.381	5.96E-01	5.7	LYM270	12871.7	A	92.601	5.14E-01	1.1
LYM178	12161.2	B	0.396	5.98E-01	9.7	LYM183	12993.7	A	92.209	5.32E-01	0.6
LYM107	12633.4	B	0.399	6.05E-01	10.7	LYM138	12562.1	A	92.298	5.80E-01	0.7
LYM149	12341.1	B	0.438	6.07E-01	21.4	LYM212	13031.6	A	92.757	5.96E-01	1.2
LYM149	12344.2	B	0.446	7.09E-01	23.7	LYM220	12852.2	A	92.225	6.15E-01	0.7
LYM147	12583.3	B	0.389	7.15E-01	7.9	LYM44	11885.4	A	92.076	6.37E-01	0.5
LYM129	12572.4	B	0.379	7.22E-01	5.2	LYM111	12251.1	A	92.235	6.39E-01	0.7
LYM88	12191.2	B	0.368	7.24E-01	1.9	LYM183	12993.5	A	92.276	6.42E-01	0.7
LYM236	12591.1	B	0.37	7.41E-01	2.6	LYM289	12491.1	A	92.318	6.45E-01	0.8
LYM159	13354.8	B	0.4	7.62E-01	10.9	LYM242	13053.7	A	92.383	6.48E-01	0.8
LYM147	12583.1	B	0.366	7.74E-01	1.5	LYM201	12833.9	A	92.111	6.51E-01	0.5
LYM175	12654.4	B	0.376	7.81E-01	4.2	LYM201	12833.7	A	92.164	6.53E-01	0.6
LYM147	12584.5	B	0.371	8.02E-01	2.9	LYM242	13051.8	A	92.232	6.65E-01	0.7
LYM256	13324.2	B	0.375	8.21E-01	3.9	LYM208	13014.7	A	92.484	6.76E-01	0.9
LYM250	12614.1	B	0.371	8.33E-01	2.7	LYM198	13002.8	A	92.042	6.93E-01	0.5
LYM6	11735.1	B	0.363	8.97E-01	0.6	LYM153	12323.2	A	91.983	7.00E-01	0.4
LYM91	13283.4	B	0.363	9.28E-01	0.6	LYM142	12802.7	A	92.044	7.19E-01	0.5
LYM73	12623.3	B	0.367	9.60E-01	1.7	LYM183	12994.8	A	92.015	7.24E-01	0.4
CONTROL	—	B	0.361	—	0	LYM142	12802.9	A	91.961	7.32E-01	0.4
LYM250	12613.4	C	4.506	3.98E-04	15.2	LYM61	13174.5	A	92.781	7.51E-01	1.3
LYM206	12601.2	C	4.463	1.11E-03	14.1	LYM107	12632.3	A	91.922	7.63E-01	0.3
LYM159	13354.6	C	4.331	2.97E-03	10.7	LYM291	12754.9	A	91.875	7.86E-01	0.3
LYM206	12603.3	C	4.438	3.26E-03	13.5	LYM201	12833.6	A	93.231	7.98E-01	1.8
LYM73	12623.2	C	4.3	4.40E-03	9.9	LYM44	11885.3	A	91.867	8.04E-01	0.3
LYM107	12633.4	C	4.356	5.15E-03	11.4	LYM130	12332.1	A	92.065	8.21E-01	0.5

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM178	12163.3	C	4.194	2.03E-02	7.2	LYM137	12153.1	A	91.968	8.65E-01	0.4
LYM250	12613.2	C	4.175	3.20E-02	6.7	LYM111	12254.4	A	91.877	8.89E-01	0.3
LYM88	12191.2	C	4.375	3.90E-02	11.9	LYM61	13172.4	A	92.025	8.90E-01	0.4
LYM159	13352.4	C	4.275	4.86E-02	9.3	LYM100	12134.1	A	91.757	8.94E-01	0.1
LYM91	13284.3	C	4.8	6.56E-02	22.7	LYM90	12392.1	A	91.79	9.06E-01	0.2
LYM206	12603.1	C	4.2	1.21E-01	7.4	LYM130	12333.1	A	91.91	9.11E-01	0.3
LYM236	12594.3	C	4.181	1.21E-01	6.9	LYM197	12824.4	A	91.779	9.37E-01	0.2
LYM178	12161.2	C	4.3	1.39E-01	9.9	LYM90	12394.2	A	91.691	9.53E-01	0.1
LYM90	12395.1	C	4.163	1.59E-01	6.4	LYM291	12753.6	A	91.669	9.65E-01	0
LYM175	12651.2	C	4.538	1.78E-01	16	LYM105	12293.1	A	91.657	9.77E-01	0
LYM99	12243.1	C	4.781	1.90E-01	22.2	LYM208	13013.6	A	91.663	9.84E-01	0
LYM157	13342.4	C	4.313	2.08E-01	10.3	LYM90	12393.4	A	91.627	9.99E-01	0
LYM236	12592.3	C	4.313	2.53E-01	10.3	CONTROL	—	A	91.624	—	0
LYM236	12591.1	C	4.075	2.73E-01	4.2	LYM152	12373.2	B	0.357	1.21E-03	50.4
LYM129	12573.5	C	4.219	2.73E-01	7.9	LYM102	12222.1	B	0.386	1.41E-03	62.7
LYM256	13321.2	C	4.188	3.23E-01	7.1	LYM174	12411.2	B	0.344	2.44E-03	44.8
LYM6	11735.1	C	4.144	3.41E-01	5.9	LYM111	12251.1	B	0.379	3.24E-03	59.8
LYM99	12241.1	C	4.013	3.48E-01	2.6	LYM100	12133.3	B	0.349	3.88E-03	47.2
LYM88	12193.1	C	4.138	3.66E-01	5.8	LYM106	12144.4	B	0.334	6.10E-03	40.6
LYM6	11736.1	C	4.638	3.77E-01	18.6	LYM107	12632.3	B	0.386	6.60E-03	62.7
LYM283	13304.4	C	4.569	3.87E-01	16.8	LYM174	12414.3	B	0.324	7.65E-03	36.4
LYM250	12611.3	C	4.569	4.20E-01	16.8	LYM102	12222.2	B	0.345	9.57E-03	45.4
LYM129	12572.4	C	4.319	4.24E-01	10.4	LYM107	12631.2	B	0.312	1.54E-02	31.4
LYM178	12163.4	C	4.266	4.25E-01	9.1	LYM102	12221.2	B	0.336	1.60E-02	41.4
LYM147	12583.3	C	4	4.32E-01	2.3	LYM105	12294.3	B	0.313	1.62E-02	31.7
LYM250	12614.1	C	4.331	4.39E-01	10.7	LYM143	12524.5	B	0.312	1.76E-02	31.4

