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

(57) Abstract: Provided are methods of increasing yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of a plant by expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 905, 882, 1-12, 15-105, 203-297, 299-523, 845- 881, 883-904, 906-925 or 933; or an exogenous polynucleotide encoding a polypeptide at least 80 % identical to SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932. Also provided isolated polynucleotide comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs:905, 882, 1- 13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933, which can be used to increase yield, biomass, growth rate, vigor, oil content, 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, BIOMASS, GROWTH RATE,
VIGOR, OIL CONTENT, ABIOTIC STRESS TOLERANCE OF PLANTS AND
NITROGEN USE EFFICIENCY

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FIELD AND BACKGROUND OF THE INVENTION

The present invention, in some embodiments thereof, relates to polypeptides, polynucleotides encoding same, transgenic plants expressing same and methods of producing and using same, and, more particularly, but not exclusively, to methods of increasing plant yield, oil yield, seed yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency.

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

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

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.

Vegetable or seed oils are the major source of energy and nutrition in human and animal diet. They are also used for the production of industrial products, such as paints, inks and lubricants. In addition, plant oils represent renewable sources of long-chain hydrocarbons which can be used as fuel. Since the currently used fossil fuels are finite resources and are gradually being depleted, fast growing biomass crops may be used as alternative fuels or for energy feedstocks and may reduce the dependence on fossil energy supplies. However, the major bottleneck for increasing consumption of plant oils as bio-fuel is the oil price, which is still higher than fossil fuel [Hypertext Transfer Protocol://World Wide Web (dot) eia (dot) doe (dot) gov/oiaf/analysispaper/biodiesel/; Hypertext Transfer Protocol://World Wide Web (dot) njbiz (dot)com/weekly article.asp?aID=19755147 (dot) 6122555 (dot) 957931 (dot) 7393254 (dot) 4337383 (dot) 561&aID2=73678]. In addition, the production rate of plant oil is limited by the availability of agricultural land and water. Thus, increasing plant oil yields from the same growing area can effectively overcome the shortage in production space and can decrease vegetable oil prices at the same time.

Studies aiming at increasing plant oil yields focus on the identification of genes involved in oil metabolism as well as in genes capable of increasing plant and seed yields in transgenic plants.

Genes known to be involved in increasing plant oil yields include those participating in fatty acid synthesis or sequestering such as desaturase [e.g., DELTA6, DELTA12 or acyl-ACP (Ssi2; Arabidopsis Information Resource (TAIR; Hypertext Transfer Protocol://World Wide Web (dot) arabidopsis (dot) org/), TAIR No. AT2G43710)], OleosinA (TAIR No. AT3G01570) or FAD3 (TAIR No. AT2G29980), and various transcription factors and activators such as Lec1 [TAIR No. AT1G21970, Lotan *et al.* 1998. *Cell.* 26;93(7):1195-205], Lec2 [TAIR No. AT1G28300, Santos Mendoza *et al.* 2005, *FEBS Lett.* 579(21):4666-70], Fus3 (TAIR No. AT3G26790), ABI3 [TAIR No. AT3G24650, Lara *et al.* 2003. *J Biol Chem.* 278(23): 21003-11] and Wri1 [TAIR No. AT3G54320, Cernac and Benning, 2004. *Plant J.* 40(4): 575-85].

Zabrouskov V., et al., 2002 (Physiol Plant. 116:172-185) describe an increase in the total lipid fraction by upregulation of endoplasmic reticulum (FAD3) and plastidal (FAD7) fatty acid desaturases in potato.

Wang HW et al., 2007 (Plant J. 52:716-29. Epub 2007 Sep 18) describe an
5 increase in the content of total fatty acids and lipids in plant seeds by over-expressing the GmDof4 and GmDof11 transcription factors.

Vigeolas H, et al. [Plant Biotechnol J. 2007, 5(3):431-41] and U.S. Pat. Appl. No. 20060168684 discloses an increase in seed oil content in oil-seed rape (*Brassica napus* L.) by over-expression of a yeast glycerol-3-phosphate dehydrogenase under the
10 control of a seed-specific promoter.

Katavic V, et al., 2000 (Biochem Soc Trans. 28:935-7) describe the use of the *Arabidopsis* FAE1 and yeast SLC1-1 genes for improvements in erucic acid and oil content in rapeseed.

U.S. Pat. Appl. No. 20080076179 discloses an isolated moss nucleic acid
15 encoding a lipid metabolism protein (LMP) and transgenic plants expressing same with increased lipid levels.

U.S. Pat. Appl. No. 20060206961 discloses a method of increasing oil content in plants (e.g., in plant seeds), by expressing in the plant the Ypr140w polypeptide.

U.S. Pat. Appl. No. 20060174373 discloses a method of increasing oil content
20 in plants by expressing a nucleic acid encoding a triacylglycerols (TAG) synthesis enhancing protein (TEP) in the plant.

U.S. Pat. Appl. Nos. 20070169219, 20070006345, 20070006346 and 20060195943, disclose transgenic plants with improved nitrogen use efficiency which can be used for the conversion into fuel or chemical feedstocks.

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

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

WO2008/122890 teaches polynucleotide sequences and methods of utilizing
same for increasing oil content, growth rate, biomass, yield and/or vigor of a plant.

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, abiotic stress tolerance and/or nitrogen use efficiency of a plant, comprising expressing within
5 the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 or 933, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

10 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, 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: 905, 882, 1-13, 15-105, 203-523, 845-881,
15 883-904, 906-925 and 933, thereby increasing the yield, biomass, growth rate, vigor, oil content, 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, abiotic stress tolerance and/or nitrogen use efficiency of a plant, comprising expressing within
20 the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least 80 % identical to SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

25 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, 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: 172, 146, 106-117,
30 120-145, 147-171, 173-202, 524-844 and 926-932, thereby increasing the yield, biomass, growth rate, vigor, oil content, 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: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 or 933, wherein said nucleic acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, 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: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933.

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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932, wherein said amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

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

According to an aspect of some embodiments of the present invention there is provided an isolated polypeptide comprising an amino acid sequence at least 80 % homologous to SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932, wherein said amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

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

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

10 According to some embodiments of the invention, the nucleic acid sequence is as set forth in SEQ ID NO: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 or 933.

 According to some embodiments of the invention, the polynucleotide consists of the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 905, 15 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933.

 According to some embodiments of the invention, the nucleic acid sequence encodes an amino acid sequence at least 80 % homologous to SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932.

20 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

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

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

 According to some embodiments of the invention, the abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, 30 nutrient excess, atmospheric pollution and UV irradiation.

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

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.

10 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 15 embodiments of the invention may be practiced.

In the drawings:

FIG. 1 is a schematic illustration of the pGI binary plasmid used for expressing the isolated polynucleotide sequences of some embodiments of the invention. RB - T-DNA right border; LB - T-DNA left border; H- *HindIII* restriction enzyme; X - *XbaI* restriction enzyme; B - *BamHI* restriction enzyme; S - *SalI* restriction enzyme; Sm - *SmaI* restriction enzyme; R-I - *EcoRI* restriction enzyme; Sc - *SacI/SstI/Ecl136II*; (numbers) - Length in base-pairs; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); GUSintron - the GUS reporter gene (coding sequence and intron) The isolated polynucleotide sequences of the invention were cloned into the vector while replacing the GUSintron reporter gene 25

FIG. 2 is a schematic illustration of the modified pGI binary plasmid 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; (numbers) - Length in base-pairs; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; 30

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.

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

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

The present invention, in some embodiments thereof, relates to polypeptides, polynucleotides encoding same, nucleic acid constructs comprising same, transgenic plants expressing same and methods of producing and using same for increasing plant yield, oil yield, seed yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency.

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

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

5 Thus, as shown in the Examples section which follows, the present inventors have utilized bioinformatics tools and microarray analyses to identify polynucleotides which enhance yield (e.g., seed yield, oil yield, oil content), growth rate, biomass, vigor, abiotic stress tolerance and/or nitrogen use efficiency of a plant. Genes which affect the trait-of-interest [Table 15; Example 5 of the Examples section which follows; SEQ ID
10 NOs:1-105 (polynucleotides) and SEQ ID NOs:106-202 (polypeptides)] were identified based on correlation analyses between expression profiles of various genes in tissues, developmental stages, fertilizer limiting conditions, abiotic stress conditions or normal conditions across several Arabidopsis ecotypes, Sorghum Accessions and Tomato accessions and various parameters of yield, biomass, vigor, growth rate and/or oil
15 content (Examples 1, 2, 3, 4, 10 and 11 of the Examples section which follows; Tables 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 28 and 29). Homologous polypeptides and polynucleotides having the same function (activity) were also identified [Table 16, Example 6 of the Examples section which follows; SEQ ID NOs:203-523 (polynucleotides), and SEQ ID NOs:524-844 (polypeptides)]. The identified genes
20 were cloned in binary vectors (see for example, Tables 17, 18, 19 and 20; Example 7 of the Examples section which follows; SEQ ID NOs:47, 845-925 and 933) and transgenic plants over-expressing the identified genes of the invention were generated (see for example, Example 8 of the Examples section which follows). These plants which are transformed with the identified polynucleotides were found to exhibit increased yield,
25 biomass, growth rate, vigor, seed yield, oil content, oil yield, flowering, harvest index and rosette area (Tables 21-27; Example 9 of the Examples section which follows). These results suggest the use of the novel polynucleotides and polypeptides of the invention for increasing yield (including oil yield, seed yield and oil content), growth rate, biomass, vigor, abiotic stress tolerance and/or nitrogen use efficiency of a plant.

30 Thus, according to an aspect of some embodiments of the invention, there is provided method of increasing yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency 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: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925, or 933, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

As used herein the phrase "plant yield" refers to the amount (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
5 % 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.

10 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
15 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
20 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.

25 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
30 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.

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

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

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

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

the exogenous polynucleotide may comprise a nucleic acid sequence which is identical or partially homologous to an endogenous nucleic acid sequence of the plant.

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

5 According to some embodiments of the invention the exogenous polynucleotide comprises a nucleic acid sequence which is at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least
10 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: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 and 933.

Identity (e.g., percent homology) can be determined using any homology
15 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
20 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID NOs: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925
25 and 933.

According to some embodiments of the invention the exogenous polynucleotide is set forth by SEQ ID NO: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 or 933.

According to an aspect of some embodiments of the invention, there is
30 provided a method of increasing yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of a plant. The method is effected by expressing within the plant an exogenous polynucleotide comprising the nucleic acid

sequence selected from the group consisting of SEQ ID NOs: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

According to some embodiments of the invention the exogenous polynucleotide is selected from the group consisting of SEQ ID NOs: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933.

5 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).

10 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.

15 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.

25 According to some embodiments of the invention, the exogenous polynucleotide of the invention encodes a polypeptide having an amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or at least about 100 %.

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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 and 932.

5 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-
10 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
15 different organisms due to ancestral relationship.

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

Transfer Protocol://en (dot) wikipedia (dot) org/wiki/Neighbor-joining) which helps visualizing the clustering.

According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide consisting of the amino acid sequence set forth by
5 SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932.

According to an aspect of some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of a plant is effected by expressing within the plant an
10 exogenous polynucleotide comprising the nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

Nucleic acid sequences encoding the polypeptides of the present invention
15 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
20 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
25 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
30 of highly expressed plant genes, followed by a calculation of the average squared deviation. The formula used is: $1 \text{ SDCU} = n = \frac{1}{N} \left[\frac{(X_n - Y_n)^2}{Y_n} \right] / N$, where X_n refers to the frequency of usage of codon n in highly expressed plant genes, where Y_n to

the frequency of usage of codon n in the gene of interest and N refers to the total number of codons in the gene of interest. A Table of codon usage from highly expressed genes of dicotyledonous plants is compiled using the data of Murray et al. (1989, Nuc Acids Res. 17:477-498).

5 One method of optimizing the nucleic acid sequence in accordance with the preferred codon usage for a particular plant cell type is based on the direct use, without performing any extra statistical calculations, of codon optimization Tables such as those provided on-line at the Codon Usage Database through the NIAS (National Institute of Agrobiological Sciences) DNA bank in Japan (Hypertext Transfer Protocol://World
10 Wide Web (dot) kazusa (dot) or (dot) jp/codon/). The Codon Usage Database contains codon usage tables for a number of different species, with each codon usage Table 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-
15 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
20 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
25 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
30 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.

5 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).

10 A non-limiting example of a non-coding RNA polynucleotide is provided in SEQ ID NO:72 (BDL90).

Thus, the invention encompasses nucleic acid sequences described hereinabove; fragments thereof, sequences hybridizable therewith, sequences homologous thereto, sequences encoding similar polypeptides with different codon
15 usage, altered sequences characterized by mutations, such as deletion, insertion or substitution of one or more nucleotides, either naturally occurring or man induced, either randomly or in a targeted fashion.

The invention provides an isolated polynucleotide comprising a nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83
20 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID
25 NOs: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 and 933.

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

According to some embodiments of the invention the isolated polynucleotide
30 comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933.

According to some embodiments of the invention the isolated polynucleotide is set forth by SEQ ID NO: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 or 933.

The invention provides an isolated polynucleotide comprising a nucleic acid
5 sequence encoding a polypeptide which comprises an amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about
10 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 and 932.

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

The invention provides an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-
20 202, 524-844 and 926-932.

The invention provides an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

The invention provides an isolated polypeptide comprising an amino acid
25 sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to an amino acid sequence selected from the group
30 consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 and 932.

According to some embodiments of the invention, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

5 According to some embodiments of the invention, the polypeptide is set forth by SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844, 926-931 or 932.

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, 10 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, 15 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, 20 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, 25 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 amplexens, Dioclea spp, Dolichos spp., Dorycnium rectum, Echinochloa pyramidalis, Ehraffia spp., Eleusine coracana, Eragrestis spp., Erythrina spp., Eucalypfus spp., Euclea schimperi, Eulalia villosa, Pagopyrum spp., Feijoa sellowiana, Fragaria spp., Flemingia spp, Freycinetia banksli, Geranium thunbergii, 30 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,
 5 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,
 10 Populus spp., Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus
 communis, Quercus spp., Rhapsioleipsis 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,
 15 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,
 20 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.

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

30 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
5 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
10 exogenous polynucleotide of some embodiments of the invention and at least one promoter for directing transcription of the exogenous polynucleotide in a host cell (a plant cell). Further details of suitable transformation approaches are provided hereinbelow.

According to some embodiments of the invention, there is provided a nucleic
15 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.

20 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
25 to initiate transcription of RNA. The promoter controls where (e.g., which portion of a plant) and/or when (e.g., at which stage or condition in the lifetime of an organism) the gene is expressed.

Any suitable promoter sequence can be used by the nucleic acid construct of the present invention. Preferably the promoter is a constitutive promoter, a tissue-specific, or an abiotic stress-inducible promoter.
30

Suitable constitutive promoters include, for example, CaMV 35S promoter (SEQ ID NO:1184; Odell et al., Nature 313:810-812, 1985); Arabidopsis At6669

promoter (SEQ ID NO:1183; see PCT Publication No. WO04081173A2); 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 ltr1 promoter, barley B1, C, D hordein (*Theor Appl Gen* 98:1253-62, 1999; *Plant J* 4:343-55, 1993; *Mol Gen Genet* 250:750- 60, 1996), 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)], embryo specific promoters [e.g., rice OSH1 (Sato et al, Proc. Nati. Acad. Sci. USA, 93: 8117-8122), KNOX (Postma-Haarsma ef al, Plant Mol. Biol. 39:257-71, 1999), rice
5 oleosin (Wu et at, J. Biochem., 123:386, 1998)], and flower-specific promoters [e.g., AtPRP4, chalcone synthase (chsA) (Van der Meer, et al., Plant Mol. Biol. 15, 95-109, 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.
10 236:331-340, 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).

15 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
20 propagation in cells. The construct according to the present invention can be, for example, a plasmid, a bacmid, a phagemid, a cosmid, a phage, a virus or an artificial chromosome.

The nucleic acid construct of some embodiments of the invention can be utilized to stably or transiently transform plant cells. In stable transformation, the
25 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
30 monocotyledonous and dicotyledonous plants (Potrykus, I., Annu. Rev. Plant. Physiol., Plant. Mol. Biol. (1991) 42:205-225; Shimamoto et al., Nature (1989) 338:274-276).

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

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

(ii) Direct DNA uptake: Paszkowski et al., in *Cell Culture and Somatic Cell Genetics of Plants*, Vol. 6, Molecular Biology of Plant Nuclear Genes eds. Schell, J., and Vasil, L. K., Academic Publishers, San Diego, Calif. (1989) p. 52-68; including methods for direct uptake of DNA into protoplasts, Toriyama, K. et al. (1988) *Bio/Technology* 6:1072-1074. DNA uptake induced by brief electric shock of plant cells: Zhang et al. *Plant Cell Rep.* (1988) 7:379-384. Fromm et al. *Nature* (1986) 319:791-793. DNA injection into plant cells or tissues by particle bombardment, Klein et al. *Bio/Technology* (1988) 6:559-563; McCabe et al. *Bio/Technology* (1988) 6:923-926; Sanford, *Physiol. Plant.* (1990) 79:206-209; by the use of micropipette systems: Neuhaus et al., *Theor. Appl. Genet.* (1987) 75:30-36; Neuhaus and Spangenberg, *Physiol. Plant.* (1990) 79:213-217; glass fibers or silicon carbide whisker transformation of cell cultures, embryos or callus tissue, U.S. Pat. No. 5,464,765 or by the direct incubation of DNA with germinating pollen, DeWet et al. in *Experimental Manipulation of Ovule Tissue*, eds. Chapman, G. P. and Mantell, S. H. and Daniels, W. Longman, London, (1985) p. 197-209; and Ohta, *Proc. Natl. Acad. Sci. USA* (1986) 83:715-719.

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

with vacuum infiltration. The *Agrobacterium* system is especially viable in the creation of transgenic dicotyledonous plants.

There are various methods of direct DNA transfer into plant cells. In electroporation, the protoplasts are briefly exposed to a strong electric field. In
5 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
10 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
15 produced such that the regenerated plant has the identical traits and characteristics of the parent transgenic plant. Therefore, it is preferred that the transformed plant be regenerated by micropropagation which provides a rapid, consistent reproduction of the transformed plants.

Micropropagation is a process of growing new generation plants from a single
20 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
25 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
30 medium or growth conditions between stages. Thus, the micropropagation process involves four basic stages: Stage one, initial tissue culturing; stage two, tissue culture multiplication; stage three, differentiation and plant formation; and stage four, greenhouse culturing and hardening. During stage one, initial tissue culturing, the tissue

culture is established and certified contaminant-free. During stage two, the initial tissue culture is multiplied until a sufficient number of tissue samples are produced to meet production goals. During stage three, the tissue samples grown in stage two are divided and grown into individual plantlets. At stage four, the transformed plantlets are transferred to a greenhouse for hardening where the plants' tolerance to light is gradually increased so that it can be grown in the natural environment.

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

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

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

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

Suitable virus strains can be obtained from available sources such as, for example, the American Type Culture Collection (ATCC) or by isolation from infected plants. Isolation of viruses from infected plant tissues can be effected by techniques well known in the art such as described, for example by Foster and Tatlor, Eds. "Plant

Virology Protocols: From Virus Isolation to Transgenic Resistance (Methods in Molecular Biology (Humana Pr), Vol 81)", Humana Press, 1998. Briefly, tissues of an infected plant believed to contain a high concentration of a suitable virus, preferably young leaves and flower petals, are ground in a buffer solution (e.g., phosphate buffer solution) to produce a virus infected sap which can be used in subsequent inoculations.

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

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

In one embodiment, a plant viral polynucleotide is provided in which the native coat protein coding sequence has been deleted from a viral polynucleotide, a non-native plant viral coat protein coding sequence and a non-native promoter, preferably the subgenomic promoter of the non-native coat protein coding sequence, capable of expression in the plant host, packaging of the recombinant plant viral polynucleotide, and ensuring a systemic infection of the host by the recombinant plant viral polynucleotide, has been inserted. Alternatively, the coat protein gene may be inactivated by insertion of the non-native polynucleotide sequence within it, such that a protein is produced. The recombinant plant viral polynucleotide may contain one or more additional non-native subgenomic promoters. Each non-native subgenomic promoter is capable of transcribing or expressing adjacent genes or polynucleotide

sequences in the plant host and incapable of recombination with each other and with native subgenomic promoters. Non-native (foreign) polynucleotide sequences may be inserted adjacent the native plant viral subgenomic promoter or the native and a non-native plant viral subgenomic promoters if more than one polynucleotide sequence is included. The non-native polynucleotide sequences are transcribed or expressed in the host plant under control of the subgenomic promoter to produce the desired products.

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

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

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

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

Techniques for inoculation of viruses to plants may be found in Foster and Taylor, eds. "Plant Virology Protocols: From Virus Isolation to Transgenic Resistance (Methods in Molecular Biology (Humana Pr), Vol 81)", Humana Press, 1998; Maramorosh and Koprowski, eds. "Methods in Virology" 7 vols, Academic Press, New

York 1967-1984; Hill, S.A. "Methods in Plant Virology", Blackwell, Oxford, 1984; Walkey, D.G.A. "Applied Plant Virology", Wiley, New York, 1985; and Kado and Agrawa, eds. "Principles and Techniques in Plant Virology", Van Nostrand-Reinhold, New York.

5 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
10 chloroplasts per cell to about one. Then, the exogenous polynucleotide is introduced via particle bombardment into the cells with the aim of introducing at least one exogenous polynucleotide molecule into the chloroplasts. The exogenous polynucleotides selected such that it is integratable into the chloroplast's genome via homologous recombination which is readily effected by enzymes inherent to the chloroplast. To this end, the
15 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
20 polynucleotide. Further details relating to this technique are found in U.S. Pat. Nos. 4,945,050; and 5,693,507 which are incorporated herein by reference. A polypeptide can thus be produced by the protein expression system of the chloroplast and become integrated into the chloroplast's inner membrane.

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

 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
5 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
10 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.
15 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.

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

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

30 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.

In addition, the endogenous homolog of the exogenous polynucleotide or polypeptide of the invention, or a fragment of the endogenous homolog (e.g. introns or untranslated regions) in the plant can be used as a marker 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, yield, abiotic stress tolerance). These genes (DNA or RNA sequence) may contain or be linked to polymorphic sites or genetic markers on the genome such as restriction fragment length polymorphism (RFLP), microsatellites and single nucleotide polymorphism (SNP), DNA fingerprinting (DFP), amplified fragment length polymorphism (AFLP), expression level polymorphism, polymorphism of the encoded polypeptide and any other polymorphism at the DNA or RNA sequence.

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

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

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

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

Abiotic stress tolerance - Transformed (*i.e.*, expressing the transgene) and
10 non-transformed (wild type) plants are exposed to an abiotic stress condition, such as water deprivation, suboptimal temperature (low temperature, high temperature), nutrient deficiency, nutrient excess, a salt stress condition, osmotic stress, heavy metal toxicity, anaerobiosis, atmospheric pollution and UV irradiation.

Salinity tolerance assay – Transgenic plants with tolerance to high salt
15 concentrations are expected to exhibit better germination, seedling vigor or growth in high salt. Salt stress can be effected in many ways such as, for example, by irrigating the plants with a hyperosmotic solution, by cultivating the plants hydroponically in a hyperosmotic growth solution (e.g., Hoagland solution), or by culturing the plants in a hyperosmotic growth medium [e.g., 50 % Murashige-Skoog medium (MS medium)].
20 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
25 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
30 example 50 mM, 100 mM, 200 mM, 400 mM NaCl) applied from the bottom and from above to ensure even dispersal of salt. Following exposure to the stress condition the plants are frequently monitored until substantial physiological and/or morphological effects appear in wild type plants. Thus, the external phenotypic appearance, degree of

wilting and overall success to reach maturity and yield progeny are compared between control and transgenic plants.

Quantitative parameters of tolerance measured include, but are not limited to, the average wet and dry weight, growth rate, leaf size, leaf coverage (overall leaf area), the weight of the seeds yielded, the average seed size and the number of seeds produced per plant. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher biomass than wild-type plants, are identified as abiotic stress tolerant plants.

Osmotic tolerance test - Osmotic stress assays (including sodium chloride and mannitol assays) are conducted to determine if an osmotic stress phenotype was sodium chloride-specific or if it was a general osmotic stress related phenotype. Plants which are tolerant to osmotic stress may have more tolerance to drought and/or freezing. For salt and osmotic stress germination experiments, the medium is supplemented for example with 50 mM, 100 mM, 200 mM NaCl or 100 mM, 200 mM NaCl, 400 mM mannitol.

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

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

controls for each of two criteria: tolerance to the drought conditions and recovery (survival) following re-watering.

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

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

Water use efficiency – can be determined as the biomass produced per unit
15 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
20 following Formula I:

Formula I

$$\text{RWC} = [(\text{FW} - \text{DW}) / (\text{TW} - \text{DW})] \times 100$$

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

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

Nitrogen use efficiency – To analyze whether the transgenic Arabidopsis plants are more responsive to nitrogen, plants 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.

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

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

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

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

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

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

Evaluation of growth rate can be done by measuring plant biomass produced, rosette area, leaf size or root length per time (can be measured in cm^2 per day of leaf area).

Relative growth rate area can be calculated using Formula II.

Formula II:

Relative growth area rate = 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.

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

The 1000 seeds weight can be calculated using formula III:

Formula III:

1000 Seed Weight = number of seed in sample/ sample weight X 1000

The Harvest Index can be calculated using Formula IV

Formula IV:

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

Grain protein concentration - Grain protein content ($\text{g grain protein m}^{-2}$) 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
5 (g grain protein kg^{-1} grain).

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

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
15 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
20 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
25 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
30 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.

5 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
10 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
15 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)];
20 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.

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

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

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

The plant oil (including the seed oil and/or the vegetative portion oil) produced according to the method of the invention may be combined with a variety of other ingredients. The specific ingredients included in a product are determined according to the intended use. Exemplary products include animal feed, raw material for chemical
5 modification, biodegradable plastic, blended food product, edible oil, biofuel, cooking oil, lubricant, biodiesel, snack food, cosmetics, and fermentation process raw material. Exemplary products to be incorporated to the plant oil include animal feeds, human food products such as extruded snack foods, breads, as a food binding agent, aquaculture feeds, fermentable mixtures, food supplements, sport drinks, nutritional
10 food bars, multi-vitamin supplements, diet drinks, and cereal foods. According to some embodiments of the invention, the oil comprises a seed oil.

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

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

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

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

20 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.

25 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
30 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 sub-ranges 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 sub-ranges 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
5 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
10 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
15 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
20 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.

25 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.

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
30 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.

EXAMPLES

Reference is now made to the following examples, which together with the
5 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
10 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
15 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);
20 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;
25 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
30 Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for

Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader.

5 All the information contained therein is incorporated herein by reference.

EXAMPLE 1

GENE IDENTIFICATION AND GENE ROLE PREDICTION USING 10 BIOINFORMATICS TOOLS

The present inventors have identified polynucleotides which can increase plant yield, seed yield, oil yield, oil content, biomass, growth rate, abiotic stress tolerance, nitrogen use efficiency and/or vigor of a plant, as follows.

15 The nucleotide sequence datasets used here were from publicly available databases or from sequences obtained 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

20 Arabidopsis genome [TAIR genome version 6 (Hypertext Transfer Protocol://World Wide Web (dot) arabidopsis (dot) org/)];

Rice genome [IRGSP build 4.0 (Hypertext Transfer Protocol://rgp (dot) dna (dot) affrc (dot) go (dot) jp/IRGSP/)];

25 Poplar [Populus trichocarpa release 1.1 from JGI (assembly release v1.0) (Hypertext Transfer Protocol://World Wide Web (dot) genome (dot) jgi-psf (dot) org/)];

Brachypodium [JGI 4x assembly, Hypertext Transfer Protocol://World Wide Web (dot) brachpodium (dot) org)];

Soybean [DOE-JGI SCP, version Glyma0 (Hypertext Transfer Protocol://World Wide Web (dot) phytozome (dot) net/)];

30 Grape [French-Italian Public Consortium for Grapevine Genome Characterization grapevine genome (Hypertext Transfer Protocol:// World Wide Web (dot) genoscope (dot) cns (dot) fr /)];

Castobean [TIGR/J Craig Venter Institute 4x assembly [(Hypertext Transfer Protocol://msc (dot) jvci (dot) org/r communis)];

Sorghum [DOE-JGI SCP, version Sbi1 [Hypertext Transfer Protocol://World Wide Web (dot) phytozome (dot) net/)];

5 Partially assembled genome of Maize [Hypertext Transfer Protocol://maizesequence (dot) org/];

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

10 GenBank versions 154, 157, 160, 161, 164, 165, 166 and 168 (Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov/dbEST/);

RefSeq (Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov/RefSeq/);

TAIR (Hypertext Transfer Protocol://World Wide Web (dot) arabidopsis (dot) org/);

15 ***Protein and pathway databases***

Uniprot [Hypertext Transfer Protocol://World Wide Web (dot) uniprot (dot) org/].

AraCyc [Hypertext Transfer Protocol://World Wide Web (dot) arabidopsis (dot) org/biocyc/index (dot) jsp].

20 ENZYME [Hypertext Transfer Protocol://expasy (dot) org/enzyme/].

Microarray datasets were downloaded from:

GEO (Hypertext Transfer Protocol://World Wide Web.ncbi.nlm.nih.gov/geo/)

TAIR (Hypertext Transfer Protocol://World Wide Web.arabidopsis.org/).

Proprietary microarray data (See WO2008/122980 and Example 3 below).

25 ***QTL and SNPs information***

Gramene [Hypertext Transfer Protocol://World Wide Web (dot) gramene (dot) org/qtl/].

Panzea [Hypertext Transfer Protocol://World Wide Web (dot) panzea (dot) org/index (dot) html].

30 ***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 [Hypertext Transfer Protocol://blast (dot) ncbi (dot) nlm (dot) nih (dot) gov /Blast (dot) cgi] against all plant UniProt [Hypertext Transfer Protocol://World Wide Web (dot) uniprot (dot) org/] 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 [Hypertext Transfer Protocol://World Wide Web (dot) ebi (dot) ac (dot) uk/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 [Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov /Blast (dot) cgi] to validate the accuracy of the predicted protein sequence, and for efficient detection of orthologs.

5 ***Gene expression profiling*** - Several data sources were exploited for gene expression profiling which combined 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 developmental stages and environmental conditions and which are associated with different phenotypes.

10 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, biomass, growth rate, vigor, oil content, abiotic stress tolerance of plants and nitrogen use efficiency.

15 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
20 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
25 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
30 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 [Hypertext Transfer Protocol://World Wide Web (dot) icugi (dot) org/] confirmed the accuracy of the sequencing and assembly. Expression patterns of selected genes fitted well their qRT-PCR data.

EXAMPLE 2

PRODUCTION OF ARABIDOPSIS TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS OF YIRLD, 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 [Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent (dot) com/Scripts/PDS (dot) asp?lPage=50879]. 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 [Hypertext Transfer Protocol://World Wide Web (dot) davidmlane (dot) com/hyperstat/A34739 (dot) html].

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 using TRIzol Reagent from Invitrogen [Hypertext Transfer Protocol://World Wide Web (dot) invitrogen (dot) com/content (dot) cfm?pageid=469]. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table 1 below.

Table 1
Tissues used for Arabidopsis transcriptom expression sets

| <i>Expression Set</i> | <i>Set ID</i> |
|------------------------------|----------------------|
| Root | A |
| Leaf | B |
| Flower | C |
| Seed 5 DAF | D |
| Seed 12 DAF | E |

Table 1: Provided are the identification (ID) letters of each of the *Arabidopsis* expression sets (A-E). DAF = days after flowering.

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.

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 grown 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 grown 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 at Hypertext Transfer Protocol://rsbweb (dot) nih (dot) gov/. 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 V.

Formula V:

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

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

Formula VI

10 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.

15 *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.

25 *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

30

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 software package.

5 **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.

10 **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 VII.

15 **Formula VII:**

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

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

Experimental Results

20 Nine different *Arabidopsis* ecotypes were grown and characterized for 18 parameters (named as vectors). Data parameters are summarized in Table 2, below.

25 **Table 2**
***Arabidopsis* correlated parameters (vectors)**

| <i>Correlated parameter with</i> | <i>Correlation ID</i> |
|--|------------------------------|
| Root length day 13 (cm) | 1 |
| Root length day 7 (cm) | 2 |
| Relative root growth (cm /day) day 13 | 3 |
| Fresh weight per plant (gr) at bolting stage | 4 |
| Dry matter per plant (gr) | 5 |
| Vegetative growth rate (cm ² / day) till 8 true leaves | 6 |
| Blade circularity | 7 |
| Lamina width (cm) | 8 |
| Lamina length (cm) | 9 |
| Total leaf area per plant (cm) | 10 |
| 1000 Seed weight (gr) | 11 |

| <i>Correlated parameter with</i> | <i>Correlation ID</i> |
|----------------------------------|-----------------------|
| 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 2. Provided are the Arabidopsis correlated parameters (correlation ID Nos. 1-18). Abbreviations: Cm = centimeter(s); gr = gram(s); mg = milligram(s).

5 The characterized values are summarized in Tables 3 and 4 below.

Table 3
Measured parameters in Arabidopsis ecotypes

| <i>Ecotype</i> | <i>Seed yield per plant (gr)</i> | <i>Oil yield per plant (mg)</i> | <i>Oil % per seed</i> | <i>1000 Seed weight (gr)</i> | <i>Dry matter per plant (gr)</i> | <i>Harvest Index</i> | <i>Total leaf area per plant (cm)</i> | <i>Seeds per silique</i> | <i>Silique length (cm)</i> |
|----------------|----------------------------------|---------------------------------|-----------------------|------------------------------|----------------------------------|----------------------|---------------------------------------|--------------------------|----------------------------|
| 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 |

10 Table 3. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: Seed yield per plant (gram); oil yield per plant (mg); oil % per seed; 1000 seed weight (gr); dry matter per plant (gr); harvest index; total leaf area per plant (cm); seeds per silique; Silique length (cm).

Table 4
Additional measured parameters in Arabidopsis ecotypes

15

| <i>Ecotype</i> | <i>Veg. GR</i> | <i>Relat. root growth</i> | <i>Root length day 7</i> | <i>Root length day 13</i> | <i>Fresh weight per plant</i> | <i>Lam. Leng.</i> | <i>Lam. width</i> | <i>Leaf width/length</i> | <i>Blade circularity</i> |
|----------------|----------------|---------------------------|--------------------------|---------------------------|-------------------------------|-------------------|-------------------|--------------------------|--------------------------|
| 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 |

| Ecotype | Veg. GR | Relat. root growth | Root length day 7 | Root length day 13 | Fresh weight per plant | Lam. Leng. | Lam. width | Leaf width/length | Blade circularity |
|----------|---------|--------------------|-------------------|--------------------|------------------------|------------|------------|-------------------|-------------------|
| Kondara | 0.645 | 0.774 | 1.163 | 6.372 | 4.338 | 4.597 | 1.650 | 0.273 | 0.376 |
| Ler-1 | 0.430 | 0.606 | 1.284 | 5.649 | 3.467 | 3.877 | 1.510 | 0.305 | 0.394 |
| Mt-0 | 0.384 | 0.701 | 1.414 | 7.060 | 3.479 | 3.717 | 1.817 | 0.335 | 0.491 |
| Shakdara | 0.471 | 0.782 | 1.251 | 7.041 | 3.710 | 4.149 | 1.668 | 0.307 | 0.409 |

Table 4. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: Veg. GR = vegetative growth rate (cm²/day) until 8 true leaves; Relat. Root growth = relative root growth (cm/day); Root length day 7 (cm); Root length day 13 (cm); fresh weight per plant (gr) at bolting stage; Lam. Leng. = Lamina length (cm); Lam. Width = Lamina width (cm); Leaf width/length; Blade circularity.

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Tables 5-7, below, provide the selected genes, 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. A positive correlation indicates that the expression of the gene in a certain tissue or developmental stage and the correlation vector (phenotype performance) are positively associated (both, expression and phenotypic performance increase or decrease simultaneously) while a negative correlation indicates a negative association (while the one is increasing the other is decreasing and vice versa).

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Table 5

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

| Gene Name | Corr. Vec. | Exp. Set | R | Corr. Vec. | Exp. Set | R | Corr. Vec. | Exp. Set | R |
|-----------|------------|----------|--------|------------|----------|--------|------------|----------|--------|
| BDL117 | 1 | C | -0.907 | 1 | A | -0.809 | 13 | D | 0.961 |
| BDL118 | 13 | A | 0.817 | 6 | A | 0.805 | 5 | D | -0.821 |
| BDL118 | 17 | D | 0.958 | 17 | D | 0.834 | 8 | D | -0.833 |
| BDL118 | 8 | D | -0.845 | 10 | D | -0.912 | 10 | D | -0.975 |
| BDL118 | 4 | D | -0.904 | | | | | | |
| BDL126 | 5 | B | 0.942 | | | | | | |
| BDL138 | 16 | C | 0.841 | 15 | C | 0.813 | 16 | B | 0.878 |
| BDL138 | 15 | B | 0.896 | 13 | A | 0.94 | | | |

| <i>Gene Name</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> |
|------------------|-------------------|-----------------|----------|-------------------|-----------------|----------|-------------------|-----------------|----------|
| BDL140 | 14 | C | 0.841 | 3 | C | 0.821 | 11 | C | 0.855 |
| BDL140 | 14 | B | 0.836 | 11 | B | 0.855 | 7 | E | -0.812 |
| BDL140 | 6 | E | 0.889 | 13 | D | 0.826 | 14 | D | 0.862 |
| BDL147 | 16 | B | 0.948 | 15 | B | 0.898 | | | |
| BDL149 | 14 | B | 0.83 | 3 | B | 0.891 | 14 | A | 0.951 |
| BDL152 | 16 | D | 0.969 | 3 | D | 0.855 | 15 | D | 0.987 |
| BDL153 | 14 | C | 0.836 | 11 | C | 0.823 | 14 | A | -0.862 |
| BDL153 | 11 | A | 0.88 | 8 | D | -0.81 | | | |
| BDL154 | 11 | C | 0.874 | | | | | | |
| BDL155 | 16 | B | 0.829 | 16 | A | 0.86 | | | |
| BDL156 | 3 | C | 0.923 | 14 | B | 0.901 | | | |
| BDL157 | 3 | B | 0.854 | 2 | B | -0.825 | 5 | D | -0.803 |
| BDL157 | 17 | D | 0.923 | 9 | D | -0.809 | 8 | D | -0.834 |
| BDL157 | 10 | D | -0.915 | 4 | D | -0.89 | | | |
| BDL158 | 8 | B | 0.953 | 10 | B | 0.945 | 4 | B | 0.899 |
| BDL158 | 11 | A | -0.833 | | | | | | |
| BDL160 | 7 | C | 0.82 | 18 | C | 0.972 | 8 | A | 0.918 |
| BDL160 | 8 | A | 0.839 | 8 | A | 0.834 | 10 | A | 0.93 |
| BDL160 | 10 | A | 0.93 | 4 | A | 0.862 | 1 | E | 0.864 |
| BDL160 | 1 | E | 0.841 | 2 | E | 0.861 | 2 | E | 0.839 |
| BDL160 | 8 | D | 0.867 | 8 | D | 0.811 | 10 | D | 0.824 |
| BDL162 | 5 | B | 0.89 | | | | | | |
| BDL163 | 16 | B | 0.925 | 15 | B | 0.884 | 18 | E | 0.828 |
| BDL165 | 8 | B | 0.952 | 10 | B | 0.902 | 4 | B | 0.821 |
| BDL165 | 8 | E | 0.807 | 15 | E | 0.816 | 11 | D | 0.846 |
| BDL167 | 16 | B | 0.899 | 15 | B | 0.946 | 17 | D | 0.859 |
| BDL167 | 2 | D | -0.806 | | | | | | |
| BDL168 | 16 | C | 0.97 | 15 | C | 0.929 | 8 | B | 0.931 |
| BDL168 | 10 | B | 0.88 | 13 | A | -0.835 | 5 | D | -0.911 |
| BDL168 | 8 | D | -0.946 | 10 | D | -0.849 | | | |
| BDL169 | 14 | B | -0.82 | 11 | B | -0.848 | 12 | A | 0.901 |
| BDL171 | 14 | C | -0.842 | 2 | B | -0.844 | 5 | A | 0.803 |
| BDL171 | 1 | A | -0.851 | 2 | A | -0.821 | 5 | D | -0.827 |
| BDL171 | 17 | D | 0.958 | 17 | D | 0.853 | 17 | D | 0.825 |
| BDL171 | 9 | D | -0.82 | 8 | D | -0.87 | 16 | D | 0.857 |
| BDL171 | 10 | D | -0.901 | 10 | D | -0.948 | 4 | D | -0.808 |
| BDL171 | 4 | D | -0.932 | 15 | D | 0.838 | | | |
| BDL173 | 7 | B | 0.892 | 9 | B | -0.874 | 18 | B | 0.816 |
| BDL173 | 17 | D | 0.948 | 8 | D | -0.888 | 10 | D | -0.974 |
| BDL173 | 4 | D | -0.871 | | | | | | |
| BDL174 | 17 | C | 0.901 | 5 | D | -0.917 | 8 | D | -0.879 |
| BDL174 | 10 | D | -0.85 | | | | | | |
| BDL176 | 5 | D | -0.907 | 8 | D | -0.913 | 13 | D | 0.93 |

| <i>Gene Name</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> |
|------------------|-------------------|-----------------|----------|-------------------|-----------------|----------|-------------------|-----------------|----------|
| BDL177 | 17 | C | 0.919 | 17 | B | 0.91 | 17 | D | 0.82 |
| BDL181 | 16 | C | 0.893 | 15 | C | 0.838 | 8 | B | 0.816 |
| BDL181 | 12 | A | 0.931 | 16 | A | 0.823 | 18 | E | 0.819 |
| BDL181 | 16 | D | 0.865 | 15 | D | 0.856 | | | |
| BDL182 | 12 | A | 0.913 | 12 | D | 0.825 | | | |
| BDL183 | 16 | B | 0.915 | 15 | B | 0.898 | | | |
| BDL186 | 12 | B | 0.944 | 11 | B | 0.833 | 8 | D | -0.807 |
| BDL187 | 16 | B | 0.908 | 15 | B | 0.835 | 5 | D | -0.803 |
| BDL187 | 8 | D | -0.892 | | | | | | |
| BDL188 | 14 | B | 0.904 | 12 | D | 0.964 | 3 | D | 0.857 |
| BDL188 | 2 | D | -0.886 | | | | | | |
| BDL189 | 16 | B | 0.951 | 15 | B | 0.907 | 6 | E | -0.854 |
| BDL189 | 8 | D | -0.821 | 1 | D | -0.938 | | | |
| BDL190 | 16 | B | 0.857 | 15 | B | 0.91 | 7 | E | -0.865 |
| BDL192 | 7 | B | 0.907 | 9 | B | -0.806 | 17 | D | 0.91 |
| BDL192 | 10 | D | -0.907 | 4 | D | -0.94 | 2 | D | -0.82 |
| BDL193 | 8 | C | 0.846 | 12 | B | 0.904 | 11 | B | 0.876 |
| BDL193 | 11 | A | 0.885 | 11 | E | 0.923 | 5 | D | -0.801 |
| BDL193 | 8 | D | -0.802 | 8 | D | -0.844 | 10 | D | -0.806 |
| BDL194 | 12 | B | 0.933 | 18 | D | 0.877 | | | |
| BDL196 | 16 | D | 0.917 | 15 | D | 0.937 | | | |
| BDL197 | 13 | A | 0.91 | 8 | D | 0.837 | | | |
| BDL200 | 2 | C | 0.818 | 16 | B | 0.864 | 15 | B | 0.832 |
| BDL200 | 14 | A | 0.917 | 1 | E | 0.815 | 3 | D | 0.851 |
| BDL201 | 9 | C | 0.846 | 5 | D | 0.916 | 17 | D | -0.906 |
| BDL201 | 8 | D | 0.954 | 10 | D | 0.947 | 4 | D | 0.865 |
| BDL203 | 10 | B | 0.926 | 4 | B | 0.893 | 14 | A | -0.828 |
| BDL219 | 1 | A | 0.879 | 2 | A | 0.821 | 9 | E | -0.801 |
| BDL220 | 8 | B | 0.822 | 10 | B | 0.844 | 4 | B | 0.839 |
| BDL221 | 12 | C | 0.897 | 16 | C | 0.917 | 15 | C | 0.814 |
| BDL221 | 3 | B | 0.936 | 9 | D | -0.936 | 6 | D | -0.897 |
| BDL221 | 4 | D | -0.808 | | | | | | |
| BDL222 | 1 | B | 0.829 | 2 | B | 0.887 | 1 | A | 0.875 |
| BDL222 | 2 | A | 0.849 | 2 | D | 0.925 | | | |
| BDL223 | 14 | C | 0.93 | 14 | B | 0.835 | 3 | B | 0.851 |
| BDL223 | 14 | A | 0.831 | | | | | | |
| BDL224 | 5 | E | -0.826 | 9 | E | -0.872 | | | |
| BDL225 | 7 | C | 0.833 | 15 | B | -0.806 | 13 | A | -0.836 |
| BDL227 | 2 | A | -0.931 | | | | | | |
| BDL229 | 10 | B | 0.858 | 2 | D | 0.832 | | | |
| BDL231 | 16 | B | 0.911 | 15 | B | 0.869 | 11 | D | 0.88 |
| BDL233 | 14 | C | -0.885 | | | | | | |
| BDL235 | 11 | E | 0.808 | 12 | D | 0.818 | 2 | D | -0.887 |

| <i>Gene Name</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> | <i>Corr. Vec.</i> | <i>Exp. Set</i> | <i>R</i> |
|------------------|-------------------|-----------------|----------|-------------------|-----------------|----------|-------------------|-----------------|----------|
| BDL240 | 1 | D | -0.808 | | | | | | |
| BDL241 | 13 | A | -0.88 | | | | | | |
| BDL242 | 11 | B | 0.889 | | | | | | |
| BDL243 | 11 | B | 0.929 | | | | | | |
| BDL245 | 3 | A | -0.863 | 11 | A | -0.832 | 16 | D | -0.806 |
| BDL247 | 16 | B | 0.816 | | | | | | |
| BDL248 | 13 | A | -0.829 | | | | | | |
| BDL249 | 8 | C | -0.84 | 16 | E | -0.808 | 15 | E | -0.892 |
| BDL250 | 9 | A | -0.805 | 2 | E | -0.85 | 17 | D | 0.815 |
| BDL250 | 10 | D | -0.809 | 4 | D | -0.804 | 1 | D | -0.9 |
| BDL251 | 18 | C | 0.802 | 7 | D | -0.861 | | | |
| BDL47 | 8 | B | 0.845 | | | | | | |
| BDL49 | 7 | E | 0.805 | 9 | E | -0.883 | 6 | E | -0.809 |
| BDL62 | 18 | A | 0.862 | 6 | E | -0.869 | 13 | D | 0.829 |
| BDL75 | 11 | C | 0.816 | 5 | B | 0.945 | 8 | B | 0.823 |
| BDL79 | 7 | B | 0.876 | 18 | B | 0.841 | 12 | D | 0.884 |
| BDL79 | 2 | D | -0.938 | | | | | | |
| BDL81 | 8 | C | 0.897 | 12 | B | 0.803 | 1 | D | -0.81 |
| BDL81 | 2 | D | -0.86 | | | | | | |
| BDL83 | 3 | C | -0.861 | 2 | C | 0.905 | | | |
| BDL85 | 8 | D | 0.82 | | | | | | |

Table 5. Provided are the correlations between the expression level of selected genes 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 2, 3 and 4. Exp. Set = expression set according to Table 1 hereinabove.

Table 6 hereinbelow provides data about the homologous of selected genes, 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).

Table 6
Correlation between the expression level of homologous of the selected genes in specific tissues or developmental stages and the phenotypic performance across Arabidopsis ecotypes

| <i>Gene Name</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> |
|------------------|-----------------|----------------------|----------|
| BDL155 H1 | leaf | relative root growth | 0.814 |
| BDL155 H1 | seed5daf | Silique length | -0.855 |
| BDL171 H0 | leaf | Leaf width/length | 0.835 |
| BDL171 H0 | seed5daf | Dry matter per plant | -0.82 |
| BDL171 H0 | seed5daf | Lamina width | -0.813 |

| <i>Gene Name</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> |
|------------------|-----------------|----------------------|----------|
| BDL183 H0 | seed12daf | Blade circularity | -0.878 |
| BDL231 H0 | flower | seed weight | 0.825 |
| BDL231 H0 | leaf | Silique length | 0.816 |
| BDL231 H0 | leaf | relative root growth | 0.854 |
| BDL231 H0 | root | seed weight | 0.92 |
| BDL248 H0 | seed5daf | relative root growth | 0.851 |
| BDL70 H0 | seed12daf | Lamina length | -0.816 |
| BDL70 H0 | seed5daf | seed yield per plant | -0.82 |

Table 6. Provided are the correlations between the expression levels of homologues of selected Arabidopsis genes 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 2, 3 and 4; Exp. Set = expression set specified in Table 1.