Gene name	**Event**	**ID**	**Mean**	**P value**	*% incr. vs. cont.*	**Gene name**	**Event**	**ID**	**Mean**	**P value**	*% incr. vs. cont.*
LYM175	12654.4	C	4.178	4.45E-01	6.8	LYM100	12133.1	B	0.325	1.79E-02	36.9
LYM6	11733.2	C	4.113	4.62E-01	5.1	LYM198	13004.6	B	0.319	2.41E-02	34.3
LYM159	13354.5	C	4.515	4.68E-01	15.4	LYM137	12153.1	B	0.305	2.82E-02	28.5
LYM91	13283.4	C	4.144	4.87E-01	5.9	LYM107	12632.1	B	0.346	3.57E-02	45.6
LYM178	12164.3	C	4.481	5.11E-01	14.6	LYM111	12254.4	B	0.404	3.60E-02	70.4
LYM283	13302.1	C	4.231	5.82E-01	8.2	LYM105	12297.2	B	0.297	4.45E-02	25.1
LYM256	13323.3	C	3.988	6.15E-01	2	LYM137	12151.1	B	0.323	4.83E-02	36.1
LYM99	12243.2	C	4.238	6.45E-01	8.3	LYM143	12523.4	B	0.293	4.91E-02	23.2
LYM107	12631.4	C	4.1	6.53E-01	4.8	LYM111	12251.3	B	0.319	5.49E-02	34.6
LYM178	12164.2	C	4.031	6.82E-01	3.1	LYM106	12142.3	B	0.336	5.57E-02	41.4
LYM147	12584.5	C	4.069	6.98E-01	4	LYM220	12851.8	B	0.301	5.77E-02	26.9
LYM256	13324.2	C	4.013	7.05E-01	2.6	LYM102	12221.1	B	0.299	6.79E-02	26.1
LYM88	12192.1	C	3.988	7.11E-01	2	LYM174	12412.1	B	0.384	7.26E-02	61.7
LYM236	12592.4	C	4.138	7.17E-01	5.8	LYM137	12152.1	B	0.286	8.50E-02	20.3
LYM89	12211.2	C	4.094	7.24E-01	4.7	LYM137	12154.5	B	0.291	8.50E-02	22.4
LYM157	13341.4	C	4.05	7.44E-01	3.5	LYM143	12524.7	B	0.289	9.00E-02	21.7
LYM89	12214.4	C	3.956	7.54E-01	1.2	LYM138	12561.3	B	0.293	9.03E-02	23.2
LYM86	12181.2	C	3.988	7.84E-01	2	LYM102	12222.3	B	0.404	9.03E-02	70.1
LYM73	12622.2	C	4.063	8.04E-01	3.9	LYM142	12804.1	B	0.285	9.32E-02	20
LYM149	12344.2	C	4.244	8.12E-01	8.5	LYM105	12293.1	B	0.283	1.01E-01	19
LYM159	13354.8	C	4.031	8.41E-01	3.1	LYM107	12631.1	B	0.326	1.10E-01	37.5
LYM86	12183.3	C	3.944	8.67E-01	0.8	LYM212	13031.6	B	0.284	1.11E-01	19.6
LYM256	13322.3	C	3.925	9.00E-01	0.4	LYM291	12754.9	B	0.516	1.24E-01	117.5
LYM283	13302.2	C	3.925	9.20E-01	0.4	LYM105	12297.1	B	0.402	1.35E-01	69.3
LYM6	11735.2	C	3.931	9.33E-01	0.5	LYM138	12562.1	B	0.278	1.36E-01	17.2
CONTROL	—	C	3.911	—	0	LYM100	12131.2	B	0.35	1.42E-01	47.4

Gene name	Event	ID	Mean	P value	% incr. vs. cont.	Gene name	Event	ID	Mean	P value	% incr. vs. cont.
LYM107	12631.4	D	0.286	2.09E-03	30.2	LYM100	12131.3	B	0.3	1.45E-01	26.4
LYM236	12592.3	D	0.282	3.12E-03	28.3	LYM289	12491.1	B	0.348	1.51E-01	46.7
LYM147	12583.3	D	0.278	7.97E-03	26.3	LYM173	12982.7	B	0.326	1.56E-01	37.5
LYM129	12572.4	D	0.27	9.42E-03	22.7	LYM106	12144.3	B	0.351	1.59E-01	48
LYM6	11736.1	D	0.268	1.07E-02	22.1	LYM174	12414.2	B	0.384	1.60E-01	61.7
LYM178	12163.4	D	0.283	1.31E-02	28.9	LYM107	12633.4	B	0.372	1.75E-01	56.7
LYM89	12211.4	D	0.269	3.53E-02	22.3	LYM212	13032.8	B	0.304	1.89E-01	28.2
LYM73	12623.2	D	0.254	4.68E-02	15.5	LYM153	12324.2	B	0.271	1.90E-01	14.3
LYM90	12395.3	D	0.285	6.11E-02	29.5	LYM143	12521.1	B	0.303	1.91E-01	27.5
LYM99	12243.2	D	0.263	6.21E-02	19.6	LYM138	12561.1	B	0.319	1.91E-01	34.3
LYM88	12193.1	D	0.288	6.59E-02	30.9	LYM100	12134.1	B	0.298	1.91E-01	25.6
LYM206	12603.1	D	0.271	6.76E-02	23.2	LYM152	12371.3	B	0.311	2.03E-01	30.9
LYM250	12613.2	D	0.251	6.95E-02	14.5	LYM289	12493.2	B	0.281	2.03E-01	18.5
LYM90	12392.1	D	0.249	7.55E-02	13.5	LYM106	12142.2	B	0.451	2.04E-01	89.9
LYM86	12182.3	D	0.247	9.53E-02	12.5	LYM106	12141.4	B	0.427	2.09E-01	79.9
LYM90	12395.1	D	0.278	1.03E-01	26.4	LYM173	12982.6	B	0.34	2.21E-01	43.3
LYM147	12584.4	D	0.244	1.25E-01	11.2	LYM107	12631.4	B	0.503	2.37E-01	112.1
LYM178	12161.2	D	0.268	1.42E-01	22.2	LYM137	12151.4	B	0.337	2.43E-01	41.9
LYM236	12594.3	D	0.245	1.49E-01	11.3	LYM288	12744.7	B	0.319	2.48E-01	34.3
LYM128	12641.3	D	0.243	1.63E-01	10.8	LYM153	12324.1	B	0.376	2.54E-01	58.3
LYM178	12164.3	D	0.242	1.63E-01	10.3	LYM111	12254.3	B	0.275	2.65E-01	15.9
LYM206	12603.3	D	0.345	1.82E-01	57	LYM197	12824.4	B	0.34	2.66E-01	43.4
LYM159	13354.6	D	0.257	1.95E-01	16.9	LYM102	12222.6	B	0.528	2.70E-01	122.3
LYM73	12623.1	D	0.247	2.14E-01	12.5	LYM152	12371.2	B	0.323	2.76E-01	35.9
LYM159	13354.5	D	0.241	2.20E-01	9.8	LYM220	12851.12	B	0.266	2.76E-01	11.9
LYM129	12573.3	D	0.267	2.33E-01	21.4	LYM138	12566.1	B	0.296	2.78E-01	24.6

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM250	12613.4	D	0.326	2.36E-01	48.2	LYM198	13002.6	B	0.401	2.91E-01	68.8
LYM107	12633.4	D	0.321	2.54E-01	45.9	LYM173	12981.5	B	0.268	2.98E-01	13
LYM88	12191.2	D	0.285	2.57E-01	29.6	LYM142	12802.9	B	0.323	3.06E-01	36.1
LYM175	12651.2	D	0.241	2.65E-01	9.5	LYM44	11884.1	B	0.263	3.14E-01	10.6
LYM6	11735.1	D	0.298	2.86E-01	35.7	LYM143	12521.2	B	0.265	3.27E-01	11.7
LYM250	12614.1	D	0.24	2.88E-01	9.2	LYM152	12372.2	B	0.284	3.43E-01	19.7
LYM157	13341.4	D	0.235	3.14E-01	7.1	LYM288	12743.9	B	0.381	3.52E-01	60.6
LYM178	12163.3	D	0.274	3.28E-01	24.7	LYM173	12981.6	B	0.327	3.64E-01	37.7
LYM99	12243.1	D	0.298	3.29E-01	35.7	LYM111	12252.2	B	0.409	3.69E-01	72.2
LYM88	12194.2	D	0.242	3.37E-01	10	LYM111	12251.4	B	0.336	3.76E-01	41.7
LYM129	12573.5	D	0.286	3.40E-01	30	LYM289	12491.4	B	0.356	3.78E-01	50.1
LYM86	12183.3	D	0.235	3.42E-01	6.9	LYM198	13002.8	B	0.276	3.80E-01	16.1
LYM89	12214.2	D	0.283	3.49E-01	29	LYM119	12463.2	B	0.336	3.81E-01	41.4
LYM206	12601.2	D	0.332	3.68E-01	51	LYM105	12294.2	B	0.309	3.82E-01	30.3
LYM128	12642.3	D	0.254	4.14E-01	15.4	LYM255	13082.5	B	0.268	3.92E-01	12.7
LYM91	13284.3	D	0.257	4.24E-01	16.8	LYM142	12803.6	B	0.426	3.92E-01	79.3
LYM236	12591.1	D	0.27	4.45E-01	23	LYM105	12295.2	B	0.326	3.98E-01	37.5
LYM91	13283.1	D	0.231	4.60E-01	5	LYM208	13013.6	B	0.359	4.05E-01	51.2
LYM89	12214.3	D	0.256	4.88E-01	16.3	LYM242	13051.8	B	0.312	4.11E-01	31.4
LYM206	12601.3	D	0.232	5.03E-01	5.4	LYM183	12991.7	B	0.258	4.18E-01	8.5
LYM86	12183.1	D	0.245	5.08E-01	11.6	LYM119	12461.1	B	0.27	4.22E-01	13.8
LYM236	12592.4	D	0.269	5.38E-01	22.2	LYM142	12801.8	B	0.258	4.22E-01	8.8
LYM175	12654.4	D	0.262	5.39E-01	19	LYM288	12743.8	B	0.269	4.37E-01	13.5
LYM90	12393.1	D	0.251	5.42E-01	14.3	LYM287	12773.7	B	0.303	4.38E-01	27.5
LYM250	12614.2	D	0.243	5.44E-01	10.5	LYM212	13031.5	B	0.266	4.43E-01	11.9
LYM250	12611.3	D	0.265	5.54E-01	20.5	LYM255	13082.7	B	0.264	4.46E-01	11.4

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM283	13304.4	D	0.251	6.17E-01	14.1	LYM143	12524.2	B	0.309	4.52E-01	30.3
LYM6	11733.2	D	0.235	6.79E-01	6.8	LYM153	12321.2	B	0.303	4.54E-01	27.5
LYM147	12584.5	D	0.227	6.93E-01	3.3	LYM270	12871.7	B	0.264	4.64E-01	11.1
LYM157	13342.4	D	0.249	7.01E-01	13.2	LYM208	13012.8	B	0.349	4.64E-01	46.9
LYM91	13283.4	D	0.248	7.12E-01	12.8	LYM220	12851.11	B	0.273	4.64E-01	15
LYM128	12641.1	D	0.236	7.33E-01	7.6	LYM255	13082.9	B	0.327	4.69E-01	37.7
LYM206	12603.2	D	0.225	7.44E-01	2.4	LYM152	12373.1	B	0.256	4.76E-01	8
LYM73	12622.2	D	0.234	8.40E-01	6.4	LYM174	12411.3	B	0.265	4.89E-01	11.7
LYM175	12654.6	D	0.226	8.63E-01	2.7	LYM173	12981.8	B	0.254	4.95E-01	7
LYM159	13352.4	D	0.225	8.63E-01	2.3	LYM288	12741.9	B	0.268	5.10E-01	12.7
LYM147	12583.1	D	0.235	8.75E-01	7.2	LYM270	12871.5	B	0.262	5.13E-01	10.5
LYM178	12164.2	D	0.226	8.77E-01	3	LYM44	11885.4	B	0.281	5.16E-01	18.5
LYM88	12191.1	D	0.225	9.11E-01	2.2	LYM119	12462.2	B	0.361	5.34E-01	52.2
LYM89	12214.4	D	0.221	9.16E-01	0.7	LYM130	12332.2	B	0.275	5.42E-01	15.9
LYM149	12344.2	D	0.227	9.29E-01	3.5	LYM212	13034.9	B	0.256	5.42E-01	8
LYM147	12581.4	D	0.223	9.55E-01	1.6	LYM142	12804.3	B	0.259	5.43E-01	9.3
LYM175	12651.4	D	0.222	9.80E-01	1	LYM197	12824.7	B	0.293	5.46E-01	23.2
CONTROL	—	D	0.22	—	0	LYM220	12851.13	B	0.262	5.67E-01	10.3
LYM107	12633.4	E	9.188	1.23E-03	8.4	LYM198	13002.5	B	0.282	5.80E-01	18.8
LYM206	12603.3	E	9.188	1.23E-03	8.4	LYM137	12151.2	B	0.252	5.93E-01	6.1
LYM88	12193.1	E	9.063	3.77E-03	6.9	LYM183	12993.7	B	0.277	6.04E-01	16.7
LYM6	11734.3	E	9.125	2.59E-02	7.7	LYM212	13034.8	B	0.294	6.34E-01	23.8
LYM157	13341.4	E	8.813	4.79E-02	4	LYM220	12852.2	B	0.261	6.54E-01	10.1
LYM283	13304.4	E	8.813	4.79E-02	4	LYM130	12331.3	B	0.284	6.60E-01	19.6
LYM178	12164.3	E	8.875	9.63E-02	4.7	LYM288	12744.6	B	0.258	6.65E-01	8.8
LYM90	12393.1	E	9.063	1.17E-01	6.9	LYM291	12753.6	B	0.249	6.65E-01	5.1

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM90	12395.1	E	9.125	1.79E-01	7.7	LYM138	12564.1	B	0.259	6.70E-01	9
LYM250	12613.4	E	8.688	1.79E-01	2.5	LYM289	12492.2	B	0.263	6.79E-01	10.6
LYM99	12243.2	E	8.688	1.79E-01	2.5	LYM201	12833.7	B	0.281	6.89E-01	18.5
LYM107	12631.4	E	8.75	2.07E-01	3.2	LYM130	12334.1	B	0.247	7.13E-01	4
LYM73	12623.2	E	8.75	2.07E-01	3.2	LYM138	12562.2	B	0.252	7.28E-01	6.1
LYM90	12395.3	E	9.188	3.34E-01	8.4	LYM142	12802.7	B	0.246	7.38E-01	3.5
LYM147	12583.3	E	8.688	4.46E-01	2.5	LYM130	12333.1	B	0.257	7.42E-01	8.2
LYM250	12614.1	E	8.688	4.46E-01	2.5	LYM153	12323.2	B	0.255	7.44E-01	7.4
LYM128	12642.3	E	8.625	4.56E-01	1.8	LYM106	12142.1	B	0.262	7.70E-01	10.3
LYM129	12573.3	E	8.625	4.56E-01	1.8	LYM270	12872.5	B	0.244	7.99E-01	2.7
LYM88	12191.2	E	8.625	4.56E-01	1.8	LYM183	12994.7	B	0.243	8.20E-01	2.4
LYM89	12211.4	E	8.625	4.56E-01	1.8	LYM242	13053.7	B	0.242	8.52E-01	1.9
LYM99	12243.1	E	8.625	4.56E-01	1.8	LYM183	12994.8	B	0.243	8.58E-01	2.2
LYM206	12603.1	E	8.563	5.62E-01	1	LYM291	12751.7	B	0.243	8.65E-01	2.4
LYM6	11733.2	E	8.563	5.62E-01	1	LYM287	12771.6	B	0.241	8.75E-01	1.6
LYM86	12182.3	E	8.563	5.62E-01	1	LYM44	11884.3	B	0.246	9.08E-01	3.8
LYM6	11735.1	E	8.813	5.79E-01	4	LYM270	12872.7	B	0.245	9.08E-01	3.2
LYM236	12591.1	E	8.75	5.95E-01	3.2	LYM255	13081.5	B	0.244	9.17E-01	3
LYM73	12623.1	E	8.75	5.95E-01	3.2	LYM270	12871.8	B	0.238	9.96E-01	0.1
LYM178	12163.3	E	8.688	6.19E-01	2.5	CONTROL	—	B	0.237	—	0
LYM147	12584.4	E	8.563	7.37E-01	1	LYM102	12221.2	C	3.181	7.20E-05	59.4
LYM91	13283.1	E	8.563	8.30E-01	1	LYM174	12411.2	C	3.1	1.24E-04	55.4
LYM236	12594.3	E	8.625	8.51E-01	1.8	LYM111	12254.4	C	3.5	1.46E-04	75.4
LYM250	12613.2	E	8.5	8.55E-01	0.3	LYM137	12151.1	C	3.044	1.55E-04	52.5
LYM128	12641.3	E	8.5	8.98E-01	0.3	LYM102	12222.2	C	3.031	2.15E-04	51.9
LYM206	12601.2	E	8.5	8.98E-01	0.3	LYM198	13004.6	C	2.969	2.68E-04	48.8