EXAMPLE 3

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 [[Hypertext Transfer Protocol://World Wide Web \(dot\) chem \(dot\) agilent \(dot\) com/Scripts/PDS \(dot\) asp?IPage=50879](http://WorldWideWeb(dot)chem(dot)agilent(dot)com/Scripts/PDS(dot)asp?IPage=50879)]. 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 [[Hypertext Transfer Protocol://World Wide Web \(dot\) davidmlane \(dot\) com/hyperstat/A34739 \(dot\) html](http://WorldWideWeb(dot) davidmlane(dot) com/hyperstat/A34739(dot)html)].

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 using TRIzol Reagent from Invitrogen [[Hypertext Transfer Protocol://World Wide Web \(dot\) invitrogen \(dot\) com/content](http://WorldWideWeb(dot) invitrogen(dot) com/content)]

(dot)cfm?pageid=469]. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in Table 7 below.

Table 7
Tissues used for Arabidopsis transcriptom expression sets

| <i>Expression Set</i> | <i>Set ID</i> |
|---|---------------|
| 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 7: Provided are the identification (ID) letters of each of the Arabidopsis expression sets.

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 μ l of TRIzol Reagent. To the homogenized lysate, 100 μ l of chloroform was added followed by precipitation using isopropanol and two washes with 75 % ethanol. The RNA was eluted in 30 μ l 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).

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 KNO₃, supplemented with 2 mM CaCl₂, 1.25 mM KH₂PO₄, 1.50 mM MgSO₄, 5 mM KCl, 0.01 mM H₃BO₃ 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 KNO₃, supplemented with 2 mM CaCl₂, 1.25 mM KH₂PO₄, 1.50 mM MgSO₄, 0.01 mM H₃BO₃ 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 [Hypertext Transfer Protocol://rsb (dot) info (dot) nih (dot) gov/ij/] 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 [Hypertext Transfer Protocol://rsbweb (dot) nih (dot) gov/]. 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 8, hereinbelow.

Table 8
Arabidopsis correlated parameters (vectors)

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

| <i>Correlated parameter with</i> | <i>Correlation Id</i> |
|--|-----------------------|
| 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 8. 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 [cm²] (measured using digital analysis); RGR (relative growth rate) of Rosette Area at the indicated day [cm²/day] (calculated using Formula II); t50 Flowering [day] (the day in which 50% of plant flower); seed yield/ rosette area at day 10 [gr/cm²] (calculated); seed yield/leaf blade [gr/cm²] (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 at Hypertext Transfer Protocol://rsbweb (dot) nih (dot) gov/. 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.

5 **Relative growth rate area:** The relative growth rate of the rosette and the leaves was calculated according to Formula II as described above.

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
10 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,
15 weighed and divided by the number of plants. Dry weight = total weight of the vegetative portion above ground (excluding roots) after drying at 30 °C in a drying chamber.

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

20 **T₅₀ 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
25 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
30 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

5 10 different Arabidopsis accessions (ecotypes) were grown and characterized for 37 parameters as described above. The average for each of the measured parameters was calculated using the JMP software and values are summarized in Table 9 below. Subsequent correlation analysis between the various transcriptom sets (Table 7) was conducted. Following are the results integrated to the database.

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Table 9

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

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| Gene Name | Exp. Set | Corr. Vec. | R | Exp. Set | Corr. Vec. | R | Exp. Set | Corr. Vec. | R |
|------------------|-----------------|-------------------|----------|-----------------|-------------------|----------|-----------------|-------------------|----------|
| BDL117 | D | 31 | -0.748 | A | 12 | -0.784 | | | |
| BDL118 | C | 11 | -0.914 | C | 10 | -0.723 | C | 14 | -0.75 |
| BDL118 | C | 8 | 0.74 | | | | | | |
| BDL118 | D | 31 | -0.766 | B | 30 | -0.752 | D | 30 | -0.794 |
| BDL118 | D | 29 | -0.715 | B | 27 | 0.791 | A | 11 | -0.747 |
| BDL126 | A | 1 | -0.719 | | | | | | |
| BDL126 | D | 25 | 0.801 | A | 6 | -0.715 | A | 2 | -0.711 |
| BDL138 | B | 28 | -0.797 | B | 27 | -0.786 | C | 9 | -0.754 |
| BDL140 | D | 28 | -0.761 | | | | | | |
| BDL147 | D | 30 | -0.703 | C | 11 | -0.7 | | | |
| BDL149 | C | 9 | -0.744 | A | 1 | 0.703 | | | |
| BDL152 | A | 14 | -0.705 | | | | | | |
| BDL154 | B | 26 | 0.896 | B | 32 | 0.76 | B | 33 | 0.861 |
| BDL155 | C | 9 | -0.719 | | | | | | |
| BDL155_H0 | B | 28 | 0.768 | D | 28 | 0.757 | D | 29 | 0.751 |
| BDL155_H0 | C | 7 | 0.743 | | | | | | |
| BDL156 | D | 24 | 0.725 | D | 21 | 0.734 | | | |
| BDL157 | B | 29 | 0.714 | | | | | | |
| BDL158 | B | 30 | -0.722 | B | 27 | 0.708 | | | |
| BDL160 | A | 12 | -0.807 | C | 9 | -0.771 | C | 5 | -0.797 |
| BDL160 | C | 2 | -0.816 | | | | | | |
| BDL162 | B | 31 | -0.792 | | | | | | |
| BDL165 | C | 11 | -0.755 | C | 8 | 0.748 | | | |

| <i>Gene Name</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> |
|------------------|-----------------|-------------------|----------|-----------------|-------------------|----------|-----------------|-------------------|----------|
| BDL117 | D | 31 | -0.748 | A | 12 | -0.784 | | | |
| BDL118 | C | 11 | -0.914 | C | 10 | -0.723 | C | 14 | -0.75 |
| BDL118 | C | 8 | 0.74 | | | | | | |
| BDL167 | C | 10 | -0.898 | C | 14 | -0.894 | C | 13 | -0.874 |
| BDL167 | C | 15 | 0.737 | | | | | | |
| BDL167 | D | 30 | -0.75 | C | 11 | -0.709 | C | 7 | -0.821 |
| BDL168 | A | 9 | 0.703 | A | 11 | -0.786 | | | |
| BDL168 | B | 30 | -0.73 | D | 21 | 0.721 | B | 27 | 0.738 |
| BDL169 | A | 11 | -0.804 | A | 10 | -0.746 | A | 14 | -0.714 |
| BDL169 | A | 13 | -0.708 | A | 8 | 0.707 | | | |
| BDL171 | B | 33 | 0.865 | A | 9 | -0.735 | | | |
| BDL171 | D | 25 | 0.879 | B | 26 | 0.891 | D | 21 | 0.765 |
| BDL171 | D | 20 | 0.711 | B | 29 | 0.735 | B | 32 | 0.741 |
| BDL171_ H0 | C | 15 | 0.719 | C | 8 | 0.78 | | | |
| BDL173 | B | 26 | 0.723 | B | 33 | 0.72 | A | 15 | 0.751 |
| BDL174 | C | 16 | 0.7 | C | 9 | -0.73 | | | |
| BDL176 | D | 25 | 0.713 | D | 24 | -0.713 | D | 26 | 0.765 |
| BDL176 | D | 21 | 0.702 | D | 20 | -0.719 | D | 32 | 0.806 |
| BDL176 | D | 33 | 0.759 | A | 7 | 0.746 | | | |
| BDL177 | B | 27 | -0.713 | A | 11 | 0.792 | | | |
| BDL181 | C | 10 | -0.75 | C | 14 | -0.795 | C | 13 | -0.805 |
| BDL181 | C | 15 | 0.72 | A | 8 | 0.794 | | | |
| BDL181 | D | 31 | -0.704 | B | 27 | 0.723 | C | 11 | -0.725 |
| BDL182 | A | 6 | 0.728 | A | 2 | 0.717 | A | 1 | 0.763 |
| BDL183 | A | 12 | -0.764 | | | | | | |
| BDL183_ H0 | A | 2 | -0.725 | | | | | | |
| BDL186 | A | 10 | -0.754 | A | 13 | -0.713 | A | 15 | 0.805 |
| BDL186 | A | 8 | 0.865 | | | | | | |
| BDL186 | B | 31 | -0.714 | B | 27 | 0.722 | A | 11 | -0.816 |
| BDL187 | A | 2 | 0.711 | A | 1 | 0.801 | A | 10 | -0.775 |
| BDL187 | A | 14 | -0.843 | A | 13 | -0.89 | A | 15 | 0.721 |
| BDL189 | A | 13 | -0.859 | A | 15 | 0.748 | A | 8 | 0.759 |
| BDL189 | B | 30 | -0.702 | B | 27 | 0.832 | A | 11 | -0.71 |
| BDL189 | C | 7 | -0.714 | A | 10 | -0.825 | A | 14 | -0.82 |
| BDL192 | B | 24 | -0.788 | B | 21 | -0.863 | B | 20 | -0.857 |
| BDL192 | B | 29 | -0.701 | B | 32 | 0.769 | | | |
| BDL192 | D | 28 | -0.764 | B | 30 | -0.785 | B | 25 | -0.802 |
| BDL193 | A | 6 | -0.754 | A | 2 | -0.781 | A | 1 | -0.875 |
| BDL193 | A | 14 | -0.732 | | | | | | |
| BDL193 | D | 30 | -0.721 | D | 29 | -0.819 | C | 11 | -0.7 |

| <i>Gene Name</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> |
|------------------|-----------------|-------------------|----------|-----------------|-------------------|----------|-----------------|-------------------|----------|
| BDL117 | D | 31 | -0.748 | A | 12 | -0.784 | | | |
| BDL118 | C | 11 | -0.914 | C | 10 | -0.723 | C | 14 | -0.75 |
| BDL118 | C | 8 | 0.74 | | | | | | |
| BDL194 | B | 25 | 0.786 | B | 21 | 0.707 | | | |
| BDL196 | D | 25 | -0.715 | D | 21 | -0.71 | D | 20 | -0.715 |
| BDL197 | A | 6 | -0.701 | A | 5 | -0.843 | A | 2 | -0.89 |
| BDL197 | A | 1 | -0.827 | | | | | | |
| BDL201 | A | 10 | -0.768 | A | 14 | -0.84 | A | 13 | -0.872 |
| BDL201 | A | 15 | 0.746 | | | | | | |
| BDL201 | B | 29 | -0.815 | A | 2 | 0.747 | A | 1 | 0.784 |
| BDL220 | C | 11 | -0.81 | | | | | | |
| BDL220 | D | 30 | -0.707 | B | 29 | -0.785 | C | 9 | 0.752 |
| BDL221 | A | 2 | 0.768 | C | 2 | 0.763 | A | 1 | 0.817 |
| BDL221 | B | 31 | -0.81 | D | 25 | -0.743 | D | 24 | -0.896 |
| BDL221 | C | 1 | 0.74 | | | | | | |
| BDL221 | D | 21 | -0.826 | D | 20 | -0.776 | A | 5 | 0.825 |
| BDL222 | D | 27 | -0.716 | A | 11 | 0.77 | A | 14 | 0.731 |
| BDL223 | C | 11 | -0.757 | C | 15 | 0.786 | C | 8 | 0.821 |
| BDL223_H0 | C | 11 | -0.736 | | | | | | |
| BDL223_H1 | C | 8 | 0.784 | | | | | | |
| BDL223_H1 | D | 24 | 0.823 | A | 12 | 0.815 | C | 15 | 0.793 |
| BDL229 | C | 11 | -0.798 | C | 10 | -0.723 | C | 14 | -0.771 |
| BDL229 | C | 13 | -0.769 | A | 8 | 0.753 | C | 8 | 0.828 |
| BDL229 | D | 30 | -0.787 | B | 27 | 0.793 | D | 27 | 0.873 |
| BDL231 | A | 11 | -0.798 | C | 6 | -0.704 | A | 10 | -0.826 |
| BDL231 | A | 14 | -0.836 | A | 13 | -0.843 | A | 15 | 0.823 |
| BDL231 | A | 8 | 0.768 | | | | | | |
| BDL231_H0 | A | 11 | -0.779 | A | 10 | -0.799 | A | 14 | -0.841 |
| BDL231_H0 | A | 13 | -0.835 | A | 15 | 0.706 | A | 8 | 0.721 |
| BDL233 | C | 8 | 0.835 | | | | | | |
| BDL233 | D | 28 | 0.755 | C | 11 | -0.768 | C | 15 | 0.725 |
| BDL235 | C | 11 | -0.87 | C | 10 | -0.749 | A | 14 | -0.741 |
| BDL235 | C | 14 | -0.726 | A | 13 | -0.702 | C | 8 | 0.802 |
| BDL240 | A | 8 | 0.742 | | | | | | |
| BDL240 | D | 24 | 0.794 | B | 27 | 0.737 | A | 11 | -0.787 |
| BDL241 | B | 27 | 0.752 | | | | | | |
| BDL242 | A | 5 | -0.719 | A | 15 | -0.722 | | | |
| BDL245 | D | 31 | -0.875 | | | | | | |

| <i>Gene Name</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> |
|------------------|-----------------|-------------------|----------|-----------------|-------------------|----------|-----------------|-------------------|----------|
| BDL117 | D | 31 | -0.748 | A | 12 | -0.784 | | | |
| BDL118 | C | 11 | -0.914 | C | 10 | -0.723 | C | 14 | -0.75 |
| BDL118 | C | 8 | 0.74 | | | | | | |
| BDL247 | D | 31 | 0.851 | | | | | | |
| BDL249 | A | 8 | -0.707 | | | | | | |
| BDL249 | C | 12 | 0.707 | A | 11 | 0.82 | A | 10 | 0.727 |
| BDL250 | A | 10 | 0.717 | A | 14 | 0.797 | A | 13 | 0.81 |
| BDL252 | C | 9 | -0.707 | C | 7 | -0.714 | | | |
| BDL49 | B | 30 | 0.866 | B | 26 | 0.85 | B | 29 | 0.933 |
| BDL49 | B | 33 | 0.762 | | | | | | |
| BDL58 | B | 26 | 0.763 | D | 26 | 0.755 | B | 29 | 0.897 |
| BDL58 | C | 14 | 0.816 | C | 13 | 0.855 | C | 15 | -0.784 |
| BDL58 | C | 8 | -0.843 | | | | | | |
| BDL58 | D | 32 | 0.758 | D | 33 | 0.778 | C | 10 | 0.8 |
| BDL62 | C | 11 | -0.858 | C | 10 | -0.739 | C | 14 | -0.77 |
| BDL62 | C | 13 | -0.747 | C | 8 | 0.819 | | | |
| BDL63 | C | 16 | -0.704 | | | | | | |
| BDL64 | B | 31 | -0.793 | C | 5 | -0.739 | | | |
| BDL70_H0 | C | 8 | 0.757 | | | | | | |
| BDL75 | C | 11 | -0.716 | C | 8 | 0.713 | | | |
| BDL75 | D | 31 | -0.776 | D | 28 | 0.75 | D | 30 | -0.832 |
| BDL79 | B | 31 | -0.77 | | | | | | |
| BDL85 | C | 10 | 0.824 | C | 14 | 0.754 | C | 13 | 0.721 |
| BDL85 | C | 15 | -0.705 | | | | | | |

Table 9. Provided are the correlations (R) between the expression levels of selected genes 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 8 hereinabove; Exp. Set = expression set according to Table 7 hereinabove.

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EXAMPLE 4

PRODUCTION OF SORGHUM TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS WITH ABST RELATED PARAMETRERS USING 44K SORGHUM 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 [Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent (dot)

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com/Scripts/PDS (dot) asp?lPage=50879]. 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
5 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 [Hypertext Transfer Protocol://World Wide Web (dot) davidmlane (dot) com/hyperstat/A34739 (dot) html].

10 ***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
15 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
20 observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test [Hypertext Transfer Protocol://World Wide Web (dot) davidmlane (dot) com/hyperstat/A34739 (dot) html].

RNA extraction – All 10 selected Sorghum varieties were sample per each
25 treatment. Plant tissues [Flag leaf and Flower meristem] growing under severe drought stress and plants grown under Normal conditions were sampled and RNA was extracted using TRIzol Reagent from Invitrogen [Hypertext Transfer Protocol://World Wide Web (dot) invitrogen (dot) com/content (dot) cfm?pageid=469]. For convenience, each micro-array expression information tissue type has received a Set ID as summarized in
30 Table 10 below.

Table 10
Sorghum transcriptom expression sets

| <i>Expression Set</i> | <i>Set ID</i> |
|------------------------------------|---------------|
| Drought Stress: Flag leaf | U |
| Normal conditions: Flag leaf | X |
| Normal conditions: Flower meristem | Y |

5 Table 10: Provided are the sorghum transcriptom expression set U, X and Y. Flag leaf = the leaf below the flower; Flower meristem = Apical meristem following panicle initiation.

The collected data parameters were as follows:

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

Plant height – Plants were characterized for height during growing period at 6
15 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.

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

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

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

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

30 ***Harvest Index (for sorghum)*** - The harvest index is calculated using Formula VIII.

Formula VIII:

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

Experimental Results

5 16 different sorghum varieties were grown and characterized for 7 parameters:
 "Seed/plant normal" = total seed weight per plant under normal conditions; "DW-5
 Inflorescence Normal" – dry weight of five complete inflorescences (seeds and rachis)
 under normal conditions; "DW all Normal" = dry weight of per plot under normal
 conditions; "Weight of seeds (5 heads) gr Normal" = dry weight of seeds from five
 10 inflorescences under normal conditions; "Plant Height 4 Drought" = plant height in the
 4th time point under drought conditions; "Plant Height 4 Normal" = plant height in the
 4th time point under normal conditions; "Plant Height 6 Normal" = plant height in the 6th
 time point under normal conditions. The average for each of the measured parameter
 was calculated using the JMP software and values are summarized in Table 11 below.
 15 Subsequent correlation analysis between the various transcriptom sets (Table 10) and
 the average parameters, was conducted (Tables 12). Results were then integrated to the
 database.

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Table 11
Measured parameters in Sorghum accessions

| Seed ID | Seed/Plant Normal | DW-5 Inflorescence Normal | DW all Normal | Weight of seeds (5 heads) gr Normal | Plant Height 4 Drought | Plant Height 4 Normal | Plant Height 6 Normal |
|----------------|--------------------------|----------------------------------|----------------------|--|-------------------------------|------------------------------|------------------------------|
| 20 | 0.031 | 0.039 | 5.408 | 0.237 | 38.000 | 37.313 | 37.313 |
| 21 | 0.026 | 0.062 | 3.091 | 0.225 | 30.833 | | |
| 22 | 0.019 | 0.033 | 21.341 | 0.142 | 110.833 | 47.750 | 47.750 |
| 24 | 0.038 | 0.030 | 5.329 | 0.352 | 42.833 | 40.083 | 40.083 |
| 25 | 0.027 | 0.074 | 20.600 | 0.161 | 49.583 | 45.938 | 45.938 |
| 26 | 0.046 | 0.049 | 21.685 | 0.332 | 49.750 | 41.438 | 41.438 |
| 27 | 0.048 | 0.046 | 11.205 | 0.317 | 46.875 | 44.875 | 44.875 |
| 28 | 0.031 | 0.033 | 9.045 | 0.222 | 41.917 | 42.125 | 42.125 |
| 29 | 0.040 | 0.048 | 10.293 | 0.283 | 46.125 | 41.000 | 41.000 |
| 30 | 0.038 | 0.038 | 9.139 | 0.300 | 50.167 | 42.500 | 42.063 |
| 31 | 0.032 | 0.023 | 9.549 | 0.227 | 43.583 | 41.875 | 41.875 |
| 32 | 0.033 | 0.039 | 10.424 | 0.277 | 50.833 | 43.375 | 43.375 |
| 33 | 0.033 | 0.049 | 10.150 | 0.353 | 42.417 | 39.813 | 39.813 |
| 34 | 0.052 | 0.050 | 8.783 | 0.351 | 45.500 | 40.625 | 40.625 |
| 35 | 0.036 | 0.038 | 10.259 | 0.270 | 50.375 | 44.375 | 44.375 |
| 36 | 0.038 | 0.042 | 12.005 | 0.299 | 48.833 | 43.250 | 43.250 |
| 37 | 0.042 | 0.063 | 15.681 | 0.263 | 49.833 | 41.000 | 41.000 |

Table 11: 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.

5

Table 12

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

| <i>Gene Name</i> | <i>Exp. Set</i> | <i>Corr. Vec.</i> | <i>R</i> |
|------------------|-----------------|-------------------------------------|----------|
| BDL102_H47 | flower | DW all Normal | -0.721 |
| BDL102_H47 | flower | FW-Inflorescence/Plant Normal | 0.717 |
| BDL102_H47 | flower | Plant Height 4 Normal | -0.722 |
| BDL102_H47 | flower | Plant Height 6 Normal | -0.718 |
| BDL83_H57 | flag leaf | DW-5 Inflorescence Normal | -0.712 |
| BDL83_H57 | flag leaf | Seed/Plant Normal | -0.708 |
| BDL83_H57 | flower | Plant Height 4 Normal | 0.858 |
| BDL83_H57 | flower | Plant Height 6 Normal | 0.853 |
| BDL83_H58 | flag leaf | Plant Height 4 Drought | 0.763 |
| BDL83_H58 | flower | Seed/Plant Low-N | 0.759 |
| BDL83_H58 | flower | Weight of seeds (5 heads) gr Normal | -0.707 |
| BDL83_H58 | Flower meristem | Leaf_No 2 Normal | 0.802 |
| BDL88_H13 | Flag leaf | Leaf_No 3 Drought | -0.893 |
| BDL88_H13 | Flag leaf | Leaf_TP 1 Drought | -0.929 |
| BDL88_H13 | Flag leaf | Plant Height 2 Drought | -0.796 |
| BDL88_H13 | Flag leaf | Plant Height 3 Drought | -0.837 |
| BDL88_H13 | Flag leaf | Seed/Plant_Normal | 0.73 |

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Table 12. Provided are the correlations (R) between the expression levels of homologues of selected genes in tissues (Flag leaf or Flower meristem; Expression sets) and the phenotypic performance in various yield, biomass, growth rate and/or vigor components [Correlation (Corr.) vector (Vec.)] under abiotic stress conditions (drought) or normal conditions across Sorghum accessions.

15

Sorghum vigor related parameters under 100 mM NaCl and low temperature (8-10 °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 (8-10 °C in the presence of Full Hogland solution) or at Normal growth solution [Full Hogland solution at 20-24 °C].

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25

Full Hogland solution consists of: KNO₃ - 0.808 grams/liter, MgSO₄ - 0.12 grams/liter, KH₂ PO₄ - 0.172 grams/liter and 0.01 % (volume/volume) of 'Super coratin' micro elements (Iron-EDDHA [ethylenediamine-N,N'-bis(2-hydroxyphenylacetic acid)]- 40.5 grams/liter; Mn - 20.2 grams/liter; Zn 10.1 grams/liter; Co 1.5 grams/liter; and Mo 1.1 grams/liter), solution's pH should be 6.5 – 6.8].

RNA extraction – All 10 selected Sorghum varieties were sampled per each treatment. Two tissues [leaves and roots] growing at 100 mM NaCl, low temperature (8-10 °C) or under Normal conditions (full Hogland at a temperature between 20-24 °C) were sampled and RNA was extracted using TRIzol Reagent from Invitrogen [Hypertext Transfer Protocol://World Wide Web (dot) invitrogen (dot) com/content (dot)cfm?pageid=469].

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 13 below. Subsequent correlation analysis between the various transcriptom sets and the average parameters was conducted (Table 14). Results were then integrated to the database.

Table 13
Measured parameters in Sorghum accessions

| <i>Seed ID</i> | <i>Plant Height T1 NaCl</i> | <i>Plant Height T1+8 NaCl</i> | <i>Plant Height T1+15 NaCl</i> | <i>Leaf number T1 NaCl</i> | <i>Leaf number T1+8 Normal</i> | <i>DW Root/Plant NaCl</i> |
|----------------|-----------------------------|-------------------------------|--------------------------------|----------------------------|--------------------------------|---------------------------|
| 20 | 7.900 | 14.200 | 21.800 | 3.000 | 4.167 | 0.05 |
| 22 | 9.500 | 16.267 | 23.167 | 3.133 | 4.500 | 0.10447479 |
| 26 | 10.933 | 20.367 | 30.367 | 3.400 | 4.800 | 0.12370635 |
| 27 | 7.933 | 13.333 | 22.833 | 3.067 | 4.600 | 0.06880519 |
| 28 | 9.700 | 15.900 | 23.700 | 3.333 | 4.533 | 0.07568254 |
| 29 | 8.533 | 16.533 | 23.300 | 3.067 | 4.967 | 0.07517045 |
| 30 | 8.900 | 15.467 | 22.467 | 3.067 | 4.600 | 0.13539542 |
| 31 | 10.367 | 18.933 | 26.833 | 3.267 | 4.933 | 0.09546434 |
| 34 | 7.000 | 13.680 | 20.280 | 3.000 | 4.500 | 0.16491667 |
| 37 | 7.833 | 15.767 | 23.567 | 3.067 | 4.567 | 0.13888278 |

Table 13: Provided are the measured parameters of the Sorghum Accessions under normal conditions or high salt conditions at the indicated time points. T1 (first day of measurements); T1+8 (8 days following the first day); T1+15 (15 days following the first day). The exact conditions are detailed above in the experiment description section.

Table 14

Correlation between the expression level of homologues of selected genes in roots and the phenotypic performance under normal or abiotic stress conditions across Sorghum accessions

| Gene Name | Exp. Set | Corr. Vec. | R |
|------------------|-----------------|--------------------------------|--------------|
| <i>BDL83_H58</i> | <i>root</i> | <i>DW Root/Plant NaCl</i> | <i>0.897</i> |
| <i>BDL83_H58</i> | <i>root</i> | <i>Leaf number T1 NaCl</i> | <i>-0.75</i> |
| <i>BDL83_H58</i> | <i>root</i> | <i>Plant Height T1 NaCl</i> | <i>-0.82</i> |
| <i>BDL83_H58</i> | <i>root</i> | <i>Plant Height T1+8 NaCl</i> | <i>-0.9</i> |
| <i>BDL83_H58</i> | <i>root</i> | <i>Plant Height T1+15 NaCl</i> | <i>-0.77</i> |
| <i>BDL83_H58</i> | <i>root</i> | <i>Leaf number T1 Normal</i> | <i>0.779</i> |

5 Table 14. Provided are the correlations (R) between the expression levels of homologues of selected genes in roots [Expression (Exp.) sets] and the phenotypic performance [yield, biomass, growth rate and/or vigor components (Correlation vector)] at the indicated time points under abiotic stress conditions (salinity) or normal conditions across Sorghum accessions. Corr. Vec. = correlation vector as described hereinabove (Table 13). T1 (first day of measurements); T1+8 (8 days following the first day);
10 T1+15 (15 days following the first day).

EXAMPLE 5

**IDENTIFICATION OF GENES WHICH INCREASE YIELD, BIOMASS,
15 GROWTH RATE, VIGOR, OIL CONTENT, ABIOTIC STRESS TOLERANCE OF
PLANTS AND NITROGEN USE EFFICIENCY**

Based on the above described bioinformatics and experimental tools, the present inventors have identified 105 genes (89 distinct gene families) which have a
20 major impact on yield, seed yield, oil yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance, and/or nitrogen 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 15, hereinbelow.

Table 15

Identified polynucleotides which affect plant yield, seed yield, oil yield, oil content, biomass, growth rate, vigor, abiotic stress tolerance and/or nitrogen use efficiency of a plant

| Serial No | Gene Name | Cluster Name | Organism | Polynucleotide SEQ ID NO: | Polypeptide SEQ ID NO: |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 1 | BDL47 | arabidopsislgb1651AT4 G38660 | arabidopsis | 1 | 106 |

30

| <i>Serial No</i> | <i>Gene Name</i> | <i>Cluster Name</i> | <i>Organism</i> | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 2 | BDL47 | arabidopsislgb165 AT4 G38660 | arabidopsis | 1 | 194 |
| 3 | BDL48 | arabidopsislgb165 AT2 G25270 | arabidopsis | 2 | 107 |
| 4 | BDL62 | arabidopsislgb165 AT1 G64390 | arabidopsis | 3 | 108 |
| 5 | BDL75 | arabidopsislgb165 AT3 G55420 | arabidopsis | 4 | 109 |
| 6 | BDL79 | arabidopsislgb165 AT3 G20010 | arabidopsis | 5 | 110 |
| 7 | BDL81 | arabidopsislgb165 AT1 G13030 | arabidopsis | 6 | 111 |
| 8 | BDL83 | arabidopsislgb165 AT1 G43670 | arabidopsis | 7 | 112 |
| 9 | BDL117 | arabidopsislgb165 AT4 G33240 | arabidopsis | 8 | 113 |
| 10 | BDL118 | arabidopsislgb165 AT2 G22125 | arabidopsis | 9 | 114 |
| 11 | BDL126 | arabidopsislgb165 AT3 G59100 | arabidopsis | 10 | 115 |
| 12 | BDL138 | arabidopsislgb165 AT3 G12180 | arabidopsis | 11 | 116 |
| 13 | BDL140 | arabidopsislgb165 AT5 G02640 | arabidopsis | 12 | 117 |
| 14 | BDL147 | arabidopsislgb165 AT2 G47930 | arabidopsis | 13 | 118 |
| 15 | BDL149 | arabidopsislgb165 AT5 G15750 | arabidopsis | 14 | 119 |
| 16 | BDL152 | arabidopsislgb165 AT1 G70420 | arabidopsis | 15 | 120 |
| 17 | BDL153 | arabidopsislgb165 AT5 G47690 | arabidopsis | 16 | 121 |
| 18 | BDL154 | arabidopsislgb165 AT1 G62940 | arabidopsis | 17 | 122 |
| 19 | BDL155 | arabidopsislgb165 AT4 G11630 | arabidopsis | 18 | 123 |

| <i>Serial No</i> | <i>Gene Name</i> | <i>Cluster Name</i> | <i>Organism</i> | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 20 | BDL156 | arabidopsislgb165 AT1 G01570 | arabidopsis | 19 | 124 |
| 21 | BDL157 | arabidopsislgb165 AT1 G14560 | arabidopsis | 20 | 125 |
| 22 | BDL158 | arabidopsislgb165 AT1 G22030 | arabidopsis | 21 | 126 |
| 23 | BDL160 | arabidopsislgb165 AT1 G28960 | arabidopsis | 22 | 127 |
| 24 | BDL162 | arabidopsislgb165 AT1 G49360 | arabidopsis | 23 | 128 |
| 25 | BDL163 | arabidopsislgb165 AT1 G51430 | arabidopsis | 24 | 129 |
| 26 | BDL165 | arabidopsislgb165 AT1 G65010 | arabidopsis | 25 | 130 |
| 27 | BDL167 | arabidopsislgb165 AT1 G79630 | arabidopsis | 26 | 131 |
| 28 | BDL168 | arabidopsislgb165 AT2 G01910 | arabidopsis | 27 | 132 |
| 29 | BDL169 | arabidopsislgb165 AT2 G19120 | arabidopsis | 28 | 133 |
| 30 | BDL171 | arabidopsislgb165 AT2 G32320 | arabidopsis | 29 | 134 |
| 31 | BDL173 | arabidopsislgb165 AT2 G36720 | arabidopsis | 30 | 135 |
| 32 | BDL174 | arabidopsislgb165 AT2 G39580 | arabidopsis | 31 | 136 |
| 33 | BDL176 | arabidopsislgb165 AT3 G10160 | arabidopsis | 32 | 137 |
| 34 | BDL177 | arabidopsislgb165 AT3 G18610 | arabidopsis | 33 | 138 |
| 35 | BDL181 | arabidopsislgb165 AT4 G12640 | arabidopsis | 34 | 139 |
| 36 | BDL182 | arabidopsislgb165 AT4 G14605 | arabidopsis | 35 | 140 |
| 37 | BDL183 | arabidopsislgb165 AT4 G15620 | arabidopsis | 36 | 141 |

| <i>Serial No</i> | <i>Gene Name</i> | <i>Cluster Name</i> | <i>Organism</i> | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 38 | BDL186 | arabidopsislgb165 AT4 G32560 | arabidopsis | 37 | 142 |
| 39 | BDL187 | arabidopsislgb165 AT4 G35130 | arabidopsis | 38 | 143 |
| 40 | BDL188 | arabidopsislgb165 AT4 G35560 | arabidopsis | 39 | 144 |
| 41 | BDL189 | arabidopsislgb165 AT5 G05560 | arabidopsis | 40 | 145 |
| 42 | BDL190 | arabidopsislgb165 AT5 G06690 | arabidopsis | 41 | 146 |
| 43 | BDL192 | arabidopsislgb165 AT5 G09880 | arabidopsis | 42 | 147 |
| 44 | BDL193 | arabidopsislgb165 AT5 G12950 | arabidopsis | 43 | 148 |
| 45 | BDL194 | arabidopsislgb165 AT5 G16540 | arabidopsis | 44 | 149 |
| 46 | BDL196 | arabidopsislgb165 AT5 G38180 | arabidopsis | 45 | 150 |
| 47 | BDL197 | arabidopsislgb165 AT5 G39240 | arabidopsis | 46 | 151 |
| 48 | BDL200 | arabidopsislgb165 AT5 G51470 | arabidopsis | 47 | 152 |
| 49 | BDL201 | arabidopsislgb165 AT5 G58250 | arabidopsis | 48 | 153 |
| 50 | BDL203 | arabidopsislgb165 AT5 G66440 | arabidopsis | 49 | 154 |
| 51 | BDL219 | arabidopsislgb165 AT1 G36095 | arabidopsis | 50 | 155 |
| 52 | BDL220 | arabidopsislgb165 AT1 G61170 | arabidopsis | 51 | 156 |
| 53 | BDL221 | arabidopsislgb165 AT1 G75860 | arabidopsis | 52 | 157 |
| 54 | BDL222 | arabidopsislgb165 AT1 G77885 | arabidopsis | 53 | 158 |
| 55 | BDL223 | arabidopsislgb165 AT2 G37975 | arabidopsis | 54 | 159 |

| <i>Serial No</i> | <i>Gene Name</i> | <i>Cluster Name</i> | <i>Organism</i> | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 56 | BDL229 | arabidopsislgb165 AT5 G53830 | arabidopsis | 55 | 160 |
| 57 | BDL230 | arabidopsislgb154 ATH PEARA | arabidopsis | 56 | 161 |
| 58 | BDL231 | arabidopsislgb165 AT1 G16350 | arabidopsis | 57 | 162 |
| 59 | BDL235 | arabidopsislgb165 AT2 G38970 | arabidopsis | 58 | 163 |
| 60 | BDL242 | arabidopsislgb165 AT3 G22740 | arabidopsis | 59 | 164 |
| 61 | BDL243 | arabidopsislgb165 AT3 G31430 | arabidopsis | 60 | 165 |
| 62 | BDL245 | arabidopsislgb165 AT4 G12690 | arabidopsis | 61 | 166 |
| 63 | BDL247 | arabidopsislgb165 AT4 G29510 | arabidopsis | 62 | 167 |
| 64 | BDL248 | arabidopsislgb165 AT4 G37360 | arabidopsis | 63 | 168 |
| 65 | BDL250 | arabidopsislgb165 AT4 G37400 | arabidopsis | 64 | 169 |
| 66 | BDL49 | arabidopsislgb165 AT3 G06180 | arabidopsis | 65 | 170 |
| 67 | BDL58 | arabidopsislgb165 AT1 G22160 | arabidopsis | 66 | 171 |
| 68 | BDL63 | arabidopsislgb165 AT2 G40550 | arabidopsis | 67 | 172 |
| 69 | BDL64 | arabidopsislgb165 AT5 G38020 | arabidopsis | 68 | 173 |
| 70 | BDL70 | cottonlgb164 AF150730 | cotton | 69 | 174 |
| 71 | BDL85 | arabidopsislgb165 AT1 G05340 | arabidopsis | 70 | 175 |
| 72 | BDL88 | ricelgb157.2 AA754446 | rice | 71 | 176 |
| 73 | BDL90 | ricelgb154 AK102950 | rice | 72 | |
| 74 | BDL94 | ricelgb157.2 BE228242 | rice | 73 | 177 |
| 75 | BDL102 | maizelgb164 AI600933 | maize | 74 | 178 |

| <i>Serial No</i> | <i>Gene Name</i> | <i>Cluster Name</i> | <i>Organism</i> | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 76 | BDL224 | arabidopsislgb165 AT4 G29780 | arabidopsis | 75 | 179 |
| 77 | BDL225 | arabidopsislgb165 AT5 G39670 | arabidopsis | 76 | 180 |
| 78 | BDL226 | arabidopsislgb165 AT5 G65470 | arabidopsis | 77 | 181 |
| 79 | BDL227 | arabidopsislgb165 AT3 G56410 | arabidopsis | 78 | 182 |
| 80 | BDL228 | castorbeanlgb160 EE25 6201 | castorbean | 79 | 183 |
| 81 | BDL232 | arabidopsislgb165 AT1 G56100 | arabidopsis | 80 | 184 |
| 82 | BDL233 | arabidopsislgb165 AT1 G66360 | arabidopsis | 81 | 185 |
| 83 | BDL234 | arabidopsislgb165 AT2 G05400 | arabidopsis | 82 | 186 |
| 84 | BDL237 | arabidopsislgb165 AT2 G45510 | arabidopsis | 83 | 187 |
| 85 | BDL238 | arabidopsislgb165 AT3 G04540 | arabidopsis | 84 | 188 |
| 86 | BDL240 | arabidopsislgb165 AT3 G18480 | arabidopsis | 85 | 189 |
| 87 | BDL241 | arabidopsislgb165 AT3 G20020 | arabidopsis | 86 | 190 |
| 88 | BDL249 | arabidopsislgb165 AT4 G37370 | arabidopsis | 87 | 191 |
| 89 | BDL251 | arabidopsislgb165 AT5 G08250 | arabidopsis | 88 | 192 |
| 90 | BDL252 | arabidopsislgb165 AT5 G18650 | arabidopsis | 89 | 193 |
| 91 | BDL79 | arabidopsislgb165 AT3 G20010 | arabidopsis | 90 | 110 |
| 92 | BDL126 | arabidopsislgb165 AT3 G59100 | arabidopsis | 91 | 115 |
| 93 | BDL153 | arabidopsislgb165 AT5 G47690 | arabidopsis | 92 | 195 |

| <i>Serial No</i> | <i>Gene Name</i> | <i>Cluster Name</i> | <i>Organism</i> | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|------------------|---------------------------------|-----------------|----------------------------------|-------------------------------|
| 94 | BDL156 | arabidopsislgb165 AT1 G01570 | arabidopsis | 93 | 124 |
| 95 | BDL167 | arabidopsislgb165 AT1 G79630 | arabidopsis | 94 | 196 |
| 96 | BDL169 | arabidopsislgb165 AT2 G19120 | arabidopsis | 95 | 197 |
| 97 | BDL171 | arabidopsislgb165 AT2 G32320 | arabidopsis | 96 | 134 |
| 98 | BDL174 | arabidopsislgb165 AT2 G39580 | arabidopsis | 97 | 198 |
| 99 | BDL187 | arabidopsislgb165 AT4 G35130 | arabidopsis | 98 | 143 |
| 100 | BDL189 | arabidopsislgb165 AT5 G05560 | arabidopsis | 99 | 199 |
| 101 | BDL197 | arabidopsislgb165 AT5 G39240 | arabidopsis | 100 | 200 |
| 102 | BDL200 | arabidopsislgb165 AT5 G51470 | arabidopsis | 101 | 152 |
| 103 | BDL231 | arabidopsislgb165 AT1 G16350 | arabidopsis | 102 | 162 |
| 104 | BDL248 | arabidopsislgb165 AT4 G37360 | arabidopsis | 103 | 168 |
| 105 | BDL70 | cottonlgb164 AF150730 | cotton | 104 | 201 |
| 106 | BDL238 | arabidopsislgb165 AT3 G04540 | arabidopsis | 105 | 202 |

Table 15: Provided are the identified genes, their annotation, organism and polynucleotide and polypeptide sequence identifiers.

5

EXAMPLE 6

IDENTIFICATION OF HOMOLOGOUS SEQUENCES THAT INCREASE SEED YIELD, OIL YIELD, GROWTH RATE, OIL CONTENT, BIOMASS, VIGOR, ABST RESISTANCE AND/OR NUE OF A PLANT

The concepts of orthology and paralogy have recently been applied to
10 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
5 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
10 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
15 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
20 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
25 identical function over evolutionary time. These methods provide different sets of indications on function similarities between two homologous genes, similarities in the sequence level - identical amino acids in the protein domains and similarity in expression profiles.

Methods for searching and identifying homologues of yield and improved
30 agronomic traits such as ABS tolerance and NUE related polypeptides or polynucleotides are well within the realm of the skilled artisan. The search and identification of homologous genes involves the screening of sequence information

available, for example, in public databases 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 (Hypertext Transfer Protocol://World Wide Web (dot) biochem (dot) ucl (dot) ac (dot) uk/bsm/dbbrowser/protocol/prodomqry (dot) html), PIR (Hypertext Transfer Protocol://pir (dot) Georgetown (dot) edu/) or Pfam (Hypertext Transfer Protocol://World Wide Web (dot) sanger (dot) ac (dot) uk/Software/Pfam/) database. Sequence analysis programs designed for motif searching may be used for identification of fragments, regions and conserved domains as mentioned above. Preferred computer programs include, but are not limited to, MEME, SIGNALSCAN, and GENESCAN.

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

Polynucleotides and polypeptides with significant homology to the identified genes described in Table 15 above have been identified from the databases using BLAST software using the Blastp and tBlastn algorithms. The query nucleotide sequences were SEQ ID NOs: 1-106 and the identified homologues are provided in Table 16, below. These genes are expected to increase plant yield, seed yield, oil yield, oil content, growth rate, biomass, vigor, ABST and/or NUE of a plant.