Gene name	**Event**	**ID**	**Mean**	**P value**	**%** ***incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	**%** ***incr. vs. cont.***
LYM236	12592.3	E	8.5	8.98E-01	0.3	LYM106	12144.4	C	2.881	4.76E-04	44.4
LYM159	13354.5	E	8.521	9.20E-01	0.5	LYM174	12414.3	C	2.856	5.73E-04	43.1
LYM129	12572.4	E	8.5	9.40E-01	0.3	LYM152	12373.2	C	2.856	6.33E-04	43.1
LYM175	12653.3	E	8.5	9.40E-01	0.3	LYM105	12297.2	C	2.869	7.57E-04	43.8
LYM178	12164.2	E	8.5	9.40E-01	0.3	LYM137	12152.1	C	2.731	1.65E-03	36.9
LYM99	12241.1	E	8.5	9.40E-01	0.3	LYM100	12134.1	C	2.881	1.87E-03	44.4
LYM157	13342.4	E	8.5	9.59E-01	0.3	LYM107	12632.1	C	2.913	2.19E-03	46
CONTROL	—	E	8.475	—	0	LYM105	12294.3	C	2.8	2.39E-03	40.3
LYM206	12603.3	F	0.579	5.70E-05	43	LYM107	12631.1	C	2.688	2.68E-03	34.7
LYM236	12592.3	F	0.487	6.32E-03	20.3	LYM107	12632.3	C	3.3	3.16E-03	65.4
LYM73	12623.1	F	0.442	1.25E-01	9.2	LYM107	12631.2	C	2.681	6.82E-03	34.4
LYM129	12572.4	F	0.442	1.62E-01	9.1	LYM100	12133.3	C	3.294	7.28E-03	65.1
LYM73	12623.2	F	0.438	1.80E-01	8	LYM197	12824.4	C	2.738	9.52E-03	37.2
LYM159	13354.6	F	0.443	1.85E-01	9.4	LYM106	12141.4	C	3.675	1.04E-02	84.2
LYM206	12603.1	F	0.456	1.88E-01	12.6	LYM152	12373.1	C	2.5	1.15E-02	25.3
LYM250	12613.4	F	0.533	2.23E-01	31.6	LYM143	12523.4	C	2.556	1.22E-02	28.1
LYM147	12583.3	F	0.434	2.25E-01	7.1	LYM111	12251.1	C	3.525	1.30E-02	76.7
LYM90	12395.3	F	0.432	2.54E-01	6.6	LYM291	12754.9	C	4.031	1.90E-02	102
LYM90	12395.1	F	0.459	2.58E-01	13.2	LYM142	12804.1	C	2.494	2.73E-02	25
LYM178	12163.4	F	0.487	2.76E-01	20.2	LYM102	12221.1	C	2.813	3.28E-02	41
LYM89	12211.4	F	0.433	2.87E-01	7	LYM288	12744.7	C	2.638	3.46E-02	32.2
LYM250	12614.1	F	0.429	3.05E-01	5.8	LYM100	12131.2	C	3.154	3.50E-02	58
LYM107	12633.4	F	0.487	3.08E-01	20.2	LYM111	12254.3	C	2.563	3.71E-02	28.4
LYM236	12591.1	F	0.481	3.14E-01	18.8	LYM105	12297.1	C	3.269	4.57E-02	63.8
LYM88	12193.1	F	0.49	3.39E-01	20.9	LYM212	13031.5	C	2.354	4.66E-02	18
LYM236	12594.3	F	0.46	3.51E-01	13.6	LYM183	12991.7	C	2.456	4.75E-02	23.1

Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*	Gene name	Event	ID	Mean	P value	*% incr. vs. cont.*
LYM99	12243.1	F	0.496	3.78E-01	22.5	LYM102	12222.1	C	3.556	5.16E-02	78.2
LYM6	11735.1	F	0.482	4.20E-01	19.1	LYM143	12524.5	C	2.756	5.74E-02	38.1
LYM178	12161.2	F	0.465	4.22E-01	14.9	LYM102	12222.3	C	3.769	6.05E-02	88.9
LYM250	12614.2	F	0.452	4.40E-01	11.5	LYM105	12293.1	C	2.419	6.23E-02	21.2
LYM157	13341.4	F	0.435	4.48E-01	7.4	LYM270	12871.5	C	2.321	6.49E-02	16.3
LYM175	12654.4	F	0.472	4.48E-01	16.5	LYM153	12324.2	C	2.313	7.05E-02	15.9
LYM129	12573.5	F	0.457	4.50E-01	12.9	LYM100	12133.1	C	3.288	7.40E-02	64.8
LYM206	12603.2	F	0.422	4.75E-01	4.3	LYM106	12142.3	C	3.038	8.14E-02	52.2
LYM128	12641.1	F	0.424	4.85E-01	4.7	LYM152	12372.2	C	2.605	9.07E-02	30.6
LYM178	12163.3	F	0.441	4.99E-01	8.9	LYM174	12414.2	C	3.1	9.40E-02	55.4
LYM206	12601.2	F	0.5	5.39E-01	23.5	LYM174	12412.1	C	3.269	1.06E-01	63.8
LYM88	12191.2	F	0.446	6.11E-01	10.2	LYM106	12144.3	C	2.813	1.07E-01	41
LYM159	13354.5	F	0.416	7.19E-01	2.8	LYM270	12872.5	C	2.375	1.14E-01	19
LYM129	12573.3	F	0.418	7.51E-01	3.1	LYM138	12566.1	C	2.838	1.14E-01	42.2
LYM89	12214.3	F	0.412	8.15E-01	1.7	LYM138	12561.3	C	2.619	1.21E-01	31.2
LYM89	12214.2	F	0.422	8.16E-01	4.1	LYM173	12981.8	C	2.263	1.25E-01	13.4
LYM283	13304.4	F	0.42	8.23E-01	3.8	LYM289	12491.1	C	2.9	1.26E-01	45.3
LYM236	12592.4	F	0.425	8.29E-01	5	LYM143	12521.1	C	2.613	1.32E-01	30.9
LYM250	12611.3	F	0.416	8.42E-01	2.7	LYM173	12982.6	C	2.863	1.34E-01	43.5
LYM107	12631.4	F	0.409	9.12E-01	0.9	LYM212	13032.8	C	2.438	1.36E-01	22.2
LYM90	12393.1	F	0.411	9.45E-01	1.4	LYM138	12562.1	C	2.569	1.40E-01	28.7
LYM159	13352.4	F	0.407	9.49E-01	0.4	LYM212	13034.9	C	2.244	1.40E-01	12.5
LYM91	13284.3	F	0.41	9.52E-01	1.2	LYM106	12142.2	C	3.731	1.41E-01	87
LYM91	13283.4	F	0.411	9.54E-01	1.4	LYM153	12324.1	C	2.831	1.48E-01	41.9
CONTROL	—	F	0.405	—	0	LYM100	12131.3	C	2.856	1.54E-01	43.1
LYM6	11734.3	G	9.53	2.63E-01	9.9	LYM107	12631.4	C	4.221	1.57E-01	111.6

Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*
LYM206	12603.3	G	9.772	3.62E-01	12.7	LYM289	12493.2	C	2.231	1.58E-01	11.8
LYM236	12591.1	G	9.157	4.16E-01	5.6	LYM152	12371.2	C	2.731	1.62E-01	36.9
LYM99	12243.1	G	9.096	4.92E-01	4.9	LYM220	12851.8	C	2.8	1.62E-01	40.3
LYM206	12601.2	G	9.11	5.79E-01	5	LYM220	12851.12	C	2.244	1.69E-01	12.5
LYM250	12614.2	G	8.905	6.05E-01	2.7	LYM138	12561.1	C	3.119	1.71E-01	56.3
LYM159	13354.5	G	8.845	6.87E-01	2	LYM137	12151.2	C	2.288	1.75E-01	14.6
LYM236	12592.3	G	9.013	8.02E-01	3.9	LYM142	12802.9	C	2.738	1.81E-01	37.2
LYM175	12654.4	G	8.974	8.11E-01	3.5	LYM111	12252.2	C	3.175	2.04E-01	59.1
LYM250	12613.4	G	8.913	8.18E-01	2.8	LYM102	12222.6	C	4.188	2.20E-01	109.9
LYM91	13284.4	G	8.877	8.65E-01	2.4	LYM142	12801.8	C	2.194	2.26E-01	9.9
LYM206	12603.1	G	8.75	8.71E-01	0.9	LYM105	12294.2	C	2.725	2.36E-01	36.6
LYM6	11733.2	G	8.891	8.75E-01	2.5	LYM288	12743.9	C	2.644	2.36E-01	32.5
LYM147	12584.4	G	8.747	9.59E-01	0.9	LYM107	12633.4	C	2.969	2.38E-01	48.8
LYM175	12651.4	G	8.748	9.72E-01	0.9	LYM111	12251.3	C	2.938	2.59E-01	47.2
LYM175	12654.6	G	8.697	9.75E-01	0.3	LYM143	12524.7	C	2.369	2.68E-01	18.7
CONTROL	—	G	8.673	—	0	LYM220	12852.4	C	2.194	2.78E-01	9.9
LYM107	12631.4	H	14.158	3.91E-03	35.7	LYM198	13002.6	C	3.356	2.79E-01	68.2
LYM147	12583.3	H	13.534	8.52E-03	29.7	LYM208	13012.8	C	2.65	2.79E-01	32.8
LYM236	12592.3	H	13.487	9.09E-03	29.3	LYM288	12743.8	C	2.356	2.80E-01	18.1
LYM90	12395.1	H	13.78	1.94E-02	32.1	LYM173	12982.7	C	2.725	2.82E-01	36.6
LYM129	12572.4	H	12.866	2.83E-02	23.3	LYM289	12491.4	C	2.775	2.83E-01	39.1
LYM206	12603.1	H	13.405	4.09E-02	28.5	LYM119	12463.2	C	2.894	2.84E-01	45
LYM147	12584.4	H	12.629	4.40E-02	21	LYM90	12392.1	C	2.475	2.89E-01	24
LYM88	12194.2	H	12.515	4.87E-02	20	LYM137	12153.1	C	2.588	2.97E-01	29.7
LYM6	11736.1	H	12.391	5.69E-02	18.8	LYM288	12741.9	C	2.319	2.97E-01	16.2
LYM89	12211.4	H	12.771	6.74E-02	22.4	LYM220	12852.2	C	2.269	3.14E-01	13.7

Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*	Gene name	Event	ID	Mean	P value	% *incr. vs. cont.*
LYM90	12395.3	H	14.316	6.99E-02	37.2	LYM142	12803.6	C	3.263	3.16E-01	63.5
LYM73	12623.2	H	12.201	8.98E-02	16.9	LYM287	12773.7	C	2.469	3.34E-01	23.7
LYM86	12182.3	H	12.123	9.17E-02	16.2	LYM143	12521.2	C	2.225	3.47E-01	11.5
LYM128	12641.3	H	12.249	1.00E-01	17.4	LYM152	12371.3	C	2.625	3.48E-01	31.6
LYM206	12603.3	H	17.874	1.01E-01	71.3	LYM212	13031.6	C	2.469	3.77E-01	23.7
LYM99	12243.2	H	12.41	1.03E-01	18.9	LYM173	12981.6	C	2.475	3.79E-01	24
LYM178	12163.4	H	12.811	1.54E-01	22.8	LYM255	13082.7	C	2.169	3.81E-01	8.7
LYM159	13354.6	H	12.193	1.55E-01	16.9	LYM105	12295.2	C	2.844	3.99E-01	42.5
LYM236	12594.3	H	11.884	1.59E-01	13.9	LYM137	12151.4	C	3.006	4.08E-01	50.7
LYM88	12193.1	H	14.778	1.60E-01	41.6	LYM119	12461.1	C	2.281	4.10E-01	14.3
LYM178	12164.3	H	12.031	1.81E-01	15.3	LYM198	13002.5	C	2.619	4.15E-01	31.2
LYM250	12614.1	H	12.094	2.04E-01	15.9	LYM111	12251.4	C	3.275	4.15E-01	64.1
LYM250	12613.4	H	16.068	2.07E-01	54	LYM138	12564.1	C	2.263	4.26E-01	13.4
LYM250	12613.2	H	11.628	2.09E-01	11.5	LYM208	13013.6	C	2.819	4.34E-01	41.3
LYM73	12623.1	H	12.001	2.10E-01	15	LYM183	12994.8	C	2.256	4.45E-01	13.1
LYM88	12191.2	H	13.605	2.15E-01	30.4	LYM153	12321.2	C	2.638	4.50E-01	32.2
LYM99	12243.1	H	14.765	2.34E-01	41.5	LYM143	12524.2	C	2.519	4.55E-01	26.2
LYM107	12633.4	H	15.436	2.76E-01	47.9	LYM289	12492.2	C	2.481	4.61E-01	24.4
LYM178	12163.3	H	13.589	2.92E-01	30.2	LYM242	13051.8	C	2.406	4.75E-01	20.6
LYM6	11735.1	H	15.004	3.12E-01	43.8	LYM183	12994.7	C	2.431	4.77E-01	21.8
LYM178	12161.2	H	12.57	3.13E-01	20.5	LYM255	13082.5	C	2.163	4.79E-01	8.4
LYM128	12642.3	H	12.501	3.37E-01	19.8	LYM287	12771.6	C	2.231	4.83E-01	11.8
LYM129	12573.3	H	12.931	3.61E-01	23.9	LYM173	12981.5	C	2.331	4.84E-01	16.8
LYM206	12601.2	H	17.033	3.65E-01	63.2	LYM288	12744.6	C	2.206	4.86E-01	10.6
LYM129	12573.5	H	13.692	3.66E-01	31.2	LYM220	12851.11	C	2.229	5.02E-01	11.7
LYM89	12214.2	H	13.553	4.00E-01	29.9	LYM291	12751.7	C	2.206	5.06E-01	10.6

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM175	12651.2	H	11.266	4.15E-01	8	LYM255	13082.9	C	2.394	5.08E-01	20
LYM6	11734.3	H	11.461	4.19E-01	9.8	LYM220	12851.13	C	2.175	5.17E-01	9
LYM90	12392.1	H	11.166	4.25E-01	7	LYM291	12753.6	C	2.225	5.20E-01	11.5
LYM236	12591.1	H	13.166	4.56E-01	26.2	LYM44	11884.1	C	2.15	5.32E-01	7.8
LYM157	13341.4	H	11.131	4.73E-01	6.7	LYM130	12332.2	C	2.219	5.39E-01	11.2
LYM90	12393.1	H	12.601	4.83E-01	20.8	LYM197	12824.7	C	2.625	5.42E-01	31.6
LYM89	12214.3	H	12.181	5.09E-01	16.7	LYM119	12462.2	C	2.925	5.45E-01	46.6
LYM250	12614.2	H	11.889	5.16E-01	14	LYM242	13053.7	C	2.094	5.53E-01	4.9
LYM91	13284.3	H	11.762	5.45E-01	12.7	LYM44	11885.4	C	2.35	5.71E-01	17.8
LYM283	13304.4	H	12.329	5.80E-01	18.2	LYM137	12154.5	C	2.319	5.87E-01	16.2
LYM86	12183.1	H	11.569	5.87E-01	10.9	LYM130	12331.3	C	2.5	6.12E-01	25.3
LYM236	12592.4	H	12.52	5.99E-01	20	LYM142	12804.3	C	2.156	6.19E-01	8.1
LYM6	11733.2	H	11.309	6.05E-01	8.4	LYM270	12871.7	C	2.2	6.64E-01	10.3
LYM250	12611.3	H	12.099	6.19E-01	16	LYM174	12411.3	C	2.15	6.66E-01	7.8
LYM175	12654.6	H	11.242	6.78E-01	7.7	LYM183	12993.7	C	2.225	6.77E-01	11.5
LYM175	12654.4	H	12.126	6.86E-01	16.2	LYM138	12562.2	C	2.181	6.86E-01	9.3
LYM206	12603.2	H	10.774	7.04E-01	3.3	LYM212	13034.8	C	2.313	6.90E-01	15.9
LYM128	12641.1	H	11.41	7.15E-01	9.4	LYM270	12872.7	C	2.169	7.14E-01	8.7
LYM91	13283.4	H	11.798	7.22E-01	13.1	LYM130	12333.1	C	2.294	7.33E-01	15
LYM147	12584.5	H	10.733	7.53E-01	2.9	LYM153	12323.2	C	2.188	7.44E-01	9.6
LYM206	12601.3	H	10.704	7.86E-01	2.6	LYM106	12142.1	C	2.363	7.50E-01	18.4
LYM157	13342.4	H	11.448	7.87E-01	9.7	LYM130	12334.1	C	2.05	7.51E-01	2.7
LYM147	12583.1	H	11.545	8.28E-01	10.7	LYM198	13002.8	C	2.213	7.61E-01	10.9
LYM86	12183.3	H	10.656	8.33E-01	2.1	LYM287	12771.7	C	2.063	8.00E-01	3.4
LYM178	12164.2	H	10.838	8.72E-01	3.9	LYM44	11882.1	C	2.106	8.42E-01	5.6
LYM91	13283.1	H	10.514	9.28E-01	0.8	LYM198	13005.6	C	2.063	8.64E-01	3.4

Gene name	**Event**	**ID**	**Mean**	**P value**	**% *incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	**% *incr. vs. cont.***
LYM73	12622.2	H	10.758	9.28E-01	3.1	LYM291	12751.2	C	2.042	8.80E-01	2.3
LYM149	12344.2	H	10.764	9.42E-01	3.2	LYM201	12833.7	C	2.088	8.82E-01	4.6
CONTROL	—	H	10.434	—	0	LYM44	11884.3	C	2.069	9.05E-01	3.7
LYM206	12603.3	J	0.042	2.32E-03	61.6	LYM44	11885.3	C	2.013	9.12E-01	0.9
LYM250	12613.4	J	0.038	1.29E-02	47.8	LYM90	12394.2	C	2.006	9.59E-01	0.5
LYM206	12601.2	J	0.039	2.60E-02	48.5	LYM255	13082.8	C	2	9.86E-01	0.2
LYM107	12633.4	J	0.037	2.93E-02	43.3	CONTROL	—	C	1.995	—	0
LYM6	11735.1	J	0.035	4.68E-02	36.2	LYM102	12222.2	D	0.265	6.00E-06	40
LYM99	12243.1	J	0.035	5.89E-02	35.2	LYM288	12743.9	D	0.264	1.70E-05	39.2
LYM88	12191.2	J	0.035	6.27E-02	32.8	LYM173	12981.6	D	0.248	9.60E-05	31
LYM129	12573.5	J	0.035	7.06E-02	33.1	LYM138	12561.3	D	0.31	1.04E-04	63.6
LYM236	12592.3	J	0.034	7.96E-02	30.2	LYM107	12631.4	D	0.239	1.13E-04	26.3
LYM89	12214.2	J	0.034	8.48E-02	31.2	LYM105	12297.2	D	0.24	2.13E-04	26.7
LYM90	12395.3	J	0.033	8.93E-02	28.3	LYM130	12332.1	D	0.283	2.74E-03	49.6
LYM129	12572.4	J	0.033	1.15E-01	27.1	LYM289	12493.1	D	0.272	3.81E-03	43.6
LYM178	12163.4	J	0.033	1.22E-01	25.9	LYM130	12334.1	D	0.23	4.39E-03	21.6
LYM147	12583.3	J	0.033	1.28E-01	25.3	LYM102	12222.1	D	0.228	5.99E-03	20.7
LYM236	12592.4	J	0.033	1.43E-01	28.1	LYM255	13082.8	D	0.252	6.25E-03	33.3
LYM107	12631.4	J	0.032	1.44E-01	24.3	LYM106	12144.4	D	0.258	6.35E-03	36.4
LYM89	12211.4	J	0.032	1.56E-01	23.7	LYM107	12631.2	D	0.216	6.37E-03	14.2
LYM6	11736.1	J	0.032	1.66E-01	24.2	LYM153	12323.2	D	0.282	7.68E-03	49
LYM90	12395.1	J	0.032	1.73E-01	22.4	LYM105	12293.1	D	0.278	1.12E-02	47
LYM88	12193.1	J	0.032	1.92E-01	21.6	LYM201	12833.7	D	0.212	1.16E-02	12.1
LYM250	12611.3	J	0.032	1.97E-01	24.5	LYM119	12461.4	D	0.301	1.22E-02	59
LYM236	12591.1	J	0.032	2.14E-01	22.8	LYM287	12771.6	D	0.219	1.38E-02	15.5
LYM99	12243.2	J	0.031	2.28E-01	20.1	LYM105	12294.2	D	0.248	1.47E-02	31.1

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM178	12161.2	J	0.031	2.32E-01	20.1	LYM173	12982.6	D	0.215	1.80E-02	13.7
LYM178	12163.3	J	0.031	2.45E-01	20	LYM137	12153.1	D	0.227	2.52E-02	19.8
LYM206	12603.1	J	0.031	2.53E-01	19	LYM152	12373.1	D	0.234	2.75E-02	23.5
LYM159	13354.6	J	0.031	2.78E-01	18.6	LYM270	12873.6	D	0.252	2.79E-02	33.2
LYM129	12573.3	J	0.031	2.87E-01	18.4	LYM138	12561.1	D	0.399	4.37E-02	110.9
LYM175	12654.4	J	0.031	2.90E-01	19.4	LYM287	12774.6	D	0.206	4.37E-02	8.8
LYM90	12392.1	J	0.03	3.06E-01	16.4	LYM242	13052.5	D	0.212	4.61E-02	12.1
LYM91	13284.3	J	0.031	3.18E-01	17.4	LYM137	12151.4	D	0.27	5.04E-02	42.4
LYM159	13354.5	J	0.03	3.56E-01	15.4	LYM100	12133.3	D	0.205	5.59E-02	8.1
LYM89	12214.3	J	0.03	3.58E-01	15.8	LYM137	12151.2	D	0.25	6.45E-02	32.1
LYM250	12613.2	J	0.03	3.76E-01	14.5	LYM289	12492.2	D	0.246	6.50E-02	29.9
LYM236	12594.3	J	0.029	4.45E-01	12.5	LYM174	12414.3	D	0.32	7.11E-02	69
LYM157	13342.4	J	0.03	4.61E-01	14	LYM153	12322.1	D	0.218	7.32E-02	15.3
LYM91	13283.4	J	0.029	4.75E-01	13.2	LYM111	12254.4	D	0.23	7.53E-02	21.3
LYM73	12623.2	J	0.029	4.77E-01	11.7	LYM119	12463.2	D	0.302	7.64E-02	59.5
LYM175	12651.2	J	0.029	4.79E-01	11.9	LYM106	12142.2	D	0.307	7.80E-02	62.1
LYM6	11733.2	J	0.029	4.88E-01	11.9	LYM153	12324.2	D	0.27	7.86E-02	42.8
LYM86	12182.3	J	0.029	4.94E-01	11	LYM106	12141.4	D	0.219	7.93E-02	15.7
LYM283	13304.4	J	0.029	5.17E-01	11.3	LYM212	13032.8	D	0.239	8.15E-02	26.2
LYM90	12393.1	J	0.029	5.43E-01	10.3	LYM119	12461.1	D	0.308	8.59E-02	62.9
LYM73	12623.1	J	0.029	5.45E-01	9.8	LYM201	12833.9	D	0.203	8.86E-02	7.2
LYM128	12642.3	J	0.029	5.62E-01	9.5	LYM100	12131.3	D	0.209	9.17E-02	10.3
LYM73	12622.2	J	0.029	5.64E-01	10.5	LYM288	12743.8	D	0.236	9.25E-02	24.6
LYM250	12614.2	J	0.028	5.82E-01	9.3	LYM220	12851.8	D	0.286	9.36E-02	51.1
LYM86	12183.1	J	0.028	6.07E-01	8.6	LYM102	12222.3	D	0.229	1.07E-01	20.9
LYM86	12183.3	J	0.028	6.17E-01	8.1	LYM105	12295.2	D	0.269	1.09E-01	41.9