Table 16
Homologous polynucleotides and polypeptides

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|------------------------------------|------------------|---------------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 203 | BDL47_H0 | radishlgb164IEW717854 | 524 | 194 | 85.15 | tblastn |
| 204 | BDL48_H0 | radishlgb164IEW735131 | 525 | 107 | 82.7 | blastp |
| 205 | BDL62_H0 | canolalgb161ICD835773 | 526 | 108 | 94.5 | blastp |
| 206 | BDL62_H1 | radishlgb164IEV543949 | 527 | 108 | 94.36 | tblastn |
| 207 | BDL75_H0 | canolalgb161IEE485008 | 528 | 109 | 84.1 | blastp |
| 208 | BDL83_H0 | applelgb171ICN494551 | 529 | 112 | 86.8 | blastp |
| 209 | BDL83_H1 | aquilegialgb157.3IDR916 286 | 530 | 112 | 85.9 | blastp |
| 210 | BDL83_H2 | artemisialgb164IEY03740 7 | 531 | 112 | 86.2 | blastp |
| 211 | BDL83_H3 | b_juncealgb164IEVGN00 808312601672 | 532 | 112 | 91.7 | blastp |
| 212 | BDL83_H4 | b_oleracalgb161IAM387 331 | 533 | 112 | 94.7 | blastp |
| 213 | BDL83_H5 | b_rapalgb162IAY161288 | 534 | 112 | 94.4 | blastp |
| 214 | BDL83_H6 | bananalgb167IAF130251 | 535 | 112 | 85 | blastp |
| 215 | BDL83_H7 | barleylgb157.3IBE420760 | 536 | 112 | 83.4 | blastp |
| 216 | BDL83_H8 | barleylgb157.3IBG365169 | 537 | 112 | 82.1 | blastp |
| 217 | BDL83_H9 | beanlgb167ICA896765 | 538 | 112 | 87.1 | blastp |
| 218 | BDL83_H1 0 | beanlgb167ICB539815 | 539 | 112 | 87.4 | blastp |
| 219 | BDL83_H1 1 | beetlgb162IBE590341 | 540 | 112 | 85.9 | blastp |
| 220 | BDL83_H1 2 | brachypodiumlgb169IBE2 13261 | 541 | 112 | 85.4 | blastp |
| 221 | BDL83_H1 3 | brachypodiumlgb169IBE4 19504 | 542 | 112 | 82.7 | blastp |
| 222 | BDL83_H1 4 | canolalgb161IBNU20179 | 543 | 112 | 94.13 | tblastn |
| 223 | BDL83_H1 5 | canolalgb161ICD818253 | 544 | 112 | 94.4 | blastp |
| 224 | BDL83_H1 6 | cassavalgb164IDV445162 | 545 | 112 | 88 | blastp |
| 225 | BDL83_H1 7 | castorbeanlgb160IEE2567 91 | 546 | 112 | 87.4 | blastp |
| 226 | BDL83_H1 8 | centaurealgb166IEH73437 5 | 547 | 112 | 87.7 | blastp |
| 227 | BDL83_H1 9 | cichoriumlgb171IEH6800 19 | 548 | 112 | 88 | blastp |
| 228 | BDL83_H2 0 | citruslgb166ICV885954 | 549 | 112 | 89.15 | tblastn |
| 229 | BDL83_H2 1 | coffealgb157.2IDV68558 9 | 550 | 112 | 87.1 | tblastn |
| 230 | BDL83_H2 2 | cottonlgb164IAI725778 | 551 | 112 | 86.8 | blastp |
| 231 | BDL83_H2 3 | cottonlgb164ICA993334 | 552 | 112 | 88.3 | blastp |

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|------------------------------------|------------------|-----------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 232 | BDL83_H2 4 | cowpealgb166 FF537383 | 553 | 112 | 87.7 | blastp |
| 233 | BDL83_H2 5 | cynaralgb167 GE584395 | 554 | 112 | 84.16 | tblastn |
| 234 | BDL83_H2 6 | dandeliongb161 DY8069 19 | 555 | 112 | 87.1 | blastp |
| 235 | BDL83_H2 7 | eucalyptusgb166 CB9676 49 | 556 | 112 | 88 | blastp |
| 236 | BDL83_H2 8 | fescuelgb161 DT696580 | 557 | 112 | 82.8 | blastp |
| 237 | BDL83_H2 9 | gingerlgb164 DY345757 | 558 | 112 | 86.5 | blastp |
| 238 | BDL83_H3 0 | grapelgb160 CD008185 | 559 | 112 | 86.8 | blastp |
| 239 | BDL83_H3 1 | iceplantlgb164 CA833792 | 560 | 112 | 87.1 | blastp |
| 240 | BDL83_H3 2 | ipomoealgb157.2 CJ7555 28 | 561 | 112 | 86.8 | blastp |
| 241 | BDL83_H3 3 | lettucelgb157.2 AF16220 6 | 562 | 112 | 87.7 | blastp |
| 242 | BDL83_H3 4 | leymuslgb166 EG375854 | 563 | 112 | 84 | blastp |
| 243 | BDL83_H3 5 | lovegrasslgb167 DN4818 48 | 564 | 112 | 82.8 | blastp |
| 244 | BDL83_H3 6 | maizelgb170 BG355384 | 565 | 112 | 83 | blastp |
| 245 | BDL83_H3 7 | maizelgb170 LLAI603703 | 566 | 112 | 83.5 | blastp |
| 246 | BDL83_H3 8 | medicagolgb157.2 AL386 990 | 567 | 112 | 80.5 | blastp |
| 247 | BDL83_H3 9 | medicagolgb157.2 AW69 5293 | 568 | 112 | 84.8 | blastp |
| 248 | BDL83_H4 0 | papayalgb165 EX248440 | 569 | 112 | 84.5 | blastp |
| 249 | BDL83_H4 1 | peanutlgb171 EE126296 | 570 | 112 | 86.8 | blastp |
| 250 | BDL83_H4 2 | peanutlgb171 ES752783 | 571 | 112 | 85.9 | blastp |
| 251 | BDL83_H4 3 | pepperlgb171 CO907209 | 572 | 112 | 86.8 | blastp |
| 252 | BDL83_H4 4 | pepperlgb171 GD064098 | 573 | 112 | 87.4 | blastp |
| 253 | BDL83_H4 5 | physcomitrellalgb157 BJ1 57670 | 574 | 112 | 82.4 | blastp |
| 254 | BDL83_H4 6 | physcomitrellalgb157 BJ1 71093 | 575 | 112 | 83.63 | tblastn |
| 255 | BDL83_H4 7 | pinelgb157.2 AW010114 | 576 | 112 | 82.7 | blastp |
| 256 | BDL83_H4 8 | pinelgb157.2 CO169305 | 577 | 112 | 86.2 | blastp |
| 257 | BDL83_H4 9 | poplarlgb170 BI068614 | 578 | 112 | 88 | blastp |

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|------------------------------------|------------------|--------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 258 | BDL83_H5 0 | poplar gb170 BU878945 | 579 | 112 | 86.05 | tblastn |
| 259 | BDL83_H5 1 | potato gb157.2 BF053889 | 580 | 112 | 86.2 | blastp |
| 260 | BDL83_H5 2 | prunus gb167 DW341878 | 581 | 112 | 88.9 | blastp |
| 261 | BDL83_H5 3 | radish gb164 EV537348 | 582 | 112 | 95 | blastp |
| 262 | BDL83_H5 4 | radish gb164 EV565372 | 583 | 112 | 94.7 | blastp |
| 263 | BDL83_H5 5 | rice gb170 OS01G64660 | 584 | 112 | 84.5 | blastp |
| 264 | BDL83_H5 6 | rice gb170 OS05G36270 | 585 | 112 | 83.3 | blastp |
| 265 | BDL83_H5 7 | sorghum gb161.crplAW5 66083 | 586 | 112 | 84.8 | blastp |
| 266 | BDL83_H5 8 | sorghum gb161.crplAW6 71091 | 587 | 112 | 83.6 | blastp |
| 267 | BDL83_H5 9 | soybean gb168 AL388391 | 588 | 112 | 81.3 | blastp |
| 268 | BDL83_H6 0 | soybean gb168 BE941320 | 589 | 112 | 86.5 | blastp |
| 269 | BDL83_H6 1 | soybean gb168 BF636881 | 590 | 112 | 87.1 | blastp |
| 270 | BDL83_H6 2 | soybean gb168 CD394856 | 591 | 112 | 86.2 | blastp |
| 271 | BDL83_H6 3 | spikemoss gb165 FE4436 31 | 592 | 112 | 83.9 | blastp |
| 272 | BDL83_H6 4 | spruce gb162 CO227794 | 593 | 112 | 87.4 | blastp |
| 273 | BDL83_H6 5 | spruce gb162 CO238226 | 594 | 112 | 83.3 | blastp |
| 274 | BDL83_H6 6 | spurge gb161 DV121804 | 595 | 112 | 87.4 | blastp |
| 275 | BDL83_H6 7 | strawberry gb164 DY671 211 | 596 | 112 | 87.4 | blastp |
| 276 | BDL83_H6 8 | sugarcane gb157.3 BQ533 620 | 597 | 112 | 85.4 | blastp |
| 277 | BDL83_H6 9 | sunflower gb162 BU6720 90 | 598 | 112 | 84.2 | blastp |
| 278 | BDL83_H7 0 | sunflower gb162 CD8477 11 | 599 | 112 | 87.7 | blastp |
| 279 | BDL83_H7 1 | switchgrass gb167 DN143 181 | 600 | 112 | 84.8 | blastp |
| 280 | BDL83_H7 2 | switchgrass gb167 DN148 413 | 601 | 112 | 82.4 | tblastn |
| 281 | BDL83_H7 3 | tomato gb164 AI486777 | 602 | 112 | 88.3 | blastp |
| 282 | BDL83_H7 4 | tomato gb164 BG123415 | 603 | 112 | 85.9 | blastp |
| 283 | BDL83_H7 5 | triphysaria gb164 EY1662 97 | 604 | 112 | 85.9 | blastp |

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|------------------------------------|------------------|--------------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 284 | BDL83_H7 6 | triphysarialgb164IEY1697 17 | 605 | 112 | 87.4 | blastp |
| 285 | BDL83_H7 7 | wheatlgb164IBE213261 | 606 | 112 | 82.8 | blastp |
| 286 | BDL83_H7 8 | wheatlgb164IBE418868 | 607 | 112 | 82.8 | blastp |
| 287 | BDL83_H7 9 | wheatlgb164IBE500460 | 608 | 112 | 82.8 | blastp |
| 288 | BDL118_H 0 | castorbeanlgb160IMDL29 877M000477 | 609 | 114 | 81.4 | blastp |
| 289 | BDL118_H 1 | poplarlgb170IAI164922 | 610 | 114 | 81.3 | blastp |
| 290 | BDL118_H 2 | poplarlgb170IBI138300 | 611 | 114 | 82 | blastp |
| 291 | BDL118_H 3 | soybeanlgb168IBE658051 | 612 | 114 | 80.1 | blastp |
| 292 | BDL118_H 4 | soybeanlgb168ICB540069 | 613 | 114 | 80 | blastp |
| 293 | BDL138_H 0 | canolalgb161ICD817345 | 614 | 116 | 92.5 | blastp |
| 294 | BDL138_H 1 | radishlgb164IEV536083 | 615 | 116 | 91.8 | blastp |
| 295 | BDL138_H 2 | radishlgb164IEW725583 | 616 | 116 | 91.1 | blastp |
| 296 | BDL147_H 0 | thellungiellalgb167IBY81 8222 | 617 | 118 | 81.6 | blastp |
| 297 | BDL149_H 0 | b_rapalgb162IDY009670 | 618 | 119 | 87.9 | blastp |
| 298 | BDL149_H 1 | canolalgb161ICD818601 | 619 | 119 | 88.5 | blastp |
| 299 | BDL149_H 2 | cowpealgb166IFF400239 | 620 | 119 | 82.4 | blastp |
| 300 | BDL154_H 0 | b_rapalgb162IEX046206 | 621 | 122 | 90.77 | tblastn |
| 301 | BDL154_H 1 | canolalgb161ICD841052 | 622 | 122 | 92.25 | tblastn |
| 302 | BDL155_H 0 | arabidopsislgb165IAT1G2 4240 | 623 | 123 | 92.9 | blastp |
| 303 | BDL155_H 1 | arabidopsislgb165IAT5G1 1750 | 624 | 123 | 91.7 | blastp |
| 304 | BDL155_H 2 | canolalgb161IEE462449 | 625 | 123 | 81.3 | blastp |
| 305 | BDL155_H 3 | radishlgb164IEV545009 | 626 | 123 | 80.34 | tblastn |
| 306 | BDL155_H 4 | radishlgb164IEV569478 | 627 | 123 | 80.4 | blastp |
| 307 | BDL158_H 0 | radishlgb164IEW715818 | 628 | 126 | 88.46 | tblastn |
| 308 | BDL160_H 0 | canolalgb161IEE418738 | 629 | 127 | 83.9 | blastp |
| 309 | BDL160_H 1 | radishlgb164IEV545765 | 630 | 127 | 85.1 | blastp |

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|------------------------------------|------------------|---------------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 310 | BDL167_H 0 | radishlgb164IEV535056 | 631 | 196 | 82.7 | tblastn |
| 311 | BDL168_H 0 | radishlgb164IEV525399 | 632 | 132 | 90.5 | blastp |
| 312 | BDL171_H 0 | arabidopsislgb165IAT2G3 1580 | 633 | 134 | 84 | blastp |
| 313 | BDL182_H 0 | canolalgb161ICX188804 | 634 | 140 | 87.5 | blastp |
| 314 | BDL183_H 0 | arabidopsislgb165IAT4G1 5630 | 635 | 141 | 81.6 | blastp |
| 315 | BDL183_H 1 | b_rapalgb162IEE526726 | 636 | 141 | 83.7 | blastp |
| 316 | BDL183_H 2 | canolalgb161ICD811977 | 637 | 141 | 80 | blastp |
| 317 | BDL183_H 3 | canolalgb161ICN735162 | 638 | 141 | 83.7 | blastp |
| 318 | BDL183_H 4 | canolalgb161ICN828640 | 639 | 141 | 83.7 | blastp |
| 319 | BDL183_H 5 | radishlgb164IEW722612 | 640 | 141 | 83.2 | blastp |
| 320 | BDL183_H 6 | radishlgb164IEX753993 | 641 | 141 | 81.6 | blastp |
| 321 | BDL183_H 7 | thellungiellalgb167IBY82 4379 | 642 | 141 | 80 | blastp |
| 322 | BDL190_H 0 | b_oleracealgb161IAM395 197 | 643 | 146 | 84.49 | tblastn |
| 323 | BDL190_H 1 | canolalgb161IEE407003 | 644 | 146 | 87.2 | blastp |
| 324 | BDL190_H 2 | radishlgb164IEV547395 | 645 | 146 | 86.6 | blastp |
| 325 | BDL190_H 3 | thellungiellalgb167IBY82 7749 | 646 | 146 | 89.8 | blastp |
| 326 | BDL192_H 0 | canolalgb161ICD827541 | 647 | 147 | 80.37 | tblastn |
| 327 | BDL201_H 0 | b_juncealgb164IEVGN00 584109703185 | 648 | 153 | 81.8 | blastp |
| 328 | BDL201_H 1 | b_oleracealgb161IDY014 784 | 649 | 153 | 80.4 | blastp |
| 329 | BDL201_H 2 | b_oleracealgb161IDY015 288 | 650 | 153 | 82.2 | blastp |
| 330 | BDL201_H 3 | b_rapalgb162IBQ791239 | 651 | 153 | 83.2 | blastp |
| 331 | BDL201_H 4 | canolalgb161IBQ704590 | 652 | 153 | 81.7 | blastp |
| 332 | BDL201_H 5 | canolalgb161ICD822183 | 653 | 153 | 80.8 | blastp |
| 333 | BDL201_H 6 | canolalgb161ICD838597 | 654 | 153 | 81.8 | blastp |
| 334 | BDL201_H 7 | radishlgb164IEV527287 | 655 | 153 | 81.6 | blastp |
| 335 | BDL201_H 8 | radishlgb164IEV534907 | 656 | 153 | 81.8 | blastp |

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|------------------------------------|------------------|---------------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 336 | BDL201_H 9 | radishlgb164IEV543313 | 657 | 153 | 81.3 | blastp |
| 337 | BDL201_H 10 | radishlgb164IEV565783 | 658 | 153 | 81.9 | blastp |
| 338 | BDL201_H 11 | thellungiellalgb167IBY81 4893 | 659 | 153 | 83.89 | tblastn |
| 339 | BDL223_H 0 | arabidopsislgb165IAT3G5 4080 | 660 | 159 | 82.05 | tblastn |
| 340 | BDL223_H 1 | arabidopsislgb165IAT3G5 4085 | 661 | 159 | 82.1 | blastp |
| 341 | BDL223_H 2 | b_juncealgb164IEVGN01 441114591370 | 662 | 159 | 96.15 | tblastn |
| 342 | BDL223_H 3 | b_juncealgb164IEVGN05 602102561055 | 663 | 159 | 85 | blastp |
| 343 | BDL223_H 4 | b_oleracealgb161IEE5349 59 | 664 | 159 | 96.2 | blastp |
| 344 | BDL223_H 5 | b_oleracealgb161IES9476 77 | 665 | 159 | 94.9 | blastp |
| 345 | BDL223_H 6 | b_rapalgb162IEE527700 | 666 | 159 | 96.2 | blastp |
| 346 | BDL223_H 7 | canolalgb161ICD812251 | 667 | 159 | 96.2 | blastp |
| 347 | BDL223_H 8 | canolalgb161ICN734091 | 668 | 159 | 96.15 | tblastn |
| 348 | BDL223_H 9 | canolalgb161IDY007214 | 669 | 159 | 96.15 | tblastn |
| 349 | BDL223_H 10 | canolalgb161IEG019597 | 670 | 159 | 97.4 | blastp |
| 350 | BDL223_H 11 | canolalgb161IES992154 | 671 | 159 | 97.4 | blastp |
| 351 | BDL223_H 12 | canolalgb161IEV087632 | 672 | 159 | 97.4 | blastp |
| 352 | BDL223_H 13 | radishlgb164IEV524950 | 673 | 159 | 96.15 | tblastn |
| 353 | BDL223_H 14 | radishlgb164IEY899056 | 674 | 159 | 96.2 | blastp |
| 354 | BDL229_H 0 | b_rapalgb162IEX066757 | 675 | 160 | 83.5 | blastp |
| 355 | BDL229_H 1 | radishlgb164IEW725388 | 676 | 160 | 82.59 | tblastn |
| 356 | BDL231_H 0 | arabidopsislgb165IAT1G7 9470 | 677 | 162 | 84.5 | blastp |
| 357 | BDL231_H 1 | canolalgb161ICD826885 | 678 | 162 | 84.7 | blastp |
| 358 | BDL231_H 2 | canolalgb161ICD827559 | 679 | 162 | 95.42 | tblastn |
| 359 | BDL242_H 0 | radishlgb164IEV539529 | 680 | 164 | 85.9 | blastp |
| 360 | BDL247_H 0 | b_oleracealgb161IDY026 136 | 681 | 167 | 90.82 | tblastn |
| 361 | BDL247_H 1 | b_rapalgb162IAY185359 | 682 | 167 | 91.1 | blastp |

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|------------------------------------|------------------|------------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 362 | BDL247_H 2 | canolalgb161 CD838112 | 683 | 167 | 89.1 | blastp |
| 363 | BDL247_H 3 | canolalgb161 EE455228 | 684 | 167 | 91.1 | blastp |
| 364 | BDL247_H 4 | maizelgb170 LEU94083 3 | 685 | 167 | 92.8 | blastp |
| 365 | BDL247_H 5 | radishlgb164 EV566311 | 686 | 167 | 92.6 | blastp |
| 366 | BDL247_H 6 | thellungiellalgb167 DN77 3706 | 687 | 167 | 93.08 | tblastn |
| 367 | BDL248_H 0 | arabidopsislgb165 AT4G3 7340 | 688 | 168 | 80.6 | blastp |
| 368 | BDL70_H0 | arabidopsislgb165 AT4G2 5960 | 689 | 201 | 80.6 | blastp |
| 369 | BDL70_H1 | poplarlgb170 CN192983 | 690 | 201 | 82.8 | blastp |
| 370 | BDL70_H2 | soybeanlgb168 BE822547 | 691 | 201 | 81.9 | blastp |
| 371 | BDL70_H3 | soybeanlgb168 CD415929 | 692 | 201 | 81.8 | blastp |
| 372 | BDL85_H0 | b_oleracealgb161 AM385 973 | 693 | 175 | 83.3 | blastp |
| 373 | BDL85_H1 | b_rapalgb162 CV544456 | 694 | 175 | 83.3 | blastp |
| 374 | BDL85_H2 | b_rapalgb162 EE523194 | 695 | 175 | 84.7 | blastp |
| 375 | BDL85_H3 | canolalgb161 CD813661 | 696 | 175 | 83.3 | blastp |
| 376 | BDL85_H4 | canolalgb161 CD822271 | 697 | 175 | 84.7 | blastp |
| 377 | BDL85_H5 | canolalgb161 CX280350 | 698 | 175 | 83.3 | blastp |
| 378 | BDL85_H6 | radishlgb164 EV527759 | 699 | 175 | 82.2 | blastp |
| 379 | BDL85_H7 | thellungiellalgb167 DN77 9034 | 700 | 175 | 83.6 | blastp |
| 380 | BDL88_H0 | barleylgb157.3 BI950587 | 701 | 176 | 82.3 | blastp |
| 381 | BDL88_H1 | barleylgb157.3 BI955547 | 702 | 176 | 88.6 | blastp |
| 382 | BDL88_H2 | brachypodiumlgb169 BE4 25841 | 703 | 176 | 82.7 | blastp |
| 383 | BDL88_H3 | brachypodiumlgb169 BM 817094 | 704 | 176 | 90 | blastp |
| 384 | BDL88_H4 | fescuelgb161 CK802755 | 705 | 176 | 88.7 | blastp |
| 385 | BDL88_H5 | leymuslgb166 EG378145 | 706 | 176 | 83.2 | blastp |
| 386 | BDL88_H6 | maizelgb170 AI622555 | 707 | 176 | 89.9 | blastp |
| 387 | BDL88_H7 | maizelgb170 AI712236 | 708 | 176 | 89.2 | blastp |
| 388 | BDL88_H8 | maizelgb170 AI855432 | 709 | 176 | 80.7 | blastp |
| 389 | BDL88_H9 | pseudoroegneria gb167 F F342352 | 710 | 176 | 88 | blastp |
| 390 | BDL88_H1 0 | pseudoroegneria gb167 F F342444 | 711 | 176 | 82.3 | blastp |
| 391 | BDL88_H1 1 | ricelgb170 OS08G43320 | 712 | 176 | 84.5 | blastp |
| 392 | BDL88_H1 2 | sorghumlgb161.crp AW5 62977 | 713 | 176 | 81.4 | blastp |
| 393 | BDL88_H1 3 | sorghumlgb161.crp BE12 9901 | 714 | 176 | 91.1 | blastp |
| 394 | BDL88_H1 4 | sugarcanelgb157.3 SCFM EMPRO | 715 | 176 | 91.4 | blastp |
| 395 | BDL88_H1 5 | switchgrasslgb167 DN144 780 | 716 | 176 | 91.7 | blastp |

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|------------------------------------|------------------|---------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 396 | BDL88_H1 6 | switchgrass gb167 FE629 824 | 717 | 176 | 92 | blastp |
| 397 | BDL88_H1 7 | wheat gb164 BE406463 | 718 | 176 | 88 | blastp |
| 398 | BDL88_H1 8 | wheat gb164 BE425841 | 719 | 176 | 82 | blastp |
| 399 | BDL88_H1 9 | wheat gb164 BF474328 | 720 | 176 | 81.2 | blastp |
| 400 | BDL88_H2 0 | wheat gb164 BQ484144 | 721 | 176 | 87.7 | blastp |
| 401 | BDL88_H2 1 | wheat gb164 CA599299 | 722 | 176 | 88 | blastp |
| 402 | BDL94_H0 | rice gb170 OS01G09220 | 723 | 177 | 96.7 | blastp |
| 403 | BDL102_H 0 | avocado gb164 CK76710 8 | 724 | 178 | 80.69 | tblastn |
| 404 | BDL102_H 1 | banana gb167 FL650176 | 725 | 178 | 82.8 | blastp |
| 405 | BDL102_H 2 | banana gb167 FL657720 | 726 | 178 | 80.4 | blastp |
| 406 | BDL102_H 3 | banana gb167 FL658383 | 727 | 178 | 83.4 | blastp |
| 407 | BDL102_H 4 | barley gb157.3 BE215743 | 728 | 178 | 84.83 | tblastn |
| 408 | BDL102_H 5 | barley gb157.3 BE411917 | 729 | 178 | 85.2 | blastp |
| 409 | BDL102_H 6 | barley gb157.3 BF627967 | 730 | 178 | 82.76 | tblastn |
| 410 | BDL102_H 7 | brachypodium gb169 BE3 98478 | 731 | 178 | 83.7 | blastp |
| 411 | BDL102_H 8 | brachypodium gb169 BE3 99017 | 732 | 178 | 87.6 | blastp |
| 412 | BDL102_H 9 | brachypodium gb169 BE4 23566 | 733 | 178 | 85.5 | blastp |
| 413 | BDL102_H 10 | cenchrus gb166 EB65550 9 | 734 | 178 | 89 | blastp |
| 414 | BDL102_H 11 | cichorium gb171 DT2119 67 | 735 | 178 | 80.1 | blastp |
| 415 | BDL102_H 12 | cichorium gb171 EH7006 64 | 736 | 178 | 80 | blastp |
| 416 | BDL102_H 13 | citrus gb166 BE208879 | 737 | 178 | 80 | blastp |
| 417 | BDL102_H 14 | clover gb162 BB906663 | 738 | 178 | 80 | blastp |
| 418 | BDL102_H 15 | cowpea gb166 FC462243 | 739 | 178 | 80.7 | blastp |
| 419 | BDL102_H 16 | dandelion gb161 DY8137 50 | 740 | 178 | 80.7 | blastp |
| 420 | BDL102_H 17 | fescue gb161 DT685902 | 741 | 178 | 85.6 | blastp |
| 421 | BDL102_H 18 | ginger gb164 DY369602 | 742 | 178 | 80.7 | blastp |
| 422 | BDL102_H 19 | ipomoea gb157.2 BJ5570 23 | 743 | 178 | 80 | tblastn |

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|------------------------------------|------------------|---------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 423 | BDL102_H 20 | ipomoealgb157.2IBU6907 07 | 744 | 178 | 80 | tblastn |
| 424 | BDL102_H 21 | lettuce gb157.2IDW04478 6 | 745 | 178 | 80 | blastp |
| 425 | BDL102_H 22 | lettuce gb157.2IDW05075 7 | 746 | 178 | 80 | tblastn |
| 426 | BDL102_H 23 | lettuce gb157.2IDW10880 9 | 747 | 178 | 81.38 | tblastn |
| 427 | BDL102_H 24 | lettuce gb157.2IDW10881 0 | 748 | 178 | 80 | tblastn |
| 428 | BDL102_H 25 | liquorice gb171IFS238664 | 749 | 178 | 80.7 | blastp |
| 429 | BDL102_H 26 | liquorice gb171IFS241892 | 750 | 178 | 80 | tblastn |
| 430 | BDL102_H 27 | liriodendron gb166 CK76 6596 | 751 | 178 | 83.4 | blastp |
| 431 | BDL102_H 28 | lotus gb157.2IAW720301 | 752 | 178 | 82.1 | blastp |
| 432 | BDL102_H 29 | lotus gb157.2ICN825142 | 753 | 178 | 81.5 | blastp |
| 433 | BDL102_H 30 | lovegrass gb167 EH18838 8 | 754 | 178 | 88.97 | tblastn |
| 434 | BDL102_H 31 | maize gb170 AI391795 | 755 | 178 | 95.2 | blastp |
| 435 | BDL102_H 32 | maize gb170 LLBE51025 4 | 756 | 178 | 95.2 | blastp |
| 436 | BDL102_H 33 | melon gb165 DV632852 | 757 | 178 | 80 | tblastn |
| 437 | BDL102_H 34 | millet gb161 CD725312 | 758 | 178 | 85.7 | blastp |
| 438 | BDL102_H 35 | nuphar gb166 CV003178 | 759 | 178 | 81.4 | blastp |
| 439 | BDL102_H 36 | oat gb164 CN815719 | 760 | 178 | 91.03 | tblastn |
| 440 | BDL102_H 37 | oil_palm gb166 EL68109 8 | 761 | 178 | 86.21 | tblastn |
| 441 | BDL102_H 38 | oil_palm gb166 EL68263 0 | 762 | 178 | 84.1 | blastp |
| 442 | BDL102_H 39 | oil_palm gb166 EL68411 9 | 763 | 178 | 82.1 | blastp |
| 443 | BDL102_H 40 | onion gb162 CF446214 | 764 | 178 | 80.4 | blastp |
| 444 | BDL102_H 41 | papaya gb165 EX258155 | 765 | 178 | 80.7 | blastp |
| 445 | BDL102_H 42 | pineapple gb157.2IDT336 701 | 766 | 178 | 84.8 | blastp |
| 446 | BDL102_H 43 | pineapple gb157.2IDT338 401 | 767 | 178 | 84.8 | blastp |
| 447 | BDL102_H 44 | poppy gb166 FE964559 | 768 | 178 | 80 | tblastn |
| 448 | BDL102_H 45 | rice gb170 OS03G31090 | 769 | 178 | 93.8 | blastp |

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|------------------------------------|------------------|--------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 449 | BDL102_H 46 | ryelgb164 BE637001 | 770 | 178 | 85.2 | blastp |
| 450 | BDL102_H 47 | sorghum gb161.crplAI673 920 | 771 | 178 | 96.6 | blastp |
| 451 | BDL102_H 48 | sorghum gb161.crplAW7 47023 | 772 | 178 | 83.3 | blastp |
| 452 | BDL102_H 49 | soybean gb168 AA66103 6 | 773 | 178 | 80 | blastp |
| 453 | BDL102_H 50 | soybean gb168 AW72030 1 | 774 | 178 | 80 | tblastn |
| 454 | BDL102_H 51 | sugarcane gb157.3 CA076 952 | 775 | 178 | 96.6 | blastp |
| 455 | BDL102_H 52 | sugarcane gb157.3 CA087 422 | 776 | 178 | 96.6 | blastp |
| 456 | BDL102_H 53 | sugarcane gb157.3 CA103 720 | 777 | 178 | 97.2 | blastp |
| 457 | BDL102_H 54 | sugarcane gb157.3 CA113 942 | 778 | 178 | 84.25 | tblastn |
| 458 | BDL102_H 55 | sugarcane gb157.3 CA114 406 | 779 | 178 | 97.2 | blastp |
| 459 | BDL102_H 56 | sugarcane gb157.3 CA116 867 | 780 | 178 | 87.6 | blastp |
| 460 | BDL102_H 57 | sugarcane gb157.3 CA119 956 | 781 | 178 | 90.34 | tblastn |
| 461 | BDL102_H 58 | sugarcane gb157.3 CA128 680 | 782 | 178 | 86.9 | blastp |
| 462 | BDL102_H 59 | sugarcane gb157.3 CA139 681 | 783 | 178 | 84.3 | blastp |
| 463 | BDL102_H 60 | sugarcane gb157.3 CA151 882 | 784 | 178 | 93.1 | tblastn |
| 464 | BDL102_H 61 | sugarcane gb157.3 CA153 401 | 785 | 178 | 96.6 | blastp |
| 465 | BDL102_H 62 | sugarcane gb157.3 CA193 794 | 786 | 178 | 97.2 | blastp |
| 466 | BDL102_H 63 | sugarcane gb157.3 CA215 946 | 787 | 178 | 80 | blastp |
| 467 | BDL102_H 64 | sugarcane gb157.3 CA235 573 | 788 | 178 | 80.3 | blastp |
| 468 | BDL102_H 65 | sugarcane gb157.3 CA241 742 | 789 | 178 | 82.76 | tblastn |
| 469 | BDL102_H 66 | sugarcane gb157.3 CA289 186 | 790 | 178 | 95.2 | blastp |
| 470 | BDL102_H 67 | sugarcane gb157.3 CF571 967 | 791 | 178 | 93.79 | tblastn |
| 471 | BDL102_H 68 | sugarcane gb157.3 CF574 520 | 792 | 178 | 97.2 | blastp |
| 472 | BDL102_H 69 | sunflower gb162 CD8485 88 | 793 | 178 | 80 | blastp |
| 473 | BDL102_H 70 | sunflower gb162 CD8509 71 | 794 | 178 | 80.7 | blastp |
| 474 | BDL102_H 71 | switchgrass gb167 DN142 384 | 795 | 178 | 95.9 | blastp |

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|------------------------------------|------------------|--------------------------------------|------------------------------------|-------------------------------------|------------------------------|---------------|
| 475 | BDL102_H 72 | switchgrasslgb167IFE598 349 | 796 | 178 | 96.6 | blastp |
| 476 | BDL102_H 73 | switchgrasslgb167IFE608 943 | 797 | 178 | 96.6 | blastp |
| 477 | BDL102_H 74 | switchgrasslgb167IFE642 870 | 798 | 178 | 96.6 | blastp |
| 478 | BDL102_H 75 | switchgrasslgb167IFL710 664 | 799 | 178 | 95.2 | blastp |
| 479 | BDL102_H 76 | tealgb171IFE861343 | 800 | 178 | 80.14 | tblastn |
| 480 | BDL102_H 77 | walnutlgb166ICV195103 | 801 | 178 | 80.7 | blastp |
| 481 | BDL102_H 78 | walnutlgb166ICV196374 | 802 | 178 | 80.7 | blastp |
| 482 | BDL102_H 79 | wheatlgb164IBE398202 | 803 | 178 | 85.2 | blastp |
| 483 | BDL102_H 80 | wheatlgb164IBE406254 | 804 | 178 | 85.2 | blastp |
| 484 | BDL102_H 81 | wheatlgb164IBE414893 | 805 | 178 | 85.2 | blastp |
| 485 | BDL102_H 82 | wheatlgb164ICA485952 | 806 | 178 | 96.6 | blastp |
| 486 | BDL102_H 83 | wheatlgb164ICA486424 | 807 | 178 | 93.8 | blastp |
| 487 | BDL226_H 0 | canolalgb161ICD835072 | 808 | 181 | 89.5 | blastp |
| 488 | BDL226_H 1 | radishlgb164IEV568139 | 809 | 181 | 91.7 | blastp |
| 489 | BDL233_H 0 | radishlgb164IEV549343 | 810 | 185 | 84.5 | blastp |
| 490 | BDL237_H 0 | arabidopsislgb165IAT2G4 4890 | 811 | 187 | 86.3 | blastp |
| 491 | BDL238_H 0 | arabidopsislgb165IAT1G3 2763 | 812 | 202 | 81.5 | blastp |
| 492 | BDL240_H 0 | castorbeanlgb160IMDL30 174M008707 | 813 | 189 | 82.4 | blastp |
| 493 | BDL240_H 1 | cottonlgb164IBG446934 | 814 | 189 | 81.4 | blastp |
| 494 | BDL240_H 2 | soybeanlgb168IAW32969 3 | 815 | 189 | 80.7 | blastp |
| 495 | BDL240_H 3 | soybeanlgb168IBE329627 | 816 | 189 | 80.1 | blastp |
| 496 | BDL241_H 0 | canolalgb161ICN825973 | 817 | 190 | 85.3 | blastp |
| 497 | BDL249_H 0 | radishlgb164IEW735252 | 818 | 191 | 86.7 | blastp |
| 498 | BDL251_H 0 | arabidopsislgb165IAT5G2 3190 | 819 | 192 | 80.07 | tblastn |
| 499 | BDL252_H 0 | applelgb171ICN489978 | 820 | 193 | 80.9 | blastp |
| 500 | BDL252_H 1 | applelgb171ICN883406 | 821 | 193 | 80.9 | blastp |

| <i>Polynuc. SEQ ID NO:</i> | <i>Gene Name</i> | <i>Organism/Cluster name</i> | <i>Polypep. SEQ ID NO:</i> | <i>Homol. to SEQ ID NO:</i> | <i>% Global identity</i> | <i>Algor.</i> |
|----------------------------|------------------|--------------------------------------|----------------------------|-----------------------------|--------------------------|---------------|
| 501 | BDL252_H 2 | b_rapalgb162 EX036871 | 822 | 193 | 91 | blastp |
| 502 | BDL252_H 3 | cacaolgb167 CU476642 | 823 | 193 | 84.3 | blastp |
| 503 | BDL252_H 4 | canolalgb161 CN732395 | 824 | 193 | 90.6 | blastp |
| 504 | BDL252_H 5 | canolalgb161 ES900668 | 825 | 193 | 86.2 | blastp |
| 505 | BDL252_H 6 | castorbeanlgb160 MDL29 726M003996 | 826 | 193 | 81.4 | blastp |
| 506 | BDL252_H 7 | citruslgb166 CB417408 | 827 | 193 | 82.8 | blastp |
| 507 | BDL252_H 8 | cottonlgb164 AI725830 | 828 | 193 | 82.8 | blastp |
| 508 | BDL252_H 9 | cottonlgb164 CO094656 | 829 | 193 | 82.5 | blastp |
| 509 | BDL252_H 10 | cowpealgb166 FC458375 | 830 | 193 | 80.5 | blastp |
| 510 | BDL252_H 11 | grapelgb160 CB920145 | 831 | 193 | 80.5 | blastp |
| 511 | BDL252_H 12 | ipomoealgb157.2 AU2238 26 | 832 | 193 | 80.2 | blastp |
| 512 | BDL252_H 13 | lettucelgb157.2 DW11675 3 | 833 | 193 | 80.22 | tblastn |
| 513 | BDL252_H 14 | medicagolgb157.2 AL371 996 | 834 | 193 | 80.9 | blastp |
| 514 | BDL252_H 15 | peachlgb157.2 BU039377 | 835 | 193 | 82.4 | blastp |
| 515 | BDL252_H 16 | poplarlgb170 BU816161 | 836 | 193 | 80.7 | blastp |
| 516 | BDL252_H 17 | prunuslgb167 BU039377 | 837 | 193 | 82.4 | blastp |
| 517 | BDL252_H 18 | radishlgb164 EV535608 | 838 | 193 | 92.1 | blastp |
| 518 | BDL252_H 19 | radishlgb164 EW723334 | 839 | 193 | 91.8 | blastp |
| 519 | BDL252_H 20 | soybeanlgb168 BF636462 | 840 | 193 | 80.1 | blastp |
| 520 | BDL252_H 21 | soybeanlgb168 BU546186 | 841 | 193 | 82.4 | blastp |
| 521 | BDL252_H 22 | soybeanlgb168 CD390334 | 842 | 193 | 82.4 | blastp |
| 522 | BDL252_H 23 | strawberylgb164 CX6613 79 | 843 | 193 | 82 | blastp |
| 523 | BDL252_H 24 | thellungiellalgb167 BY81 2142 | 844 | 193 | 92.1 | blastp |

Table 16: Provided are polynucleotides and polypeptides which are homologous to the identified polynucleotides or polypeptides of Table 15. Homol. = homologue; Algor. = Algorithm;

EXAMPLE 7**GENE CLONING AND GENERATION OF BINARY VECTORS FOR PLANT
EXPRESSION**

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

Cloning strategy

Genes listed in Examples 5 and 6 hereinabove were cloned into binary vectors
for the generation of transgenic plants. For cloning, the full-length open reading frame
10 (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
15 leaves, flowers, siliques or other plant tissues, growing under normal conditions. Total
RNA was extracted as described in Example 2 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
20 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 Ambion,
Clontech or Invitrogen (RACE = Rapid Access to cDNA Ends) was used to access the
full cDNA transcript of the gene from the RNA samples described above. The RACE
procedure was performed for the genes BDL197 (SEQ ID NO:46), BDL156 (SEQ ID
25 NO:19), BDL169 (SEQ ID NO:28), BDL189 (SEQ ID NO:40), BDL200 (SEQ ID
NO:47), BDL79 (SEQ ID NO:5), BDL231 (SEQ ID NO:57), BDL238 (SEQ ID NO:84)
and BDL248 (SEQ ID NO:103) using the primers sequences listed in Table 17, below.
RACE products were cloned into high copy vector followed by sequencing or directly
sequenced. RACE products were sequenced as described hereinbelow for the genes
30 specified in Table 17.

The information from the RACE procedure was used for cloning of the full
length ORF of the corresponding genes.

Table 17
RACE primers used for sequencing of the identified genes of the invention

5

| <i>Gene Name</i> | <i>Primers used for amplification</i> | <i>High copy plasmid used for cloning of RACE products</i> |
|------------------|---|--|
| BDL197_5'Race | BDL197_NGSP1_R2 (SEQ ID NO:934) (CGCCTGAAGCTTCTCCGAGAAC) | TopoTA |
| BDL156_5'Race | BDL156_NGSP1_R (SEQ ID NO:937) (ACGGTGTTTCCAGAATTTCCGACAG) | |
| BDL156_3'Race | BDL156_NGSP2_F (SEQ ID NO:938) (CTGAATGTGACTGGGATATGTCCGG) | TopoTA |
| BDL169_5'Race | BDL169_NGSP1_R (SEQ ID NO:939) (TGCACTGGAGCGTGTAGGGACAG) | |
| BDL169_3'Race | BDL169_NGSP1_F (SEQ ID NO:940) (GGCAGAAACTGTTTTATGGAAATGG) | |
| BDL189_5'Race | BDL189_NGSP1_R (SEQ ID NO:941) (TTCTGTCCCTCGACCAAGGTTG) | TopoTA |
| BDL189_3'Race | BDL189_GSP2_F (SEQ ID NO:942) (CAGTCAATCTTCTTAGCATCGCTGAG) | |
| BDL200_5'Race | BDL200_NGSP_Rb (SEQ ID NO:943) (CCAATGCCAATACGATGGTCCG) | TopoTA |
| BDL200_3'Race | BDL200_NGSP2_F (SEQ ID NO:944) (GAGCTTTGGAGATAAGATTGGTGCAG) | |
| BDL79_5'Race | BDL79_GSP1_R (SEQ ID NO:945) (GTATCACTCGAGGCACCATTTGGG) | TopoTA |
| BDL231_3'Race | BDL231_NGSP_R (SEQ ID NO:946) (ATGTGGGATTCGAGACAGTGTC) | TopoTA |
| BDL238_5'Race | BDL238_NGSP_R (SEQ ID NO:947) (TTTACCGTCCCAAACGTTGCCG) | |
| BDL238_3'Race | BDL238_NGSP_F (SEQ ID NO:948) (CTCATCCGGACGATGTCTTACTTCTTCTCC) | |
| BDL248_5'Race | BDL248_NGSP_R (SEQ ID NO:949) (GAGGTGACCGATCACTGGTAACGC) | |
| BDL215_5'Race | BDL215_NGSP1_R (SEQ ID NO:950) (TGGCTTTGAAAACGTAACATGCC) | |
| BDL215_3'Race | BDL215_NGSP2_F (SEQ ID NO:951) (TATTGGGATTTTCGGATCGATGG) | TopoTA |

Table 17. Provided are the PCR primers used for RACE sequencing. Fwd = forward primer; Rev = reverse primer;

10 In case genomic DNA was cloned, as in the case of BDL90 and BDL94 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 18 below provides primers used for cloning of selected genes.

5

Table 18
The PCR primers used for cloning the genes of the invention

| Gene Name | Restriction Enzymes used for cloning | Primers used for amplification |
|------------------|---|---|
| BDL102 | Sall, XbaI | BDL102_NF_Sall(SEQ ID NO:952) AATGTCGACTACCTGCCTTTCTCTCGTCC |
| | | BDL102_EF_Sall(SEQ ID NO:953) AAAGTCGACACTCTACCTGCCTTTCTCTCG |
| | | BDL102_NR_XbaI(SEQ ID NO:954) ATTCTAGACTATGTAGCCATCTCAACAATCAAAC |
| | | BDL102_ER_XbaI(SEQ ID NO:955) ATTCTAGAGGTTTTGATAAATAGGTAAGTACTCAGG |
| BDL117 | | BDL117_EF_SmaI(SEQ ID NO:956) CCCCGGGTCTCGGAGGTATCTTATTCCAG |
| | | BDL117_ER_SmaI(SEQ ID NO:957) CCCCGGGATGCCACACTTAAGGCCAAG |
| BDL118 | SmaI, SmaI | BDL118_NF_SmaI(SEQ ID NO:958) TCCCCGGGTCTGGGTCTACTTTTGATTGAG |
| | | BDL118_NR_SmaI(SEQ ID NO:959) TCCCCGGGTGAAGCAGAAGTTTCGATTAAAG |
| BDL138 | Sall, XbaI | BDL138_NF_Sall(SEQ ID NO:960) AAAGTCGACCGAATCGTAATTGTTGAAGAGAG |
| | | BDL138_EF_Sall(SEQ ID NO:961) ATTGTCGACTTTAAGGAGAAGAGTTCGCAGTC |
| | | BDL138_NR_XbaI(SEQ ID NO:962) ATTCTAGATTAGAGAGTGGTTGATAACGCAGAG |
| | | BDL138_ER_XbaI(SEQ ID NO:963) ACTCTAGACTACCTGTCACAATTTTCTAAAACAC |
| BDL140 | XbaI, SacI | BDL140_NF_XbaI(SEQ ID NO:964) TATCTAGATTGAGAATGAACTCAGTGTGTATC |
| | | BDL140_EF_XbaI(SEQ ID NO:965) AATCTAGAACTAAACATTGAGAATGAACTCAG |
| | | BDL140_NR_SacI(SEQ ID NO:966) TGAGCTCTTAAGTCATTTAGTTTGGATCAACAAC |
| | | BDL140_ER_SacI(SEQ ID NO:967) CGAGCTCAGACCATGCATTTAAGGATCAC |
| | | BDL147_NF_Sall(SEQ ID NO:968) TTAGTCGACCACAGTAACCATGTCCGTCTC |
| BDL147 | Sall, XbaI | BDL147_NR_XbaI(SEQ ID NO:969) TATCTAGAGTGCTGCTTACTCGCTGTTTC |
| | | BDL149_NF_Sall(SEQ ID NO:970) AAAGTCGACCTCAAACCCAAGAACCCTCATC |
| BDL149 | Sall, XbaI | BDL149_NR_XbaI(SEQ ID NO:971) ATTCTAGATGCAATAGTAGTAGCAGTGAACC |
| | | BDL152_NF_XbaI(SEQ ID NO:972) TATCTAGATTCAGACAAAAACAGAGAGAAACT |
| BDL152 | XbaI, SacI | BDL152_NR_SacI(SEQ ID NO:973) TGAGCTCCTAAGATCGGTTTAAATCAATAGGG |
| | | BDL153_NF_Sall(SEQ ID NO:974) AAAGTCGACAACAGCTTCGGTTTAAAGAGTTC |
| BDL153 | Sall, SmaI | |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|--|
| | | BDL153_NF_SmaI(SEQ ID NO:975) TCCCCGGTCTACATTACGGCATAACGGC |
| BDL154 | Sall, SacI | BDL154_NF_Sall(SEQ ID NO:976) TTAGTCGACTTAAAAATGGAGAGTCAAAGC |
| | | BDL154_NR_SacI(SEQ ID NO:977) TGAGCTCCTACTACTTCTTGTGATGCTGAGG |
| BDL155 | Sall, XbaI | BDL155_NF_Sall(SEQ ID NO:978) AATGTCGACTCCTCTTGC GGAGAGATGC |
| | | BDL155_NR_XbaI(SEQ ID NO:979) ATTCTAGATCTCCTTTTGAGAGAGTGCAAC |
| BDL156 | Sall, XbaI | BDL156_NF_Sall(SEQ ID NO:980) AATGTCGACTCGTCGTCTTCTCATTTCG |
| | | BDL156_ER_XbaI(SEQ ID NO:981) ATTCTAGACTAATACGATTGGTAACAAGAAAACG |
| BDL157 | Sall, XbaI | BDL157_NF_Sall(SEQ ID NO:982) ATTGTCGACTTTCAATAAGAAATCTGCGTCC |
| | | BDL157_EF_Sall(SEQ ID NO:983) AAAGTCGACGAATCTGCTTTTAAAGCTTCTCG |
| | | BDL157_NR_XbaI(SEQ ID NO:984) ATTCTAGACTAAAGAGAGTGAAGGAACAAAGACC |
| | | BDL157_ER_XbaI(SEQ ID NO:985) ATTCTAGACTATTTTCTTCTGTCTTCTGTGTCTTC |
| BDL158 | | BDL158_EF_XbaI(SEQ ID NO:986) AATCTAGACCTCACTTCTCTCTCTCTCTCTTC |
| | | BDL158_ER_SmaI(SEQ ID NO:987) CCCCGGGAGCCTAAAGCCTAACCCAAC |
| BDL160 | Sall, XbaI | BDL160_NF_Sall(SEQ ID NO:988) AAAGTCGACTGATCTACACAGAATCCATTTCC |
| | | BDL160_NR_XbaI(SEQ ID NO:989) AATCTAGATCATTACAGCCATTACATTTTAGG |
| BDL162 | Sall, XbaI | BDL162_NF_Sall(SEQ ID NO:990) TTAGTCGACCCTAATAATGGCTTGCAGAGC |
| | | BDL162_NR_XbaI(SEQ ID NO:991) TATCTAGAAAATCTTGAGACTAAATCAAGCTG |
| BDL167 | Sall, XbaI | BDL167_NF_Sall(SEQ ID NO:992) AAAGTCGACGCAAGAAAGGGACTAACCAAG |
| | | BDL167_NR_XbaI(SEQ ID NO:993) ACTCTAGACTATGTCGGCATTAACTTAGAATCAC |
| BDL168 | XbaI, SmaI | BDL168_NF_XbaI(SEQ ID NO:994) AATCTAGACTTGCTTCAAGATTTCGAGTGAG |
| | | BDL168_EF_XbaI(SEQ ID NO:995) AATCTAGAATTAACCACCATTTCTGTGAAG |
| | | BDL168_NR_SmaI(SEQ ID NO:996) TCCCCGGGCTACCTTCTTCTTCTTCACTTCC |
| | | BDL168_ER_SmaI(SEQ ID NO:997) TCCCCGGGTCTTAAAAGTCAGTCACCTTCTG |
| BDL169 | Sall, XbaI | BDL169_NF_Sall(SEQ ID NO:998) AAAGTCGACGAAGGTGAAGTGATGGATTCTG |
| | | BDL169_EF_Sall(SEQ ID NO:999) AATGTCGACTGTTACCGATAAGAAGGTGAAG |
| | | BDL169_NR_XbaI(SEQ ID NO:1000) ATTCTAGACTAACAGCTTCAACGTAATTTGGTG |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|---|
| | | BDL169_ER_XbaI(SEQ ID NO:1001) ATTCTAGATCAACGTCATTTTGTGCATATC |
| BDL173 | XbaI, SmaI | BDL173_EF_XbaI(SEQ ID NO:1002) ATTCTAGATTTTCCCGAATCTATTTCATCAC |
| | | BDL173_ER_SmaI(SEQ ID NO:1003) CCCCGGGAACGCTTCACCCTTTAATCC |
| BDL174 | Sall, SacI | BDL174_NF_Sall(SEQ ID NO:1004) AAAGTCGACCCGAGGAAGATGACGACAC |
| | | BDL174_NR_SacI(SEQ ID NO:1005) TGAGCTCCTAGTTTCAAGCAAGAGTGATTCC |
| BDL176 | SmaI, SmaI | BDL176_NF_SmaI(SEQ ID NO:1006) TCCCGGTATTGAGCAGCCGTGAAATC |
| | | BDL176_NR_SmaI(SEQ ID NO:1007) TCCCGGTGGACCAAAGAATCAAATAGTAAC |
| BDL177 | Sall, SacI | BDL177_NF_Sall(SEQ ID NO:1008) AATGTCGACTCAGGATCTATGGCAAGTC |
| | | BDL177_EF_Sall(SEQ ID NO:1009) AAAGTCGACGCTTGTGATCAGGATCTATGG |
| | | BDL177_NR_SacI(SEQ ID NO:1010) TGAGCTCCTAAACAGCTTTCCTTCTACTCTTCATC |
| | | BDL177_ER_SacI(SEQ ID NO:1011) CGAGCTCACAGAAAACAAAAGAACTAGGC |
| BDL181 | Sall, SacI | BDL181_NF_Sall(SEQ ID NO:1012) AAAGTCGACGCGATAGATCTGACGAATGC |
| | | BDL181_NR_SacI(SEQ ID NO:1013) TGAGCTCCTAGATTTTCATACTCAGGAAGCCAC |
| BDL182 | Sall, SacI | BDL182_NF_Sall(SEQ ID NO:1014) AACGTCGACTCTACCATCGACAACGAGAAAC |
| | | BDL182_NR_SacI_new(SEQ ID NO:1015) TGAGCTCCTACATTCAACAACAAACCACACTAC |
| BDL183 | Sall, XbaI | BDL183_NF_Sall(SEQ ID NO:1016) AATGTCGACTTATTTTGATCTTCCTCACTTCTG |
| | | BDL183_EF_Sall(SEQ ID NO:1017) AAAGTCGACGATCAATCTTTGTTATCTCTCACTC |
| | | BDL183_NR_XbaI(SEQ ID NO:1018) ATTCTAGACTAATCACACAAAACGACAAGAACAG |
| | | BDL183_ER_XbaI(SEQ ID NO:1019) ACTCTAGAACGATGTGATAAAACATTAGAAGC |
| BDL186 | Sall, XbaI | BDL186_NF_Sall(SEQ ID NO:1020) AAAGTCGACCGAAGTGAAAGTCGTGATGG |
| | | BDL186_EF_Sall(SEQ ID NO:1021) AAAGTCGACACGCAAACGTGATCCTAAAC |
| | | BDL186_NR_XbaI(SEQ ID NO:1022) ATTCTAGACTCAAGGGGACGAGATATCAG |
| | | BDL186_ER_XbaI(SEQ ID NO:1023) ACTCTAGAAGGTAGAGAGCATCAAGGAAGC |
| BDL187 | Sall, SmaI | BDL187_NF_Sall(SEQ ID NO:1024) ATAGTCGACATTCCTTCAGTTTCCGGTG |
| | | BDL187_EF_Sall(SEQ ID NO:1025) AAAGTCGACGCTTGAATTCCTTCAGTTTCC |
| | | BDL187_NR_SmaI(SEQ ID NO:1026) TCCCGGGCTATTTTACCAGTAATTTCCACAC |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|---|
| | | BDL187_ER_SmaI(SEQ ID NO:1027) TCCCGGGTTACTTTAGCCACAATCTGTGTTTTTC |
| BDL188 | XbaI, SmaI | BDL188_NF_XbaI(SEQ ID NO:1028) AATCTAGAATTTTCATTTGTTTCGCTTCG |
| | | BDL188_NR_SmaI(SEQ ID NO:1029) TCCCGGGCTAACAGTAGGTAATTTTGACATCCAG |
| BDL189 | | BDL189_NF_SmaI(SEQ ID NO:1030) ACCCGGGCATTGCCTGTTGGCTTCG |
| | | BDL189_NR_SmaI(SEQ ID NO:1031) ACCCGGGTTACAATACAATTGTTAATTCGAGG |
| BDL190 | SalI, XbaI | BDL190_NF_SalI(SEQ ID NO:1032) TTAGTCGACAAAATAATGGCAGCTTTGGC |
| | | BDL190_EF_SalI(SEQ ID NO:1033) TTAGTCGACTCTCGTCACATATCTTCATCGAC |
| | | BDL190_NR_XbaI(SEQ ID NO:1034) TATCTAGACTACTAGACAAATTTGTTGATCAATTC |
| | | BDL190_ER_XbaI(SEQ ID NO:1035) TATCTAGACTAAAGAGAGAACTAGACAAATTTGTTG |
| BDL192 | SalI, XbaI | BDL192_NF_SalI(SEQ ID NO:1036) ATTGTCGACTTTACGAAATACGCCGAATC |
| | | BDL192_EF_SalI(SEQ ID NO:1037) AATGTCGACTTCGAAACCCTAACAAAAGC |
| | | BDL192_NR_XbaI(SEQ ID NO:1038) ACTCTAGAATCTGCATAGCAGTTAGAACAAG |
| | | BDL192_ER_XbaI(SEQ ID NO:1039) ATTCTAGAGAAAGGTCCTCATTCAATCC |
| BDL193 | XbaI, SacI | BDL193_EF_XbaI(SEQ ID NO:1040) AATCTAGACTTCATATTCAAATCTCCTCTCC |
| | | BDL193_ER_SacI (SEQ ID NO:1041) CGAGCTCATCACAAACAAACCTAAGAGGC |
| BDL194 | EcoRV, EcoRV | BDL194_NF_EcoRV(SEQ ID NO:1042) AAGATATCAGCCATTGTTCTTCATCATCTC |
| | | BDL194_NR_EcoRV(SEQ ID NO:1043) ACGATATCCTAACAGGGTTTTTCAGTGCTGTG |
| BDL196 | SalI, XbaI | BDL196_NF_salI(SEQ ID NO:1044) TTAGTCGACAAGACATGAAGTTCATGACACTAATG |
| | | BDL196_EF_SalI(SEQ ID NO:1045) TTAGTCGACAACCTGAAACAAAAGAAGAGTCATC |
| | | BDL196_NR_XbaI(SEQ ID NO:1046) TATCTAGATTATGAGCTTTAACAACCTAGTATAAGGAAC |
| | | BDL196_ER_XbaI(SEQ ID NO:1047) TATCTAGACACCACAATTTTAAGCTTCAAC |
| BDL197 | SalI, XbaI | BDL197_NF_SalI(SEQ ID NO:1048) AAAGTCGACTGTTCTTGTTCCTTCACGATGAG |
| | | BDL197_EF_SalI(SEQ ID NO:1049) AAAGTCGACTCTAAATCCTATGTTCTTGTTCCTTC |
| | | BDL197_NR_XbaI(SEQ ID NO:1050) AATTCTAGAGGTTCAAATACGTAACACATTG |
| | | BDL197_ER_XbaI(SEQ ID NO:1051) AACTCTAGAACCATATTAGGTTCAAATACGTAAC |
| BDL201 | SalI, XbaI | BDL201_NF_SalI(SEQ ID NO:1052) AAAGTCGACCGATCAACAGACTCTAATCAGC |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|--|
| | | BDL201_NF_XbaI(SEQ ID NO:1053) ATTCTAGATTAGTTCTATACTGCAGATTCTTGGG |
| BDL203 | SalI, XbaI | BDL203_NF_SalI(SEQ ID NO:1054) AATGTCGACTTCTCTCTGTTCTTGCCTCG |
| | | BDL203_EF_SalI(SEQ ID NO:1055) AAAGTCGACCTTCTTCTTTTCTCAATCTTTC |
| | | BDL203_NR_XbaI(SEQ ID NO:1056) ATTCTAGATCTGTATCATTAAAACTGAGGAAG |
| | | BDL203_ER_XbaI(SEQ ID NO:1057) ATTCTAGAGTGGCGAGACAACATTTCTAC |
| | | BDL220_NF_SalI(SEQ ID NO:1058) AAAGTCGACCTCTCTCTCTAATGGGTAATTG |
| BDL220 | SalI, XbaI | BDL220_EF_SalI(SEQ ID NO:1059) AATGTCGACTCACACACAACACAACCAAG |
| | | BDL220_NR_XbaI(SEQ ID NO:1060) ACTCTAGAAATCCAACGTCAAATGAGAAG |
| | | BDL220_NF_SalI(SEQ ID NO:1061) AAAGTCGACCTCTCTCTCTAATGGGTAATTG |
| | | BDL221_NF_SalI(SEQ ID NO:1062) AATGTCGACTTGGATCAGAGAAAATATGTCTG |
| BDL221 | SalI, XbaI | BDL221_EF_SalI(SEQ ID NO:1063) ATAGTCGACCTTGAATCTGAAGCTAATCTTGG |
| | | BDL221_NR_XbaI(SEQ ID NO:1064) ATTCTAGATTAGCATTAGAACGGGACAGTATAAG |
| | | BDL221_ER_XbaI(SEQ ID NO:1065) ACTCTAGATCAAAGAATCGAGCATTAGAACGG |
| | | BDL222_NF_SalI(SEQ ID NO:1066) AAAGTCGACCTAAACCGTAAAAGATGTCTG |
| BDL222 | SalI, XbaI | BDL222_EF_SalI(SEQ ID NO:1067) AACGTCGACACTTTTGTGTTTTGCCTTTCTC |
| | | BDL222_NR_XbaI(SEQ ID NO:1068) ATTCTAGATCTTCTTCATCACTCAATCGC |
| | | BDL222_ER_XbaI(SEQ ID NO:1069) ATTCTAGACTGTGGTATTTAGGGAATACATCC |
| | | BDL223_NF_SalI(SEQ ID NO:1070) AAAGTCGACCACAGAGAAATCATGGGGTTC |
| BDL223 | SalI, XbaI | BDL223_EF_SalI(SEQ ID NO:1071) AACGTCGACAGATATCGTTGGCTTCGTCTC |
| | | BDL223_NR_XbaI(SEQ ID NO:1072) ATTCTAGATTAGGTTTGTATCATTTTAACCAGAG |
| | | BDL223_ER_XbaI(SEQ ID NO:1073) ATTCTAGACTATGCAGAAATGTTTGGATTGAG |
| | | BDL224_NF_XbaI(SEQ ID NO:1074) AATCTAGACCACAAAATTCGTCAAAGCTC |
| BDL224 | XbaI, SmaI | BDL224_EF_XbaI(SEQ ID NO:1075) ATTCTAGATTTTCAAACCACAAAATTCGTC |
| | | BDL224_NR_SmaI(SEQ ID NO:1076) CCCCGGGATCCAACCAATCCCTAAAATG |
| | | BDL224_ER_SmaI(SEQ ID NO:1077) CCCCGGGATCAGCCACTTCTACTCTCAATTC |
| | | BDL225_NF_SalI(SEQ ID NO:1078) AATGTCGACTCCTTGTGATTCATTATTTTGC |
| BDL225 | SalI, XbaI | |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|---|
| | | BDL225_EF_SalI(SEQ ID NO:1079) AAAGTCGACCAACATCTCCTCCAAAACATTC |
| | | BDL225_NR_XbaI(SEQ ID NO:1080) ACTCTAGATTAGCAAGAAGAAAAGAAGTGCAG |
| | | BDL225_ER_XbaI(SEQ ID NO:1081) ATTCTAGATTAGTAGTTTATACAAGGTGCGGAGAC |
| BDL226 | EcoRV, EcoRV | BDL226_NF_EcoRV(SEQ ID NO:1082) AAGATATCGAAACTGGATCTGGGTTTATCC |
| | | BDL226_NR_EcoRV(SEQ ID NO:1083) ATGATATCCTAAACTAATCAAACATGGCACATAC |
| BDL227 | | BDL227_NF_SalI(SEQ ID NO:1084) AAAGTCGACAGAGTTAAGTCAATCACCAAACC |
| | | BDL227_NR_SmaI(SEQ ID NO:1085) TCCCGGGTTACCATCAAGTTTTCTTGCTGAAG |
| BDL228 | SalI, XbaI | BDL228_NF_SalI(SEQ ID NO:1086) AAAGTCGACCCAACACTATATCATGGCTACTATC |
| | | BDL228_NR_XbaI(SEQ ID NO:1087) ATTCTAGACTAACCTCACTTGATGCTCTTGC |
| BDL229 | SalI, XbaI | BDL229_NR_XbaI(SEQ ID NO:1088) TATCTAGAGCTAAACAAAATCCGGAGATAG |
| | | BDL229_ER_XbaI(SEQ ID NO:1089) TATCTAGACAGTCACTCCATAACTATGATCAAAC |
| | | BDL229_F_SalI(SEQ ID NO:1090) TTAGTCGACCTCATTAATGGAAGTTTCAACATC |
| | | BDL229_F_SalI(SEQ ID NO:1091) TTAGTCGACCTCATTAATGGAAGTTTCAACATC |
| BDL230 | SmaI, SmaI | BDL230_NF_SmaI(SEQ ID NO:1092) TCCCGGGTAAGTTTGTGAGATGGAATTAGTG |
| | | BDL230_NR_SmaI(SEQ ID NO:1093) TCCCGGGCTAATTGGTTGGTTACAAGATGC |
| BDL231 | SalI, XbaI | BDL231_NF_SalI(SEQ ID NO:1094) AATGTCGACTGGACTGAAGATGTCAGGATTC |
| | | BDL231_EF_SalI(SEQ ID NO:1095) ATAGTCGACATTTCTCTCTATTGGCATCGAC |
| | | BDL231_NR_XbaI(SEQ ID NO:1096) AATTCTAGACTAAACTGGGGAAAGCTAAAACG |
| | | BDL231_ER_XbaI(SEQ ID NO:1097) AATTCTAGATCATAACATAAGAAAGTAAACTGGGG |
| BDL232 | XbaI, SacI | BDL232_NF_XbaI(SEQ ID NO:1098) AATCTAGACACCCCCTCAAAGAAATATAAC |
| | | BDL232_EF_XbaI(SEQ ID NO:1099) AATCTAGAAAGAAATTCACACCCCCTCAAAG |
| | | BDL232_NR_SacI(SEQ ID NO:1100) TGAGCTCCTAAAGGTGGAGTAATTAGAAGCG |
| | | BDL232_ER_SacI(SEQ ID NO:1101) TGAGCTCTGGTGAAGTGTTAAGTAATTGTCG |
| BDL233 | SalI, SacI | BDL233_NF_SalI(SEQ ID NO:1102) AAAGTCGACGAAAGAGAGAAAATGGAGAATATG |
| | | BDL233_EF_SalI(SEQ ID NO:1103) AAAGTCGACCGATCTAAAGAAAGAGAGAAAATG |
| | | BDL233_NR_SacI(SEQ ID NO:1104) TGAGCTCCTAAGAGTCGATCTAGAAAGCAACATC |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|--|
| | | BDL233_ER_SacI(SEQ ID NO:1105) TGAGCTCGAATTAGTCCTTGTGGTTCTACTC |
| BDL234 | Sall, SmaI | BDL234_NF_Sall(SEQ ID NO:1106) AATGTGCGACTGATAAGAATGCTCCTGACTGG |
| | | BDL234_EF_Sall(SEQ ID NO:1107) AATGTGCGACTCTTTCTCTGTATCTCGACGTTCT |
| | | BDL234_NR_SmaI(SEQ ID NO:1108) TCCCGGGCTAAAATCCAAGTGCCCAAGAAC |
| | | BDL234_ER_SmaI(SEQ ID NO:1109) TCCCGGGCTAGCAAAACATAAAATCCAAGTGC |
| | | |
| BDL235 | Sall, SmaI | BDL235_NF_Sall(SEQ ID NO:1110) AATGTGCGACTCTTACTCAATCCGAAGAATGG |
| | | BDL235_NR_SmaI(SEQ ID NO:1111) CCCCGGGACTTCGATTCACATTTCTCCTC |
| BDL237 | Sall, XbaI | BDL237_NF_Sall(SEQ ID NO:1112) AAAGTCGACCGAAGTAAGAAAAGAAAATGGAG |
| | | BDL237_EF_Sall(SEQ ID NO:1113) AAAGTCGACCTTCGAAGTAAGAAAAGAAAATG |
| | | BDL237_NR_XbaI(SEQ ID NO:1114) AATCTAGATCATACTCAAGTGCTTGTCTCGG |
| | | BDL237_ER_XbaI(SEQ ID NO:1115) ATTCTAGAGTTATTGGTGTCTTGTTCACC |
| BDL238 | Sall, XbaI | BDL238_NF_Sall(SEQ ID NO:1116) AAAGTCGACCAACGAGCAAGAGAAAATGG |
| | | BDL238_EF_Sall(SEQ ID NO:1117) AAAGTCGACGATACAACGAGCAAGAGAAAATG |
| | | BDL238_NR_XbaI(SEQ ID NO:1118) AATTCTAGATGGTTCTAGCTATCACTAGGTGC |
| | | BDL238_ER_XbaI(SEQ ID NO:1119) AATTCTAGAGGCAATACAACAAGAGAAAACCTC |
| BDL240 | Sall, XbaI | BDL240_NF_Sall(SEQ ID NO:1120) AAAGTCGACCGAGTACAATGGAGGTTTCG |
| | | BDL240_NR_XbaI(SEQ ID NO:1121) ATTCTAGATCAAGCTTAAAGACCGTGAGGAAG |
| BDL241 | XbaI, SmaI | BDL241_NF_XbaI(SEQ ID NO:1122) AATCTAGAACAGTCGTCGTCGTCGAAGC |
| | | BDL241_NR_SmaI(SEQ ID NO:1123) TCCCGGGCTAAAGGTAAGGATGAATTGTCAGAG |
| BDL242 | Sall, XbaI | BDL242_NF_Sall(SEQ ID NO:1124) AATGTGCGACTCAAATCAATATGGGATCTTTC |
| | | BDL242_NR_XbaI(SEQ ID NO:1125) ATTCTAGATTATTGACAAGTCTATTGCCCG |
| BDL245 | Sall, SmaI | BDL245_NF_Sall(SEQ ID NO:1126) AATGTGCGACTTCGTTAAATTATGTCTTTGAGG |
| | | BDL245_EF_Sall(SEQ ID NO:1127) AAAGTCGACTGACTCAGAGATCAACAAAACC |
| | | BDL245_NR_SmaI(SEQ ID NO:1128) ACCCGGGTTAGACTTACTCCAATTTCCAAGC |
| | | BDL245_ER_SmaI(SEQ ID NO:1129) TCCCGGGTCAAGAGTCGGTCACACGC |
| | | |
| BDL247 | SmaI, SacI | BDL247_NF_SmaI(SEQ ID NO:1130) TCCCGGGTCCCTTCTTGTGTGAGACCGAG |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|---|
| | | BDL247_NF_SacI(SEQ ID NO:1131) TGAGCTCCTAAGAACTTTAACGCATTTTGTAGTG |
| BDL248 | Sall, XbaI | BDL248_NF_Sall(SEQ ID NO:1132) AAAGTCGACAACGTGATCAATATGGAAGCTC |
| | | BDL248_EF_Sall(SEQ ID NO:1133) AAAGTCGACACTCACCAAATCCAACGTG |
| | | BDL248_NR_XbaI(SEQ ID NO:1134) AATTCTAGACTAAACTCAAGAGGAGTCGGGTAAG |
| | | BDL248_ER_XbaI(SEQ ID NO:1135) AATTCTAGATTAATTCGTTACCGTTGCTAAG |
| | | BDL249_NF_Sall(SEQ ID NO:1136) AAAGTCGACACCAAATAGATCTAAAACATGG |
| BDL249 | Sall, XbaI | BDL249_EF_Sall(SEQ ID NO:1137) AATGTCGACTTCACTCACCAAATAGATCTAAAAC |
| | | BDL249_NR_XbaI(SEQ ID NO:1138) AATCTAGATCAACGTCAAACGGACTCGTTG |
| | | BDL249_ER_XbaI(SEQ ID NO:1139) AATCTAGATCACCAAAGTCTAAACGTCAAACG |
| | | BDL250_NF_Sall(SEQ ID NO:1140) TTAGTCGACCAAAGATGTTTTACTATGTGATTGTC |
| BDL250 | Sall, XbaI | BDL250_EF_Sall(SEQ ID NO:1141) TTAGTCGACAGGAAGAGAAAGGTCAAAGATG |
| | | BDL250_NR_XbaI(SEQ ID NO:1142) TATCTAGATCAAATCTCACATCTCCATGCATAG |
| | | BDL250_ER_XbaI(SEQ ID NO:1143) TATCTAGATCATGTTTCGCATTACACAAATATCC |
| | | BDL252_NF_XbaI(SEQ ID NO:1144) ATTCTAGATTCTCTGTCTCTTTGGCTTTTC |
| BDL252 | XbaI, SmaI | BDL252_EF_XbaI(SEQ ID NO:1145) ATTCTAGATAAACTCTCAGCTTCCATTC |
| | | BDL252_NR_SmaI(SEQ ID NO:1146) TCCCGGGCTATTGTTCATTGAGGAAGAACAGG |
| | | BDL252_ER_SmaI(SEQ ID NO:1147) TCCCGGGCTAAAAGTTCTTGCTTGCTTTCTG |
| | | BDL48_NF_Sall(SEQ ID NO:1148) AAAGTCGACAGATTGCGTCACTGTAGTAGTAGTAG |
| BDL48 | Sall, XbaI | BDL48_EF_Sall(SEQ ID NO:1149) AAAGTCGACCTGCAACTCTTTCTCACTTTCAC |
| | | BDL48_NR_XbaI(SEQ ID NO:1150) AGTCTAGAAAACATTTTGCTTAAGATCTACAGAG |
| | | BDL48_ER_XbaI(SEQ ID NO:1151) ACTCTAGAAGACATGAAAGCACAAATCAAG |
| | | BDL49_NF_SmaI(SEQ ID NO:1152) ACCCGGGCTAACATGCTCCATCTCCTTC |
| BDL49 | SmaI, SacI | BDL49_NR_SacI(SEQ ID NO:1153) TGAGCTCTCAACCTGATCAGCGATGGTGC |
| | | BDL58_NF_Sall(SEQ ID NO:1154) AAAGTCGACCACACAAGACTAACGATGTTGC |
| BDL58 | Sall, XbaI | BDL58_NR_XbaI(SEQ ID NO:1155) ATTCTAGATTA AAAAGAGACCTACACGGCG |
| | | BDL62_NF_Sall(SEQ ID NO:1156) AATGTCGACTCTCTGGTCTCCCTATATCAGC |
| BDL62 | Sall, SacI | |

| <i>Gene Name</i> | <i>Restriction Enzymes used for cloning</i> | <i>Primers used for amplification</i> |
|------------------|---|--|
| | | BDL62_NF_SacI(SEQ ID NO:1157) TGAGCTCCTATTTGATGTTGTTGTTGTTGTCTG |
| BDL63 | Sall, XbaI | BDL63_NF_Sall(SEQ ID NO:1158) ATAGTCGACGTTTTGAGATATGGGAGGACC |
| | | BDL63_EF_Sall(SEQ ID NO:1159) AAAGTCGACCTCTAGATTCTTGCCGATTCTC |
| | | BDL63_NR_XbaI(SEQ ID NO:1160) ATTCTAGATTAGTGGTTTTACTTGAGCCTCTCC |
| | | BDL63_ER_SacI(SEQ ID NO:1161) TGAGCTCCTATTGTTTCGTTACGGTGGTTTTAC |
| | | BDL64 |
| | | BDL64_NR_XbaI(SEQ ID NO:1163) ATTCTAGACTACTCATAGGTTTGTACTTCCTTG |
| BDL75 | Sall, XbaI | BDL75_NF_Sall(SEQ ID NO:1164) AAAGTCGACAAGAAGAAAGAAACAGAGAATCG |
| | | BDL75_NR_XbaI(SEQ ID NO:1165) ATTCTAGACTAATTGTTCAAAGTTCAGTGAGCC |
| BDL79 | XbaI, SmaI | BDL79_NF_XbaI(SEQ ID NO:1166) ATTCTAGAGGAGATTTTGTAATGGATTCTGC |
| | | BDL79_EF_XbaI(SEQ ID NO:1167) ATTCTAGAGAAGGAGATTTTGTAATGGATTCTC |
| | | BDL79_NR_SmaI(SEQ ID NO:1168) TCCCGGGTTACGCTTAGACCATAACAACGAGTAG |
| | | BDL79_ER_SmaI(SEQ ID NO:1169) TCCCGGGTTATTTACTTATGGCCTGTTTC |
| BDL81 | Sall, SacI | BDL81_EF_Sall(SEQ ID NO:1170) AAAGTCGACCAGGGGTTTAAGGATTTTCTC |
| | | BDL81_ER_SacI(SEQ ID NO:1171) CGAGCTCAAATGGCTTTCTCTACCCTTTG |
| BDL83 | Sall, XbaI | BDL83_NF_Sall(SEQ ID NO:1172) AATGTCGACTGGTAGGCTGAGAGAAAGAAAG |
| | | BDL83_NR_XbaI(SEQ ID NO:1173) AGTCTAGATTAGAGAATAAAAGAAGAATGAGAAGC |
| BDL85 | XbaI, Sall | BDL85_NF_Sall(SEQ ID NO:1174) AATGTCGACTTAATCGTTAGAAGATGAGCCAG |
| | | BDL85_NR_XbaI(SEQ ID NO:1175) ATTCTAGATCAGGCTTAGAAGCAAATGTCCAG |
| BDL88 | Sall, XbaI | BDL88_NF_Sall(SEQ ID NO:1176) AATGTCGACGAGGAGATGGCGAGCAAC |
| | | BDL88_NR_XbaI(SEQ ID NO:1177) TATCTAGATTATTAGGTATTGCACTTCCACTTC |
| BDL90 | | BDL90_EF_Sall(SEQ ID NO:1178) AAAGTCGACCACCAGAAACAAAGAGAGAGTG |
| | | BDL90_ER_XbaI(SEQ ID NO:1179) ATTCTAGATATCATGCAACCACAAACAATAG |
| BDL94 | XbaI, SmaI | BDL94_EF_XbaI_new(SEQ ID NO:1180) AATCTAGAAAGTCCAAGTGACCAACCATC |
| | | BDL94_ER_SmaI_new(SEQ ID NO:1181) TCCCGGGGGGATACAAGATTATGCAGGC |

Table 18. 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
5 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 [pBlue-script KS plasmid vector, Hypertext Transfer
10 Protocol://World Wide Web (dot) stratagene (dot) com/manuals/212205 (dot) pdf] or into plasmids originating from this vector. In cases where the pGXN high copy vector (originated from pBlue-script KS) was used, the PCR product was inserted upstream to the NOS terminator (SEQ ID NO:1182) originated from pBI 101.3 binary vector (GenBank Accession No. U12640, nucleotides 4356 to 4693) and downstream to the
15 35S promoter (Table 20 below). The digested products and the linearized plasmid vector were ligated using T4 DNA ligase enzyme (Roche, Switzerland).

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
20 introduced into the pGI binary vector [pBXYN or pQXYN containing the 35S CaMV promoter] according to Table 19 hereinabove, via digestion with appropriate restriction endonucleases. In any case the insert was followed by single copy of the NOS terminator (SEQ ID NO:1182x).

High copy plasmids containing the cloned genes were digested with the
25 restriction endonucleases (New England BioLabs Inc) according to the sites designed in the primers (Table 18, above) and cloned into binary vectors according to Table 19, below.

Binary vectors used for cloning: The plasmid pPI was constructed by inserting a synthetic poly-(A) signal sequence, originating from pGL3 basic plasmid
30 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) (Figure 1) 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:1182) (Vancanneyt. G, *et al* MGG 220, 245-50, 1990). pGI was used to clone the polynucleotide sequences, initially under the control of 35S promoter [Odell, JT, et al. Nature 313, 810 - 812 (28 February 1985); SEQ ID NO:1184.

- 5 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.

10

Table 19
Restriction enzyme sites used to clone the identified genes into binary vector

| <i>Gene name</i> | <i>Binary vector</i> | <i>Restriction enzymes used for cloning into binary vector- FORWARD</i> | <i>Restriction enzymes used for cloning into binary vector- REVERSE</i> | <i>Restriction enzymes used for digesting the binary vector</i> |
|------------------|----------------------|---|---|---|
| BDL62 | pQXYN | Sall | SacI | Sall, SacI |
| BDL75 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL79 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL81 | pQXYN | Sall | SacI | Sall, SacI |
| BDL83 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL117 | pQXYN | SmaI | SmaI | SmaI, Ecl136II |
| BDL118 | pQXYN | SmaI | SmaI | SmaI, Ecl136II |
| BDL138 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL140 | pQXYN | XbaI | SacI | XbaI, SacI |
| BDL147 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL149 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL152 | pQXYN | XbaI | SacI | XbaI, SacI |
| BDL153 | pQXYN | Sall | SmaI | Sall, Ecl136II |
| BDL154 | pQXYN | Sall | SacI | Sall, SacI |
| BDL155 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL156 | pQXYN | Sall | SacI | SacI, Sall |
| BDL157 | pQXYN | Sall | SacI | Sall, SacI |
| BDL158 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL160 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL162 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL167 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL168 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL169 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL171 | pQXYN | XbaI | SacI | XbaI, SacI |
| BDL173 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL174 | pQXYN | Sall | SacI | Sall, SacI |
| BDL176 | pQXYN | SmaI | SmaI | SmaI, Ecl136II |
| BDL177 | pQXYN | Sall | SacI | Sall, SacI |
| BDL181 | pQXYN | Sall | SacI | Sall, SacI |
| BDL182 | pQXYN | Sall | SacI | Sall, SacI |
| BDL183 | pQXYN | Sall | EcoRI | Sall, EcoRI |
| BDL186 | pQXYN | Sall | SacI | Sall, SacI |
| BDL187 | pQXYN | Sall | SmaI | Sall, Ecl136II |

| <i>Gene name</i> | <i>Binary vector</i> | <i>Restriction enzymes used for cloning into binary vector- FORWARD</i> | <i>Restriction enzymes used for cloning into binary vector- REVERSE</i> | <i>Restriction enzymes used for digesting the binary vector</i> |
|------------------|----------------------|---|---|---|
| BDL188 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL189 | pQXYN | SmaI | BamHI | SmaI, Ecl136II |
| BDL190 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL192 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL193 | pQXYN | XbaI | SacI | XbaI, SacI |
| BDL194 | pQXYN | EcoRV | EcoRV | SmaI, Ecl136II |
| BDL196 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL197 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL201 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL203 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL220 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL221 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL222 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL223 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL229 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL230 | pQXYN | SmaI | SmaI | SmaI, Ecl136II |
| BDL231 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL235 | pQXYN | Sall | SmaI | SaII, Ecl136II |
| BDL242 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL245 | pQXYN | Sall | SmaI | SaII, Ecl136II |
| BDL247 | pQXYN | SmaI | SacI | SmaI, SacI |
| BDL248 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL250 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL49 | pQXYN | EcoRV | SacI | SmaI, SacI |
| BDL58 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL63 | pQXYN | Sall | SacI | SaII, SacI |
| BDL64 | pQXYN | Sall | XbaI | SaII, Ecl136II |
| BDL85 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL88 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL90 | pQXYN | XbaI | SaII | SaII, Ecl136II |
| BDL94 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL102 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL224 | pQXYN | XbaI | EcoRI | XbaI, EcoRI |
| BDL225 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL226 | pQXYN | EcoRV | EcoRV | SmaI, Ecl136II |
| BDL227 | pQXYN | Sall | SmaI | SaII, Ecl136II |
| BDL228 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL232 | pQXYN | XbaI | EcoRI | XbaI, EcoRI |
| BDL233 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL234 | pQXYN | Sall | SmaI | SaII, Ecl136II |
| BDL237 | pQXYN | Sall | SacI | SaII, SacI |
| BDL238 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL240 | pQXYN | Sall | SacI | SaII, SacI |
| BDL241 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL249 | pQXYN | Sall | EcoRI | SaII, EcoRI |
| BDL252 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL47 | pQXYN | XbaI | SmaI | XbaI, Ecl136II |
| BDL48 | pQXYN | Sall | EcoRI | SaII, EcoRI |

Table 19.

Table 20
Genes cloned from cDNA libraries or genomic DNA in a High copy number plasmid

| <i>Gene Name</i> | <i>High copy plasmid</i> | <i>Amplified from</i> | | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|--------------------------|----------------------------|---------------|----------------------------------|-------------------------------|
| | | <i>Organism</i> | <i>Origin</i> | | |
| BDL62 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 847 | 108 |
| BDL75 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 848 | 109 |
| BDL79 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 849 | 110 |
| BDL81 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 850 | 111 |
| BDL83 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 851 | 112 |
| BDL117 | Topo B | Arabidopsis thaliana ND | RNA | 852 | 926 |
| BDL118 | Topo B | Arabidopsis thaliana ND | RNA | 853 | 114 |
| BDL138 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 854 | 116 |
| BDL140 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 855 | 117 |
| BDL147 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 856 | 118 |
| BDL149 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 857 | 119 |
| BDL152 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 858 | 120 |
| BDL153 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 859 | 121 |
| BDL154 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 860 | 122 |
| BDL155 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 861 | 123 |
| BDL156 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 862 | 124 |
| BDL157 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 863 | 125 |
| BDL158 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 864 | 126 |
| BDL160 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 865 | 127 |
| BDL162 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 866 | 128 |
| BDL167 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 867 | 196 |
| BDL168 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 868 | 132 |
| BDL169 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 869 | 133 |
| BDL171 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 870 | 927 |
| BDL173 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 871 | 135 |

| <i>Gene Name</i> | <i>High copy plasmid</i> | <i>Amplified from</i> | | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|--------------------------|----------------------------|---------------|----------------------------------|-------------------------------|
| | | <i>Organism</i> | <i>Origin</i> | | |
| BDL174 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 872 | 136 |
| BDL176 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 873 | 137 |
| BDL177 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 874 | 138 |
| BDL181 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 875 | 139 |
| BDL182 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 876 | 140 |
| BDL183 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 877 | 141 |
| BDL186 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 878 | 928 |
| BDL187 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 879 | 929 |
| BDL188 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 880 | 144 |
| BDL189 | Topo B | Arabidopsis thaliana ND | RNA | 881 | 145 |
| BDL190 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 882 | 146 |
| BDL192 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 883 | 147 |
| BDL193 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 884 | 148 |
| BDL194 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 885 | 149 |
| BDL196 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 886 | 150 |
| BDL197 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 887 | 151 |
| BDL201 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 888 | 153 |
| BDL203 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 889 | 154 |
| BDL220 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 890 | 156 |
| BDL221 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 891 | 157 |
| BDL222 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 892 | 158 |
| BDL223 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 893 | 159 |
| BDL229 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 894 | 160 |
| BDL230 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 895 | 161 |
| BDL231 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 896 | 162 |
| BDL235 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 897 | 163 |

| <i>Gene Name</i> | <i>High copy plasmid</i> | <i>Amplified from</i> | | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|--------------------------|--|---------------|----------------------------------|----------------------------------|
| | | <i>Organism</i> | <i>Origin</i> | | |
| BDL242 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 898 | 164 |
| BDL245 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 899 | 166 |
| BDL247 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 900 | 167 |
| BDL248 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 901 | 168 |
| BDL250 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 902 | 169 |
| BDL49 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 903 | 170 |
| BDL58 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 904 | 171 |
| BDL63 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 905 | 172 |
| BDL64 | Topo B | Arabidopsis thaliana ND | RNA | 906 | 173 |
| BDL85 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 907 | 175 |
| BDL88 | pGXN (pKG+Nos+35S) | RICE Oryza sativa L. Japonica ND | RNA | 908 | 176 |
| BDL90 | Topo B | RICE Oryza sativa L.Japonica ND | gDNA | 909 | Non Coding polynucleoti de |
| BDL94 | pGXN (pKG+Nos+35S) | Rice Japonica ND leaves | gDNA | 910 | 930 |
| BDL102 | pGXN (pKG+Nos+35S) | MAIZE Zea mays L. ND | RNA | 911 | 178 |
| BDL224 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 912 | 179 |
| BDL225 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 913 | 180 |
| BDL226 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 914 | 181 |
| BDL227 | Topo B | Arabidopsis thaliana ND | RNA | 915 | 182 |
| BDL228 | pGXN (pKG+Nos+35S) | CASTOR BEAN Ricinus communis L. ND | RNA | 916 | 931 |
| BDL232 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 917 | 184 |
| BDL233 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 918 | 932 |
| BDL234 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 919 | 186 |
| BDL237 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 920 | 187 |
| BDL238 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 921 | 188 |
| BDL240 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 922 | 189 |

| <i>Gene Name</i> | <i>High copy plasmid</i> | <i>Amplified from</i> | | <i>Polynucleotide SEQ ID NO:</i> | <i>Polypeptide SEQ ID NO:</i> |
|------------------|--------------------------|----------------------------|---------------|----------------------------------|-------------------------------|
| | | <i>Organism</i> | <i>Origin</i> | | |
| BDL241 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 923 | 190 |
| BDL249 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 924 | 191 |
| BDL252 | pKS(Pks_J) | Arabidopsis thaliana ND | RNA | 925 | 193 |
| BDL47 | High copy plasmid pMA | Synthetic DNA | | 845 | 106 |
| BDL48 | pGXN (pKG+Nos+35S) | Arabidopsis thaliana ND | RNA | 846 | 107 |
| BDL200 | High copy plasmid | Synthetic DNA | | 47 | 152 |

Table 20: 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.

5 Selected DNA sequences were synthesized by a commercial supplier GeneArt, GmbH [Hypertext Transfer Protocol://World Wide Web (dot) geneart (dot) com/]. 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 pBXYN/ pQXYN binary downstream of the CaMV 35S promoter (SEQ ID NO:1184).
10 For example BDL47 (SEQ ID NO:1 was synthesized and the XbaI and SmaI restriction enzymes were added to the synthetic sequence in order to facilitate cloning.

For 7 genes, namely BDL117, BDL171, BDL186, BDL187, BDL94, BDL228 and BDL233, the protein translation of the amplified cDNA sequence did not match the initial bioinformatics prediction of the protein sequences. The polypeptide sequences
15 encoded by the cloned sequence were predicted and are provided in SEQ ID NO: 926-932.

EXAMPLE 8

PRODUCING TRANSGENIC ARABIDOPSIS PLANTS EXPRESSING THE IDENTIFIED POLYNUCLEOTIDES OF THE INVENTION

Materials and Experimental Methods

Plant transformation - The *Arabidopsis thaliana* var Columbia (T₀ plants) were transformed according to the Floral Dip procedure [Clough SJ, Bent AF. (1998) Floral dip: a simplified method for Agrobacterium-mediated transformation of
25 *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) T₀ plants were sown in 250 ml pots filled with wet peat-based growth mix. The pots were covered with aluminum foil and a plastic dome, kept at 4 °C for 3–4 days, then uncovered and incubated in a growth chamber at 18–24 °C under 16/8 hours light/dark cycles. The T₀ plants were ready for transformation six days before anthesis.

Single colonies of *Agrobacterium* carrying the binary vectors harboring the seed oil 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 T₀ 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 T₀ 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 T₀ 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 T₁ and T₂ transgenic plants harboring the genes, seeds collected from transgenic T₀ 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 Murashige-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 T₁ *Arabidopsis* plants were

transferred to a fresh culture plates for another week of incubation. Following incubation the T₁ 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 T₁ plants were cultured and grown to maturity as T₂ plants under the same conditions as used for culturing and growing the T₁ plants.

EXAMPLE 9

IMPROVED TRANSGENIC PLANT PERFORMANCE

To analyze the effect of expression of the isolated polynucleotides in plants, plants were grown in pots with an adequate amount of nutrients and water. The plants were analyzed for their overall size, growth rate, time to inflorescence emergence (bolting) and 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 with an empty vector or expressing the uidA reporter gene (GUS-Intron) under the same promoter were used as control.

Parameters were measured as described in Examples 2, 3 and 4 above.

Statistical analyses - Plant growth rate, plant area, time to bolt, time to flower, weight of 1,000 seeds, seed yield, oil yield, dry matter, and harvest index area data were analyzed using t-test. To identify outperforming genes and constructs, results from mix of transformation events or independent events were analyzed. For gene versus control analysis t- test was applied, using significance of $p < 0.1$. 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 invention were assayed for a number of commercially desired traits. Results are presented in Tables 21 and 22.

Analysis of plants in tissue culture assay - Tables 21 and 22, hereinbelow, depict analyses of seed yield in plants overexpressing the polynucleotides of the invention under the regulation of the constitutive 35S (SEQ ID NO:1184) or At6669 (SEQ ID NO:1183) promoters. In cases where a certain event appears more than once, the event was tested in several independent experiments.