Gene name	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***	**Gene name**	**Event**	**ID**	**Mean**	**P value**	***% incr. vs. cont.***
LYM91	13283.1	J	0.028	6.19E-01	8	LYM174	12411.2	D	0.276	1.10E-01	45.9
LYM250	12614.1	J	0.028	6.33E-01	7.7	LYM289	12491.1	D	0.201	1.29E-01	6.1
LYM157	13341.4	J	0.028	6.74E-01	7.2	LYM137	12151.1	D	0.253	1.36E-01	33.5
LYM178	12164.3	J	0.028	6.96E-01	6.2	LYM138	12562.2	D	0.246	1.48E-01	29.8
LYM128	12641.1	J	0.028	6.98E-01	6.8	LYM107	12632.3	D	0.298	1.51E-01	57.5
LYM147	12584.4	J	0.028	7.13E-01	5.8	LYM105	12294.3	D	0.226	1.59E-01	19.4
LYM175	12651.4	J	0.028	7.62E-01	5.8	LYM119	12462.1	D	0.278	1.80E-01	47
LYM159	13352.4	J	0.027	7.80E-01	4.6	LYM153	12324.1	D	0.283	1.89E-01	49.3
LYM88	12194.2	J	0.027	7.86E-01	4.4	LYM288	12743.5	D	0.274	1.92E-01	44.7
LYM175	12654.6	J	0.027	8.01E-01	4.3	LYM174	12412.1	D	0.282	2.01E-01	48.9
LYM147	12583.1	J	0.027	8.50E-01	3.7	LYM212	13031.6	D	0.211	2.07E-01	11.6
LYM149	12344.2	J	0.027	8.67E-01	3.2	LYM197	12821.6	D	0.224	2.15E-01	18.1
LYM128	12641.3	J	0.027	8.88E-01	2.2	LYM107	12631.1	D	0.225	2.32E-01	18.8
LYM88	12191.1	J	0.027	9.00E-01	2.1	LYM90	12395.3	D	0.23	2.34E-01	21.4
LYM206	12601.3	J	0.027	9.12E-01	1.8	LYM242	13051.8	D	0.223	2.35E-01	17.6
LYM89	12214.4	J	0.026	9.25E-01	1.5	LYM173	12981.5	D	0.227	2.35E-01	19.7
LYM147	12584.5	J	0.026	9.58E-01	0.9	LYM130	12332.2	D	0.246	2.46E-01	29.8
LYM178	12164.2	J	0.026	9.69E-01	0.6	LYM111	12251.1	D	0.203	2.49E-01	7.1
LYM147	12581.4	J	0.026	9.95E-01	0.1	LYM174	12411.3	D	0.299	2.57E-01	57.9
CONTROL	—	J	0.026	—	0	LYM198	13005.8	D	0.2	2.58E-01	5.8
LYM157	13341.4	K	0.697	6.89E-02	22.1	LYM119	12462.2	D	0.25	2.82E-01	32
LYM88	12193.1	K	0.617	4.88E-01	8.1	LYM153	12321.2	D	0.235	2.89E-01	24.2
LYM73	12623.2	K	0.605	6.11E-01	6	LYM111	12252.2	D	0.239	2.92E-01	26.1
LYM107	12633.4	K	0.604	6.16E-01	5.8	LYM242	13053.7	D	0.215	3.07E-01	13.4
LYM159	13354.8	K	0.603	6.36E-01	5.6	LYM102	12221.1	D	0.221	3.09E-01	16.5
LYM90	12395.3	K	0.6	6.64E-01	5.1	LYM255	13082.9	D	0.22	3.26E-01	16

DEMANDES OU BREVETS VOLUMINEUX

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

CECI EST LE TOME __2___ 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 __2___ OF __2___

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

WHAT IS CLAIMED IS:

1. A method of increasing yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of a plant, comprising over-expressing within the plant a polypeptide comprising an amino acid sequence at least 80% identical to the full length amino acid sequence set forth by SEQ ID NO: 264, wherein said polypeptide increases yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of a plant, thereby increasing the yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of the plant.

2. A method of increasing yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress , and/or nitrogen use efficiency of a plant, comprising over-expressing within the plant a polypeptide comprising an amino acid sequence set forth by SEQ ID NO: 264 or 2425, thereby increasing the yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of the plant.

3. A method of increasing yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, 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 the full length nucleic acid sequence set forth by SEQ ID NO: 3505 or 25, wherein said polynucleotide increases yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of a plant, thereby increasing the yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress , and/or nitrogen use efficiency of the plant.

4. A method of increasing yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO: 3505, or 25, or 918, thereby increasing the yield, biomass, growth rate, vigor, oil content, tolerance to abiotic stress, and/or nitrogen use efficiency of the plant.

5. The method of claim 1, wherein said amino acid sequence is at least 85% identical to the full length amino acid sequence set forth by SEQ ID NO: 264.

6. The method of claim 1, wherein said amino acid sequence is at least 90% identical to the full length amino acid sequence set forth by SEQ ID NO: 264.

7. The method of claim 1, wherein said amino acid sequence is at least 95% identical to the full length amino acid sequence set forth by SEQ ID NO: 264.

8. The method of claim 1, wherein said amino acid sequence is at least 98% identical to the full length amino acid sequence set forth by SEQ ID NO: 264.

9. The method of claim 1, wherein said amino acid sequence is set forth by SEQ ID NO: 264 or 2425.

10. The method of claim 3, wherein said nucleic acid sequence is at least 90% identical to the full length nucleic acid sequence set forth in SEQ ID NO: 3505 or 25.

11. The method of claim 3, wherein said nucleic acid sequence is at least 95% identical to the full length nucleic acid sequence set forth in SEQ ID NO: 3505 or 25.

12. The method of claim 3, wherein said nucleic acid sequence is set forth in SEQ ID NO: 3505 or 25.

13. The method of any one of claims 1 to 4, wherein the abiotic stress is selected from the group consisting of salinity, drought, water deprivation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

14. The method of any one of claims 1 to 4, further comprising growing the plant under the abiotic stress.

15. The method of any one of claims 1 to 4, further comprising growing the plant under nitrogen-limiting conditions.

16. The method of any one of claims 1 to 15, further comprising selecting said plant for an increased trait as compared to a native plant of the same species which is grown under the same growth conditions, said trait being selected from the group consisting of: yield, oil content, biomass, growth rate, abiotic stress tolerance, and nitrogen use efficiency.

17. The method of any one of claims 1 to 15, further comprising selecting said plant for an increased trait as compared to a native plant of the same species which is grown under the same growth conditions, said trait being selected from the group consisting of: yield, biomass, growth rate, and oil content.