Table 21
Results obtained in a tissue culture assay

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TPI</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL102 | 10471.1 | P | | 0.24 | | 0.01 | 0.02 | 0.13 | 0.05 |
| BDL102 | 10471.1 | Av | | 1.15 | | 1.59 | 1.39 | 1.23 | 2.34 |
| BDL102 | 10471.3 | P | | 0.6 | | 0.03 | 0.01 | 0.09 | 0.01 |
| BDL102 | 10471.3 | Av | | 1.1 | | 1.43 | 1.37 | 1.24 | 1.72 |
| BDL102 | 10472.1 | P | | | | 0.04 | 0.15 | | 0.03 |
| BDL102 | 10472.1 | Av | | | | 1.27 | 1.1 | | 1.54 |
| BDL102 | 10474.2 | P | <0.01 | <0.01 | <0.01 | | 0.23 | 0.13 | |
| BDL102 | 10474.2 | Av | 2.02 | 1.61 | 1.51 | | 1.1 | 1.13 | |
| BDL102 | 10474.6 | P | | 0.13 | 0.29 | | | | |
| BDL102 | 10474.6 | Av | | 1.21 | 1.14 | | | | |
| BDL118 | 10481.2 | P | <0.01 | 0.01 | 0.01 | | | 0.46 | |
| BDL118 | 10481.2 | Av | 2.02 | 1.91 | 2 | | | 1.1 | |
| BDL118 | 10481.5 | P | | 0.2 | 0.01 | | | | |
| BDL118 | 10481.5 | Av | | 1.15 | 1.29 | | | | |
| BDL118 | 10484.3 | P | <0.01 | <0.01 | <0.01 | | | | |
| BDL118 | 10484.3 | Av | 1.51 | 1.41 | 1.58 | | | | |
| BDL140 | 10421.3 | P | 0.03 | 0.01 | 0.05 | | | | 0.39 |
| BDL140 | 10421.3 | Av | 1.61 | 1.72 | 1.68 | | | | 1.18 |
| BDL140 | 10423.1 | P | 0.21 | 0.09 | 0.28 | 0.01 | 0.11 | | 0.19 |
| BDL140 | 10423.1 | Av | 1.24 | 1.31 | 1.21 | 1.38 | 1.21 | | 1.28 |
| BDL140 | 10424.4 | P | <0.01 | <0.01 | 0.01 | | | | |
| BDL140 | 10424.4 | Av | 1.43 | 1.48 | 1.62 | | | | |
| BDL152 | 10431.4 | P | 0.15 | 0.12 | 0.12 | | | | |
| BDL152 | 10431.4 | Av | 1.17 | 1.18 | 1.18 | | | | |
| BDL152 | 10432.5 | P | 0.37 | 0.01 | | 0.07 | 0.14 | | 0.35 |
| BDL152 | 10432.5 | Av | 1.16 | 1.28 | | 1.22 | 1.13 | | 1.25 |
| BDL152 | 10434.1 | P | | 0.43 | | | | | |
| BDL152 | 10434.1 | Av | | 1.12 | | | | | |
| BDL152 | 10434.4 | P | | 0.08 | | 0.04 | 0.01 | <0.01 | 0.08 |
| BDL152 | 10434.4 | Av | | 1.18 | | 1.52 | 1.48 | 1.31 | 2.33 |
| BDL153 | 10142.2 | P | | | | <0.01 | <0.01 | | 0.03 |
| BDL153 | 10142.2 | Av | | | | 1.83 | 1.43 | | 1.99 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|--------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL153 | 10144.1 | P | <0.01 | 0.02 | 0.07 | | 0.31 | 0.15 | 0.7 |
| BDL153 | 10144.1 | Av | 1.3 | 1.31 | 1.38 | | 1.13 | 1.12 | 1.1 |
| BDL153 | 10144.4 | P | | | | | | | 0.03 |
| BDL153 | 10144.4 | Av | | | | | | | 1.28 |
| BDL154 | 10703.1 | P | | | | 0.09 | 0.14 | 0.05 | 0.09 |
| BDL154 | 10703.1 | Av | | | | 1.36 | 1.14 | 1.2 | 1.77 |
| BDL154 | 10703.1 1 | P | | | | 0.01 | 0.17 | 0.3 | 0.5 |
| BDL154 | 10703.1 1 | Av | | | | 1.37 | 1.21 | 1.16 | 1.18 |
| BDL154 | 10703.6 | P | | | | | | | 0.42 |
| BDL154 | 10703.6 | Av | | | | | | | 1.23 |
| BDL154 | 10703.1 | P | <0.01 | <0.01 | <0.01 | | 0.11 | 0.02 | |
| BDL154 | 10703.1 | Av | 1.34 | 1.5 | 1.61 | | 1.14 | 1.18 | |
| BDL154 | 10703.5 | P | | 0.46 | 0.36 | | 0.02 | 0.02 | 0.21 |
| BDL154 | 10703.5 | Av | | 1.1 | 1.16 | | 1.47 | 1.39 | 1.52 |
| BDL154 | 10703.6 | P | | | | 0.24 | 0.06 | 0.07 | 0.15 |
| BDL154 | 10703.6 | Av | | | | 1.19 | 1.33 | 1.24 | 1.59 |
| BDL155 | 9994.3 | P | 0.22 | | | | | | |
| BDL155 | 9994.3 | Av | 1.15 | | | | | | |
| BDL156 | 10853.6 | P | | | 0.08 | | | | |
| BDL156 | 10853.6 | Av | | | 1.12 | | | | |
| BDL156 | 10852.6 | P | | | 0.15 | | | | |
| BDL156 | 10852.6 | Av | | | 1.15 | | | | |
| BDL156 | 10853.6 | P | | 0.07 | 0.01 | | | 0.24 | |
| BDL156 | 10853.6 | Av | | 1.34 | 1.71 | | | 1.22 | |
| BDL156 | 10854.4 | P | 0.11 | 0.11 | <0.01 | | | 0.01 | |
| BDL156 | 10854.4 | Av | 1.13 | 1.26 | 1.66 | | | 1.24 | |
| BDL156 | 10855.3 | P | | | 0.01 | | | 0.1 | |
| BDL156 | 10855.3 | Av | | | 1.35 | | | 1.2 | |
| BDL158 | 9973.3 | P | | | | 0.01 | 0.03 | 0.17 | 0.09 |
| BDL158 | 9973.3 | Av | | | | 1.21 | 1.27 | 1.1 | 1.21 |
| BDL158 | 9971.3 | P | 0.42 | 0.32 | 0.27 | | | | |
| BDL158 | 9971.3 | Av | 1.13 | 1.13 | 1.11 | | | | |
| BDL158 | 9973.1 | P | | | | 0.08 | 0.24 | 0.17 | 0.02 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL158 | 9973.1 | Av | | | | 1.27 | 1.16 | 1.13 | 1.37 |
| BDL158 | 9973.3 | P | | | | <0.01 | 0.02 | 0.06 | 0.01 |
| BDL158 | 9973.3 | Av | | | | 1.66 | 1.39 | 1.17 | 2.06 |
| BDL158 | 9974.2 | P | <0.01 | <0.01 | 0.09 | | | | |
| BDL158 | 9974.2 | Av | 1.68 | 1.58 | 1.23 | | | | |
| BDL158 | 9974.3 | P | <0.01 | <0.01 | 0.13 | | | | |
| BDL158 | 9974.3 | Av | 1.76 | 1.62 | 1.58 | | | | |
| BDL158 | 9971.3 | P | | 0.07 | 0.15 | | | 0.02 | |
| BDL158 | 9971.3 | Av | | 1.22 | 1.2 | | | 1.15 | |
| BDL158 | 9973.1 | P | 0.01 | 0.41 | 0.03 | <0.01 | <0.01 | 0.08 | 0.02 |
| BDL158 | 9973.1 | Av | 1.28 | 1.11 | 1.35 | 1.49 | 1.35 | 1.26 | 1.8 |
| BDL158 | 9973.3 | P | | | | <0.01 | <0.01 | <0.01 | 0.02 |
| BDL158 | 9973.3 | Av | | | | 1.36 | 1.52 | 1.39 | 1.51 |
| BDL160 | 10011.5 | P | 0.01 | 0.22 | 0.15 | | | | |
| BDL160 | 10011.5 | Av | 1.41 | 1.2 | 1.26 | | | | |
| BDL160 | 10011.5 | P | | | | | | | 0.45 |
| BDL160 | 10011.5 | Av | | | | | | | 1.25 |
| BDL160 | 10011.7 | P | | | | 0.04 | | | 0.01 |
| BDL160 | 10011.7 | Av | | | | 1.34 | | | 1.95 |
| BDL160 | 10013.1 | P | | | 0.53 | | | | |
| BDL160 | 10013.1 | Av | | | 1.11 | | | | |
| BDL160 | 10014.9 | P | 0.2 | 0.39 | 0.61 | | | | |
| BDL160 | 10014.9 | Av | 1.17 | 1.15 | 1.11 | | | | |
| BDL160 | 10015.2 | P | | 0.07 | 0.12 | | | | |
| BDL160 | 10015.2 | Av | | 1.19 | 1.22 | | | | |
| BDL167 | 10042.3 | P | <0.01 | | | | | | |
| BDL167 | 10042.3 | Av | 1.3 | | | | | | |
| BDL167 | 10043.1 | P | <0.01 | 0.02 | 0.14 | | | | |
| BDL167 | 10043.1 | Av | 1.37 | 1.18 | 1.2 | | | | |
| BDL167 | 10043.2 | P | 0.06 | 0.13 | 0.03 | | | | |
| BDL167 | 10043.2 | Av | 1.61 | 1.29 | 1.23 | | | | |
| BDL167 | 10043.3 | P | 0.01 | 0.01 | <0.01 | | | 0.01 | |
| BDL167 | 10043.3 | Av | 1.93 | 1.58 | 1.61 | | | 1.25 | |
| BDL167 | 10044.2 | P | <0.01 | 0.01 | 0.02 | 0.05 | 0.04 | 0.03 | |
| BDL167 | 10044.2 | Av | 1.63 | 1.43 | 1.43 | 1.28 | 1.23 | 1.23 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL167 | 10043.1 | P | <0.01 | <0.01 | 0.15 | | <0.01 | 0.12 | 0.47 |
| BDL167 | 10043.1 | Av | 1.56 | 1.53 | 1.43 | | 1.22 | 1.1 | 1.1 |
| BDL167 | 10044.2 | P | | | | <0.01 | <0.01 | | <0.01 |
| BDL167 | 10044.2 | Av | | | | 1.45 | 1.18 | | 2.16 |
| BDL168 | 9881.3 | P | | | | 0.15 | | | 0.04 |
| BDL168 | 9881.3 | Av | | | | 1.23 | | | 1.67 |
| BDL168 | 9881.4 | P | | | | <0.01 | <0.01 | <0.01 | 0.02 |
| BDL168 | 9881.4 | Av | | | | 1.89 | 1.72 | 1.38 | 2.28 |
| BDL168 | 9882.1 | P | | | | 0.01 | 0.01 | 0.04 | <0.01 |
| BDL168 | 9882.1 | Av | | | | 1.9 | 1.68 | 1.29 | 2.57 |
| BDL168 | 9883.3 | P | | | | | | | 0.2 |
| BDL168 | 9883.3 | Av | | | | | | | 1.38 |
| BDL168 | 9884.1 | P | | | | <0.01 | <0.01 | 0.02 | 0.02 |
| BDL168 | 9884.1 | Av | | | | 2.05 | 1.73 | 1.38 | 2.61 |
| BDL169 | 10744.2 | P | | | | 0.08 | 0.02 | 0.08 | 0.29 |
| BDL169 | 10744.2 | Av | | | | 1.24 | 1.23 | 1.19 | 1.11 |
| BDL169 | 10747.1 | P | | | | 0.03 | 0.09 | 0.13 | |
| BDL169 | 10747.1 | Av | | | | 1.15 | 1.12 | 1.11 | |
| BDL169 | 10747.5 | P | | | | 0.06 | 0.01 | <0.01 | 0.12 |
| BDL169 | 10747.5 | Av | | | | 1.62 | 1.59 | 1.4 | 1.73 |
| BDL171 | 10661.2 | P | | 0.25 | 0.28 | <0.01 | <0.01 | <0.01 | 0.03 |
| BDL171 | 10661.2 | Av | | 1.19 | 1.23 | 1.62 | 1.65 | 1.39 | 1.8 |
| BDL171 | 10661.5 | P | 0.02 | 0.04 | 0.12 | | | | |
| BDL171 | 10661.5 | Av | 1.45 | 1.35 | 1.24 | | | | |
| BDL171 | 10664.1 | P | 0.31 | 0.3 | 0.25 | 0.15 | 0.27 | 0.31 | 0.44 |
| BDL171 | 10664.1 | Av | 1.17 | 1.18 | 1.23 | 1.23 | 1.15 | 1.14 | 1.17 |
| BDL173 | 9951.2 | P | | 0.18 | | | 0.42 | | 0.3 |
| BDL173 | 9951.2 | Av | | 1.17 | | | 1.11 | | 1.17 |
| BDL173 | 9952.1 | P | | | | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL173 | 9952.1 | Av | | | | 2.17 | 1.99 | 1.45 | 3.32 |
| BDL173 | 9952.2 | P | | 0.35 | | <0.01 | <0.01 | 0.01 | 0.02 |
| BDL173 | 9952.2 | Av | | 1.12 | | 1.72 | 1.63 | 1.24 | 2.07 |
| BDL174 | 11082.1 | P | | | | | 0.2 | 0.06 | 0.42 |
| BDL174 | 11082.1 | Av | | | | | 1.14 | 1.17 | 1.18 |
| BDL174 | 11083.1 | P | <0.01 | <0.01 | 0.07 | <0.01 | <0.01 | 0.01 | 0.01 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL174 | 11083.1 | Av | 1.64 | 1.32 | 1.2 | 1.78 | 1.67 | 1.39 | 1.66 |
| BDL174 | 11083.2 | P | 0.04 | 0.17 | 0.12 | | 0.14 | 0.18 | |
| BDL174 | 11083.2 | Av | 1.2 | 1.16 | 1.25 | | 1.34 | 1.32 | |
| BDL174 | 11084.1 | P | <0.01 | <0.01 | <0.01 | | 0.03 | 0.1 | 0.03 |
| BDL174 | 11084.1 | Av | 2.56 | 2.29 | 2.1 | | 1.31 | 1.31 | 1.68 |
| BDL174 | 11085.1 | P | | 0.41 | 0.07 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL174 | 11085.1 | Av | | 1.11 | 1.24 | 1.95 | 2.33 | 1.98 | 1.71 |
| BDL174 | 11083.2 | P | <0.01 | <0.01 | 0.01 | 0.3 | | | 0.31 |
| BDL174 | 11083.2 | Av | 1.41 | 1.35 | 1.21 | 1.16 | | | 1.27 |
| BDL174 | 11084.1 | P | | | | 0.15 | | | <0.01 |
| BDL174 | 11084.1 | Av | | | | 1.22 | | | 2.13 |
| BDL174 | 11085.1 | P | | | | <0.01 | 0.01 | 0.04 | 0.01 |
| BDL174 | 11085.1 | Av | | | | 2.04 | 1.36 | 1.16 | 2.33 |
| BDL176 | 9891.4 | P | 0.1 | 0.05 | 0.06 | | | | |
| BDL176 | 9891.4 | Av | 1.1 | 1.17 | 1.36 | | | | |
| BDL176 | 9893.2 | P | 0.04 | <0.01 | 0.27 | | | | |
| BDL176 | 9893.2 | Av | 1.28 | 1.26 | 1.22 | | | | |
| BDL176 | 9893.3 | P | | | | 0.38 | | | |
| BDL176 | 9893.3 | Av | | | | 1.13 | | | |
| BDL176 | 9893.2 | P | | | | 0.15 | | | |
| BDL176 | 9893.2 | Av | | | | 1.2 | | | |
| BDL176 | 9893.3 | P | 0.05 | 0.01 | | 0.36 | | | 0.16 |
| BDL176 | 9893.3 | Av | 1.42 | 1.34 | | 1.16 | | | 1.42 |
| BDL177 | 10521.3 | P | | | | | | 0.23 | |
| BDL177 | 10521.3 | Av | | | | | | 1.16 | |
| BDL177 | 10524.2 | P | | | | 0.13 | | | |
| BDL177 | 10524.2 | Av | | | | 1.16 | | | |
| BDL181 | 11293.6 | P | | | 0.32 | | | | |
| BDL181 | 11293.6 | Av | | | 1.18 | | | | |
| BDL181 | 11294.7 | P | | | 0.36 | | | | |
| BDL181 | 11294.7 | Av | | | 1.13 | | | | |
| BDL181 | 11293.1 | P | | | 0.6 | | | | |
| BDL181 | 11293.1 | Av | | | 1.11 | | | | |
| BDL181 | 11293.6 | P | | 0.01 | <0.01 | | | | |
| BDL181 | 11293.6 | Av | | 1.2 | 1.27 | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL181 | 11294.7 | P | | | | | 0.16 | 0.17 | |
| BDL181 | 11294.7 | Av | | | | | 1.1 | 1.1 | |
| BDL182 | 10691.8 | P | 0.03 | 0.07 | 0.16 | | | | |
| BDL182 | 10691.8 | Av | 1.32 | 1.24 | 1.18 | | | | |
| BDL182 | 10692.2 | P | 0.17 | 0.08 | 0.19 | | | | |
| BDL182 | 10692.2 | Av | 1.19 | 1.27 | 1.2 | | | | |
| BDL182 | 10693.3 | P | 0.01 | 0.07 | 0.1 | 0.17 | 0.1 | 0.11 | |
| BDL182 | 10693.3 | Av | 1.55 | 1.44 | 1.31 | 1.17 | 1.17 | 1.1 | |
| BDL182 | 10693.5 | P | 0.04 | 0.24 | 0.12 | <0.01 | <0.01 | <0.01 | 0.48 |
| BDL182 | 10693.5 | Av | 1.33 | 1.15 | 1.22 | 1.39 | 1.33 | 1.21 | 1.1 |
| BDL183 | 9943.4 | P | | | | 0.02 | 0.11 | | 0.02 |
| BDL183 | 9943.4 | Av | | | | 1.26 | 1.17 | | 1.61 |
| BDL183 | 9944.4 | P | | | | 0.01 | <0.01 | 0.02 | 0.36 |
| BDL183 | 9944.4 | Av | | | | 1.24 | 1.36 | 1.21 | 1.26 |
| BDL189 | 11351.2 | P | 0.05 | | | | | | |
| BDL189 | 11351.2 | Av | 1.17 | | | | | | |
| BDL189 | 11353.3 | P | 0.22 | 0.04 | 0.11 | | | | |
| BDL189 | 11353.3 | Av | 1.19 | 1.2 | 1.17 | | | | |
| BDL189 | 11353.5 | P | 0.26 | | | | | | |
| BDL189 | 11353.5 | Av | 1.1 | | | | | | |
| BDL189 | 11355.4 | P | 0.12 | 0.12 | 0.1 | | | | |
| BDL189 | 11355.4 | Av | 1.12 | 1.11 | 1.11 | | | | |
| BDL189 | 11356.7 | P | 0.27 | | | | | | |
| BDL189 | 11356.7 | Av | 1.11 | | | | | | |
| BDL196 | 10242.2 | P | 0.02 | 0.09 | | 0.05 | 0.03 | 0.09 | |
| BDL196 | 10242.2 | Av | 1.18 | 1.13 | | 1.29 | 1.28 | 1.16 | |
| BDL196 | 10243.4 | P | 0.09 | 0.25 | 0.24 | 0.13 | 0.05 | 0.17 | <0.01 |
| BDL196 | 10243.4 | Av | 1.16 | 1.23 | 1.24 | 1.11 | 1.25 | 1.15 | 1.74 |
| BDL196 | 10244.1 | P | <0.01 | 0.07 | | | 0.23 | | 0.21 |
| BDL196 | 10244.1 | Av | 1.21 | 1.19 | | | 1.22 | | 1.33 |
| BDL196 | 10243.3 | P | | | | 0.02 | | | 0.68 |
| BDL196 | 10243.3 | Av | | | | 1.16 | | | 1.1 |
| BDL196 | 10243.4 | P | | 0.01 | <0.01 | | | 0.23 | |
| BDL196 | 10243.4 | Av | | 1.24 | 1.49 | | | 1.12 | |
| BDL197 | 11362.2 | P | | | 0.14 | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL197 | 11362.2 | Av | | | 1.17 | | | | |
| BDL197 | 11363.1 | P | | | | | | 0.04 | |
| BDL197 | 11363.1 | Av | | | | | | 1.17 | |
| BDL197 | 11363.6 | P | | | 0.15 | | | | |
| BDL197 | 11363.6 | Av | | | 1.17 | | | | |
| BDL197 | 11364.1 | P | | 0.08 | 0.01 | | | 0.09 | |
| BDL197 | 11364.1 | Av | | 1.14 | 1.42 | | | 1.15 | |
| BDL197 | 11364.5 | P | | 0.09 | 0.04 | | | | |
| BDL197 | 11364.5 | Av | | 1.12 | 1.25 | | | | |
| BDL197 | 11363.6 | P | | 0.2 | 0.07 | | | | |
| BDL197 | 11363.6 | Av | | 1.11 | 1.19 | | | | |
| BDL201 | 9961.2 | P | 0.02 | 0.18 | 0.39 | | | | |
| BDL201 | 9961.2 | Av | 1.41 | 1.18 | 1.18 | | | | |
| BDL201 | 9961.3 | P | 0.08 | 0.13 | | | | | |
| BDL201 | 9961.3 | Av | 1.21 | 1.28 | | | | | |
| BDL201 | 9961.4 | P | | | | 0.06 | 0.15 | 0.43 | 0.02 |
| BDL201 | 9961.4 | Av | | | | 1.37 | 1.25 | 1.11 | 1.76 |
| BDL201 | 9964.3 | P | | | | <0.01 | 0.01 | | 0.02 |
| BDL201 | 9964.3 | Av | | | | 1.34 | 1.24 | | 1.84 |
| BDL220 | 10331.2 | P | <0.01 | <0.01 | 0.15 | | | | |
| BDL220 | 10331.2 | Av | 1.75 | 1.37 | 1.15 | | | | |
| BDL220 | 10331.5 | P | 0.01 | 0.02 | 0.05 | | | | |
| BDL220 | 10331.5 | Av | 1.48 | 1.64 | 1.75 | | | | |
| BDL220 | 10334.2 | P | <0.01 | <0.01 | 0.04 | | | | |
| BDL220 | 10334.2 | Av | 1.58 | 1.37 | 1.21 | | | | |
| BDL221 | 10341.3 | P | 0.13 | 0.13 | 0.06 | | | | |
| BDL221 | 10341.3 | Av | 1.26 | 1.19 | 1.44 | | | | |
| BDL221 | 10341.4 | P | <0.01 | 0.01 | <0.01 | | | | |
| BDL221 | 10341.4 | Av | 1.57 | 1.3 | 1.35 | | | | |
| BDL221 | 10343.3 | P | | 0.11 | 0.06 | 0.01 | <0.01 | <0.01 | 0.13 |
| BDL221 | 10343.3 | Av | | 1.1 | 1.16 | 1.37 | 1.4 | 1.4 | 1.55 |
| BDL221 | 10341.1 | P | 0.26 | 0.45 | 0.19 | | | | |
| BDL221 | 10341.1 | Av | 1.18 | 1.15 | 1.26 | | | | |
| BDL221 | 10342.1 | P | <0.01 | <0.01 | 0.02 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL221 | 10342.1 | Av | 1.9 | 1.46 | 1.32 | 2.02 | 2.08 | 1.68 | 4.31 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL221 | 10343.1 | P | 0.18 | 0.05 | 0.07 | 0.26 | <0.01 | <0.01 | <0.01 |
| BDL221 | 10343.1 | Av | 1.3 | 1.51 | 1.58 | 1.12 | 1.35 | 1.32 | 1.67 |
| BDL221 | 10343.3 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL221 | 10343.3 | Av | 2.7 | 1.8 | 1.59 | 1.75 | 2.12 | 1.87 | 2.4 |
| BDL221 | 10343.4 | P | 0.05 | 0.11 | 0.19 | 0.01 | <0.01 | 0.05 | 0.02 |
| BDL221 | 10343.4 | Av | 1.88 | 1.56 | 1.57 | 1.46 | 1.65 | 1.49 | 2.07 |
| BDL221 | 10344.3 | P | 0.02 | 0.01 | 0.05 | | 0.1 | 0.18 | <0.01 |
| BDL221 | 10344.3 | Av | 1.9 | 1.61 | 1.56 | | 1.14 | 1.12 | 1.63 |
| BDL223 | 10793.5 | P | | | | | | 0.11 | |
| BDL223 | 10793.5 | Av | | | | | | 1.14 | |
| BDL223 | 10793.8 | P | | | | 0.21 | 0.17 | 0.08 | |
| BDL223 | 10793.8 | Av | | | | 1.18 | 1.17 | 1.18 | |
| BDL223 | 10796.2 | P | <0.01 | 0.06 | | | | | |
| BDL223 | 10796.2 | Av | 1.22 | 1.14 | | | | | |
| BDL223 | 10791.1 | P | | | 0.07 | | 0.12 | 0.03 | |
| BDL223 | 10791.1 | Av | | | 1.21 | | 1.17 | 1.2 | |
| BDL223 | 10793.3 | P | 0.01 | 0.04 | 0.02 | | | 0.14 | |
| BDL223 | 10793.3 | Av | 1.33 | 1.3 | 1.55 | | | 1.18 | |
| BDL223 | 10793.5 | P | | | | | 0.07 | 0.04 | |
| BDL223 | 10793.5 | Av | | | | | 1.14 | 1.18 | |
| BDL223 | 10793.8 | P | | 0.08 | 0.08 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL223 | 10793.8 | Av | | 1.17 | 1.19 | 1.54 | 1.65 | 1.5 | 1.64 |
| BDL223 | 10796.1 | P | | | 0.11 | | | | |
| BDL223 | 10796.1 | Av | | | 1.15 | | | | |
| BDL224 | 10451.3 | P | | 0.29 | | | | | |
| BDL224 | 10451.3 | Av | | 1.11 | | | | | |
| BDL224 | 10451.5 | P | | | 0.1 | | | | |
| BDL224 | 10451.5 | Av | | | 1.15 | | | | |
| BDL224 | 10451.7 | P | <0.01 | <0.01 | 0.01 | 0.03 | 0.07 | 0.23 | 0.16 |
| BDL224 | 10451.7 | Av | 1.58 | 1.69 | 1.8 | 1.39 | 1.26 | 1.19 | 1.41 |
| BDL226 | 10861.2 | P | | | | | | 0.4 | |
| BDL226 | 10861.2 | Av | | | | | | 1.1 | |
| BDL227 | 11491.1 | P | | | | <0.01 | <0.01 | 0.03 | 0.01 |
| BDL227 | 11491.1 | Av | | | | 1.5 | 1.46 | 1.21 | 1.95 |
| BDL227 | 11491.3 | P | <0.01 | <0.01 | <0.01 | 0.01 | <0.01 | 0.02 | 0.04 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL227 | 11491.3 | Av | 2.12 | 1.6 | 1.42 | 1.64 | 1.65 | 1.56 | 2.26 |
| BDL227 | 11491.5 | P | <0.01 | <0.01 | 0.02 | <0.01 | <0.01 | 0.01 | <0.01 |
| BDL227 | 11491.5 | Av | 1.84 | 1.53 | 1.42 | 1.78 | 1.85 | 1.64 | 2.73 |
| BDL227 | 11492.5 | P | <0.01 | <0.01 | 0.01 | 0.26 | 0.03 | 0.04 | 0.01 |
| BDL227 | 11492.5 | Av | 2.13 | 1.91 | 1.72 | 1.17 | 1.48 | 1.32 | 1.58 |
| BDL227 | 11493.5 | P | <0.01 | <0.01 | 0.02 | 0.33 | <0.01 | <0.01 | 0.02 |
| BDL227 | 11493.5 | Av | 1.55 | 1.63 | 1.74 | 1.1 | 1.47 | 1.47 | 1.53 |
| BDL230 | 10671.3 | P | <0.01 | 0.06 | 0.01 | | | | |
| BDL230 | 10671.3 | Av | 1.36 | 1.44 | 1.81 | | | | |
| BDL230 | 10671.5 | P | | | | 0.33 | 0.49 | 0.46 | |
| BDL230 | 10671.5 | Av | | | | 1.22 | 1.16 | 1.11 | |
| BDL231 | 11111.1 | P | <0.01 | <0.01 | <0.01 | | | | |
| BDL231 | 11111.1 | Av | 1.55 | 1.53 | 1.51 | | | | |
| BDL231 | 11111.2 | P | 0.11 | 0.15 | 0.04 | 0.19 | | 0.04 | |
| BDL231 | 11111.2 | Av | 1.12 | 1.12 | 1.28 | 1.15 | | 1.19 | |
| BDL231 | 11111.3 | P | <0.01 | 0.04 | 0.05 | | | | |
| BDL231 | 11111.3 | Av | 1.35 | 1.26 | 1.37 | | | | |
| BDL231 | 11112.2 | P | <0.01 | 0.01 | 0.03 | <0.01 | <0.01 | <0.01 | 0.01 |
| BDL231 | 11112.2 | Av | 1.72 | 1.43 | 1.38 | 2.08 | 1.68 | 1.48 | 2.34 |
| BDL231 | 11116.5 | P | <0.01 | <0.01 | <0.01 | <0.01 | 0.01 | 0.03 | <0.01 |
| BDL231 | 11116.5 | Av | 1.82 | 1.77 | 1.76 | 1.67 | 1.38 | 1.31 | 1.92 |
| BDL231 | 11111.1 | P | <0.01 | <0.01 | <0.01 | | 0.36 | | 0.07 |
| BDL231 | 11111.1 | Av | 1.88 | 1.78 | 1.49 | | 1.11 | | 1.43 |
| BDL231 | 11111.2 | P | 0.01 | 0.03 | 0.01 | 0.01 | 0.1 | | 0.05 |
| BDL231 | 11111.2 | Av | 1.66 | 1.6 | 1.45 | 1.28 | 1.15 | | 1.51 |
| BDL231 | 11111.3 | P | | | | 0.01 | 0.26 | | 0.53 |
| BDL231 | 11111.3 | Av | | | | 1.31 | 1.1 | | 1.1 |
| BDL231 | 11112.2 | P | 0.24 | 0.17 | | <0.01 | <0.01 | | <0.01 |
| BDL231 | 11112.2 | Av | 1.12 | 1.12 | | 1.51 | 1.3 | | 1.97 |
| BDL231 | 11116.5 | P | | | | 0.11 | | | 0.24 |
| BDL231 | 11116.5 | Av | | | | 1.19 | | | 1.35 |
| BDL232 | 10904.1 | P | | 0.61 | 0.54 | | 0.43 | 0.23 | |
| BDL232 | 10904.1 | Av | | 1.17 | 1.2 | | 1.1 | 1.14 | |
| BDL232 | 10905.1 | P | | | | 0.02 | <0.01 | 0.05 | 0.02 |
| BDL232 | 10905.1 | Av | | | | 1.5 | 1.46 | 1.25 | 1.4 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL232 | 10906.3 | P | | 0.25 | 0.14 | | 0.59 | 0.25 | |
| BDL232 | 10906.3 | Av | | 1.29 | 1.45 | | 1.1 | 1.21 | |
| BDL232 | 10902.2 | P | | | | <0.01 | <0.01 | 0.06 | 0.01 |
| BDL232 | 10902.2 | Av | | | | 1.7 | 1.47 | 1.24 | 2.1 |
| BDL232 | 10905.1 | P | | | | <0.01 | 0.01 | 0.09 | 0.03 |
| BDL232 | 10905.1 | Av | | | | 1.59 | 1.42 | 1.2 | 2.17 |
| BDL233 | 10825.4 | P | | | | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL233 | 10825.4 | Av | | | | 1.47 | 1.45 | 1.35 | 2.01 |
| BDL233 | 10822.4 | P | | | 0.14 | | | | |
| BDL233 | 10822.4 | Av | | | 1.23 | | | | |
| BDL233 | 10824.2 | P | | | | | | 0.05 | |
| BDL233 | 10824.2 | Av | | | | | | 1.16 | |
| BDL233 | 10825.3 | P | | | | | | | 0.26 |
| BDL233 | 10825.3 | Av | | | | | | | 1.27 |
| BDL233 | 10825.4 | P | | | 0.24 | <0.01 | <0.01 | <0.01 | 0.19 |
| BDL233 | 10825.4 | Av | | | 1.17 | 1.56 | 1.59 | 1.51 | 1.3 |
| BDL235 | 11413.2 | P | | | | <0.01 | 0.01 | 0.03 | 0.18 |
| BDL235 | 11413.2 | Av | | | | 1.63 | 1.3 | 1.19 | 1.43 |
| BDL235 | 11413.2 | P | | | | <0.01 | <0.01 | 0.05 | 0.01 |
| BDL235 | 11413.2 | Av | | | | 1.57 | 1.45 | 1.29 | 2.12 |
| BDL237 | 10892.2 | P | 0.16 | | | | 0.28 | 0.12 | 0.09 |
| BDL237 | 10892.2 | Av | 1.21 | | | | 1.1 | 1.12 | 1.4 |
| BDL237 | 10893.1 | P | <0.01 | 0.02 | 0.14 | | 0.19 | 0.28 | |
| BDL237 | 10893.1 | Av | 1.96 | 1.39 | 1.24 | | 1.13 | 1.14 | |
| BDL237 | 10895.3 | P | <0.01 | <0.01 | 0.01 | 0.01 | <0.01 | <0.01 | 0.02 |
| BDL237 | 10895.3 | Av | 2.2 | 1.99 | 1.9 | 1.84 | 1.97 | 1.79 | 2.09 |
| BDL237 | 10896.1 | P | 0.19 | | 0.49 | | | | |
| BDL237 | 10896.1 | Av | 1.29 | | 1.1 | | | | |
| BDL238 | 10951.4 | P | | | | 0.08 | | | 0.01 |
| BDL238 | 10951.4 | Av | | | | 1.2 | | | 1.69 |
| BDL238 | 10952.3 | P | 0.05 | | | | | | |
| BDL238 | 10952.3 | Av | 1.2 | | | | | | |
| BDL238 | 10953.3 | P | | | | | | | 0.32 |
| BDL238 | 10953.3 | Av | | | | | | | 1.5 |
| BDL238 | 10954.2 | P | | | | 0.05 | | | 0.59 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL238 | 10954.2 | Av | | | | 1.24 | | | 1.13 |
| BDL238 | 10954.3 | P | 0.09 | | | 0.03 | 0.17 | 0.26 | 0.17 |
| BDL238 | 10954.3 | Av | 1.16 | | | 1.3 | 1.12 | 1.1 | 1.45 |
| BDL238 | 10951.4 | P | | | | 0.13 | 0.04 | 0.23 | 0.17 |
| BDL238 | 10951.4 | Av | | | | 1.22 | 1.24 | 1.11 | 1.39 |
| BDL238 | 10952.3 | P | | | | 0.02 | 0.01 | 0.02 | 0.11 |
| BDL238 | 10952.3 | Av | | | | 1.44 | 1.43 | 1.37 | 1.54 |
| BDL238 | 10954.2 | P | | | | 0.02 | 0.08 | 0.17 | 0.22 |
| BDL238 | 10954.2 | Av | | | | 1.26 | 1.2 | 1.17 | 1.2 |
| BDL240 | 10802.2 | P | <0.01 | 0.2 | 0.31 | | 0.16 | 0.1 | 0.1 |
| BDL240 | 10802.2 | Av | 1.57 | 1.23 | 1.17 | | 1.17 | 1.19 | 1.25 |
| BDL240 | 10803.5 | P | 0.11 | 0.4 | 0.31 | | | | |
| BDL240 | 10803.5 | Av | 1.4 | 1.11 | 1.16 | | | | |
| BDL240 | 10806.4 | P | <0.01 | 0.18 | | | | | |
| BDL240 | 10806.4 | Av | 1.29 | 1.16 | | | | | |
| BDL240 | 10806.6 | P | 0.02 | 0.02 | 0.04 | 0.02 | 0.01 | 0.01 | 0.03 |
| BDL240 | 10806.6 | Av | 2.29 | 1.87 | 1.52 | 1.59 | 1.63 | 1.49 | 3.75 |
| BDL241 | 10873.1 | P | | | | | | | 0.51 |
| BDL241 | 10873.1 | Av | | | | | | | 1.2 |
| BDL241 | 10874.3 | P | | | | | | | 0.32 |
| BDL241 | 10874.3 | Av | | | | | | | 1.42 |
| BDL241 | 10875.1 | P | | | | 0.04 | 0.01 | 0.13 | <0.01 |
| BDL241 | 10875.1 | Av | | | | 1.4 | 1.34 | 1.21 | 2.29 |
| BDL241 | 10874.3 | P | <0.01 | <0.01 | 0.02 | | | 0.1 | |
| BDL241 | 10874.3 | Av | 1.34 | 1.34 | 1.43 | | | 1.15 | |
| BDL241 | 10875.1 | P | | | | <0.01 | 0.03 | 0.3 | 0.03 |
| BDL241 | 10875.1 | Av | | | | 1.32 | 1.29 | 1.16 | 1.52 |
| BDL242 | 10731.3 | P | | 0.03 | | | 0.06 | 0.18 | 0.11 |
| BDL242 | 10731.3 | Av | | 1.12 | | | 1.14 | 1.13 | 1.36 |
| BDL242 | 10731.5 | P | | | | 0.4 | 0.11 | 0.18 | 0.32 |
| BDL242 | 10731.5 | Av | | | | 1.13 | 1.16 | 1.1 | 1.23 |
| BDL242 | 10731.2 | P | 0.36 | | | | | | |
| BDL242 | 10731.2 | Av | 1.2 | | | | | | |
| BDL242 | 10731.3 | P | <0.01 | <0.01 | <0.01 | | 0.02 | <0.01 | 0.03 |
| BDL242 | 10731.3 | Av | 3.13 | 2.79 | 2.3 | | 1.26 | 1.27 | 1.65 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL249 | 11401.2 | Av | 3.01 | 2.92 | 2.73 | 1.78 | 1.84 | 1.71 | 3.51 |
| BDL249 | 11401.5 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL249 | 11401.5 | Av | 2.17 | 1.83 | 1.52 | 1.66 | 1.64 | 1.41 | 3.31 |
| BDL249 | 11402.4 | P | 0.01 | 0.01 | 0.03 | 0.18 | <0.01 | <0.01 | 0.04 |
| BDL249 | 11402.4 | Av | 1.49 | 1.44 | 1.39 | 1.14 | 1.64 | 1.49 | 1.54 |
| BDL249 | 11403.2 | P | | | 0.48 | | 0.19 | 0.26 | |
| BDL249 | 11403.2 | Av | | | 1.12 | | 1.2 | 1.16 | |
| BDL249 | 11404.3 | P | | | | 0.09 | 0.07 | 0.02 | 0.12 |
| BDL249 | 11404.3 | Av | | | | 1.41 | 1.4 | 1.26 | 1.57 |
| BDL249 | 11401.2 | P | | | | 0.29 | 0.2 | | 0.17 |
| BDL249 | 11401.2 | Av | | | | 1.11 | 1.1 | | 1.21 |
| BDL249 | 11401.5 | P | | | | 0.17 | | | 0.46 |
| BDL249 | 11401.5 | Av | | | | 1.2 | | | 1.21 |
| BDL249 | 11403.2 | P | | | | 0.04 | 0.15 | | 0.35 |
| BDL249 | 11403.2 | Av | | | | 1.3 | 1.13 | | 1.23 |
| BDL249 | 11404.3 | P | | | | 0.21 | 0.04 | 0.12 | 0.35 |
| BDL249 | 11404.3 | Av | | | | 1.11 | 1.27 | 1.19 | 1.14 |
| BDL250 | 10841.3 | P | | | | 0.01 | 0.12 | 0.17 | |
| BDL250 | 10841.3 | Av | | | | 1.26 | 1.23 | 1.12 | |
| BDL250 | 10842.3 | P | | 0.05 | 0.23 | <0.01 | <0.01 | <0.01 | 0.03 |
| BDL250 | 10842.3 | Av | | 1.16 | 1.12 | 1.55 | 1.5 | 1.38 | 1.39 |
| BDL250 | 10846.2 | P | | | | <0.01 | <0.01 | <0.01 | |
| BDL250 | 10846.2 | Av | | | | 1.36 | 1.37 | 1.29 | |
| BDL250 | 10846.3 | P | | | | 0.09 | <0.01 | <0.01 | 0.12 |
| BDL250 | 10846.3 | Av | | | | 1.33 | 1.39 | 1.29 | 1.44 |
| BDL250 | 10841.3 | P | 0.01 | 0.1 | 0.09 | <0.01 | <0.01 | <0.01 | 0.01 |
| BDL250 | 10841.3 | Av | 1.23 | 1.21 | 1.22 | 1.82 | 1.89 | 1.68 | 2.37 |
| BDL250 | 10842.3 | P | 0.05 | 0.15 | 0.26 | <0.01 | 0.23 | 0.48 | 0.02 |
| BDL250 | 10842.3 | Av | 1.73 | 1.59 | 1.5 | 1.4 | 1.26 | 1.14 | 2.03 |
| BDL250 | 10843.2 | P | 0.01 | 0.02 | 0.04 | <0.01 | 0.01 | 0.01 | <0.01 |
| BDL250 | 10843.2 | Av | 1.97 | 1.67 | 1.61 | 1.37 | 1.44 | 1.37 | 2.33 |
| BDL250 | 10846.2 | P | <0.01 | 0.01 | <0.01 | 0.11 | 0.02 | <0.01 | 0.08 |
| BDL250 | 10846.2 | Av | 2.3 | 1.59 | 1.69 | 1.21 | 1.33 | 1.36 | 1.39 |
| BDL250 | 10846.3 | P | <0.01 | <0.01 | <0.01 | 0.01 | <0.01 | <0.01 | 0.01 |
| BDL250 | 10846.3 | Av | 1.92 | 1.69 | 1.78 | 1.66 | 1.98 | 1.79 | 2.83 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL252 | 10881.1 | P | <0.01 | <0.01 | <0.01 | 0.13 | 0.01 | <0.01 | 0.04 |
| BDL252 | 10881.1 | Av | 1.96 | 1.94 | 1.72 | 1.29 | 1.48 | 1.42 | 1.52 |
| BDL252 | 10882.1 | P | <0.01 | <0.01 | <0.01 | 0.05 | 0.01 | 0.01 | 0.02 |
| BDL252 | 10882.1 | Av | 2.97 | 2.36 | 2.12 | 1.65 | 1.88 | 1.77 | 3.43 |
| BDL252 | 10882.2 | P | <0.01 | <0.01 | <0.01 | 0.03 | 0.04 | <0.01 | 0.03 |
| BDL252 | 10882.2 | Av | 1.89 | 1.48 | 1.43 | 1.47 | 1.54 | 1.45 | 2.04 |
| BDL252 | 10882.4 | P | 0.03 | <0.01 | 0.11 | <0.01 | 0.01 | 0.03 | 0.01 |
| BDL252 | 10882.4 | Av | 1.64 | 1.4 | 1.3 | 1.7 | 1.48 | 1.31 | 2.99 |
| BDL252 | 10884.1 | P | <0.01 | 0.02 | 0.13 | | | | |
| BDL252 | 10884.1 | Av | 1.55 | 1.31 | 1.17 | | | | |
| BDL58 | 10281.5 | P | 0.23 | 0.48 | 0.16 | | | | |
| BDL58 | 10281.5 | Av | 1.25 | 1.18 | 1.3 | | | | |
| BDL58 | 10282.3 | P | <0.01 | <0.01 | 0.01 | 0.12 | <0.01 | <0.01 | 0.26 |
| BDL58 | 10282.3 | Av | 1.79 | 1.72 | 1.77 | 1.27 | 1.62 | 1.62 | 1.43 |
| BDL62 | 10682.1 | P | | | | | | | 0.53 |
| BDL62 | 10682.1 | Av | | | | | | | 1.16 |
| BDL62 | 10684.2 | P | | | | 0.01 | | | 0.22 |
| BDL62 | 10684.2 | Av | | | | 1.43 | | | 1.3 |
| BDL62 | 10682.1 | P | | 0.37 | 0.56 | | | | |
| BDL62 | 10682.1 | Av | | 1.17 | 1.16 | | | | |
| BDL62 | 10684.2 | P | | | | | | 0.09 | |
| BDL62 | 10684.2 | Av | | | | | | 1.13 | |
| BDL64 | 10651.5 | P | | 0.08 | 0.27 | | | | |
| BDL64 | 10651.5 | Av | | 1.26 | 1.56 | | | | |
| BDL64 | 10653.1 | P | 0.01 | 0.06 | 0.01 | | | | |
| BDL64 | 10653.1 | Av | 1.24 | 1.23 | 1.53 | | | | |
| BDL64 | 10654.3 | P | | 0.32 | 0.3 | 0.2 | 0.04 | 0.09 | |
| BDL64 | 10654.3 | Av | | 1.21 | 1.38 | 1.11 | 1.4 | 1.4 | |
| BDL64 | 10651.1 | P | | 0.53 | | | | | |
| BDL64 | 10651.1 | Av | | 1.11 | | | | | |
| BDL64 | 10653.1 | P | 0.11 | 0.02 | 0.05 | 0.01 | <0.01 | 0.01 | 0.14 |
| BDL64 | 10653.1 | Av | 1.34 | 1.57 | 1.61 | 1.34 | 1.42 | 1.28 | 1.34 |
| BDL64 | 10654.3 | P | 0.01 | <0.01 | <0.01 | <0.01 | <0.01 | 0.01 | 0.29 |
| BDL64 | 10654.3 | Av | 1.41 | 1.49 | 1.46 | 1.28 | 1.29 | 1.23 | 1.27 |
| BDL64 | 10651.1 | P | <0.01 | <0.01 | | 0.02 | 0.15 | | 0.2 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL64 | 10651.1 | Av | 1.5 | 1.31 | | 1.41 | 1.13 | | 1.44 |
| BDL64 | 10651.3 | P | | | | <0.01 | <0.01 | 0.13 | <0.01 |
| BDL64 | 10651.3 | Av | | | | 1.96 | 1.41 | 1.15 | 3.02 |
| BDL64 | 10653.1 | P | | | | 0.03 | 0.3 | | 0.08 |
| BDL64 | 10653.1 | Av | | | | 1.64 | 1.18 | | 1.64 |
| BDL64 | 10654.3 | P | | | | <0.01 | 0.22 | | 0.04 |
| BDL64 | 10654.3 | Av | | | | 1.82 | 1.23 | | 2.34 |
| BDL79 | 11041.1 | P | | | | | | | 0.62 |
| BDL79 | 11041.1 | Av | | | | | | | 1.12 |
| BDL79 | 11042.1 | P | | | | | | | 0.61 |
| BDL79 | 11042.1 | Av | | | | | | | 1.13 |
| BDL79 | 11043.1 | P | | | | | | | 0.08 |
| BDL79 | 11043.1 | Av | | | | | | | 1.64 |
| BDL79 | 11042.3 | P | | | | | | 0.33 | |
| BDL79 | 11042.3 | Av | | | | | | 1.12 | |
| BDL79 | 11043.1 | P | | | 0.04 | 0.17 | <0.01 | 0.01 | 0.37 |
| BDL79 | 11043.1 | Av | | | 1.23 | 1.19 | 1.36 | 1.29 | 1.19 |
| BDL81 | 10372.2 | P | <0.01 | 0.35 | 0.43 | | | | |
| BDL81 | 10372.2 | Av | 1.25 | 1.11 | 1.13 | | | | |
| BDL81 | 10374.1 | P | | | | | | | 0.3 |
| BDL81 | 10374.1 | Av | | | | | | | 1.24 |
| BDL85 | 10411.3 | P | | | | | 0.08 | 0.03 | |
| BDL85 | 10411.3 | Av | | | | | 1.15 | 1.12 | |
| BDL85 | 10414.1 | P | 0.2 | | 0.04 | | | | |
| BDL85 | 10414.1 | Av | 1.16 | | 1.26 | | | | |
| BDL85 | 10414.2 | P | 0.19 | 0.02 | <0.01 | | | | |
| BDL85 | 10414.2 | Av | 1.1 | 1.2 | 1.35 | | | | |
| BDL88 | 10291.2 | P | 0.01 | 0.03 | 0.03 | | | 0.07 | |
| BDL88 | 10291.2 | Av | 1.88 | 1.59 | 1.52 | | | 1.13 | |
| BDL88 | 10291.4 | P | 0.02 | <0.01 | <0.01 | | 0.03 | <0.01 | |
| BDL88 | 10291.4 | Av | 1.45 | 1.43 | 1.53 | | 1.21 | 1.28 | |
| BDL88 | 10291.5 | P | 0.12 | 0.15 | 0.37 | | | | 0.67 |
| BDL88 | 10291.5 | Av | 1.43 | 1.35 | 1.17 | | | | 1.11 |
| BDL88 | 10293.3 | P | <0.01 | <0.01 | <0.01 | | | | 0.57 |
| BDL88 | 10293.3 | Av | 2.76 | 2.34 | 2.24 | | | | 1.12 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Leaf Area TP1</i> | <i>Leaf Area TP2</i> | <i>Leaf Area TP3</i> | <i>Roots Length TP1</i> | <i>Roots Length TP2</i> | <i>Roots Length TP3</i> | <i>Roots Coverage TP1</i> |
|-------------|------------|-------------|----------------------|----------------------|----------------------|-------------------------|-------------------------|-------------------------|---------------------------|
| BDL88 | 10291.2 | P | <0.01 | <0.01 | <0.01 | | | | |
| BDL88 | 10291.2 | Av | 1.64 | 1.57 | 1.58 | | | | |
| BDL88 | 10291.4 | P | <0.01 | <0.01 | <0.01 | | | | |
| BDL88 | 10291.4 | Av | 1.67 | 1.5 | 1.53 | | | | |
| BDL88 | 10291.5 | P | <0.01 | <0.01 | <0.01 | | | | |
| BDL88 | 10291.5 | Av | 1.8 | 1.7 | 1.84 | | | | |
| BDL88 | 10293.3 | P | 0.03 | 0.05 | 0.06 | | | | |
| BDL88 | 10293.3 | Av | 1.19 | 1.16 | 1.22 | | | | |
| BDL88 | 10294.2 | P | <0.01 | 0.01 | 0.02 | | | | |
| BDL88 | 10294.2 | Av | 1.82 | 1.66 | 1.78 | | | | |
| BDL90 | 10924.2 | P | | | | 0.05 | 0.01 | <0.01 | 0.16 |
| BDL90 | 10924.2 | Av | | | | 1.43 | 1.55 | 1.48 | 1.9 |
| BDL90 | 10925.4 | P | | | | <0.01 | <0.01 | <0.01 | 0.07 |
| BDL90 | 10925.4 | Av | | | | 1.95 | 1.91 | 1.62 | 2.22 |
| BDL90 | 10924.2 | P | 0.12 | 0.2 | 0.09 | 0.02 | 0.01 | 0.01 | 0.04 |
| BDL90 | 10924.2 | Av | 1.32 | 1.23 | 1.22 | 1.31 | 1.31 | 1.31 | 1.93 |
| BDL90 | 10925.4 | P | 0.04 | 0.12 | | <0.01 | <0.01 | <0.01 | 0.02 |
| BDL90 | 10925.4 | Av | 1.25 | 1.15 | | 1.68 | 1.61 | 1.51 | 2.25 |
| BDL90 | 10921.6 | P | | | 0.1 | | | | |
| BDL90 | 10921.6 | Av | | | 1.19 | | | | |
| BDL90 | 10924.2 | P | | | 0.38 | <0.01 | <0.01 | <0.01 | 0.03 |
| BDL90 | 10924.2 | Av | | | 1.13 | 1.48 | 1.6 | 1.51 | 1.41 |
| BDL90 | 10925.4 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL90 | 10925.4 | Av | 1.6 | 1.66 | 1.8 | 1.85 | 1.81 | 1.71 | 2.9 |
| BDL94 | 11721.4 | P | 0.04 | 0.03 | 0.07 | | | | |
| BDL94 | 11721.4 | Av | 1.41 | 1.39 | 1.16 | | | | |
| BDL94 | 11725.2 | P | 0.04 | | | | | | |
| BDL94 | 11725.2 | Av | 1.16 | | | | | | |
| BDL94 | 11725.3 | P | 0.04 | | | | | | |
| BDL94 | 11725.3 | Av | 1.21 | | | | | | |
| BDL94 | 11725.5 | P | 0.14 | | | | | | |
| BDL94 | 11725.5 | Av | 1.1 | | | | | | |
| BDL94 | 11725.3 | P | 0.01 | | | | | | |
| BDL94 | 11725.3 | Av | 1.29 | | | | | | |

Table 21. "P" = P-value; "Av" = ratio between the averages of event and control. Note that when the average ratio is higher than "1" the effect of exogenous expression of the gene is an increase of

the desired trait; "Par" = Parameter according to the measured parameters; "Ev" = event. TP1 = Time point 1; TP2 = Time point 2; TP3 = Time point 3.

Table 22
Results obtained in a tissue culture assay

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| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL102 | 10471.1 | P | 0.08 | 0.05 | | 0.11 | 0.36 | | |
| BDL102 | 10471.1 | Av | 1.58 | 1.35 | | 1.26 | 1.11 | | |
| BDL102 | 10471.3 | P | 0.08 | 0.15 | | 0.02 | 0.15 | | |
| BDL102 | 10471.3 | Av | 1.72 | 1.58 | | 1.57 | 1.18 | | |
| BDL102 | 10472.1 | P | 0.19 | 0.28 | | 0.25 | | 0.29 | |
| BDL102 | 10472.1 | Av | 1.28 | 1.22 | | 1.19 | | 1.18 | |
| BDL102 | 10474.2 | P | 0.33 | 0.16 | 0.01 | 0.02 | 0.07 | 0.21 | 0.26 |
| BDL102 | 10474.2 | Av | 1.22 | 1.38 | 1.4 | 1.44 | 1.19 | 1.53 | 1.5 |
| BDL102 | 10474.6 | P | | 0.2 | 0.31 | 0.14 | | | |
| BDL102 | 10474.6 | Av | | 1.19 | 1.15 | 1.22 | | | |
| BDL118 | 10481.2 | P | 0.13 | 0.24 | <0.01 | 0.14 | 0.28 | 0.03 | 0.01 |
| BDL118 | 10481.2 | Av | 1.2 | 1.19 | 1.99 | 1.23 | 1.15 | 2.14 | 1.99 |
| BDL118 | 10481.5 | P | | | 0.01 | | | 0.02 | 0.01 |
| BDL118 | 10481.5 | Av | | | 1.36 | | | 2.03 | 1.97 |
| BDL118 | 10483.4 | P | | | | | | 0.07 | 0.03 |
| BDL118 | 10483.4 | Av | | | | | | 1.93 | 1.65 |
| BDL118 | 10484.3 | P | | | <0.01 | | | <0.01 | <0.01 |
| BDL118 | 10484.3 | Av | | | 1.6 | | | 1.98 | 2.01 |
| BDL140 | 10421.3 | P | 0.14 | 0.06 | <0.01 | <0.01 | | 0.03 | 0.13 |
| BDL140 | 10421.3 | Av | 1.45 | 1.64 | 1.7 | 1.68 | | 1.81 | 1.57 |
| BDL140 | 10423.1 | P | 0.21 | 0.28 | 0.22 | 0.16 | | 0.41 | 0.33 |
| BDL140 | 10423.1 | Av | 1.31 | 1.25 | 1.21 | 1.25 | | 1.17 | 1.16 |
| BDL140 | 10424.4 | P | | 0.18 | <0.01 | 0.2 | | 0.08 | 0.45 |
| BDL140 | 10424.4 | Av | | 1.13 | 1.66 | 1.18 | | 1.46 | 1.2 |
| BDL152 | 10431.4 | P | | 0.21 | 0.24 | 0.13 | | 0.23 | 0.02 |
| BDL152 | 10431.4 | Av | | 1.23 | 1.18 | 1.27 | | 1.18 | 1.27 |
| BDL152 | 10432.5 | P | 0.1 | 0.04 | | 0.03 | | | |
| BDL152 | 10432.5 | Av | 1.25 | 1.31 | | 1.32 | | | |
| BDL152 | 10434.4 | P | 0.02 | <0.01 | | <0.01 | 0.03 | | |
| BDL152 | 10434.4 | Av | 1.76 | 1.51 | | 1.44 | 1.23 | | |
| BDL153 | 10142.2 | P | 0.04 | 0.58 | | | | | |
| BDL153 | 10142.2 | Av | 1.57 | 1.1 | | | | | |
| BDL153 | 10144.1 | P | 0.09 | 0.12 | 0.02 | 0.09 | 0.12 | 0.36 | |
| BDL153 | 10144.1 | Av | 1.51 | 1.32 | 1.42 | 1.35 | 1.18 | 1.18 | |
| BDL154 | 10703.1 | P | 0.38 | 0.47 | | 0.52 | 0.44 | | |
| BDL154 | 10703.1 | Av | 1.13 | 1.18 | | 1.15 | 1.13 | | |
| BDL154 | 10703.3 | P | | | | | 0.34 | | |
| BDL154 | 10703.3 | Av | | | | | 1.17 | | |
| BDL154 | 10703.5 | P | | | | | | 0.38 | 0.16 |
| BDL154 | 10703.5 | Av | | | | | | 1.11 | 1.16 |
| BDL154 | 10703.1 | P | 0.03 | 0.05 | <0.01 | 0.01 | 0.01 | 0.01 | 0.01 |
| BDL154 | 10703.1 | Av | 1.48 | 1.55 | 1.71 | 1.7 | 1.37 | 1.36 | 1.57 |
| BDL154 | 10703.5 | P | 0.1 | 0.04 | 0.11 | 0.01 | <0.01 | 0.34 | 0.11 |
| BDL154 | 10703.5 | Av | 1.75 | 1.7 | 1.29 | 1.73 | 1.59 | 1.24 | 1.38 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL154 | 10703.6 | P | 0.07 | 0.04 | | 0.07 | 0.14 | | |
| BDL154 | 10703.6 | Av | 1.63 | 1.47 | | 1.45 | 1.28 | | |
| BDL155 | 9991.2 | P | | | | | | 0.22 | 0.45 |
| BDL155 | 9991.2 | Av | | | | | | 1.44 | 1.27 |
| BDL155 | 9993.2 | P | | | | | | 0.55 | |
| BDL155 | 9993.2 | Av | | | | | | 1.45 | |
| BDL155 | 9994.4 | P | | | | | 0.19 | | |
| BDL155 | 9994.4 | Av | | | | | 1.13 | | |
| BDL156 | 10852.6 | P | 0.41 | 0.51 | | 0.19 | 0.09 | | |
| BDL156 | 10852.6 | Av | 1.1 | 1.12 | | 1.21 | 1.22 | | |
| BDL156 | 10852.7 | P | | | | | 0.35 | | |
| BDL156 | 10852.7 | Av | | | | | 1.13 | | |
| BDL156 | 10853.6 | P | 0.58 | 0.25 | 0.07 | 0.07 | 0.16 | 0.28 | 0.04 |
| BDL156 | 10853.6 | Av | 1.13 | 1.24 | 1.21 | 1.33 | 1.19 | 1.2 | 1.26 |
| BDL156 | 10852.6 | P | | | 0.05 | 0.59 | 0.33 | 0.35 | 0.21 |
| BDL156 | 10852.6 | Av | | | 1.29 | 1.13 | 1.16 | 1.12 | 1.24 |
| BDL156 | 10853.6 | P | 0.42 | 0.25 | <0.01 | 0.05 | 0.06 | <0.01 | 0.01 |
| BDL156 | 10853.6 | Av | 1.29 | 1.69 | 1.97 | 1.83 | 1.43 | 1.78 | 2.26 |
| BDL156 | 10854.4 | P | | 0.03 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL156 | 10854.4 | Av | | 1.59 | 1.87 | 1.76 | 1.53 | 1.61 | 1.94 |
| BDL156 | 10855.3 | P | 0.32 | <0.01 | <0.01 | <0.01 | 0.01 | 0.46 | 0.05 |
| BDL156 | 10855.3 | Av | 1.17 | 1.78 | 1.49 | 1.99 | 1.44 | 1.18 | 1.42 |
| BDL158 | 9973.3 | P | 0.26 | | | | | | |
| BDL158 | 9973.3 | Av | 1.22 | | | | | | |
| BDL158 | 9971.3 | P | | 0.12 | 0.45 | 0.03 | 0.3 | | |
| BDL158 | 9971.3 | Av | | 1.27 | 1.11 | 1.34 | 1.11 | | |
| BDL158 | 9973.1 | P | | 0.04 | | 0.1 | | | |
| BDL158 | 9973.1 | Av | | 1.25 | | 1.24 | | | |
| BDL158 | 9973.3 | P | 0.04 | 0.27 | | 0.32 | | | |
| BDL158 | 9973.3 | Av | 1.43 | 1.23 | | 1.16 | | | |
| BDL158 | 9974.2 | P | 0.01 | 0.03 | 0.34 | <0.01 | | | 0.49 |
| BDL158 | 9974.2 | Av | 1.48 | 1.41 | 1.14 | 1.45 | | | 1.1 |
| BDL158 | 9974.3 | P | 0.08 | 0.05 | 0.02 | <0.01 | | 0.01 | 0.01 |
| BDL158 | 9974.3 | Av | 1.5 | 1.49 | 1.54 | 1.54 | | 1.5 | 1.54 |
| BDL158 | 9971.3 | P | | 0.33 | 0.06 | 0.13 | <0.01 | | |
| BDL158 | 9971.3 | Av | | 1.13 | 1.25 | 1.24 | 1.46 | | |
| BDL158 | 9973.1 | P | 0.09 | 0.25 | 0.02 | 0.45 | 0.29 | | 0.16 |
| BDL158 | 9973.1 | Av | 1.22 | 1.22 | 1.37 | 1.13 | 1.13 | | 1.2 |
| BDL158 | 9973.3 | P | 0.02 | 0.1 | | 0.03 | <0.01 | | |
| BDL158 | 9973.3 | Av | 1.62 | 1.43 | | 1.42 | 1.4 | | |
| BDL158 | 9974.2 | P | 0.06 | 0.02 | | 0.03 | | | |
| BDL158 | 9974.2 | Av | 1.21 | 1.24 | | 1.32 | | | |
| BDL158 | 9974.3 | P | | | 0.51 | | | | |
| BDL158 | 9974.3 | Av | | | 1.11 | | | | |
| BDL160 | 10011.5 | P | | | 0.24 | | | <0.01 | 0.53 |
| BDL160 | 10011.5 | Av | | | 1.23 | | | 1.48 | 1.33 |
| BDL160 | 10011.6 | P | | | | | | 0.51 | 0.66 |
| BDL160 | 10011.6 | Av | | | | | | 1.18 | 1.1 |
| BDL160 | 10011.7 | P | | | | | | 0.56 | |
| BDL160 | 10011.7 | Av | | | | | | 1.28 | |
| BDL160 | 10015.1 | P | | | | | | 0.03 | 0.12 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL160 | 10015.1 | Av | | | | | | 1.57 | 1.25 |
| BDL160 | 10011.5 | P | 0.61 | 0.38 | | 0.42 | | | |
| BDL160 | 10011.5 | Av | 1.11 | 1.14 | | 1.14 | | | |
| BDL160 | 10013.1 | P | | | 0.32 | | | | |
| BDL160 | 10013.1 | Av | | | 1.16 | | | | |
| BDL160 | 10014.9 | P | | 0.52 | | 0.37 | | | |
| BDL160 | 10014.9 | Av | | 1.16 | | 1.18 | | | |
| BDL160 | 10015.2 | P | | | 0.05 | | | 0.1 | 0.11 |
| BDL160 | 10015.2 | Av | | | 1.28 | | | 1.29 | 1.42 |
| BDL167 | 10042.3 | P | | | | | 0.12 | | |
| BDL167 | 10042.3 | Av | | | | | 1.17 | | |
| BDL167 | 10043.1 | P | | 0.58 | 0.13 | 0.21 | 0.23 | | |
| BDL167 | 10043.1 | Av | | 1.17 | 1.16 | 1.25 | 1.18 | | |
| BDL167 | 10043.2 | P | | | 0.18 | 0.34 | 0.09 | | |
| BDL167 | 10043.2 | Av | | | 1.14 | 1.1 | 1.19 | | |
| BDL167 | 10043.3 | P | 0.1 | <0.01 | <0.01 | <0.01 | <0.01 | | |
| BDL167 | 10043.3 | Av | 1.27 | 1.67 | 1.54 | 1.79 | 1.46 | | |
| BDL167 | 10044.2 | P | 0.05 | <0.01 | <0.01 | <0.01 | 0.08 | | 0.61 |
| BDL167 | 10044.2 | Av | 1.26 | 1.48 | 1.38 | 1.55 | 1.2 | | 1.12 |
| BDL167 | 10043.1 | P | <0.01 | 0.17 | 0.04 | 0.16 | 0.14 | 0.06 | |
| BDL167 | 10043.1 | Av | 1.63 | 1.27 | 1.4 | 1.3 | 1.17 | 1.6 | |
| BDL167 | 10044.2 | P | 0.01 | | | | | | |
| BDL167 | 10044.2 | Av | 1.39 | | | | | | |
| BDL168 | 9881.4 | P | <0.01 | 0.14 | | 0.08 | 0.05 | | |
| BDL168 | 9881.4 | Av | 1.74 | 1.47 | | 1.42 | 1.21 | | |
| BDL168 | 9882.1 | P | 0.08 | 0.69 | | | | | |
| BDL168 | 9882.1 | Av | 1.85 | 1.11 | | | | | |
| BDL168 | 9884.1 | P | <0.01 | 0.11 | | 0.34 | 0.22 | | |
| BDL168 | 9884.1 | Av | 1.84 | 1.29 | | 1.2 | 1.15 | | |
| BDL169 | 10744.2 | P | 0.02 | 0.17 | | 0.13 | 0.24 | | |
| BDL169 | 10744.2 | Av | 1.34 | 1.21 | | 1.22 | 1.16 | | |
| BDL169 | 10747.1 | P | 0.39 | | | 0.4 | | | |
| BDL169 | 10747.1 | Av | 1.1 | | | 1.11 | | | |
| BDL169 | 10747.5 | P | 0.04 | 0.02 | | 0.02 | 0.07 | | |
| BDL169 | 10747.5 | Av | 1.59 | 1.41 | | 1.37 | 1.28 | | |
| BDL171 | 10661.2 | P | 0.03 | 0.01 | 0.19 | <0.01 | 0.01 | 0.06 | 0.02 |
| BDL171 | 10661.2 | Av | 2.26 | 2.17 | 1.28 | 2.22 | 1.3 | 1.73 | 2.47 |
| BDL171 | 10661.5 | P | | 0.14 | 0.32 | 0.04 | | 0.02 | <0.01 |
| BDL171 | 10661.5 | Av | | 1.33 | 1.19 | 1.38 | | 1.35 | 2.02 |
| BDL171 | 10662.3 | P | | 0.32 | | 0.19 | | | 0.56 |
| BDL171 | 10662.3 | Av | | 1.12 | | 1.18 | | | 1.13 |
| BDL171 | 10663.3 | P | | | | 0.45 | | | 0.39 |
| BDL171 | 10663.3 | Av | | | | 1.14 | | | 1.19 |
| BDL171 | 10664.1 | P | | 0.26 | 0.25 | 0.1 | 0.46 | 0.03 | 0.03 |
| BDL171 | 10664.1 | Av | | 1.33 | 1.24 | 1.35 | 1.1 | 1.39 | 1.89 |
| BDL173 | 9951.2 | P | 0.37 | | | | | 0.27 | |
| BDL173 | 9951.2 | Av | 1.32 | | | | | 1.43 | |
| BDL173 | 9952.1 | P | 0.04 | 0.02 | | 0.01 | 0.08 | | |
| BDL173 | 9952.1 | Av | 2.68 | 1.72 | | 1.61 | 1.21 | | |
| BDL173 | 9952.2 | P | 0.15 | 0.56 | | | | | |
| BDL173 | 9952.2 | Av | 1.44 | 1.11 | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL173 | 9954.3 | P | | | | | | 0.14 | |
| BDL173 | 9954.3 | Av | | | | | | 1.46 | |
| BDL174 | 11082.1 | P | 0.29 | 0.39 | | 0.43 | 0.05 | | |
| BDL174 | 11082.1 | Av | 1.24 | 1.15 | | 1.14 | 1.26 | | |
| BDL174 | 11083.1 | P | 0.07 | 0.11 | 0.41 | 0.05 | 0.15 | 0.48 | 0.37 |
| BDL174 | 11083.1 | Av | 1.76 | 1.43 | 1.13 | 1.42 | 1.21 | 1.1 | 1.2 |
| BDL174 | 11083.2 | P | 0.17 | 0.25 | 0.13 | 0.09 | 0.04 | 0.2 | 0.4 |
| BDL174 | 11083.2 | Av | 1.27 | 1.36 | 1.26 | 1.38 | 1.44 | 1.21 | 1.19 |
| BDL174 | 11084.1 | P | 0.04 | 0.06 | <0.01 | <0.01 | 0.01 | 0.06 | 0.05 |
| BDL174 | 11084.1 | Av | 2.13 | 1.94 | 2.01 | 1.96 | 1.42 | 2.06 | 2.27 |
| BDL174 | 11085.1 | P | <0.01 | <0.01 | 0.1 | <0.01 | <0.01 | 0.2 | 0.24 |
| BDL174 | 11085.1 | Av | 2.66 | 2.13 | 1.27 | 2.17 | 2 | 1.24 | 1.37 |
| BDL174 | 11083.2 | P | | | 0.19 | | | 0.12 | 0.29 |
| BDL174 | 11083.2 | Av | | | 1.15 | | | 1.2 | 1.14 |
| BDL174 | 11084.1 | P | 0.6 | | | | | | |
| BDL174 | 11084.1 | Av | 1.1 | | | | | | |
| BDL174 | 11085.1 | P | 0.05 | 0.32 | | | | | |
| BDL174 | 11085.1 | Av | 1.42 | 1.14 | | | | | |
| BDL176 | 9891.4 | P | | 0.67 | 0.01 | 0.47 | | 0.06 | |
| BDL176 | 9891.4 | Av | | 1.11 | 1.45 | 1.17 | | 2.02 | |
| BDL176 | 9893.2 | P | 0.21 | 0.4 | 0.22 | 0.26 | | 0.15 | |
| BDL176 | 9893.2 | Av | 1.37 | 1.22 | 1.21 | 1.25 | | 1.38 | |
| BDL176 | 9893.3 | P | 0.47 | 0.23 | | 0.12 | | 0.14 | 0.48 |
| BDL176 | 9893.3 | Av | 1.17 | 1.31 | | 1.3 | | 1.29 | 1.22 |
| BDL177 | 10521.3 | P | 0.66 | 0.34 | | 0.28 | 0.06 | | |
| BDL177 | 10521.3 | Av | 1.1 | 1.15 | | 1.17 | 1.3 | | |
| BDL181 | 11293.6 | P | | 0.59 | 0.1 | 0.37 | 0.45 | 0.39 | 0.37 |
| BDL181 | 11293.6 | Av | | 1.15 | 1.3 | 1.24 | 1.15 | 1.17 | 1.26 |
| BDL181 | 11294.7 | P | | | 0.04 | | 0.12 | 0.11 | 0.1 |
| BDL181 | 11294.7 | Av | | | 1.36 | | 1.28 | 1.26 | 1.38 |
| BDL181 | 11293.1 | P | | | 0.25 | 0.4 | 0.02 | 0.05 | 0.02 |
| BDL181 | 11293.1 | Av | | | 1.19 | 1.11 | 1.22 | 1.59 | 1.58 |
| BDL181 | 11293.6 | P | 0.23 | 0.15 | <0.01 | 0.09 | 0.03 | <0.01 | <0.01 |
| BDL181 | 11293.6 | Av | 1.23 | 1.22 | 1.34 | 1.25 | 1.18 | 1.48 | 1.45 |
| BDL181 | 11294.7 | P | 0.02 | 0.21 | 0.3 | 0.05 | 0.01 | | 0.57 |
| BDL181 | 11294.7 | Av | 1.55 | 1.26 | 1.11 | 1.3 | 1.23 | | 1.1 |
| BDL182 | 10691.8 | P | | | 0.42 | | | 0.06 | 0.01 |
| BDL182 | 10691.8 | Av | | | 1.15 | | | 1.53 | 2.11 |
| BDL182 | 10692.2 | P | 0.53 | 0.2 | 0.28 | 0.07 | | 0.28 | 0.15 |
| BDL182 | 10692.2 | Av | 1.12 | 1.21 | 1.21 | 1.28 | | 1.47 | 1.93 |
| BDL182 | 10692.3 | P | | 0.63 | | 0.3 | 0.43 | | |
| BDL182 | 10692.3 | Av | | 1.13 | | 1.21 | 1.1 | | |
| BDL182 | 10693.3 | P | 0.02 | 0.03 | 0.22 | <0.01 | | 0.17 | 0.01 |
| BDL182 | 10693.3 | Av | 1.37 | 1.55 | 1.25 | 1.62 | | 1.41 | 1.88 |
| BDL182 | 10693.5 | P | 0.02 | <0.01 | 0.32 | <0.01 | 0.13 | 0.06 | 0.01 |
| BDL182 | 10693.5 | Av | 1.47 | 1.72 | 1.19 | 1.8 | 1.13 | 1.38 | 1.91 |
| BDL183 | 9943.4 | P | 0.19 | 0.3 | | 0.48 | | | |
| BDL183 | 9943.4 | Av | 1.3 | 1.16 | | 1.13 | | | |
| BDL183 | 9944.4 | P | 0.02 | 0.52 | | 0.46 | 0.06 | 0.44 | |
| BDL183 | 9944.4 | Av | 1.37 | 1.15 | | 1.15 | 1.2 | 1.16 | |
| BDL189 | 11353.3 | P | | 0.17 | 0.18 | 0.18 | | | 0.46 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL189 | 11353.3 | Av | | 1.18 | 1.16 | 1.2 | | | 1.1 |
| BDL189 | 11351.2 | P | | | 0.43 | | | | 0.4 |
| BDL189 | 11351.2 | Av | | | 1.1 | | | | 1.17 |
| BDL189 | 11353.3 | P | | 0.24 | 0.22 | 0.11 | | | 0.33 |
| BDL189 | 11353.3 | Av | | 1.15 | 1.11 | 1.22 | | | 1.1 |
| BDL189 | 11353.5 | P | | | | | | 0.65 | |
| BDL189 | 11353.5 | Av | | | | | | 1.1 | |
| BDL189 | 11355.4 | P | | | 0.22 | | | 0.28 | 0.32 |
| BDL189 | 11355.4 | Av | | | 1.11 | | | 1.36 | 1.13 |
| BDL196 | 10242.2 | P | | | | | 0.28 | 0.49 | |
| BDL196 | 10242.2 | Av | | | | | 1.13 | 1.15 | |
| BDL196 | 10243.4 | P | <0.01 | 0.12 | 0.12 | 0.13 | 0.17 | 0.57 | |
| BDL196 | 10243.4 | Av | 1.45 | 1.36 | 1.27 | 1.34 | 1.17 | 1.11 | |
| BDL196 | 10244.1 | P | 0.16 | 0.43 | | 0.28 | | 0.02 | |
| BDL196 | 10244.1 | Av | 1.65 | 1.27 | | 1.27 | | 1.45 | |
| BDL196 | 10242.2 | P | | | 0.47 | | | | |
| BDL196 | 10242.2 | Av | | | 1.1 | | | | |
| BDL196 | 10243.3 | P | | | 0.6 | | | 0.43 | 0.23 |
| BDL196 | 10243.3 | Av | | | 1.1 | | | 1.13 | 1.23 |
| BDL196 | 10243.4 | P | 0.51 | 0.15 | <0.01 | 0.11 | 0.16 | 0.13 | 0.03 |
| BDL196 | 10243.4 | Av | 1.12 | 1.23 | 1.65 | 1.27 | 1.18 | 1.42 | 1.69 |
| BDL197 | 11362.2 | P | | 0.33 | 0.03 | 0.18 | 0.14 | | 0.38 |
| BDL197 | 11362.2 | Av | | 1.18 | 1.35 | 1.32 | 1.24 | | 1.19 |
| BDL197 | 11363.1 | P | | 0.23 | | 0.12 | <0.01 | | |
| BDL197 | 11363.1 | Av | | 1.25 | | 1.38 | 1.53 | | |
| BDL197 | 11363.6 | P | 0.39 | 0.01 | 0.05 | <0.01 | 0.04 | 0.02 | 0.04 |
| BDL197 | 11363.6 | Av | 1.19 | 1.59 | 1.31 | 1.77 | 1.36 | 1.41 | 1.61 |
| BDL197 | 11364.1 | P | | 0.04 | <0.01 | <0.01 | <0.01 | 0.08 | <0.01 |
| BDL197 | 11364.1 | Av | | 1.67 | 1.63 | 1.85 | 1.48 | 1.44 | 1.91 |
| BDL197 | 11364.5 | P | | | 0.02 | 0.47 | | 0.11 | 0.04 |
| BDL197 | 11364.5 | Av | | | 1.37 | 1.16 | | 1.18 | 1.42 |
| BDL197 | 11363.1 | P | | | | | 0.1 | 0.53 | 0.17 |
| BDL197 | 11363.1 | Av | | | | | 1.12 | 1.1 | 1.23 |
| BDL197 | 11363.6 | P | 0.11 | 0.03 | 0.01 | <0.01 | <0.01 | 0.06 | 0.04 |
| BDL197 | 11363.6 | Av | 1.39 | 1.49 | 1.3 | 1.58 | 1.24 | 1.45 | 1.55 |
| BDL197 | 11364.1 | P | 0.3 | | | 0.53 | | 0.62 | 0.07 |
| BDL197 | 11364.1 | Av | 1.18 | | | 1.11 | | 1.16 | 1.75 |
| BDL197 | 11364.5 | P | | | | | 0.12 | | 0.49 |
| BDL197 | 11364.5 | Av | | | | | 1.12 | | 1.13 |
| BDL201 | 9961.2 | P | | | 0.47 | | | 0.57 | 0.47 |
| BDL201 | 9961.2 | Av | | | 1.13 | | | 1.1 | 1.15 |
| BDL201 | 9961.3 | P | | | | | | 0.13 | |
| BDL201 | 9961.3 | Av | | | | | | 1.39 | |
| BDL201 | 9961.4 | P | 0.19 | 0.41 | | | | | |
| BDL201 | 9961.4 | Av | 1.3 | 1.14 | | | | | |
| BDL201 | 9964.3 | P | 0.17 | 0.05 | | 0.27 | | | |
| BDL201 | 9964.3 | Av | 1.25 | 1.21 | | 1.15 | | | |
| BDL203 | 9831.14 | P | | | | | | 0.62 | 0.42 |
| BDL203 | 9831.14 | Av | | | | | | 1.13 | 1.27 |
| BDL203 | 9831.7 | P | | | | | 0.11 | | |
| BDL203 | 9831.7 | Av | | | | | 1.22 | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL203 | 9833.6 | P | | | | | | 0.71 | |
| BDL203 | 9833.6 | Av | | | | | | 1.14 | |
| BDL203 | 9835.2 | P | | | | | 0.33 | | |
| BDL203 | 9835.2 | Av | | | | | 1.14 | | |
| BDL220 | 10331.2 | P | | | | | | <0.01 | 0.06 |
| BDL220 | 10331.2 | Av | | | | | | 1.51 | 1.25 |
| BDL220 | 10331.5 | P | | 0.22 | <0.01 | 0.1 | 0.27 | 0.05 | 0.11 |
| BDL220 | 10331.5 | Av | | 1.22 | 1.81 | 1.28 | 1.11 | 1.97 | 1.6 |
| BDL220 | 10333.5 | P | | | | | | 0.47 | 0.41 |
| BDL220 | 10333.5 | Av | | | | | | 1.16 | 1.18 |
| BDL220 | 10334.2 | P | | | 0.34 | | | 0.35 | |
| BDL220 | 10334.2 | Av | | | 1.13 | | | 1.14 | |
| BDL221 | 10341.1 | P | | | | | | 0.19 | |
| BDL221 | 10341.1 | Av | | | | | | 1.3 | |
| BDL221 | 10341.3 | P | | | 0.01 | | | 0.01 | <0.01 |
| BDL221 | 10341.3 | Av | | | 1.5 | | | 1.92 | 2.18 |
| BDL221 | 10341.4 | P | | | 0.02 | | | <0.01 | 0.01 |
| BDL221 | 10341.4 | Av | | | 1.29 | | | 1.98 | 2.04 |
| BDL221 | 10343.3 | P | 0.03 | 0.01 | 0.07 | <0.01 | <0.01 | | |
| BDL221 | 10343.3 | Av | 1.55 | 1.6 | 1.21 | 1.6 | 1.41 | | |
| BDL221 | 10344.3 | P | | | | | | 0.41 | |
| BDL221 | 10344.3 | Av | | | | | | 1.11 | |
| BDL221 | 10341.1 | P | | | 0.15 | | | | 0.59 |
| BDL221 | 10341.1 | Av | | | 1.27 | | | | 1.16 |
| BDL221 | 10342.1 | P | <0.01 | <0.01 | 0.17 | <0.01 | <0.01 | 0.25 | 0.42 |
| BDL221 | 10342.1 | Av | 3.03 | 2.06 | 1.22 | 1.88 | 1.52 | 1.24 | 1.24 |
| BDL221 | 10343.1 | P | 0.01 | <0.01 | 0.01 | <0.01 | <0.01 | 0.15 | 0.33 |
| BDL221 | 10343.1 | Av | 1.8 | 1.61 | 1.62 | 1.6 | 1.41 | 1.46 | 1.51 |
| BDL221 | 10343.3 | P | 0.01 | 0.02 | 0.03 | <0.01 | <0.01 | | |
| BDL221 | 10343.3 | Av | 3.03 | 2.69 | 1.4 | 2.71 | 1.92 | | |
| BDL221 | 10343.4 | P | 0.03 | 0.08 | 0.07 | <0.01 | 0.01 | 0.14 | 0.08 |
| BDL221 | 10343.4 | Av | 2.15 | 2.07 | 1.51 | 2.07 | 1.49 | 1.44 | 1.53 |
| BDL221 | 10344.3 | P | 0.01 | 0.07 | 0.02 | 0.02 | 0.09 | 0.17 | 0.12 |
| BDL221 | 10344.3 | Av | 1.67 | 1.49 | 1.49 | 1.48 | 1.23 | 1.39 | 1.33 |
| BDL223 | 10791.1 | P | | | | | 0.33 | | |
| BDL223 | 10791.1 | Av | | | | | 1.13 | | |
| BDL223 | 10793.5 | P | 0.1 | 0.01 | | 0.01 | 0.02 | | |
| BDL223 | 10793.5 | Av | 1.21 | 1.32 | | 1.38 | 1.33 | | |
| BDL223 | 10793.8 | P | | | | | 0.21 | | |
| BDL223 | 10793.8 | Av | | | | | 1.18 | | |
| BDL223 | 10796.1 | P | | | | 0.58 | 0.41 | | |
| BDL223 | 10796.1 | Av | | | | 1.1 | 1.12 | | |
| BDL223 | 10796.2 | P | 0.41 | | | | 0.33 | 0.34 | 0.16 |
| BDL223 | 10796.2 | Av | 1.11 | | | | 1.13 | 1.14 | 1.4 |
| BDL223 | 10791.1 | P | | 0.03 | 0.02 | 0.05 | 0.06 | | 0.3 |
| BDL223 | 10791.1 | Av | | 1.38 | 1.34 | 1.43 | 1.3 | | 1.24 |
| BDL223 | 10793.3 | P | | 0.34 | <0.01 | 0.08 | 0.01 | 0.24 | 0.16 |
| BDL223 | 10793.3 | Av | | 1.45 | 1.64 | 1.62 | 1.48 | 1.15 | 1.39 |
| BDL223 | 10793.5 | P | 0.47 | 0.23 | 0.44 | 0.15 | 0.04 | | |
| BDL223 | 10793.5 | Av | 1.13 | 1.29 | 1.11 | 1.34 | 1.31 | | |
| BDL223 | 10793.8 | P | <0.01 | <0.01 | 0.07 | <0.01 | <0.01 | | 0.21 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL223 | 10793.8 | Av | 1.75 | 1.71 | 1.26 | 1.72 | 1.47 | | 1.26 |
| BDL223 | 10796.1 | P | | 0.01 | 0.03 | 0.01 | 0.07 | | 0.3 |
| BDL223 | 10796.1 | Av | | 1.47 | 1.31 | 1.61 | 1.29 | | 1.2 |
| BDL224 | 10451.5 | P | | | 0.17 | | | 0.21 | 0.2 |
| BDL224 | 10451.5 | Av | | | 1.19 | | | 1.28 | 1.25 |
| BDL224 | 10451.7 | P | 0.11 | 0.16 | <0.01 | 0.01 | 0.35 | 0.11 | 0.19 |
| BDL224 | 10451.7 | Av | 1.48 | 1.67 | 1.85 | 1.69 | 1.13 | 1.48 | 1.29 |
| BDL224 | 10451.8 | P | | | | 0.5 | | | |
| BDL224 | 10451.8 | Av | | | | 1.13 | | | |
| BDL226 | 10861.2 | P | | 0.41 | 0.41 | 0.15 | 0.08 | | |
| BDL226 | 10861.2 | Av | | 1.18 | 1.1 | 1.26 | 1.26 | | |
| BDL226 | 10861.4 | P | | 0.18 | | 0.03 | 0.04 | | 0.23 |
| BDL226 | 10861.4 | Av | | 1.27 | | 1.37 | 1.28 | | 1.2 |
| BDL226 | 10862.2 | P | | 0.56 | | 0.23 | 0.19 | | |
| BDL226 | 10862.2 | Av | | 1.11 | | 1.2 | 1.18 | | |
| BDL227 | 11491.1 | P | <0.01 | 0.12 | | 0.25 | | | |
| BDL227 | 11491.1 | Av | 1.59 | 1.25 | | 1.2 | | | |
| BDL227 | 11491.3 | P | 0.01 | 0.05 | 0.06 | <0.01 | <0.01 | 0.42 | 0.35 |
| BDL227 | 11491.3 | Av | 1.87 | 1.71 | 1.29 | 1.66 | 1.52 | 1.12 | 1.23 |
| BDL227 | 11491.5 | P | 0.01 | 0.03 | 0.04 | <0.01 | <0.01 | 0.36 | 0.15 |
| BDL227 | 11491.5 | Av | 2.24 | 2 | 1.34 | 1.94 | 1.58 | 1.24 | 1.34 |
| BDL227 | 11492.5 | P | <0.01 | 0.03 | <0.01 | <0.01 | 0.02 | 0.13 | 0.12 |
| BDL227 | 11492.5 | Av | 2.09 | 1.71 | 1.64 | 1.72 | 1.39 | 2.07 | 1.86 |
| BDL227 | 11493.5 | P | <0.01 | 0.01 | <0.01 | <0.01 | <0.01 | 0.16 | 0.08 |
| BDL227 | 11493.5 | Av | 2.13 | 2.02 | 1.78 | 2.05 | 1.64 | 1.55 | 1.73 |
| BDL230 | 10671.3 | P | | | <0.01 | | | <0.01 | <0.01 |
| BDL230 | 10671.3 | Av | | | 1.95 | | | 1.84 | 2.02 |
| BDL231 | 11111.1 | P | 0.58 | 0.12 | <0.01 | 0.1 | 0.51 | 0.14 | 0.55 |
| BDL231 | 11111.1 | Av | 1.1 | 1.24 | 1.5 | 1.27 | 1.1 | 1.24 | 1.1 |
| BDL231 | 11111.2 | P | 0.24 | 0.09 | <0.01 | 0.09 | 0.16 | | |
| BDL231 | 11111.2 | Av | 1.18 | 1.24 | 1.31 | 1.27 | 1.2 | | |
| BDL231 | 11111.3 | P | 0.33 | 0.08 | <0.01 | 0.03 | | 0.31 | 0.35 |
| BDL231 | 11111.3 | Av | 1.13 | 1.36 | 1.38 | 1.39 | | 1.15 | 1.2 |
| BDL231 | 11112.2 | P | <0.01 | 0.01 | 0.01 | <0.01 | 0.05 | | 0.52 |
| BDL231 | 11112.2 | Av | 1.89 | 1.61 | 1.3 | 1.55 | 1.27 | | 1.21 |
| BDL231 | 11116.5 | P | <0.01 | <0.01 | <0.01 | <0.01 | 0.23 | 0.21 | 0.05 |
| BDL231 | 11116.5 | Av | 1.97 | 1.79 | 1.74 | 1.78 | 1.18 | 1.28 | 1.45 |
| BDL231 | 11111.1 | P | 0.09 | 0.31 | <0.01 | 0.38 | 0.51 | 0.1 | 0.16 |
| BDL231 | 11111.1 | Av | 1.25 | 1.18 | 1.41 | 1.16 | 1.1 | 1.23 | 1.2 |
| BDL231 | 11111.2 | P | 0.02 | 0.2 | 0.01 | 0.32 | | 0.07 | 0.28 |
| BDL231 | 11111.2 | Av | 1.31 | 1.19 | 1.4 | 1.17 | | 1.46 | 1.24 |
| BDL231 | 11112.2 | P | 0.1 | | | | | | |
| BDL231 | 11112.2 | Av | 1.42 | | | | | | |
| BDL232 | 10904.1 | P | 0.6 | 0.26 | 0.33 | 0.16 | 0.11 | 0.71 | 0.5 |
| BDL232 | 10904.1 | Av | 1.25 | 1.36 | 1.29 | 1.44 | 1.29 | 1.14 | 1.37 |
| BDL232 | 10905.1 | P | 0.27 | 0.24 | | 0.3 | | | |
| BDL232 | 10905.1 | Av | 1.18 | 1.26 | | 1.23 | | | |
| BDL232 | 10906.3 | P | 0.48 | 0.24 | 0.02 | 0.07 | 0.06 | 0.14 | 0.13 |
| BDL232 | 10906.3 | Av | 1.37 | 1.63 | 1.61 | 1.75 | 1.44 | 1.48 | 1.77 |
| BDL232 | 10902.2 | P | 0.02 | 0.22 | | 0.43 | | | |
| BDL232 | 10902.2 | Av | 1.65 | 1.24 | | 1.12 | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL232 | 10905.1 | P | 0.18 | | | | | | |
| BDL232 | 10905.1 | Av | 1.28 | | | | | | |
| BDL232 | 10906.4 | P | | | | | 0.06 | | |
| BDL232 | 10906.4 | Av | | | | | 1.15 | | |
| BDL233 | 10822.4 | P | | | | | 0.28 | | |
| BDL233 | 10822.4 | Av | | | | | 1.13 | | |
| BDL233 | 10824.2 | P | | | | | 0.05 | | |
| BDL233 | 10824.2 | Av | | | | | 1.25 | | |
| BDL233 | 10825.3 | P | | | | | 0.1 | | |
| BDL233 | 10825.3 | Av | | | | | 1.21 | | |
| BDL233 | 10825.4 | P | <0.01 | 0.01 | | <0.01 | 0.03 | | |
| BDL233 | 10825.4 | Av | 1.78 | 1.49 | | 1.43 | 1.29 | | |
| BDL233 | 10822.4 | P | | | 0.04 | | 0.19 | 0.26 | 0.37 |
| BDL233 | 10822.4 | Av | | | 1.37 | | 1.21 | 1.18 | 1.24 |
| BDL233 | 10824.1 | P | | | 0.43 | | 0.48 | | |
| BDL233 | 10824.1 | Av | | | 1.11 | | 1.1 | | |
| BDL233 | 10824.2 | P | | 0.38 | 0.3 | 0.19 | <0.01 | | |
| BDL233 | 10824.2 | Av | | 1.16 | 1.16 | 1.29 | 1.5 | | |
| BDL233 | 10825.4 | P | 0.22 | 0.02 | 0.18 | 0.04 | 0.01 | | 0.42 |
| BDL233 | 10825.4 | Av | 1.23 | 1.44 | 1.23 | 1.46 | 1.47 | | 1.14 |
| BDL235 | 11412.2 | P | | 0.34 | | 0.33 | 0.4 | | |
| BDL235 | 11412.2 | Av | | 1.14 | | 1.17 | 1.11 | | |
| BDL235 | 11413.2 | P | 0.07 | 0.06 | | 0.03 | | | |
| BDL235 | 11413.2 | Av | 1.43 | 1.39 | | 1.38 | | | |
| BDL235 | 11413.3 | P | | | | | | 0.51 | 0.3 |
| BDL235 | 11413.3 | Av | | | | | | 1.15 | 1.18 |
| BDL235 | 11411.2 | P | | | | | 0.08 | | 0.62 |
| BDL235 | 11411.2 | Av | | | | | 1.16 | | 1.15 |
| BDL235 | 11413.2 | P | <0.01 | 0.08 | | 0.12 | 0.15 | | |
| BDL235 | 11413.2 | Av | 1.61 | 1.33 | | 1.22 | 1.15 | | |
| BDL235 | 11413.3 | P | | | | | 0.09 | | |
| BDL235 | 11413.3 | Av | | | | | 1.16 | | |
| BDL237 | 10892.1 | P | | | | | | 0.05 | 0.14 |
| BDL237 | 10892.1 | Av | | | | | | 1.43 | 1.33 |
| BDL237 | 10892.2 | P | 0.18 | 0.19 | | 0.4 | 0.18 | | |
| BDL237 | 10892.2 | Av | 1.23 | 1.16 | | 1.14 | 1.18 | | |
| BDL237 | 10893.1 | P | 0.23 | 0.29 | 0.51 | 0.28 | 0.09 | | |
| BDL237 | 10893.1 | Av | 1.2 | 1.17 | 1.11 | 1.19 | 1.25 | | |
| BDL237 | 10895.3 | P | 0.01 | 0.01 | <0.01 | <0.01 | <0.01 | 0.09 | 0.05 |
| BDL237 | 10895.3 | Av | 2.68 | 2.3 | 1.85 | 2.32 | 1.77 | 1.59 | 1.71 |
| BDL237 | 10896.1 | P | | 0.71 | | 0.57 | 0.27 | | |
| BDL237 | 10896.1 | Av | | 1.11 | | 1.13 | 1.21 | | |
| BDL238 | 10951.4 | P | 0.51 | | | | | | |
| BDL238 | 10951.4 | Av | 1.13 | | | | | | |
| BDL238 | 10952.3 | P | 0.12 | 0.12 | | 0.25 | 0.09 | | |
| BDL238 | 10952.3 | Av | 1.3 | 1.29 | | 1.25 | 1.32 | | |
| BDL238 | 10953.1 | P | | | 0.37 | | 0.37 | | |
| BDL238 | 10953.1 | Av | | | 1.14 | | 1.15 | | |
| BDL238 | 10954.2 | P | | 0.52 | | 0.61 | 0.5 | | |
| BDL238 | 10954.2 | Av | | 1.13 | | 1.11 | 1.12 | | |
| BDL238 | 10954.3 | P | | | | | | | 0.67 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL238 | 10954.3 | Av | | | | | | | 1.12 |
| BDL240 | 10802.2 | P | | | | | 0.47 | | |
| BDL240 | 10802.2 | Av | | | | | 1.1 | | |
| BDL240 | 10806.6 | P | 0.33 | 0.43 | | 0.27 | 0.19 | | |
| BDL240 | 10806.6 | Av | 1.28 | 1.19 | | 1.2 | 1.18 | | |
| BDL240 | 10802.2 | P | 0.38 | | | | 0.1 | | |
| BDL240 | 10802.2 | Av | 1.17 | | | | 1.24 | | |
| BDL240 | 10803.5 | P | | | 0.48 | | 0.17 | | |
| BDL240 | 10803.5 | Av | | | 1.12 | | 1.18 | | |
| BDL240 | 10806.6 | P | 0.01 | 0.03 | 0.05 | <0.01 | 0.01 | 0.15 | 0.26 |
| BDL240 | 10806.6 | Av | 2.85 | 2.11 | 1.38 | 1.97 | 1.44 | 1.32 | 1.34 |
| BDL241 | 10875.1 | P | 0.1 | | | | 0.46 | | |
| BDL241 | 10875.1 | Av | 1.25 | | | | 1.13 | | |
| BDL241 | 10873.1 | P | | | | | 0.22 | | 0.61 |
| BDL241 | 10873.1 | Av | | | | | 1.19 | | 1.11 |
| BDL241 | 10874.2 | P | | | | | 0.45 | | |
| BDL241 | 10874.2 | Av | | | | | 1.11 | | |
| BDL241 | 10874.3 | P | 0.54 | 0.05 | 0.01 | 0.03 | 0.05 | 0.08 | 0.01 |
| BDL241 | 10874.3 | Av | 1.1 | 1.43 | 1.47 | 1.53 | 1.32 | 1.21 | 1.55 |
| BDL241 | 10875.1 | P | 0.09 | 0.53 | | | | | |
| BDL241 | 10875.1 | Av | 1.36 | 1.13 | | | | | |
| BDL242 | 10731.3 | P | <0.01 | 0.2 | | 0.19 | 0.12 | | 0.2 |
| BDL242 | 10731.3 | Av | 1.38 | 1.21 | | 1.19 | 1.21 | | 1.22 |
| BDL242 | 10731.5 | P | 0.1 | 0.31 | | 0.32 | | | |
| BDL242 | 10731.5 | Av | 1.34 | 1.16 | | 1.15 | | | |
| BDL242 | 10737.1 | P | | | | | 0.32 | | |
| BDL242 | 10737.1 | Av | | | | | 1.14 | | |
| BDL242 | 10731.3 | P | <0.01 | 0.01 | <0.01 | <0.01 | <0.01 | 0.05 | 0.04 |
| BDL242 | 10731.3 | Av | 1.75 | 1.62 | 2.15 | 1.62 | 1.39 | 2.12 | 2.23 |
| BDL242 | 10731.5 | P | 0.06 | | | | | | |
| BDL242 | 10731.5 | Av | 1.29 | | | | | | |
| BDL242 | 10731.7 | P | <0.01 | <0.01 | 0.01 | 0.01 | 0.03 | 0.01 | 0.04 |
| BDL242 | 10731.7 | Av | 1.85 | 1.49 | 1.45 | 1.47 | 1.28 | 1.64 | 1.86 |
| BDL242 | 10737.2 | P | 0.47 | 0.23 | <0.01 | 0.07 | 0.05 | <0.01 | 0.01 |
| BDL242 | 10737.2 | Av | 1.26 | 1.38 | 1.86 | 1.43 | 1.32 | 1.91 | 2.05 |
| BDL245 | 10811.2 | P | 0.54 | 0.17 | | 0.08 | 0.21 | | 0.3 |
| BDL245 | 10811.2 | Av | 1.1 | 1.22 | | 1.28 | 1.16 | | 1.14 |
| BDL245 | 10813.3 | P | | | | | 0.09 | | |
| BDL245 | 10813.3 | Av | | | | | 1.22 | | |
| BDL245 | 10816.3 | P | | | | | 0.14 | | |
| BDL245 | 10816.3 | Av | | | | | 1.18 | | |
| BDL247 | 10912.1 | P | | 0.08 | | 0.02 | 0.01 | | |
| BDL247 | 10912.1 | Av | | 1.31 | | 1.4 | 1.37 | | |
| BDL247 | 10912.2 | P | | | | | 0.08 | | |
| BDL247 | 10912.2 | Av | | | | | 1.22 | | |
| BDL247 | 10915.1 | P | | 0.45 | 0.22 | 0.14 | 0.02 | | 0.53 |
| BDL247 | 10915.1 | Av | | 1.19 | 1.2 | 1.28 | 1.4 | | 1.12 |
| BDL247 | 10911.1 | P | 0.15 | 0.1 | 0.01 | 0.01 | 0.02 | 0.3 | 0.23 |
| BDL247 | 10911.1 | Av | 1.96 | 1.8 | 1.6 | 1.79 | 1.45 | 1.38 | 1.5 |
| BDL247 | 10912.1 | P | 0.32 | 0.4 | 0.24 | 0.25 | 0.13 | 0.32 | 0.14 |
| BDL247 | 10912.1 | Av | 1.15 | 1.22 | 1.2 | 1.24 | 1.21 | 1.27 | 1.56 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL247 | 10912.2 | P | 0.04 | 0.01 | 0.03 | <0.01 | <0.01 | 0.09 | 0.3 |
| BDL247 | 10912.2 | Av | 1.73 | 1.74 | 1.36 | 1.81 | 1.62 | 1.41 | 1.35 |
| BDL247 | 10912.6 | P | | 0.61 | | 0.57 | 0.39 | 0.21 | 0.48 |
| BDL247 | 10912.6 | Av | | 1.11 | | 1.11 | 1.13 | 1.37 | 1.3 |
| BDL247 | 10915.1 | P | 0.23 | 0.14 | <0.01 | 0.03 | 0.08 | 0.02 | 0.06 |
| BDL247 | 10915.1 | Av | 1.47 | 1.52 | 1.81 | 1.54 | 1.3 | 1.74 | 1.58 |
| BDL248 | 11051.2 | P | <0.01 | 0.01 | 0.03 | 0.02 | <0.01 | 0.21 | |
| BDL248 | 11051.2 | Av | 1.61 | 1.45 | 1.36 | 1.43 | 1.42 | 1.22 | |
| BDL248 | 11052.2 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | 0.04 | 0.01 |
| BDL248 | 11052.2 | Av | 1.89 | 1.68 | 1.89 | 1.7 | 1.44 | 1.74 | 1.81 |
| BDL248 | 11053.3 | P | <0.01 | <0.01 | 0.07 | <0.01 | 0.03 | 0.46 | 0.65 |
| BDL248 | 11053.3 | Av | 2.04 | 1.62 | 1.29 | 1.57 | 1.34 | 1.13 | 1.14 |
| BDL248 | 11054.3 | P | 0.15 | 0.15 | | 0.24 | 0.04 | | |
| BDL248 | 11054.3 | Av | 1.18 | 1.18 | | 1.19 | 1.29 | | |
| BDL248 | 11051.2 | P | | | | | 0.18 | | |
| BDL248 | 11051.2 | Av | | | | | 1.1 | | |
| BDL248 | 11054.2 | P | | | | | 0.18 | | |
| BDL248 | 11054.2 | Av | | | | | 1.1 | | |
| BDL249 | 11401.2 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL249 | 11401.2 | Av | 3.19 | 2.43 | 2.68 | 2.35 | 1.67 | 2.55 | 3.02 |
| BDL249 | 11401.5 | P | <0.01 | 0.01 | 0.02 | <0.01 | 0.02 | 0.39 | 0.44 |
| BDL249 | 11401.5 | Av | 2.63 | 1.94 | 1.4 | 1.83 | 1.3 | 1.19 | 1.23 |
| BDL249 | 11402.4 | P | <0.01 | <0.01 | 0.03 | <0.01 | <0.01 | 0.03 | 0.1 |
| BDL249 | 11402.4 | Av | 2.42 | 1.99 | 1.38 | 2.02 | 1.65 | 1.37 | 1.43 |
| BDL249 | 11403.2 | P | | 0.46 | 0.34 | 0.27 | 0.2 | 0.56 | |
| BDL249 | 11403.2 | Av | | 1.22 | 1.17 | 1.25 | 1.21 | 1.11 | |
| BDL249 | 11404.3 | P | 0.01 | 0.07 | | 0.23 | 0.22 | | |
| BDL249 | 11404.3 | Av | 1.43 | 1.22 | | 1.19 | 1.19 | | |
| BDL249 | 11401.5 | P | | 0.31 | | 0.45 | | | |
| BDL249 | 11401.5 | Av | | 1.1 | | 1.11 | | | |
| BDL249 | 11404.3 | P | 0.03 | 0.22 | | 0.2 | 0.04 | | |
| BDL249 | 11404.3 | Av | 1.33 | 1.18 | | 1.18 | 1.23 | | |
| BDL250 | 10842.3 | P | <0.01 | 0.01 | 0.21 | <0.01 | 0.02 | | 0.34 |
| BDL250 | 10842.3 | Av | 1.69 | 1.54 | 1.15 | 1.56 | 1.29 | | 1.24 |
| BDL250 | 10846.2 | P | 0.01 | <0.01 | 0.29 | <0.01 | 0.05 | 0.4 | 0.21 |
| BDL250 | 10846.2 | Av | 1.43 | 1.41 | 1.12 | 1.45 | 1.25 | 1.19 | 1.33 |
| BDL250 | 10846.3 | P | 0.02 | 0.36 | | | 0.05 | | |
| BDL250 | 10846.3 | Av | 1.37 | 1.11 | | | 1.26 | | |
| BDL250 | 10841.3 | P | 0.01 | 0.02 | 0.17 | <0.01 | <0.01 | | |
| BDL250 | 10841.3 | Av | 1.99 | 1.66 | 1.22 | 1.61 | 1.62 | | |
| BDL250 | 10842.3 | P | 0.23 | 0.52 | 0.12 | 0.44 | | 0.41 | 0.59 |
| BDL250 | 10842.3 | Av | 1.57 | 1.28 | 1.45 | 1.22 | | 1.6 | 1.27 |
| BDL250 | 10843.2 | P | 0.03 | 0.07 | 0.01 | 0.01 | 0.01 | 0.02 | 0.1 |
| BDL250 | 10843.2 | Av | 1.85 | 1.67 | 1.55 | 1.62 | 1.37 | 1.53 | 1.6 |
| BDL250 | 10846.2 | P | 0.04 | <0.01 | <0.01 | <0.01 | <0.01 | 0.45 | 0.67 |
| BDL250 | 10846.2 | Av | 1.46 | 1.68 | 1.58 | 1.7 | 1.43 | 1.22 | 1.15 |
| BDL250 | 10846.3 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | 0.05 | 0.03 |
| BDL250 | 10846.3 | Av | 2.79 | 2.32 | 1.76 | 2.28 | 1.84 | 1.8 | 1.87 |
| BDL252 | 10881.1 | P | 0.01 | <0.01 | <0.01 | <0.01 | <0.01 | 0.09 | 0.19 |
| BDL252 | 10881.1 | Av | 2.1 | 1.87 | 1.68 | 1.9 | 1.48 | 1.43 | 1.68 |
| BDL252 | 10882.1 | P | 0.01 | 0.01 | <0.01 | <0.01 | <0.01 | 0.18 | 0.18 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL252 | 10882.1 | Av | 3.11 | 2.51 | 1.97 | 2.43 | 1.82 | 1.4 | 1.51 |
| BDL252 | 10882.2 | P | 0.05 | <0.01 | 0.04 | <0.01 | 0.01 | | 0.62 |
| BDL252 | 10882.2 | Av | 1.87 | 1.74 | 1.35 | 1.72 | 1.44 | | 1.11 |
| BDL252 | 10882.4 | P | 0.01 | 0.01 | 0.17 | 0.01 | 0.38 | | |
| BDL252 | 10882.4 | Av | 2.06 | 1.62 | 1.24 | 1.52 | 1.13 | | |
| BDL252 | 10884.1 | P | | | 0.5 | | | 0.24 | 0.24 |
| BDL252 | 10884.1 | Av | | | 1.1 | | | 1.22 | 1.3 |
| BDL58 | 10281.5 | P | | | 0.07 | 0.46 | 0.15 | 0.55 | 0.02 |
| BDL58 | 10281.5 | Av | | | 1.32 | 1.15 | 1.18 | 1.14 | 1.37 |
| BDL58 | 10282.3 | P | <0.01 | 0.01 | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL58 | 10282.3 | Av | 1.94 | 2.18 | 1.77 | 2.29 | 1.81 | 1.79 | 1.83 |
| BDL58 | 10285.3 | P | | | | | 0.06 | | |
| BDL58 | 10285.3 | Av | | | | | 1.21 | | |
| BDL62 | 10682.1 | P | | 0.31 | 0.43 | 0.12 | | | 0.4 |
| BDL62 | 10682.1 | Av | | 1.35 | 1.19 | 1.46 | | | 1.33 |
| BDL62 | 10684.2 | P | | 0.43 | | 0.33 | 0.08 | | 0.58 |
| BDL62 | 10684.2 | Av | | 1.17 | | 1.23 | 1.26 | | 1.11 |
| BDL62 | 10684.5 | P | | | 0.41 | 0.64 | 0.31 | 0.67 | 0.64 |
| BDL62 | 10684.5 | Av | | | 1.14 | 1.11 | 1.15 | 1.13 | 1.13 |
| BDL64 | 10651.5 | P | | | 0.02 | 0.39 | 0.07 | 0.17 | 0.26 |
| BDL64 | 10651.5 | Av | | | 1.77 | 1.14 | 1.19 | 1.54 | 1.52 |
| BDL64 | 10653.1 | P | | 0.14 | <0.01 | 0.13 | | <0.01 | 0.03 |
| BDL64 | 10653.1 | Av | | 1.21 | 1.62 | 1.24 | | 1.42 | 1.51 |
| BDL64 | 10653.3 | P | | | | | 0.01 | | |
| BDL64 | 10653.3 | Av | | | | | 1.25 | | |
| BDL64 | 10654.3 | P | 0.15 | 0.23 | 0.06 | 0.02 | <0.01 | 0.37 | 0.27 |
| BDL64 | 10654.3 | Av | 1.53 | 1.6 | 1.5 | 1.71 | 1.55 | 1.45 | 1.44 |
| BDL64 | 10651.1 | P | | | 0.5 | | | 0.31 | 0.16 |
| BDL64 | 10651.1 | Av | | | 1.13 | | | 1.45 | 1.91 |
| BDL64 | 10651.2 | P | | | | | | | 0.62 |
| BDL64 | 10651.2 | Av | | | | | | | 1.13 |
| BDL64 | 10651.5 | P | | | | | | | 0.48 |
| BDL64 | 10651.5 | Av | | | | | | | 1.15 |
| BDL64 | 10653.1 | P | 0.01 | 0.02 | 0.01 | <0.01 | 0.02 | 0.05 | 0.03 |
| BDL64 | 10653.1 | Av | 2.18 | 2.28 | 1.69 | 2.43 | 1.25 | 2.27 | 3.13 |
| BDL64 | 10654.3 | P | <0.01 | <0.01 | 0.02 | <0.01 | 0.03 | 0.01 | <0.01 |
| BDL64 | 10654.3 | Av | 1.78 | 1.9 | 1.46 | 1.97 | 1.2 | 1.7 | 2.53 |
| BDL64 | 10651.1 | P | 0.11 | | | | | | |
| BDL64 | 10651.1 | Av | 1.27 | | | | | | |
| BDL64 | 10651.3 | P | 0.14 | 0.32 | | 0.46 | | | |
| BDL64 | 10651.3 | Av | 1.43 | 1.22 | | 1.14 | | | |
| BDL79 | 11042.3 | P | | | | | 0.5 | | |
| BDL79 | 11042.3 | Av | | | | | 1.1 | | |
| BDL79 | 11042.3 | P | | 0.44 | | 0.28 | 0.04 | | |
| BDL79 | 11042.3 | Av | | 1.18 | | 1.26 | 1.36 | | |
| BDL79 | 11042.7 | P | | | 0.4 | | | | 0.55 |
| BDL79 | 11042.7 | Av | | | 1.12 | | | | 1.11 |
| BDL79 | 11043.1 | P | | 0.27 | 0.03 | 0.25 | 0.03 | 0.29 | 0.22 |
| BDL79 | 11043.1 | Av | | 1.28 | 1.35 | 1.3 | 1.35 | 1.18 | 1.22 |
| BDL85 | 10411.1 | P | 0.74 | 0.55 | | 0.42 | | | |
| BDL85 | 10411.1 | Av | 1.1 | 1.14 | | 1.16 | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL85 | 10411.3 | P | 0.14 | 0.01 | | 0.03 | 0.17 | | |
| BDL85 | 10411.3 | Av | 1.24 | 1.28 | | 1.32 | 1.13 | | |
| BDL85 | 10412.2 | P | | | 0.44 | | | 0.06 | 0.15 |
| BDL85 | 10412.2 | Av | | | 1.1 | | | 1.22 | 1.24 |
| BDL85 | 10414.1 | P | | 0.01 | 0.05 | 0.02 | 0.08 | 0.38 | 0.47 |
| BDL85 | 10414.1 | Av | | 1.3 | 1.29 | 1.39 | 1.18 | 1.17 | 1.11 |
| BDL85 | 10414.2 | P | | 0.27 | <0.01 | 0.07 | 0.07 | <0.01 | 0.08 |
| BDL85 | 10414.2 | Av | | 1.15 | 1.42 | 1.28 | 1.17 | 1.55 | 1.5 |
| BDL88 | 10291.2 | P | 0.31 | 0.15 | 0.02 | 0.08 | 0.08 | 0.06 | 0.11 |
| BDL88 | 10291.2 | Av | 1.26 | 1.33 | 1.45 | 1.36 | 1.24 | 1.35 | 1.36 |
| BDL88 | 10291.4 | P | 0.01 | 0.02 | <0.01 | <0.01 | <0.01 | 0.23 | 0.25 |
| BDL88 | 10291.4 | Av | 1.72 | 1.57 | 1.54 | 1.62 | 1.42 | 1.44 | 1.35 |
| BDL88 | 10291.5 | P | 0.59 | 0.44 | 0.48 | 0.38 | | | |
| BDL88 | 10291.5 | Av | 1.13 | 1.17 | 1.13 | 1.17 | | | |
| BDL88 | 10293.3 | P | 0.14 | 0.28 | <0.01 | 0.11 | 0.26 | 0.16 | 0.08 |
| BDL88 | 10293.3 | Av | 1.34 | 1.35 | 2.15 | 1.36 | 1.19 | 1.58 | 1.97 |
| BDL88 | 10291.2 | P | 0.16 | 0.05 | <0.01 | 0.01 | 0.21 | 0.33 | 0.47 |
| BDL88 | 10291.2 | Av | 1.32 | 1.45 | 1.56 | 1.48 | 1.18 | 1.17 | 1.16 |
| BDL88 | 10291.4 | P | | | <0.01 | | | | |
| BDL88 | 10291.4 | Av | | | 1.49 | | | | |
| BDL88 | 10291.5 | P | | | <0.01 | | | 0.15 | 0.38 |
| BDL88 | 10291.5 | Av | | | 1.84 | | | 1.25 | 1.22 |
| BDL88 | 10293.3 | P | | | 0.02 | | | | 0.47 |
| BDL88 | 10293.3 | Av | | | 1.23 | | | | 1.15 |
| BDL88 | 10294.2 | P | | | <0.01 | | | 0.3 | 0.55 |
| BDL88 | 10294.2 | Av | | | 1.76 | | | 1.23 | 1.16 |
| BDL90 | 10921.3 | P | | | | | 0.22 | | |
| BDL90 | 10921.3 | Av | | | | | 1.18 | | |
| BDL90 | 10921.6 | P | | | | | 0.09 | | |
| BDL90 | 10921.6 | Av | | | | | 1.28 | | |
| BDL90 | 10924.2 | P | 0.06 | 0.04 | | <0.01 | <0.01 | | |
| BDL90 | 10924.2 | Av | 2 | 1.75 | | 1.73 | 1.5 | | |
| BDL90 | 10924.4 | P | | | | | 0.33 | | |
| BDL90 | 10924.4 | Av | | | | | 1.12 | | |
| BDL90 | 10925.4 | P | 0.02 | 0.03 | | <0.01 | <0.01 | | |
| BDL90 | 10925.4 | Av | 2.27 | 1.81 | | 1.76 | 1.46 | | |
| BDL90 | 10923.4 | P | | | | | 0.27 | | |
| BDL90 | 10923.4 | Av | | | | | 1.17 | | |
| BDL90 | 10924.2 | P | 0.06 | 0.28 | 0.22 | 0.33 | 0.06 | | |
| BDL90 | 10924.2 | Av | 1.43 | 1.26 | 1.19 | 1.22 | 1.3 | | |
| BDL90 | 10925.4 | P | 0.02 | 0.04 | | 0.03 | 0.01 | | |
| BDL90 | 10925.4 | Av | 1.7 | 1.58 | | 1.54 | 1.43 | | |
| BDL90 | 10921.6 | P | | 0.75 | 0.04 | 0.42 | 0.02 | | 0.13 |
| BDL90 | 10921.6 | Av | | 1.11 | 1.32 | 1.24 | 1.41 | | 1.28 |
| BDL90 | 10923.4 | P | | | | 0.51 | 0.12 | | 0.58 |
| BDL90 | 10923.4 | Av | | | | 1.15 | 1.25 | | 1.15 |
| BDL90 | 10924.2 | P | 0.16 | 0.01 | 0.28 | 0.01 | <0.01 | | |
| BDL90 | 10924.2 | Av | 1.4 | 1.65 | 1.18 | 1.7 | 1.54 | | |
| BDL90 | 10925.4 | P | <0.01 | <0.01 | <0.01 | <0.01 | <0.01 | 0.05 | 0.03 |
| BDL90 | 10925.4 | Av | 2.34 | 2.48 | 1.88 | 2.4 | 1.61 | 1.55 | 1.78 |
| BDL94 | 11721.4 | P | | | 0.45 | | | 0.09 | 0.26 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par.</i> | <i>Roots Coverage TP2</i> | <i>Roots Coverage TP3</i> | <i>RGR Of Leaf Area</i> | <i>RGR Of Root Coverage</i> | <i>RGR Of Roots Length</i> | <i>Fresh Weight</i> | <i>Dry Weight</i> |
|-------------|------------|-------------|---------------------------|---------------------------|-------------------------|-----------------------------|----------------------------|---------------------|-------------------|
| BDL94 | 11721.4 | Av | | | 1.11 | | | 1.29 | 1.16 |
| BDL94 | 11725.3 | P | | | | | | 0.17 | |
| BDL94 | 11725.3 | Av | | | | | | 1.2 | |
| BDL94 | 11725.3 | P | | | | | | 0.31 | |
| BDL94 | 11725.3 | Av | | | | | | 1.29 | |