18. The method of claim 3 or claim 4, wherein said polynucleotide is operably linked to a heterologous promoter.

19. The method of claim 18, wherein said promoter is a constitutive promoter.

20. The method of claim 18, wherein said promoter is an abiotic stress-inducible promoter.

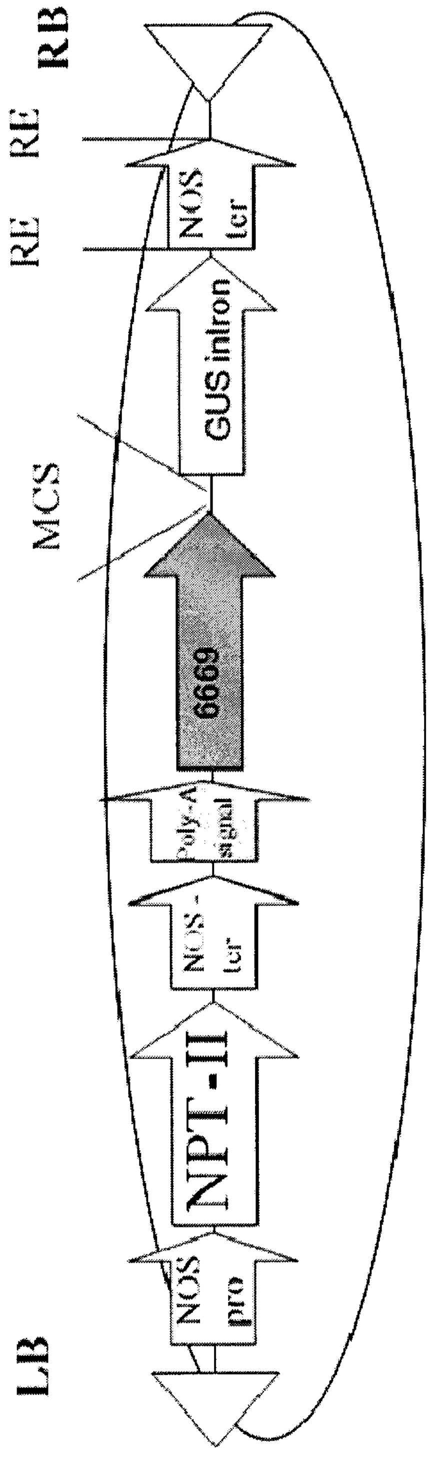

LB
NOS pro
NPT-II
NOS - ter
Poly-A signal
6669
MCS
GUS intron
NOS ter
RE
RE
RB

FIG. 1

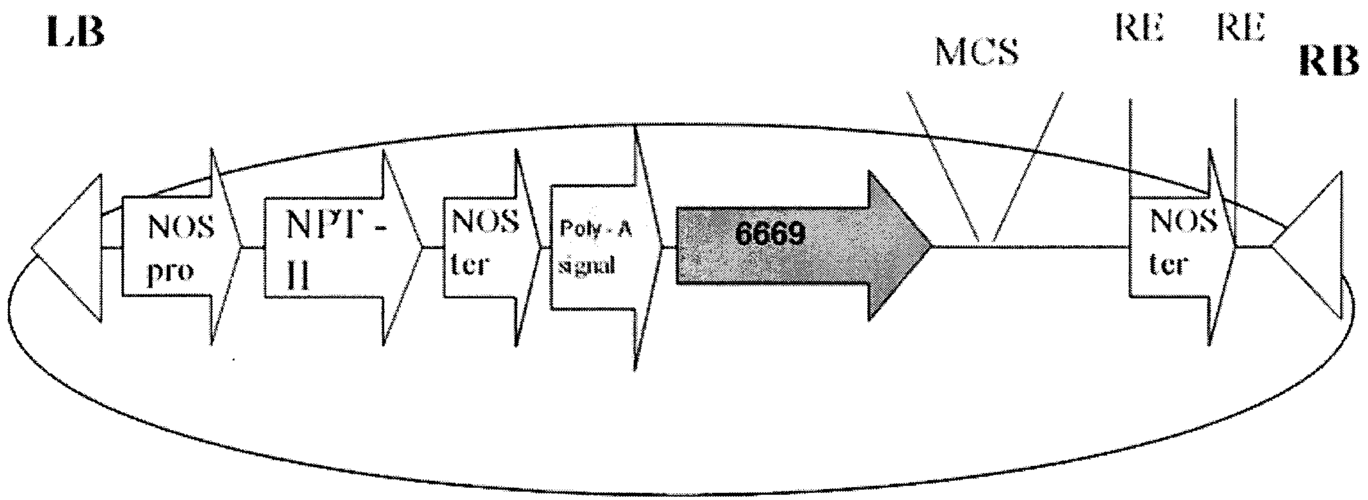


FIG. 2

Normal conditions

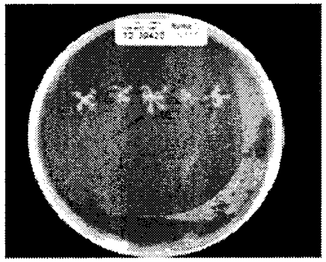


FIG. 3A

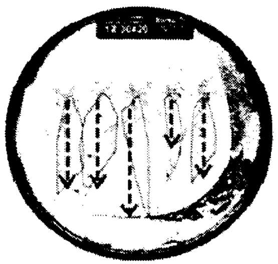


FIG. 3B

Osmotic stress (15 % PEG)

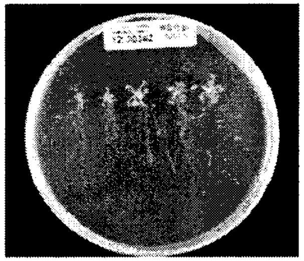


FIG. 3C

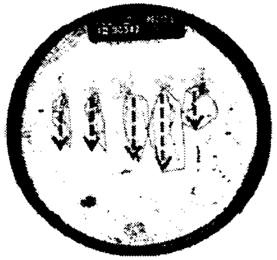


FIG. 3D

Nitrogen limiting conditions

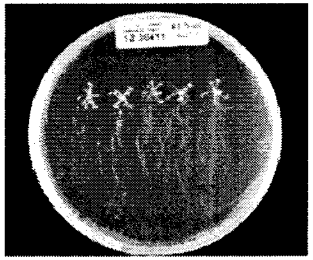


FIG. 3E

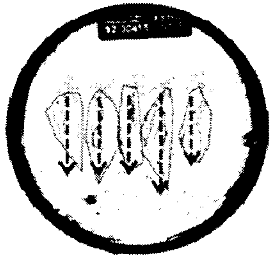
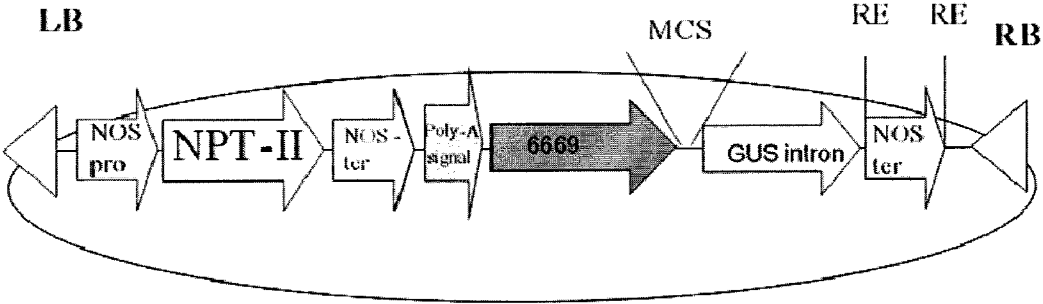


FIG. 3F


LB
NOS pro
NPT-II
NOS - ter
Poly-A signal
6669
MCS
GUS intron
RE
RE
NOS ter
RB