Table 22. "P" = P-value; "Av" = ratio between the averages of event and control. Note that when the average ratio is higher than "1" the effect of exogenous expression of the gene is an increase of the desired trait; "Par" = Parameter according to the measured parameters; "Ev" = event. TP1 = Time point 1; TP2 = Time point 2; TP3 = Time point 3; RGR = relative growth rate.

5

Greenhouse assays - Table 23 specifies the parameters that were measured in the greenhouse assays and which are presented in Tables 24, 25, 26 and 27. In cases where a certain event appears more than once, the event was tested in several independent experiments. The parameters were measured as follows:

10 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.

15 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.

20 **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.

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

An image analysis system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.39

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

Leaf 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 IX, X, XI and XII.

Formula IX:

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

Formula X:

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

Formula XI

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

Formula XII

Relative growth rate of plot coverage = Regression coefficient of plot 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.

5 ***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
10 °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)
15 and its MultiQuant software package.

Oil yield - The oil yield was calculated using Formula VII (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
20 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
25 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).

Table 23
Parameters measured in greenhouse assays

| <i>Parameter</i> | <i>Number</i> |
|---------------------------|---------------|
| Rosette Diameter TP2 | 1 |
| Rosette Diameter TP3 | 2 |
| Rosette Diameter TP4 | 3 |
| Rosette Area TP2 | 4 |
| Rosette Area TP3 | 5 |
| Rosette Area TP4 | 6 |
| Plot Coverage TP2 | 7 |
| Plot Coverage TP3 | 8 |
| Plot Coverage TP4 | 9 |
| Leaf Number TP2 | 10 |
| Leaf Number TP3 | 11 |
| Leaf Number TP4 | 12 |
| Leaf Blade Area TP2 | 13 |
| Leaf Blade Area TP3 | 14 |
| Leaf Blade Area TP4 | 15 |
| Leaf Petiole Length TP2 | 16 |
| Leaf Petiole Length TP3 | 17 |
| Leaf Petiole Length TP4 | 18 |
| Blade Relative Area TP2 | 19 |
| Blade Relative Area TP3 | 20 |
| Blade Relative Area TP4 | 21 |
| Petiole Relative Area TP2 | 22 |
| Petiole Relative Area TP3 | 23 |
| Petiole Relative Area TP4 | 24 |
| RGR Of Leaf Blade Area | 25 |
| RGR Of Leaf Number | 26 |
| RGR Of Rosette Area | 27 |
| RGR Of Rosette Diameter | 28 |
| RGR Of Plot Coverage | 29 |
| Dry Weight | 30 |
| Fresh Weight | 31 |
| Inflorescence Emergence | 32 |
| Flowering | 33 |
| Seed Yield | 34 |
| Harvest Index | 35 |
| Seeds Weight | 36 |
| Oil Content | 37 |

5 Table 23. Provided are the parameters measured in greenhouse experiments which are presented in Tables 24-27 hereinbelow. TP1 = Time point 1; TP2 = Time point 2; TP3 = Time point 3; RGR = relative growth rate.

Table 24
Results from greenhouse experiments

10

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL102 | 10471.1 | P | <0.01 | <0.01 | | 0.13 | 0.34 | 0.03 | 0.13 | 0.34 | 0.03 | |
| BDL102 | 10471.1 | Av | 1.24 | 1.14 | | 1.31 | 1.21 | 1.15 | 1.31 | 1.21 | 1.15 | |
| BDL102 | 10472.1 | P | 0.13 | 0.11 | 0.33 | 0.25 | 0.02 | 0.32 | 0.25 | 0.02 | 0.32 | |
| BDL102 | 10472.1 | Av | 1.26 | 1.19 | 1.14 | 1.37 | 1.26 | 1.26 | 1.37 | 1.26 | 1.26 | |
| BDL102 | 10474.1 | P | 0.22 | 0.23 | 0.26 | 0.19 | 0.2 | 0.23 | 0.19 | 0.2 | 0.23 | 0.19 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL102 | 10474.1 | Av | 1.35 | 1.33 | 1.2 | 1.65 | 1.87 | 1.49 | 1.65 | 1.87 | 1.49 | 1.1 |
| BDL102 | 10474.2 | P | 0.17 | 0.02 | 0.01 | 0.1 | 0.05 | <0.01 | 0.1 | 0.05 | <0.01 | <0.01 |
| BDL102 | 10474.2 | Av | 1.3 | 1.23 | 1.11 | 1.59 | 1.53 | 1.27 | 1.59 | 1.53 | 1.27 | 1.11 |
| BDL102 | 10474.6 | P | 0.02 | | | 0.23 | | | 0.23 | | | |
| BDL102 | 10474.6 | Av | 1.11 | | | 1.15 | | | 1.15 | | | |
| BDL117 | 10071.2 | P | | | | 0.62 | | | 0.59 | | | |
| BDL117 | 10071.2 | Av | | | | 1.14 | | | 1.16 | | | |
| BDL117 | 10074.1 | P | 0.28 | 0.22 | 0.16 | 0.29 | 0.3 | 0.3 | 0.28 | 0.29 | 0.29 | 0.34 |
| BDL117 | 10074.1 | Av | 1.26 | 1.23 | 1.24 | 1.58 | 1.47 | 1.44 | 1.6 | 1.49 | 1.46 | 1.15 |
| BDL117 | 10074.4 | P | 0.35 | 0.34 | 0.41 | 0.38 | 0.39 | 0.41 | 0.38 | 0.37 | 0.39 | 0.28 |
| BDL117 | 10074.4 | Av | 1.21 | 1.14 | 1.15 | 1.41 | 1.29 | 1.26 | 1.43 | 1.3 | 1.28 | 1.13 |
| BDL117 | 10073.1 | P | | | | 0.57 | 0.58 | 0.64 | | | | |
| BDL117 | 10073.1 | Av | | | | 1.13 | 1.17 | 1.14 | | | | |
| BDL117 | 10073.2 | P | | | 0.45 | 0.7 | 0.55 | 0.48 | 0.7 | 0.55 | 0.48 | |
| BDL117 | 10073.2 | Av | | | 1.14 | 1.1 | 1.21 | 1.22 | 1.1 | 1.21 | 1.22 | |
| BDL117 | 10074.1 | P | 0.41 | 0.4 | 0.39 | 0.44 | 0.37 | 0.38 | 0.44 | 0.37 | 0.38 | 0.13 |
| BDL117 | 10074.1 | Av | 1.1 | 1.15 | 1.15 | 1.17 | 1.32 | 1.29 | 1.17 | 1.32 | 1.29 | 1.15 |
| BDL117 | 10074.4 | P | | | 0.1 | | 0.4 | 0.34 | | 0.4 | 0.34 | |
| BDL117 | 10074.4 | Av | | | 1.09 | | 1.1 | 1.13 | | 1.1 | 1.13 | |
| BDL138 | 9812.1 | P | 0.04 | | | | | | | | | |
| BDL138 | 9812.1 | Av | 1.06 | | | | | | | | | |
| BDL138 | 9812.3 | P | | | | 0.06 | | | 0.04 | | | |
| BDL138 | 9812.3 | Av | | | | 1.18 | | | 1.19 | | | |
| BDL140 | 10423.1 | P | 0.02 | | | 0.01 | 0.22 | | 0.01 | 0.22 | | |
| BDL140 | 10423.1 | Av | 1.16 | | | 1.39 | 1.22 | | 1.39 | 1.22 | | |
| BDL140 | 10424.4 | P | | | | 0.62 | | | 0.62 | | | 0.1 |
| BDL140 | 10424.4 | Av | | | | 1.18 | | | 1.18 | | | 1.08 |
| BDL147 | 10301.5 | P | | | | | | | | | | 0.1 |
| BDL147 | 10301.5 | Av | | | | | | | | | | 1.08 |
| BDL147 | 10303.1 | P | <0.01 | 0.01 | | 0.06 | 0.04 | 0.08 | 0.06 | 0.04 | 0.08 | 0.05 |
| BDL147 | 10303.1 | Av | 1.23 | 1.21 | | 1.65 | 1.36 | 1.24 | 1.65 | 1.36 | 1.24 | 1.11 |
| BDL147 | 10303.6 | P | | | | 0.63 | 0.4 | | 0.63 | 0.4 | | |
| BDL147 | 10303.6 | Av | | | | 1.14 | 1.11 | | 1.14 | 1.11 | | |
| BDL147 | 10304.2 | P | | | | 0.33 | | | 0.33 | | | |
| BDL147 | 10304.2 | Av | | | | 1.19 | | | 1.19 | | | |
| BDL147 | 10304.2 | P | | | | | 0.44 | 0.36 | | 0.44 | 0.36 | |
| BDL147 | 10304.2 | Av | | | | | 1.17 | 1.11 | | 1.17 | 1.11 | |
| BDL149 | 9823.3 | P | 0.22 | 0.08 | | 0.33 | 0.13 | 0.29 | | 0.03 | | |
| BDL149 | 9823.3 | Av | 1.14 | 1.1 | | 1.14 | 1.18 | 1.14 | | 1.11 | | |
| BDL149 | 9824.4 | P | 0.01 | <0.01 | <0.01 | 0.08 | <0.01 | 0.04 | 0.09 | <0.01 | 0.04 | 0.03 |
| BDL149 | 9824.4 | Av | 1.16 | 1.13 | 1.13 | 1.35 | 1.26 | 1.29 | 1.37 | 1.28 | 1.31 | 1.05 |
| BDL149 | 9823.3 | P | | | | 0.65 | 0.67 | 0.63 | 0.65 | 0.67 | 0.63 | |
| BDL149 | 9823.3 | Av | | | | 1.17 | 1.1 | 1.13 | 1.17 | 1.1 | 1.13 | |
| BDL152 | 10431.1 | P | | | | 0.28 | | | 0.28 | | | |
| BDL152 | 10431.1 | Av | | | | 1.13 | | | 1.13 | | | |
| BDL152 | 10431.4 | P | | | | | 0.2 | 0.45 | | 0.2 | 0.45 | |
| BDL152 | 10431.4 | Av | | | | | 1.12 | 1.11 | | 1.12 | 1.11 | |
| BDL152 | 10434.4 | P | | | 0.22 | 0.72 | | 0.41 | 0.72 | | 0.41 | 0.09 |
| BDL152 | 10434.4 | Av | | | 1.12 | 1.12 | | 1.2 | 1.12 | | 1.2 | 1.07 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL153 | 10141.3 | P | <0.01 | <0.01 | <0.01 | 0.04 | <0.01 | <0.01 | 0.05 | <0.01 | <0.01 | |
| BDL153 | 10141.3 | Av | 1.21 | 1.17 | 1.17 | 1.41 | 1.33 | 1.34 | 1.43 | 1.34 | 1.36 | |
| BDL153 | 10142.2 | P | 0.21 | 0.41 | 0.38 | 0.33 | 0.38 | 0.38 | 0.32 | 0.37 | 0.38 | 0.49 |
| BDL153 | 10142.2 | Av | 1.33 | 1.2 | 1.25 | 1.64 | 1.55 | 1.57 | 1.66 | 1.58 | 1.6 | 1.15 |
| BDL153 | 10143.1 | P | 0.03 | | | 0.14 | 0.07 | 0.37 | 0.14 | 0.04 | 0.34 | |
| BDL153 | 10143.1 | Av | 1.07 | | | 1.22 | 1.12 | 1.14 | 1.23 | 1.13 | 1.16 | |
| BDL153 | 10144.1 | P | | | | 0.08 | 0.08 | 0.1 | 0.03 | 0.03 | 0.04 | |
| BDL153 | 10144.1 | Av | | | | 1.11 | 1.1 | 1.11 | 1.13 | 1.11 | 1.13 | |
| BDL153 | 10141.3 | P | 0.1 | <0.01 | 0.01 | | | 0.01 | | | 0.01 | |
| BDL153 | 10141.3 | Av | 1.14 | 1.15 | 1.06 | | | 1.14 | | | 1.14 | |
| BDL153 | 10142.2 | P | 0.01 | 0.01 | 0.14 | 0.15 | 0.44 | 0.14 | 0.15 | 0.44 | 0.14 | |
| BDL153 | 10142.2 | Av | 1.17 | 1.16 | 1.16 | 1.18 | 1.19 | 1.31 | 1.18 | 1.19 | 1.31 | |
| BDL153 | 10142.3 | P | | | | | | 0.4 | | | 0.4 | |
| BDL153 | 10142.3 | Av | | | | | | 1.15 | | | 1.15 | |
| BDL153 | 10143.1 | P | | | | | | | | | | 0.38 |
| BDL153 | 10143.1 | Av | | | | | | | | | | 1.12 |
| BDL153 | 10143.2 | P | | | | | 0.25 | 0.11 | | 0.25 | 0.11 | |
| BDL153 | 10143.2 | Av | | | | | 1.11 | 1.12 | | 1.11 | 1.12 | |
| BDL153 | 10144.1 | P | | 0.3 | 0.17 | | 0.39 | 0.34 | | 0.39 | 0.34 | |
| BDL153 | 10144.1 | Av | | 1.23 | 1.1 | | 1.44 | 1.13 | | 1.44 | 1.13 | |
| BDL154 | 10703.8 | P | <0.01 | 0.03 | | 0.12 | 0.07 | 0.43 | 0.12 | 0.07 | 0.43 | |
| BDL154 | 10703.8 | Av | 1.29 | 1.2 | | 1.53 | 1.37 | 1.13 | 1.53 | 1.37 | 1.13 | |
| BDL155 | 9991.5 | P | 0.22 | 0.07 | 0.1 | 0.31 | | 0.31 | 0.31 | | 0.31 | 0.03 |
| BDL155 | 9991.5 | Av | 1.13 | 1.12 | 1.12 | 1.14 | | 1.12 | 1.14 | | 1.12 | 1.09 |
| BDL155 | 9994.3 | P | 0.17 | 0.02 | 0.08 | 0.16 | 0.06 | 0.17 | 0.16 | 0.06 | 0.17 | 0.09 |
| BDL155 | 9994.3 | Av | 1.15 | 1.17 | 1.12 | 1.17 | 1.27 | 1.21 | 1.17 | 1.27 | 1.21 | 1.07 |
| BDL162 | 10492.2 | P | | | 0.32 | 0.16 | 0.25 | 0.11 | 0.16 | 0.25 | 0.11 | 0.59 |
| BDL162 | 10492.2 | Av | | | 1.13 | 1.22 | 1.15 | 1.34 | 1.22 | 1.15 | 1.34 | 1.11 |
| BDL167 | 10044.2 | P | | | | | 0.17 | | | 0.6 | | |
| BDL167 | 10044.2 | Av | | | | | 1.17 | | | 1.1 | | |
| BDL167 | 10043.3 | P | | | | | 0.39 | | | 0.39 | | |
| BDL167 | 10043.3 | Av | | | | | 1.1 | | | 1.1 | | |
| BDL167 | 10044.2 | P | | | | 0.21 | 0.17 | 0.31 | 0.21 | 0.17 | 0.31 | 0.03 |
| BDL167 | 10044.2 | Av | | | | 1.14 | 1.15 | 1.2 | 1.14 | 1.15 | 1.2 | 1.09 |
| BDL168 | 9881.3 | P | 0.1 | 0.11 | 0.09 | 0.18 | 0.14 | 0.09 | 0.18 | 0.14 | 0.1 | 0.22 |
| BDL168 | 9881.3 | Av | 1.22 | 1.19 | 1.24 | 1.48 | 1.44 | 1.49 | 1.5 | 1.46 | 1.52 | 1.14 |
| BDL168 | 9881.4 | P | 0.14 | 0.24 | 0.18 | 0.05 | 0.11 | 0.27 | 0.05 | 0.11 | 0.26 | 0.4 |
| BDL168 | 9881.4 | Av | 1.23 | 1.17 | 1.19 | 1.43 | 1.38 | 1.34 | 1.45 | 1.4 | 1.35 | 1.1 |
| BDL168 | 9882.1 | P | | | | 0.04 | 0.05 | 0.12 | 0.01 | 0.02 | 0.05 | |
| BDL168 | 9882.1 | Av | | | | 1.14 | 1.12 | 1.1 | 1.15 | 1.13 | 1.11 | |
| BDL168 | 9882.3 | P | 0.58 | 0.64 | 0.49 | 0.51 | 0.55 | 0.51 | 0.49 | 0.53 | 0.5 | 0.54 |
| BDL168 | 9882.3 | Av | 1.1 | 1.11 | 1.17 | 1.3 | 1.24 | 1.33 | 1.32 | 1.26 | 1.35 | 1.1 |
| BDL168 | 9884.4 | P | | | 0.72 | | | 0.76 | | | 0.74 | |
| BDL168 | 9884.4 | Av | | | 1.11 | | | 1.13 | | | 1.15 | |
| BDL168 | 9881.4 | P | | 0.02 | | | | 0.51 | | | 0.51 | |
| BDL168 | 9881.4 | Av | | 1.09 | | | | 1.15 | | | 1.15 | |
| BDL168 | 9882.1 | P | | 0.04 | | | 0.15 | 0.22 | | | | |
| BDL168 | 9882.1 | Av | | 1.07 | | | 1.12 | 1.13 | | | | |
| BDL168 | 9884.1 | P | | | 0.01 | | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL168 | 9884.1 | Av | | | 1.1 | | | | | | | |
| BDL169 | 10743.4 | P | | | | 0.43 | 0.55 | 0.56 | 0.54 | 0.7 | 0.72 | |
| BDL169 | 10743.4 | Av | | | | 1.27 | 1.2 | 1.19 | 1.17 | 1.11 | 1.1 | |
| BDL169 | 10744.1 | P | 0.41 | | | 0.37 | 0.55 | | 0.3 | 0.45 | 0.69 | 0.43 |
| BDL169 | 10744.1 | Av | 1.1 | | | 1.27 | 1.18 | | 1.35 | 1.25 | 1.1 | 1.13 |
| BDL169 | 10747.1 | P | 0.29 | | | 0.47 | 0.64 | | 0.42 | 0.54 | | <0.01 |
| BDL169 | 10747.1 | Av | 1.15 | | | 1.34 | 1.15 | | 1.42 | 1.22 | | 1.17 |
| BDL169 | 10747.5 | P | | 0.08 | | 0.01 | 0.02 | 0.24 | 0.01 | 0.01 | 0.13 | <0.01 |
| BDL169 | 10747.5 | Av | | 1.09 | | 1.4 | 1.28 | 1.11 | 1.49 | 1.36 | 1.18 | 1.16 |
| BDL169 | 10741.3 | P | 0.58 | | | 0.43 | | | 0.43 | | | |
| BDL169 | 10741.3 | Av | 1.13 | | | 1.2 | | | 1.2 | | | |
| BDL169 | 10744.2 | P | 0.43 | 0.25 | 0.18 | 0.34 | 0.31 | 0.33 | 0.34 | 0.31 | 0.33 | 0.44 |
| BDL169 | 10744.2 | Av | 1.24 | 1.26 | 1.21 | 1.6 | 1.61 | 1.42 | 1.6 | 1.61 | 1.42 | 1.12 |
| BDL169 | 10747.1 | P | 0.01 | 0.14 | | 0.33 | 0.09 | 0.53 | 0.33 | 0.09 | 0.53 | |
| BDL169 | 10747.1 | Av | 1.16 | 1.15 | | 1.44 | 1.3 | 1.17 | 1.44 | 1.3 | 1.17 | |
| BDL169 | 10747.5 | P | 0.05 | 0.1 | 0.01 | 0.16 | 0.19 | 0.05 | 0.16 | 0.19 | 0.05 | |
| BDL169 | 10747.5 | Av | 1.13 | 1.08 | 1.09 | 1.28 | 1.24 | 1.12 | 1.28 | 1.24 | 1.12 | |
| BDL171 | 10661.2 | P | 0.7 | | 0.44 | 0.59 | 0.7 | 0.56 | 0.59 | 0.7 | 0.56 | |
| BDL171 | 10661.2 | Av | 1.1 | | 1.1 | 1.23 | 1.17 | 1.22 | 1.23 | 1.17 | 1.22 | |
| BDL171 | 10662.3 | P | 0.48 | 0.44 | | 0.35 | 0.53 | | 0.35 | 0.53 | | |
| BDL171 | 10662.3 | Av | 1.12 | 1.13 | | 1.26 | 1.19 | | 1.26 | 1.19 | | |
| BDL171 | 10664.1 | P | 0.01 | <0.01 | 0.24 | <0.01 | 0.01 | 0.42 | <0.01 | 0.01 | 0.42 | <0.01 |
| BDL171 | 10664.1 | Av | 1.36 | 1.31 | 1.23 | 1.72 | 1.56 | 1.49 | 1.72 | 1.56 | 1.49 | 1.21 |
| BDL171 | 10664.3 | P | 0.16 | 0.16 | 0.38 | 0.24 | 0.15 | 0.42 | 0.24 | 0.15 | 0.42 | 0.03 |
| BDL171 | 10664.3 | Av | 1.26 | 1.22 | 1.14 | 1.49 | 1.44 | 1.36 | 1.49 | 1.44 | 1.36 | 1.19 |
| BDL171 | 10661.5 | P | | | | | | | 0.29 | 0.38 | | 0.42 |
| BDL171 | 10661.5 | Av | | | | | | | 1.15 | 1.1 | | 1.12 |
| BDL171 | 10662.2 | P | 0.01 | 0.07 | | 0.18 | | | 0.11 | | | 0.15 |
| BDL171 | 10662.2 | Av | 1.16 | 1.1 | | 1.2 | | | 1.28 | | | 1.18 |
| BDL171 | 10662.3 | P | 0.02 | <0.01 | <0.01 | <0.01 | <0.01 | 0.01 | <0.01 | <0.01 | <0.01 | <0.01 |
| BDL171 | 10662.3 | Av | 1.28 | 1.29 | 1.2 | 1.57 | 1.52 | 1.33 | 1.67 | 1.61 | 1.41 | 1.25 |
| BDL171 | 10663.3 | P | <0.01 | <0.01 | | <0.01 | 0.04 | | <0.01 | 0.02 | | 0.03 |
| BDL171 | 10663.3 | Av | 1.26 | 1.18 | | 1.32 | 1.21 | | 1.4 | 1.28 | | 1.18 |
| BDL171 | 10664.1 | P | | | | 0.76 | 0.81 | | 0.69 | 0.75 | 0.85 | |
| BDL171 | 10664.1 | Av | | | | 1.19 | 1.14 | | 1.26 | 1.21 | 1.11 | |
| BDL171 | 10664.3 | P | 0.01 | 0.12 | | 0.14 | 0.17 | 0.58 | 0.11 | 0.12 | 0.47 | 0.07 |
| BDL171 | 10664.3 | Av | 1.23 | 1.15 | | 1.44 | 1.3 | 1.16 | 1.52 | 1.37 | 1.23 | 1.25 |
| BDL173 | 9952.1 | P | | | | | | 0.67 | | | 0.64 | |
| BDL173 | 9952.1 | Av | | | | | | 1.11 | | | 1.13 | |
| BDL177 | 10521.3 | P | | | | 0.56 | | | 0.56 | | | |
| BDL177 | 10521.3 | Av | | | | 1.15 | | | 1.15 | | | |
| BDL177 | 10524.2 | P | | | | 0.09 | | 0.44 | 0.09 | | 0.44 | |
| BDL177 | 10524.2 | Av | | | | 1.2 | | 1.1 | 1.2 | | 1.1 | |
| BDL182 | 10691.2 | P | | | | | 0.27 | | | 0.27 | | 0.46 |
| BDL182 | 10691.2 | Av | | | | | 1.12 | | | 1.12 | | 1.11 |
| BDL182 | 10692.3 | P | 0.44 | | | 0.43 | 0.37 | | 0.43 | 0.37 | | 0.05 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL182 | 10692.3 | Av | 1.11 | | | 1.25 | 1.12 | | 1.25 | 1.12 | | 1.08 |
| BDL182 | 10693.2 | P | | | | | 0.65 | | | 0.65 | | |
| BDL182 | 10693.2 | Av | | | | | 1.1 | | | 1.1 | | |
| BDL182 | 10693.3 | P | 0.03 | 0.08 | | 0.16 | 0.06 | 0.38 | 0.16 | 0.06 | 0.38 | |
| BDL182 | 10693.3 | Av | 1.19 | 1.15 | | 1.22 | 1.18 | 1.12 | 1.22 | 1.18 | 1.12 | |
| BDL182 | 10693.5 | P | | | | 0.48 | | | 0.48 | | | |
| BDL182 | 10693.5 | Av | | | | 1.1 | | | 1.1 | | | |
| BDL182 | 10691.4 | P | 0.51 | 0.43 | | 0.39 | 0.44 | | 0.47 | 0.6 | | 0.32 |
| BDL182 | 10691.4 | Av | 1.11 | 1.11 | | 1.36 | 1.21 | | 1.26 | 1.13 | | 1.19 |
| BDL182 | 10691.8 | P | | | | | | | 0.87 | | | |
| BDL182 | 10691.8 | Av | | | | | | | 1.1 | | | |
| BDL183 | 9941.1 | P | | | | | | 0.21 | 0.16 | | 0.16 | |
| BDL183 | 9941.1 | Av | | | | | | 1.11 | 1.11 | | 1.13 | |
| BDL183 | 9943.4 | P | | | | | | 0.3 | | | | |
| BDL183 | 9943.4 | Av | | | | | | 1.1 | | | | |
| BDL183 | 9944.1 | P | 0.09 | 0.03 | | 0.1 | 0.15 | 0.22 | 0.1 | 0.15 | 0.21 | |
| BDL183 | 9944.1 | Av | 1.16 | 1.12 | | 1.27 | 1.23 | 1.22 | 1.29 | 1.25 | 1.24 | |
| BDL183 | 9941.1 | P | | | | | | 0.65 | | | 0.65 | |
| BDL183 | 9941.1 | Av | | | | | | 1.11 | | | 1.11 | |
| BDL183 | 9942.1 | P | 0.02 | 0.02 | | 0.16 | 0.33 | 0.38 | 0.16 | 0.33 | 0.38 | |
| BDL183 | 9942.1 | Av | 1.16 | 1.1 | | 1.12 | 1.17 | 1.13 | 1.12 | 1.17 | 1.13 | |
| BDL186 | 10002.2 | P | | | 0.1 | | 0.05 | <0.01 | | 0.02 | <0.01 | |
| BDL186 | 10002.2 | Av | | | 1.07 | | 1.13 | 1.25 | | 1.14 | 1.27 | |
| BDL186 | 10004.3 | P | | | 0.6 | | | 0.69 | | | 0.66 | |
| BDL186 | 10004.3 | Av | | | 1.11 | | | 1.15 | | | 1.17 | |
| BDL186 | 10001.3 | P | | | | | | | | | | 0.53 |
| BDL186 | 10001.3 | Av | | | | | | | | | | 1.11 |
| BDL186 | 10004.6 | P | | | | 0.43 | | | 0.43 | | | 0.1 |
| BDL186 | 10004.6 | Av | | | | 1.2 | | | 1.2 | | | 1.08 |
| BDL187 | 10502.2 | P | | | | 0.29 | | | 0.6 | | | |
| BDL187 | 10502.2 | Av | | | | 1.2 | | | 1.13 | | | |
| BDL187 | 10503.1 | P | | | | 0.09 | 0.27 | | 0.09 | 0.27 | | |
| BDL187 | 10503.1 | Av | | | | 1.26 | 1.1 | | 1.26 | 1.1 | | |
| BDL187 | 10503.3 | P | | | | 0.66 | | | 0.66 | | | |
| BDL187 | 10503.3 | Av | | | | 1.16 | | | 1.16 | | | |
| BDL187 | 10503.5 | P | 0.26 | | | | | | | | | |
| BDL187 | 10503.5 | Av | 1.1 | | | | | | | | | |
| BDL188 | 10462.4 | P | | | | 0.14 | 0.07 | | 0.14 | 0.07 | | 0.32 |
| BDL188 | 10462.4 | Av | | | | 1.13 | 1.09 | | 1.13 | 1.09 | | 1.13 |
| BDL188 | 10462.1 | P | 0.02 | 0.11 | | 0.04 | 0.11 | 0.4 | 0.04 | 0.11 | 0.4 | |
| BDL188 | 10462.1 | Av | 1.2 | 1.14 | | 1.3 | 1.27 | 1.21 | 1.3 | 1.27 | 1.21 | |
| BDL188 | 10462.4 | P | 0.03 | 0.03 | 0.14 | | 0.09 | 0.1 | | 0.09 | 0.1 | |
| BDL188 | 10462.4 | Av | 1.16 | 1.16 | 1.1 | | 1.24 | 1.23 | | 1.24 | 1.23 | |
| BDL190 | 10232.2 | P | 0.01 | 0.01 | <0.01 | 0.43 | 0.09 | 0.14 | 0.43 | 0.09 | 0.14 | |
| BDL190 | 10232.2 | Av | 1.18 | 1.15 | 1.13 | 1.17 | 1.25 | 1.24 | 1.17 | 1.25 | 1.24 | |
| BDL190 | 10233.2 | P | 0.03 | <0.01 | 0.09 | 0.03 | 0.01 | <0.01 | 0.03 | 0.01 | <0.01 | |
| BDL190 | 10233.2 | Av | 1.14 | 1.16 | 1.18 | 1.19 | 1.35 | 1.29 | 1.19 | 1.35 | 1.29 | |
| BDL190 | 10233.4 | P | | | 0.11 | 0.18 | | <0.01 | 0.18 | | <0.01 | |
| BDL190 | 10233.4 | Av | | | 1.11 | 1.11 | | 1.17 | 1.11 | | 1.17 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL190 | 10234.2 | P | | 0.09 | | | 0.05 | | | 0.05 | | |
| BDL190 | 10234.2 | Av | | 1.06 | | | 1.18 | | | 1.18 | | |
| BDL192 | 9921.6 | P | | | | 0.26 | 0.4 | 0.48 | 0.23 | 0.37 | 0.44 | |
| BDL192 | 9921.6 | Av | | | | 1.14 | 1.14 | 1.13 | 1.16 | 1.15 | 1.14 | |
| BDL192 | 9922.1 | P | 0.11 | | | 0.35 | 0.33 | 0.28 | 0.33 | 0.3 | 0.22 | |
| BDL192 | 9922.1 | Av | 1.1 | | | 1.21 | 1.14 | 1.1 | 1.23 | 1.15 | 1.12 | |
| BDL192 | 9921.6 | P | | | | 0.21 | 0.14 | 0.41 | 0.21 | 0.14 | 0.41 | |
| BDL192 | 9921.6 | Av | | | | 1.12 | 1.14 | 1.14 | 1.12 | 1.14 | 1.14 | |
| BDL192 | 9922.5 | P | | | | 0.35 | 0.33 | 0.3 | 0.65 | 0.62 | | |
| BDL192 | 9922.5 | Av | | | | 1.18 | 1.2 | 1.13 | 1.11 | 1.13 | | |
| BDL193 | 10152.2 | P | | | | 0.08 | | | 0.06 | 0.17 | | 0.01 |
| BDL193 | 10152.2 | Av | | | | 1.15 | | | 1.16 | 1.1 | | 1.06 |
| BDL193 | 10153.2 | P | | | | | | | 0.6 | | | |
| BDL193 | 10153.2 | Av | | | | | | | 1.11 | | | |
| BDL193 | 10153.4 | P | | | 0.04 | 0.4 | 0.37 | 0.21 | 0.38 | 0.34 | 0.18 | |
| BDL193 | 10153.4 | Av | | | 1.08 | 1.23 | 1.16 | 1.16 | 1.25 | 1.18 | 1.17 | |
| BDL193 | 10153.3 | P | 0.41 | 0.14 | | 0.4 | 0.01 | 0.4 | 0.4 | 0.01 | 0.4 | 0.33 |
| BDL193 | 10153.3 | Av | 1.12 | 1.15 | | 1.21 | 1.31 | 1.14 | 1.21 | 1.31 | 1.14 | 1.13 |
| BDL193 | 10153.4 | P | 0.33 | 0.25 | | 0.51 | 0.27 | 0.17 | 0.51 | 0.27 | 0.17 | |
| BDL193 | 10153.4 | Av | 1.1 | 1.11 | | 1.14 | 1.23 | 1.14 | 1.14 | 1.23 | 1.14 | |
| BDL196 | 10243.1 | P | 0.61 | 0.66 | | 0.6 | 0.66 | 0.66 | 0.6 | 0.66 | 0.66 | |
| BDL196 | 10243.1 | Av | 1.14 | 1.1 | | 1.2 | 1.16 | 1.15 | 1.2 | 1.16 | 1.15 | |
| BDL196 | 10243.1 | P | | | 0.02 | | | | | | | |
| BDL196 | 10243.1 | Av | | | 1.05 | | | | | | | |
| BDL201 | 9961.3 | P | 0.26 | 0.22 | 0.38 | 0.11 | 0.23 | 0.44 | 0.11 | 0.23 | 0.44 | 0.09 |
| BDL201 | 9961.3 | Av | 1.13 | 1.11 | 1.16 | 1.33 | 1.23 | 1.35 | 1.33 | 1.23 | 1.35 | 1.07 |
| BDL220 | 10333.5 | P | | | 0.48 | | | | | | | |
| BDL220 | 10333.5 | Av | | | 1.1 | | | | | | | |
| BDL223 | 10793.5 | P | 0.09 | 0.01 | 0.01 | 0.39 | 0.12 | 0.26 | 0.39 | 0.12 | 0.26 | 0.02 |
| BDL223 | 10793.5 | Av | 1.15 | 1.12 | 1.1 | 1.12 | 1.25 | 1.13 | 1.12 | 1.25 | 1.13 | 1.06 |
| BDL223 | 10793.8 | P | <0.01 | 0.01 | | 0.2 | 0.19 | | 0.2 | 0.19 | | |
| BDL223 | 10793.8 | Av | 1.17 | 1.1 | | 1.31 | 1.18 | | 1.31 | 1.18 | | |
| BDL224 | 10451.7 | P | | | | 0.59 | | | 0.59 | | | 0.05 |
| BDL224 | 10451.7 | Av | | | | 1.12 | | | 1.12 | | | 1.08 |
| BDL226 | 10861.2 | P | 0.05 | 0.05 | | 0.01 | 0.07 | | 0.01 | 0.04 | | 0.03 |
| BDL226 | 10861.2 | Av | 1.12 | 1.12 | | 1.26 | 1.17 | | 1.34 | 1.24 | | 1.21 |
| BDL226 | 10861.4 | P | | | | | | | 0.65 | | | 0.31 |
| BDL226 | 10861.4 | Av | | | | | | | 1.13 | | | 1.12 |
| BDL226 | 10864.2 | P | 0.01 | 0.01 | 0.09 | <0.01 | <0.01 | 0.07 | <0.01 | <0.01 | 0.04 | 0.22 |
| BDL226 | 10864.2 | Av | 1.2 | 1.15 | 1.09 | 1.49 | 1.34 | 1.21 | 1.59 | 1.42 | 1.29 | 1.13 |
| BDL227 | 11491.3 | P | 0.21 | 0.01 | 0.08 | 0.27 | 0.07 | | 0.27 | 0.07 | | |
| BDL227 | 11491.3 | Av | 1.11 | 1.09 | 1.09 | 1.12 | 1.21 | | 1.12 | 1.21 | | |
| BDL227 | 11492.3 | P | <0.01 | <0.01 | | | 0.01 | 0.05 | | 0.01 | 0.05 | |
| BDL227 | 11492.3 | Av | 1.17 | 1.12 | | | 1.23 | 1.12 | | 1.23 | 1.12 | |
| BDL233 | 10822.1 | P | | | | | 0.63 | | | 0.63 | | |
| BDL233 | 10822.1 | Av | | | | | 1.12 | | | 1.12 | | |
| BDL233 | 10825.4 | P | 0.4 | 0.4 | 0.37 | 0.63 | 0.35 | 0.48 | 0.63 | 0.35 | 0.48 | |
| BDL233 | 10825.4 | Av | 1.16 | 1.16 | 1.16 | 1.14 | 1.39 | 1.25 | 1.14 | 1.39 | 1.25 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL237 | 10893.1 | P | | | | 0.09 | | | 0.09 | | | |
| BDL237 | 10893.1 | Av | | | | 1.12 | | | 1.12 | | | |
| BDL237 | 10895.1 | P | 0.37 | 0.29 | | 0.05 | 0.56 | 0.55 | 0.05 | 0.56 | 0.55 | |
| BDL237 | 10895.1 | Av | 1.13 | 1.1 | | 1.13 | 1.15 | 1.11 | 1.13 | 1.15 | 1.11 | |
| BDL237 | 10895.2 | P | | | | 0.29 | | | 0.29 | | | |
| BDL237 | 10895.2 | Av | | | | 1.12 | | | 1.12 | | | |
| BDL237 | 10895.3 | P | 0.55 | | | 0.56 | | | 0.56 | | | |
| BDL237 | 10895.3 | Av | 1.13 | | | 1.12 | | | 1.12 | | | |
| BDL238 | 10951.4 | P | 0.35 | | | | 0.1 | | | 0.1 | | |
| BDL238 | 10951.4 | Av | 1.11 | | | | 1.14 | | | 1.14 | | |
| BDL238 | 10952.3 | P | | | | | 0.68 | | | 0.68 | | |
| BDL238 | 10952.3 | Av | | | | | 1.1 | | | 1.1 | | |
| BDL238 | 10954.2 | P | 0.04 | <0.01 | <0.01 | 0.08 | <0.01 | <0.01 | 0.08 | <0.01 | <0.01 | <0.01 |
| BDL238 | 10954.2 | Av | 1.33 | 1.28 | 1.23 | 1.73 | 1.76 | 1.52 | 1.73 | 1.76 | 1.52 | 1.13 |
| BDL238 | 10954.3 | P | | | | 0.74 | | | 0.74 | | | |
| BDL238 | 10954.3 | Av | | | | 1.13 | | | 1.13 | | | |
| BDL240 | 10802.2 | P | 0.02 | 0.03 | 0.12 | 0.1 | 0.02 | 0.04 | 0.1 | 0.02 | 0.04 | |
| BDL240 | 10802.2 | Av | 1.22 | 1.26 | 1.18 | 1.34 | 1.54 | 1.35 | 1.34 | 1.54 | 1.35 | |
| BDL241 | 10873.1 | P | 0.02 | 0.13 | 0.11 | <0.01 | 0.38 | 0.02 | <0.01 | 0.38 | 0.02 | |
| BDL241 | 10873.1 | Av | 1.19 | 1.18 | 1.15 | 1.41 | 1.3 | 1.34 | 1.41 | 1.3 | 1.34 | |
| BDL242 | 10731.2 | P | 0.4 | 0.52 | | 0.14 | 0.46 | 0.58 | 0.14 | 0.46 | 0.58 | |
| BDL242 | 10731.2 | Av | 1.13 | 1.12 | | 1.22 | 1.28 | 1.14 | 1.22 | 1.28 | 1.14 | |
| BDL242 | 10731.5 | P | | | | 0.1 | | | 0.1 | | | |
| BDL242 | 10731.5 | Av | | | | 1.11 | | | 1.11 | | | |
| BDL242 | 10731.6 | P | <0.01 | <0.01 | 0.18 | 0.03 | 0.25 | 0.08 | 0.03 | 0.25 | 0.08 | |
| BDL242 | 10731.6 | Av | 1.21 | 1.22 | 1.19 | 1.48 | 1.45 | 1.36 | 1.48 | 1.45 | 1.36 | |
| BDL242 | 10731.7 | P | | | | 0.06 | | | 0.06 | | | |
| BDL242 | 10731.7 | Av | | | | 1.12 | | | 1.12 | | | |
| BDL245 | 10813.3 | P | | 0.03 | | | | | | | | |
| BDL245 | 10813.3 | Av | | 1.08 | | | | | | | | |
| BDL250 | 10841.3 | P | 0.02 | 0.18 | 0.26 | 0.06 | 0.22 | 0.32 | 0.06 | 0.22 | 0.32 | 0.05 |
| BDL250 | 10841.3 | Av | 1.24 | 1.18 | 1.11 | 1.36 | 1.41 | 1.17 | 1.36 | 1.41 | 1.17 | 1.08 |
| BDL250 | 10846.2 | P | 0.48 | | | 0.64 | 0.41 | | 0.64 | 0.41 | | |
| BDL250 | 10846.2 | Av | 1.1 | | | 1.12 | 1.16 | | 1.12 | 1.16 | | |
| BDL250 | 10846.3 | P | 0.38 | 0.36 | 0.48 | 0.58 | 0.46 | 0.62 | 0.58 | 0.46 | 0.62 | |
| BDL250 | 10846.3 | Av | 1.11 | 1.17 | 1.11 | 1.17 | 1.34 | 1.19 | 1.17 | 1.34 | 1.19 | |
| BDL252 | 10882.1 | P | 0.3 | 0.41 | 0.44 | 0.32 | 0.26 | 0.34 | 0.32 | 0.26 | 0.34 | <0.01 |
| BDL252 | 10882.1 | Av | 1.19 | 1.19 | 1.17 | 1.38 | 1.42 | 1.24 | 1.38 | 1.42 | 1.24 | 1.1 |
| BDL48 | 10274.4 | P | 0.23 | 0.02 | 0.02 | 0.81 | 0.09 | 0.08 | 0.81 | 0.09 | 0.08 | |
| BDL48 | 10274.4 | Av | 1.14 | 1.15 | 1.2 | 1.1 | 1.23 | 1.36 | 1.1 | 1.23 | 1.36 | |
| BDL48 | 10271.1 | P | | 0.06 | <0.01 | 0.27 | 0.03 | <0.01 | 0.27 | 0.03 | <0.01 | |
| BDL48 | 10271.1 | Av | | 1.08 | 1.16 | 1.11 | 1.22 | 1.27 | 1.11 | 1.22 | 1.27 | |
| BDL48 | 10274.3 | P | 0.07 | 0.01 | <0.01 | 0.02 | 0.01 | <0.01 | 0.02 | 0.01 | <0.01 | |
| BDL48 | 10274.3 | Av | 1.21 | 1.19 | 1.09 | 1.25 | 1.35 | 1.22 | 1.25 | 1.35 | 1.22 | |
| BDL48 | 10274.4 | P | 0.29 | 0.2 | 0.13 | 0.22 | 0.03 | 0.22 | 0.22 | 0.03 | 0.22 | |
| BDL48 | 10274.4 | Av | 1.14 | 1.15 | 1.14 | 1.14 | 1.21 | 1.26 | 1.14 | 1.21 | 1.26 | |
| BDL48 | 10274.5 | P | 0.04 | 0.28 | 0.45 | 0.26 | 0.49 | 0.44 | 0.26 | 0.49 | 0.44 | |
| BDL48 | 10274.5 | Av | 1.11 | 1.13 | 1.11 | 1.14 | 1.22 | 1.22 | 1.14 | 1.22 | 1.22 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par:</i> | <i>1</i> | <i>2</i> | <i>3</i> | <i>4</i> | <i>5</i> | <i>6</i> | <i>7</i> | <i>8</i> | <i>9</i> | <i>10</i> |
|-------------|------------|-------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|-----------|
| BDL63 | 10381.1 | P | 0.12 | 0.02 | <0.01 | 0.11 | 0.21 | <0.01 | 0.11 | 0.21 | <0.01 | |
| BDL63 | 10381.1 | Av | 1.2 | 1.18 | 1.17 | 1.2 | 1.39 | 1.37 | 1.2 | 1.39 | 1.37 | |
| BDL63 | 10381.2 | P | 0.03 | 0.25 | 0.37 | 0.31 | 0.6 | 0.42 | 0.31 | 0.6 | 0.42 | |
| BDL63 | 10381.2 | Av | 1.13 | 1.15 | 1.19 | 1.19 | 1.26 | 1.32 | 1.19 | 1.26 | 1.32 | |
| BDL63 | 10384.8 | P | | 0.02 | <0.01 | | 0.06 | <0.01 | | 0.06 | <0.01 | |
| BDL63 | 10384.8 | Av | | 1.09 | 1.14 | | 1.2 | 1.24 | | 1.2 | 1.24 | |
| BDL79 | 11042.1 | P | | 0.08 | | | 0.04 | 0.52 | | 0.04 | 0.52 | |
| BDL79 | 11042.1 | Av | | 1.06 | | | 1.16 | 1.1 | | 1.16 | 1.1 | |
| BDL79 | 11044.3 | P | <0.01 | 0.03 | | | 0.14 | | | 0.14 | | |
| BDL79 | 11044.3 | Av | 1.17 | 1.11 | | | 1.14 | | | 1.14 | | |
| BDL81 | 10371.8 | P | | | | 0.34 | | | 0.34 | | | |
| BDL81 | 10371.8 | Av | | | | 1.12 | | | 1.12 | | | |
| BDL81 | 10374.1 | P | | | | 0.22 | | | 0.22 | | | |
| BDL81 | 10374.1 | Av | | | | 1.16 | | | 1.16 | | | |
| BDL81 | 10371.5 | P | | 0.02 | 0.17 | | | 0.21 | | | 0.21 | |
| BDL81 | 10371.5 | Av | | 1.08 | 1.11 | | | 1.13 | | | 1.13 | |
| BDL81 | 10371.8 | P | | | 0.6 | | 0.8 | 0.57 | | 0.8 | 0.57 | |
| BDL81 | 10371.8 | Av | | | 1.13 | | 1.13 | 1.22 | | 1.13 | 1.22 | |
| BDL81 | 10374.1 | P | 0.26 | 0.31 | 0.44 | 0.16 | 0.19 | 0.32 | 0.16 | 0.19 | 0.32 | 0.26 |
| BDL81 | 10374.1 | Av | 1.23 | 1.22 | 1.19 | 1.44 | 1.45 | 1.49 | 1.44 | 1.45 | 1.49 | 1.12 |
| BDL85 | 10411.1 | P | 0.25 | 0.34 | 0.15 | 0.13 | 0.39 | 0.33 | 0.13 | 0.39 | 0.33 | 0.12 |
| BDL85 | 10411.1 | Av | 1.2 | 1.16 | 1.14 | 1.39 | 1.29 | 1.28 | 1.39 | 1.29 | 1.28 | 1.16 |

Table 24. Results of the greenhouse experiments. Provided are the measured values of each parameter [parameters (Par.) 1-10 according to the parameters described in Table 23 above] in plants expressing the indicated polynucleotides. “Ev” = event; “P” = P-value; “Av” = ratio between the averages of event and control. Note that when the average ratio is higher than “1” the effect of exogenous expression of the gene is an increase of the desired trait;

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Table 25
Results from greenhouse experiments

| <i>Gene</i> | <i>Ev.</i> | <i>Pa</i> <i>r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL102 | 10471.1 | P | | | 0.1 | 0.27 | 0.03 | 0.04 | 0.29 | | | |
| BDL102 | 10471.1 | Av | | | 1.35 | 1.23 | 1.18 | 1.27 | 1.1 | | | |
| BDL102 | 10472.1 | P | | | 0.17 | 0.35 | 0.25 | 0.21 | 0.22 | | | |
| BDL102 | 10472.1 | Av | | | 1.36 | 1.23 | 1.3 | 1.29 | 1.15 | | | |
| BDL102 | 10474.1 | P | | | 0.18 | 0.19 | 0.16 | 0.17 | 0.3 | | | 0.02 |
| BDL102 | 10474.1 | Av | | | 1.56 | 1.82 | 1.54 | 1.4 | 1.3 | | | 1.03 |
| BDL102 | 10474.2 | P | | | 0.04 | <0.01 | 0.01 | 0.15 | <0.01 | | | |
| BDL102 | 10474.2 | Av | | | 1.51 | 1.48 | 1.34 | 1.42 | 1.22 | | | |
| BDL102 | 10474.6 | P | | | 0.23 | | | 0.11 | | | | |
| BDL102 | 10474.6 | Av | | | 1.19 | | | 1.12 | | | | |
| BDL117 | 10071.2 | P | | | | | | | | | | 0.1 |
| BDL117 | 10071.2 | Av | | | | | | | | | | 1.03 |
| BDL117 | 10073.2 | P | | | | | | 0.02 | 0.15 | | | |
| BDL117 | 10073.2 | Av | | | | | | 1.1 | 1.1 | | | |
| BDL117 | 10074.1 | P | | 0.21 | 0.27 | 0.29 | 0.26 | 0.18 | 0.12 | 0.04 | | |
| BDL117 | 10074.1 | Av | | 1.19 | 1.46 | 1.38 | 1.33 | 1.59 | 1.35 | 1.17 | | |
| BDL117 | 10074.4 | P | 0.05 | 0.37 | 0.38 | 0.49 | 0.3 | 0.25 | 0.31 | | | 0.03 |
| BDL117 | 10074.4 | Av | 1.06 | 1.12 | 1.28 | 1.16 | 1.19 | 1.43 | 1.28 | | | 1.02 |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL117 | 10073.1 | P | | | 0.62 | 0.52 | 0.63 | | | | | |
| BDL117 | 10073.1 | Av | | | 1.1 | 1.16 | 1.15 | | | | | |
| BDL117 | 10073.2 | P | | | | 0.56 | 0.37 | 0.35 | 0.53 | 0.51 | | |
| BDL117 | 10073.2 | Av | | | | 1.19 | 1.25 | 1.14 | 1.13 | 1.15 | | |
| BDL117 | 10074.1 | P | | 0.01 | 0.53 | 0.37 | 0.36 | 0.33 | 0.42 | 0.43 | | |
| BDL117 | 10074.1 | Av | | 1.09 | 1.11 | 1.29 | 1.24 | 1.21 | 1.17 | 1.2 | | |
| BDL117 | 10074.4 | P | | | | 0.37 | 0.26 | | 0.24 | 0.16 | | |
| BDL117 | 10074.4 | Av | | | | 1.1 | 1.12 | | 1.13 | 1.11 | | |
| BDL138 | 9811.4 | P | | | | | | 0.06 | | | | |
| BDL138 | 9811.4 | Av | | | | | | 1.09 | | | | |
| BDL138 | 9812.1 | P | | | | | | <0.01 | 0.02 | | | |
| BDL138 | 9812.1 | Av | | | | | | 1.16 | 1.11 | | | |
| BDL138 | 9812.3 | P | 0.05 | | 0.11 | | | 0.37 | 0.52 | | 0.01 | |
| BDL138 | 9812.3 | Av | 1.04 | | 1.13 | | | 1.14 | 1.1 | | 1.03 | |
| BDL138 | 9811.1 | P | | | | | | | | | 0.02 | <0.01 |
| BDL138 | 9811.1 | Av | | | | | | | | | 1.04 | 1.04 |
| BDL138 | 9813.4 | P | | | | | | | | | | <0.01 |
| BDL138 | 9813.4 | Av | | | | | | | | | | 1.04 |
| BDL140 | 10423.1 | P | | | 0.01 | 0.22 | | | | | | |
| BDL140 | 10423.1 | Av | | | 1.29 | 1.19 | | | | | | |
| BDL140 | 10424.3 | P | | | | | | | | | | 0.49 |
| BDL140 | 10424.3 | Av | | | | | | | | | | 1.27 |
| BDL140 | 10424.4 | P | | | | | | 0.64 | 0.68 | | | |
| BDL140 | 10424.4 | Av | | | | | | 1.14 | 1.17 | | | |
| BDL140 | 10423.1 | P | | | | | | | | | 0.03 | |
| BDL140 | 10423.1 | Av | | | | | | | | | 1.04 | |
| BDL147 | 10303.1 | P | | | 0.11 | 0.07 | 0.11 | 0.12 | 0.01 | | | |
| BDL147 | 10303.1 | Av | | | 1.49 | 1.31 | 1.18 | 1.28 | 1.43 | | | |
| BDL147 | 10303.6 | P | | | | | | 0.38 | 0.37 | | | |
| BDL147 | 10303.6 | Av | | | | | | 1.11 | 1.12 | | | |
| BDL147 | 10304.2 | P | | | 0.33 | | | | | | | 0.05 |
| BDL147 | 10304.2 | Av | | | 1.18 | | | | | | | 1.04 |
| BDL147 | 10303.5 | P | | | | 0.41 | | | | | | |
| BDL147 | 10303.5 | Av | | | | 1.1 | | | | | | |
| BDL147 | 10304.2 | P | | | | 0.48 | | | | | | |
| BDL147 | 10304.2 | Av | | | | 1.17 | | | | | | |
| BDL149 | 9823.3 | P | | | 0.23 | | | <0.01 | 0.01 | | | |
| BDL149 | 9823.3 | Av | | | 1.13 | | | 1.38 | 1.21 | | | |
| BDL149 | 9824.3 | P | | 0.09 | | | | | | | | |
| BDL149 | 9824.3 | Av | | 1.04 | | | | | | | | |
| BDL149 | 9824.4 | P | | 0.02 | 0.12 | 0.03 | 0.17 | <0.01 | <0.01 | 0.02 | | |
| BDL149 | 9824.4 | Av | | 1.1 | 1.28 | 1.12 | 1.2 | 1.23 | 1.22 | 1.11 | | |
| BDL149 | 9823.3 | P | | | 0.62 | 0.47 | 0.56 | | | | | |
| BDL149 | 9823.3 | Av | | | 1.13 | 1.16 | 1.12 | | | | | |
| BDL152 | 10431.1 | P | | | 0.31 | | | | | | | |
| BDL152 | 10431.1 | Av | | | 1.1 | | | | | | | |
| BDL152 | 10431.4 | P | | | | 0.16 | 0.47 | 0.27 | | 0.09 | | 0.03 |
| BDL152 | 10431.4 | Av | | | | 1.1 | 1.1 | 1.18 | | 1.18 | | 1.02 |
| BDL152 | 10432.5 | P | | | | 0.18 | 0.62 | | | | | |
| BDL152 | 10432.5 | Av | | | | 1.1 | 1.16 | | | | | |
| BDL152 | 10434.1 | P | | | | | | | 0.76 | | | |
| BDL152 | 10434.1 | Av | | | | | | | 1.11 | | | |
| BDL152 | 10434.4 | P | | | | | 0.32 | 0.25 | 0.04 | 0.16 | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL152 | 10434.4 | Av | | | | | 1.2 | 1.13 | 1.37 | 1.12 | | |
| BDL152 | 10434.1 | P | | | | | | | | | 0.03 | |
| BDL152 | 10434.1 | Av | | | | | | | | | 1.04 | |
| BDL152 | 10434.4 | P | | | | | | | | | 0.05 | |
| BDL152 | 10434.4 | Av | | | | | | | | | 1.04 | |
| BDL153 | 10141.3 | P | | | <0.0 1 | <0.01 | <0.0 1 | 0.25 | 0.05 | <0.0 1 | | |
| BDL153 | 10141.3 | Av | | | 1.32 | 1.24 | 1.27 | 1.33 | 1.26 | 1.15 | | |
| BDL153 | 10142.2 | P | 0.03 | 0.33 | 0.28 | 0.54 | 0.41 | 0.2 | 0.33 | 0.55 | | 0.07 |
| BDL153 | 10142.2 | Av | 1.15 | 1.16 | 1.44 | 1.28 | 1.41 | 1.54 | 1.34 | 1.12 | | 1.02 |
| BDL153 | 10143.1 | P | 0.01 | | 0.21 | | 0.32 | | 0.05 | | 0.01 | <0.01 |
| BDL153 | 10143.1 | Av | 1.12 | | 1.2 | | 1.14 | | 1.11 | | 1.02 | 1.02 |
| BDL153 | 10144.1 | P | | <0.01 | 0.05 | 0.08 | 0.07 | | | | | |
| BDL153 | 10144.1 | Av | | 1.09 | 1.13 | 1.1 | 1.1 | | | | | |
| BDL153 | 10141.3 | P | | | | 0.06 | 0.02 | 0.02 | 0.24 | | | |
| BDL153 | 10141.3 | Av | | | | 1.14 | 1.1 | 1.26 | 1.19 | | | |
| BDL153 | 10142.2 | P | | 0.1 | 0.17 | 0.35 | 0.06 | 0.02 | 0.05 | 0.04 | | |
| BDL153 | 10142.2 | Av | | 1.05 | 1.1 | 1.17 | 1.22 | 1.48 | 1.31 | 1.26 | | |
| BDL153 | 10142.3 | P | | | | | 0.36 | 0.23 | | | | |
| BDL153 | 10142.3 | Av | | | | | 1.14 | 1.1 | | | | |
| BDL153 | 10143.1 | P | | | | | | 0.15 | | | | |
| BDL153 | 10143.1 | Av | | | | | | 1.14 | | | | |
| BDL153 | 10143.2 | P | | 0.04 | | 0.15 | | 0.07 | | <0.0 1 | | |
| BDL153 | 10143.2 | Av | | 1.06 | | 1.11 | | 1.2 | | 1.15 | | |
| BDL153 | 10144.1 | P | | | | 0.4 | 0.48 | | 0.24 | 0.08 | | |
| BDL153 | 10144.1 | Av | | | | 1.43 | 1.11 | | 1.34 | 1.13 | | |
| BDL153 | 10144.4 | P | | | | | | | 0.54 | | | |
| BDL153 | 10144.4 | Av | | | | | | | 1.1 | | | |
| BDL154 | 10703.6 | P | | | | | | 0.66 | | | | |
| BDL154 | 10703.6 | Av | | | | | | 1.1 | | | | |
| BDL154 | 10703.8 | P | | | 0.08 | 0.09 | 0.54 | <0.01 | 0.09 | | | |
| BDL154 | 10703.8 | Av | | | 1.47 | 1.41 | 1.13 | 1.47 | 1.22 | | | |
| BDL155 | 9991.5 | P | | | 0.36 | | 0.09 | 0.31 | 0.41 | | | |
| BDL155 | 9991.5 | Av | | | 1.11 | | 1.18 | 1.29 | 1.35 | | | |
| BDL155 | 9991.9 | P | | | | | | | 0.27 | | | |
| BDL155 | 9991.9 | Av | | | | | | | 1.17 | | | |
| BDL155 | 9993.2 | P | | | | | | | 0.64 | | | |
| BDL155 | 9993.2 | Av | | | | | | | 1.12 | | | |
| BDL155 | 9994.3 | P | 0.16 | | 0.31 | 0.08 | 0.12 | 0.12 | 0.09 | 0.41 | | |
| BDL155 | 9994.3 | Av | 1.14 | | 1.1 | 1.16 | 1.17 | 1.43 | 1.44 | 1.12 | | |
| BDL155 | 9993.2 | P | | | | | | | | | 0.06 | |
| BDL155 | 9993.2 | Av | | | | | | | | | 1.03 | |
| BDL155 | 9994.3 | P | | | | | | | | | 0.03 | |
| BDL155 | 9994.3 | Av | | | | | | | | | 1.04 | |
| BDL157 | 9911.4 | P | | | | | | | | | | 0.09 |
| BDL157 | 9911.4 | Av | | | | | | | | | | 1.03 |
| BDL157 | 9914.2 | P | | | | | | | 0.12 | 0.09 | | |
| BDL157 | 9914.2 | Av | | | | | | | 1.11 | 1.06 | | |
| BDL162 | 10492.2 | P | | | | | 0.12 | | 0.44 | | | |
| BDL162 | 10492.2 | Av | | | | | 1.39 | | 1.15 | | | |
| BDL162 | 10492.4 | P | | | | | | | 0.82 | | | |
| BDL162 | 10492.4 | Av | | | | | | | 1.13 | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL162 | 10494.1 | P | | | | | | 0.1 | 0.13 | | | |
| BDL162 | 10494.1 | Av | | | | | | 1.21 | 1.21 | | | |
| BDL167 | 10043.1 | P | | | | | | | | | 0.17 | |
| BDL167 | 10043.1 | Av | | | | | | | | | 1.21 | |
| BDL167 | 10043.2 | P | | | | | | | | | <0.01 | 0.01 |
| BDL167 | 10043.2 | Av | | | | | | | | | 1.04 | 1.03 |
| BDL167 | 10044.2 | P | | | 0.05 | 0.07 | | | | | | 0.03 |
| BDL167 | 10044.2 | Av | | | 1.15 | 1.16 | | | | | | 1.02 |
| BDL167 | 10042.3 | P | | 0.1 | | | | | | 0.2 | | |
| BDL167 | 10042.3 | Av | | 1.05 | | | | | | 1.12 | | |
| BDL167 | 10043.3 | P | | | | 0.35 | 0.19 | 0.38 | | 0.41 | | |
| BDL167 | 10043.3 | Av | | | | 1.11 | 1.1 | 1.14 | | 1.11 | | |
| BDL167 | 10044.2 | P | | | 0.51 | 0.28 | 0.27 | 0.31 | 0.18 | | | |
| BDL167 | 10044.2 | Av | | | 1.1 | 1.14 | 1.15 | 1.17 | 1.17 | | | |
| BDL168 | 9881.3 | P | 0.08 | <0.01 | 0.24 | 0.17 | 0.1 | 0.11 | 0.21 | 0.3 | | <0.01 |
| BDL168 | 9881.3 | Av | 1.09 | 1.1 | 1.32 | 1.36 | 1.44 | 1.17 | 1.21 | 1.15 | | 1.02 |
| BDL168 | 9881.4 | P | | 0.01 | 0.1 | 0.32 | 0.05 | 0.16 | 0.36 | 0.44 | | |
| BDL168 | 9881.4 | Av | | 1.15 | 1.3 | 1.23 | 1.32 | 1.45 | 1.25 | 1.14 | | |
| BDL168 | 9882.3 | P | | | 0.61 | 0.54 | 0.49 | 0.66 | 0.71 | 0.66 | | |
| BDL168 | 9882.3 | Av | | | 1.15 | 1.2 | 1.3 | 1.2 | 1.13 | 1.1 | | |
| BDL168 | 9884.4 | P | | | | | 0.7 | | | | | |
| BDL168 | 9884.4 | Av | | | | | 1.15 | | | | | |
| BDL168 | 9881.4 | P | | | | | 0.57 | 0.57 | 0.37 | 0.4 | | |
| BDL168 | 9881.4 | Av | | | | | 1.11 | 1.1 | 1.17 | 1.14 | | |
| BDL168 | 9882.1 | P | | | | 0.1 | 0.22 | 0.48 | | <0.01 | | |
| BDL168 | 9882.1 | Av | | | | 1.12 | 1.11 | 1.14 | | 1.16 | | |
| BDL168 | 9882.3 | P | | | | | | 0.39 | 0.22 | | | |
| BDL168 | 9882.3 | Av | | | | | | 1.12 | 1.11 | | | |
| BDL168 | 9884.1 | P | | | | | | | 0.11 | | | |
| BDL168 | 9884.1 | Av | | | | | | | 1.12 | | | |
| BDL169 | 10743.4 | P | | | 0.55 | 0.5 | 0.69 | 0.44 | | | | |
| BDL169 | 10743.4 | Av | | | 1.16 | 1.19 | 1.12 | 1.17 | | | | |
| BDL169 | 10744.1 | P | 0.41 | | 0.38 | | | 0.29 | 0.31 | | | |
| BDL169 | 10744.1 | Av | 1.15 | | 1.19 | | | 1.4 | 1.24 | | | |
| BDL169 | 10747.1 | P | 0.09 | | 0.58 | | | 0.01 | | | | |
| BDL169 | 10747.1 | Av | 1.11 | | 1.22 | | | 1.42 | | | | |
| BDL169 | 10747.5 | P | <0.01 | | 0.14 | 0.06 | | | | | | |
| BDL169 | 10747.5 | Av | 1.11 | | 1.29 | 1.15 | | | | | | |
| BDL169 | 10741.3 | P | | | 0.42 | 0.68 | | 0.53 | | | | |
| BDL169 | 10741.3 | Av | | | 1.17 | 1.11 | | 1.16 | | | | |
| BDL169 | 10744.2 | P | 0.02 | | 0.26 | 0.31 | 0.32 | 0.37 | 0.24 | 0.02 | | 0.02 |
| BDL169 | 10744.2 | Av | 1.04 | | 1.48 | 1.56 | 1.44 | 1.37 | 1.26 | 1.23 | | 1.03 |
| BDL169 | 10747.1 | P | | | 0.34 | <0.01 | 0.36 | 0.02 | 0.02 | | | |
| BDL169 | 10747.1 | Av | | | 1.39 | 1.32 | 1.2 | 1.16 | 1.17 | | | |
| BDL169 | 10747.3 | P | | | | | | | | | | 0.45 |
| BDL169 | 10747.3 | Av | | | | | | | | | | 1.1 |
| BDL169 | 10747.5 | P | | | 0.11 | 0.14 | <0.01 | <0.01 | | | | |
| BDL169 | 10747.5 | Av | | | 1.2 | 1.26 | 1.27 | 1.22 | | | | |
| BDL171 | 10661.2 | P | 0.6 | | 0.63 | 0.74 | 0.35 | 0.84 | 0.55 | | | |
| BDL171 | 10661.2 | Av | 1.11 | | 1.17 | 1.1 | 1.19 | 1.1 | 1.33 | | | |
| BDL171 | 10662.3 | P | | | 0.4 | 0.67 | | 0.5 | 0.15 | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL171 | 10662.3 | Av | | | 1.21 | 1.11 | | 1.18 | 1.46 | | | |
| BDL171 | 10664.1 | P | 0.09 | | <0.0 1 | <0.01 | 0.48 | 0.03 | <0.01 | 0.01 | | |
| BDL171 | 10664.1 | Av | 1.15 | | 1.56 | 1.44 | 1.42 | 1.57 | 1.6 | 1.29 | | |
| BDL171 | 10664.3 | P | 0.34 | 0.47 | 0.24 | 0.04 | 0.46 | 0.08 | 0.38 | 0.48 | | |
| BDL171 | 10664.3 | Av | 1.19 | 1.12 | 1.3 | 1.29 | 1.18 | 1.39 | 1.43 | 1.26 | | |
| BDL171 | 10661.5 | P | 0.51 | | | | | 0.76 | 0.68 | | | |
| BDL171 | 10661.5 | Av | 1.1 | | | | | 1.11 | 1.12 | | | |
| BDL171 | 10662.2 | P | | | 0.39 | | | 0.06 | 0.42 | | | |
| BDL171 | 10662.2 | Av | | | 1.11 | | | 1.47 | 1.14 | | | |
| BDL171 | 10662.3 | P | 0.09 | | <0.0 1 | 0.02 | <0.0 1 | 0.24 | 0.17 | <0.0 1 | | |
| BDL171 | 10662.3 | Av | 1.3 | | 1.39 | 1.5 | 1.33 | 1.46 | 1.37 | 1.23 | | |
| BDL171 | 10663.3 | P | <0.01 | | 0.04 | 0.07 | | <0.01 | 0.08 | | | |
| BDL171 | 10663.3 | Av | 1.2 | | 1.2 | 1.17 | | 1.54 | 1.24 | | | |
| BDL171 | 10664.1 | P | | | 0.71 | 0.79 | | | | | | 0.01 |
| BDL171 | 10664.1 | Av | | | 1.18 | 1.13 | | | | | | 1.03 |
| BDL171 | 10664.3 | P | 0.08 | | 0.18 | 0.22 | | 0.01 | 0.33 | | 0.09 | |
| BDL171 | 10664.3 | Av | 1.18 | | 1.29 | 1.22 | | 1.54 | 1.23 | | 1.03 | |
| BDL173 | 9951.2 | P | | | | | | | | | <0.01 | |
| BDL173 | 9951.2 | Av | | | | | | | | | 1.03 | |
| BDL173 | 9952.1 | P | | | | | 0.61 | | | | | |
| BDL173 | 9952.1 | Av | | | | | 1.13 | | | | | |
| BDL173 | 9954.3 | P | | | | | | | | | <0.01 | 0.02 |
| BDL173 | 9954.3 | Av | | | | | | | | | 1.05 | 1.04 |
| BDL173 | 9953.4 | P | | | | | | | | | | <0.01 |
| BDL173 | 9953.4 | Av | | | | | | | | | | 1.03 |
| BDL177 | 10521.3 | P | | | 0.37 | | 0.2 | | | | | |
| BDL177 | 10521.3 | Av | | | 1.22 | | 1.16 | | | | | |
| BDL177 | 10522.2 | P | | | | | | | | | | <0.01 |
| BDL177 | 10522.2 | Av | | | | | | | | | | 1.05 |
| BDL177 | 10524.2 | P | | | 0.16 | | | 0.21 | 0.28 | | | |
| BDL177 | 10524.2 | Av | | | 1.14 | | | 1.14 | 1.17 | | | |
| BDL182 | 10691.2 | P | | | | 0.14 | 0.59 | 0.08 | | | | |
| BDL182 | 10691.2 | Av | | | | 1.11 | 1.12 | 1.2 | | | | |
| BDL182 | 10692.3 | P | | | 0.53 | 0.2 | | | 0.73 | | | |
| BDL182 | 10692.3 | Av | | | 1.16 | 1.15 | | | 1.13 | | | |
| BDL182 | 10693.2 | P | | | | 0.34 | | 0.18 | | 0.67 | | |
| BDL182 | 10693.2 | Av | | | | 1.13 | | 1.24 | | 1.11 | | |
| BDL182 | 10693.3 | P | | | 0.25 | 0.07 | | 0.05 | 0.25 | | | |
| BDL182 | 10693.3 | Av | | | 1.18 | 1.14 | | 1.42 | 1.35 | | | |
| BDL182 | 10693.5 | P | | | | | | 0.15 | 0.05 | | | |
| BDL182 | 10693.5 | Av | | | | | | 1.18 | 1.29 | | | |
| BDL182 | 10691.2 | P | | | | | | | | | 0.02 | 0.01 |
| BDL182 | 10691.2 | Av | | | | | | | | | 1.06 | 1.04 |
| BDL182 | 10691.4 | P | <0.01 | 0.2 | 0.56 | 0.65 | | <0.01 | 0.13 | | | |
| BDL182 | 10691.4 | Av | 1.25 | 1.15 | 1.19 | 1.12 | | 1.48 | 1.29 | | | |
| BDL182 | 10691.8 | P | | | 0.79 | | | 0.84 | | | | |
| BDL182 | 10691.8 | Av | | | 1.14 | | | 1.14 | | | | |
| BDL182 | 10693.2 | P | | | | | | | | | 0.02 | |
| BDL182 | 10693.2 | Av | | | | | | | | | 1.05 | |
| BDL182 | 10693.3 | P | | | | | | 0.85 | | | | |
| BDL182 | 10693.3 | Av | | | | | | 1.13 | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL183 | 9941.1 | P | | <0.01 | | | 0.26 | | | | | |
| BDL183 | 9941.1 | Av | | 1.09 | | | 1.13 | | | | | |
| BDL183 | 9942.4 | P | | | | | | 0.02 | <0.01 | | | |
| BDL183 | 9942.4 | Av | | | | | | 1.17 | 1.16 | | | |
| BDL183 | 9943.4 | P | | | | 0.21 | 0.15 | | | | | |
| BDL183 | 9943.4 | Av | | | | 1.11 | 1.14 | | | | | |
| BDL183 | 9944.1 | P | 0.05 | <0.01 | 0.09 | 0.01 | 0.3 | <0.01 | 0.02 | | | |
| BDL183 | 9944.1 | Av | 1.04 | 1.1 | 1.19 | 1.15 | 1.13 | 1.31 | 1.21 | | | |
| BDL183 | 9941.1 | P | | | | | 0.64 | | | 0.56 | | |
| BDL183 | 9941.1 | Av | | | | | 1.11 | | | 1.16 | | |
| BDL183 | 9942.1 | P | | | 0.12 | 0.31 | 0.46 | 0.02 | | | | |
| BDL183 | 9942.1 | Av | | | 1.13 | 1.19 | 1.12 | 1.26 | | | | |
| BDL186 | 10002.2 | P | | | | 0.01 | <0.01 | | | 0.1 | | |
| BDL186 | 10002.2 | Av | | | | 1.14 | 1.21 | | | 1.12 | | |
| BDL186 | 10004.3 | P | | | | 0.71 | 0.59 | | | | 0.09 | <0.01 |
| BDL186 | 10004.3 | Av | | | | 1.13 | 1.15 | | | | 1.02 | 1.02 |
| BDL186 | 10001.3 | P | | | | | | 0.3 | | | | |
| BDL186 | 10001.3 | Av | | | | | | 1.25 | | | | |
| BDL186 | 10004.6 | P | | | 0.54 | | | | | | | |
| BDL186 | 10004.6 | Av | | | 1.16 | | | | | | | |
| BDL187 | 10502.2 | P | | | 0.38 | | | | | | | |
| BDL187 | 10502.2 | Av | | | 1.12 | | | | | | | |
| BDL187 | 10502.4 | P | | | | | | 0.59 | | | | |
| BDL187 | 10502.4 | Av | | | | | | 1.1 | | | | |
| BDL187 | 10503.1 | P | | | 0.05 | | | | 0.26 | | | |
| BDL187 | 10503.1 | Av | | | 1.26 | | | | 1.15 | | | |
| BDL187 | 10503.3 | P | | | 0.29 | | | | 0.3 | | | |
| BDL187 | 10503.3 | Av | | | 1.25 | | | | 1.14 | | | |
| BDL187 | 10503.5 | P | | | | | | 0.2 | 0.08 | | | |
| BDL187 | 10503.5 | Av | | | | | | 1.36 | 1.25 | | | |
| BDL188 | 10462.4 | P | | | | 0.09 | | | | | | |
| BDL188 | 10462.4 | Av | | | | 1.06 | | | | | | |
| BDL188 | 10462.1 | P | | | 0.02 | 0.11 | 0.44 | 0.25 | 0.29 | | | |
| BDL188 | 10462.1 | Av | | | 1.28 | 1.32 | 1.19 | 1.15 | 1.14 | | | |
| BDL188 | 10462.4 | P | | | | 0.02 | 0.09 | 0.01 | 0.25 | | | |
| BDL188 | 10462.4 | Av | | | | 1.19 | 1.22 | 1.36 | 1.24 | | | |
| BDL188 | 10464.5 | P | | | | | | 0.33 | | | | |
| BDL188 | 10464.5 | Av | | | | | | 1.19 | | | | |
| BDL190 | 10234.1 | P | | | | 0.5 | | | | | | |
| BDL190 | 10234.1 | Av | | | | 1.11 | | | | | | |
| BDL190 | 10234.2 | P | | | | 0.57 | | | | | 0.01 | |
| BDL190 | 10234.2 | Av | | | | 1.1 | | | | | 1.03 | |
| BDL190 | 10231.1 | P | | | | | | 0.21 | | | | |
| BDL190 | 10231.1 | Av | | | | | | 1.13 | | | | |
| BDL190 | 10231.2 | P | | | | | | 0.02 | | | | |
| BDL190 | 10231.2 | Av | | | | | | 1.24 | | | | |
| BDL190 | 10232.2 | P | | | 0.44 | 0.08 | 0.16 | 0.1 | 0.39 | 0.25 | | |
| BDL190 | 10232.2 | Av | | | 1.18 | 1.23 | 1.18 | 1.29 | 1.16 | 1.16 | | |
| BDL190 | 10233.2 | P | | | 0.05 | 0.02 | <0.01 | 0.02 | 0.05 | 0.05 | | 0.04 |
| BDL190 | 10233.2 | Av | | | 1.18 | 1.31 | 1.21 | 1.25 | 1.15 | 1.31 | | 1.02 |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL190 | 10233.4 | P | | | | | 0.02 | 0.45 | 0.5 | <0.01 | | |
| BDL190 | 10233.4 | Av | | | | | 1.2 | 1.16 | 1.12 | 1.16 | | |
| BDL190 | 10234.2 | P | | | | 0.07 | | 0.05 | | | | |
| BDL190 | 10234.2 | Av | | | | 1.17 | | 1.19 | | | | |
| BDL192 | 9921.3 | P | | | | | | 0.38 | | | | |
| BDL192 | 9921.3 | Av | | | | | | 1.13 | | | | |
| BDL192 | 9921.6 | P | | | 0.12 | 0.36 | 0.55 | | | | | |
| BDL192 | 9921.6 | Av | | | 1.15 | 1.13 | 1.11 | | | | | |
| BDL192 | 9922.1 | P | | | 0.11 | 0.12 | | 0.57 | 0.56 | | | |
| BDL192 | 9922.1 | Av | | | 1.18 | 1.11 | | 1.17 | 1.11 | | | |
| BDL192 | 9921.6 | P | | 0.09 | 0.19 | | 0.51 | | | | | |
| BDL192 | 9921.6 | Av | | 1.07 | 1.1 | | 1.13 | | | | | |
| BDL192 | 9922.5 | P | | 0.01 | 0.35 | 0.29 | | | | 0.5 | | |
| BDL192 | 9922.5 | Av | | 1.06 | 1.18 | 1.2 | | | | 1.11 | | |
| BDL193 | 10152.2 | P | 0.05 | 0.23 | | | | 0.05 | 0.14 | | | |
| BDL193 | 10152.2 | Av | 1.04 | 1.1 | | | | 1.17 | 1.11 | | | |
| BDL193 | 10152.3 | P | | | | | | | | | | 0.02 |
| BDL193 | 10152.3 | Av | | | | | | | | | | 1.02 |
| BDL193 | 10153.2 | P | | | | | | 0.32 | | | | |
| BDL193 | 10153.2 | Av | | | | | | 1.1 | | | | |
| BDL193 | 10153.4 | P | | | 0.37 | | 0.29 | | 0.46 | 0.09 | <0.01 | |
| BDL193 | 10153.4 | Av | | | 1.14 | | 1.15 | | 1.1 | 1.09 | 1.02 | |
| BDL193 | 10153.2 | P | | | | 0.42 | | | | | 0.07 | <0.01 |
| BDL193 | 10153.2 | Av | | | | 1.12 | | | | | 1.02 | 1.03 |
| BDL193 | 10153.3 | P | 0.07 | | 0.37 | 0.01 | | 0.2 | 0.22 | 0.09 | | |
| BDL193 | 10153.3 | Av | 1.1 | | 1.15 | 1.27 | | 1.2 | 1.18 | 1.16 | | |
| BDL193 | 10153.4 | P | | | 0.41 | 0.24 | 0.16 | 0.63 | | | | |
| BDL193 | 10153.4 | Av | | | 1.13 | 1.16 | 1.1 | 1.11 | | | | |
| BDL196 | 10243.1 | P | | | 0.65 | 0.77 | | 0.63 | 0.71 | | | |
| BDL196 | 10243.1 | Av | | | 1.2 | 1.11 | | 1.22 | 1.11 | | | |
| BDL201 | 9961.3 | P | 0.22 | 0.04 | 0.18 | 0.29 | 0.43 | | 0.46 | 0.07 | | 0.09 |
| BDL201 | 9961.3 | Av | 1.1 | 1.06 | 1.28 | 1.16 | 1.33 | | 1.12 | 1.25 | | 1.02 |
| BDL220 | 10331.5 | P | | | | | | | | | | <0.01 |
| BDL220 | 10331.5 | Av | | | | | | | | | | 1.05 |
| BDL220 | 10331.7 | P | | | | | | | | | | 0.39 |
| BDL220 | 10331.7 | Av | | | | | | | | | | 1.1 |
| BDL220 | 10333.5 | P | | | | | 0.49 | | | | | |
| BDL220 | 10333.5 | Av | | | | | 1.18 | | | | | |
| BDL223 | 10793.3 | P | | | | | 0.1 | | | | | |
| BDL223 | 10793.3 | Av | | | | | 1.1 | | | | | |
| BDL223 | 10793.5 | P | <0.01 | | 0.47 | 0.01 | 0.02 | 0.1 | 0.21 | 0.12 | | 0.08 |
| BDL223 | 10793.5 | Av | 1.08 | | 1.1 | 1.23 | 1.15 | 1.22 | 1.16 | 1.12 | | 1.02 |
| BDL223 | 10793.8 | P | 0.08 | | 0.08 | 0.09 | 0.06 | 0.1 | 0.23 | | | |
| BDL223 | 10793.8 | Av | 1.03 | | 1.28 | 1.2 | 1.11 | 1.21 | 1.1 | | | |
| BDL224 | 10451.7 | P | | | | | | 0.57 | | | | |
| BDL224 | 10451.7 | Av | | | | | | 1.11 | | | | |
| BDL224 | 10453.3 | P | | | | | | | | | | 0.5 |
| BDL224 | 10453.3 | Av | | | | | | | | | | 1.12 |
| BDL225 | 10401.4 | P | 0.07 | | | | | | | | | |
| BDL225 | 10401.4 | Av | 1.04 | | | | | | | | | |
| BDL226 | 10861.2 | P | 0.03 | | 0.04 | 0.08 | | 0.25 | 0.08 | 0.29 | 0.01 | |
| BDL226 | 10861.2 | Av | 1.19 | | 1.17 | 1.14 | | 1.37 | 1.31 | 1.12 | 1.06 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL226 | 10864.2 | P | <0.01 | 0.07 | <0.01 | 0.01 | 0.11 | 0.06 | <0.01 | | | |
| BDL226 | 10864.2 | Av | 1.17 | 1.08 | 1.38 | 1.24 | 1.13 | 1.43 | 1.36 | | | |
| BDL227 | 11491.3 | P | | | | <0.01 | | 0.5 | 0.37 | | | |
| BDL227 | 11491.3 | Av | | | | 1.23 | | 1.12 | 1.12 | | | |
| BDL227 | 11492.3 | P | | | 0.04 | <0.01 | 0.06 | 0.03 | 0.04 | 0.35 | | |
| BDL227 | 11492.3 | Av | | | 1.16 | 1.25 | 1.14 | 1.21 | 1.19 | 1.14 | | |
| BDL233 | 10822.1 | P | | | | | | | <0.01 | | | |
| BDL233 | 10822.1 | Av | | | | | | | 1.21 | | | |
| BDL233 | 10825.4 | P | | | | 0.39 | 0.47 | 0.32 | 0.5 | 0.02 | | |
| BDL233 | 10825.4 | Av | | | | 1.32 | 1.29 | 1.27 | 1.18 | 1.12 | | |
| BDL237 | 10893.1 | P | | | 0.07 | | | | | | | |
| BDL237 | 10893.1 | Av | | | 1.17 | | | | | | | |
| BDL237 | 10895.1 | P | | | 0.09 | 0.44 | | 0.16 | 0.26 | | | |
| BDL237 | 10895.1 | Av | | | 1.11 | 1.18 | | 1.22 | 1.1 | | | |
| BDL237 | 10895.2 | P | | | 0.2 | 0.66 | | | | | | |
| BDL237 | 10895.2 | Av | | | 1.13 | 1.12 | | | | | | |
| BDL237 | 10895.3 | P | | | 0.51 | | | 0.36 | 0.64 | | | |
| BDL237 | 10895.3 | Av | | | 1.12 | | | 1.26 | 1.11 | | | |
| BDL237 | 10896.1 | P | | | | 0.11 | | | | 0.52 | | |
| BDL237 | 10896.1 | Av | | | | 1.13 | | | | 1.1 | | |
| BDL238 | 10951.4 | P | | | | 0.09 | | 0.22 | 0.18 | | | |
| BDL238 | 10951.4 | Av | | | | 1.11 | | 1.13 | 1.12 | | | |
| BDL238 | 10952.3 | P | | | | 0.69 | | | | 0.7 | | |
| BDL238 | 10952.3 | Av | | | | 1.1 | | | | 1.1 | | |
| BDL238 | 10954.2 | P | | | 0.08 | <0.01 | <0.01 | 0.11 | <0.01 | | | |
| BDL238 | 10954.2 | Av | | | 1.59 | 1.7 | 1.46 | 1.34 | 1.29 | | | |
| BDL238 | 10954.3 | P | | | 0.67 | | | 0.58 | | | | |
| BDL238 | 10954.3 | Av | | | 1.15 | | | 1.1 | | | | |
| BDL240 | 10802.2 | P | | | 0.05 | 0.04 | <0.01 | <0.01 | 0.08 | 0.05 | | |
| BDL240 | 10802.2 | Av | | | 1.34 | 1.61 | 1.3 | 1.22 | 1.27 | 1.17 | | |
| BDL240 | 10806.2 | P | | | | 0.3 | | | | | | |
| BDL240 | 10806.2 | Av | | | | 1.1 | | | | | | |
| BDL240 | 10806.6 | P | 0.01 | | | | | | | | | 0.09 |
| BDL240 | 10806.6 | Av | 1.06 | | | | | | | | | 1.04 |
| BDL241 | 10873.1 | P | | | <0.01 | 0.52 | 0.1 | 0.09 | 0.06 | | | |
| BDL241 | 10873.1 | Av | | | 1.41 | 1.24 | 1.33 | 1.23 | 1.23 | | | |
| BDL242 | 10731.2 | P | | | 0.05 | 0.45 | 0.62 | 0.49 | 0.45 | | | |
| BDL242 | 10731.2 | Av | | | 1.26 | 1.27 | 1.11 | 1.11 | 1.11 | | | |
| BDL242 | 10731.5 | P | | | 0.05 | | | | | | | |
| BDL242 | 10731.5 | Av | | | 1.13 | | | | | | | |
| BDL242 | 10731.6 | P | | | 0.01 | 0.19 | 0.02 | <0.01 | 0.09 | | 0.03 | |
| BDL242 | 10731.6 | Av | | | 1.46 | 1.43 | 1.37 | 1.29 | 1.21 | | 1.02 | |
| BDL242 | 10731.7 | P | | | 0.04 | | | 0.25 | | | | |
| BDL242 | 10731.7 | Av | | | 1.14 | | | 1.15 | | | | |
| BDL245 | 10813.3 | P | 0.04 | 0.02 | | | | 0.27 | 0.08 | 0.2 | | |
| BDL245 | 10813.3 | Av | 1.07 | 1.08 | | | | 1.14 | 1.2 | 1.15 | | |
| BDL245 | 10816.3 | P | | | | | | | | | | 0.02 |
| BDL245 | 10816.3 | Av | | | | | | | | | | 1.03 |
| BDL245 | 10812.3 | P | | | | | | | | 0.07 | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Pa r</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL245 | 10812.3 | Av | | | | | | | | 1.09 | | |
| BDL245 | 10813.3 | P | | | | | | 0.12 | 0.03 | 0.01 | | |
| BDL245 | 10813.3 | Av | | | | | | 1.14 | 1.11 | 1.16 | | |
| BDL247 | 10911.4 | P | | | | | | | | | | 0.01 |
| BDL247 | 10911.4 | Av | | | | | | | | | | 1.03 |
| BDL247 | 10912.6 | P | | | | | | | | | | 0.02 |
| BDL247 | 10912.6 | Av | | | | | | | | | | 1.02 |
| BDL248 | 11051.1 | P | | | | | | | | | 0.04 | |
| BDL248 | 11051.1 | Av | | | | | | | | | 1.03 | |
| BDL248 | 11054.1 | P | | | | | | | | | 0.06 | |
| BDL248 | 11054.1 | Av | | | | | | | | | 1.04 | |
| BDL250 | 10841.3 | P | | | 0.05 | 0.23 | 0.45 | 0.05 | 0.01 | 0.21 | | |
| BDL250 | 10841.3 | Av | | | 1.31 | 1.31 | 1.12 | 1.38 | 1.32 | 1.1 | | |
| BDL250 | 10842.3 | P | | | | 0.17 | | | | | | |
| BDL250 | 10842.3 | Av | | | | 1.11 | | | | | | |
| BDL250 | 10846.2 | P | | | | 0.47 | | 0.32 | 0.41 | | | |
| BDL250 | 10846.2 | Av | | | | 1.13 | | 1.2 | 1.11 | | | |
| BDL250 | 10846.3 | P | | | 0.54 | 0.46 | 0.51 | | 0.14 | 0.26 | | |
| BDL250 | 10846.3 | Av | | | 1.15 | 1.3 | 1.22 | | 1.25 | 1.15 | | |
| BDL252 | 10882.1 | P | | | 0.26 | 0.25 | 0.24 | 0.33 | 0.51 | 0.54 | 0.01 | |
| BDL252 | 10882.1 | Av | | | 1.35 | 1.36 | 1.22 | 1.35 | 1.28 | 1.21 | 1.02 | |
| BDL252 | 10882.4 | P | | | 0.49 | | | | | | | |
| BDL252 | 10882.4 | Av | | | 1.14 | | | | | | | |
| BDL48 | 10274.4 | P | 0.04 | | | | 0.01 | 0.06 | 0.01 | 0.13 | | |
| BDL48 | 10274.4 | Av | 1.11 | | | | 1.33 | 1.4 | 1.49 | 1.14 | | |
| BDL48 | 10271.1 | P | | | 0.18 | 0.02 | <0.0 1 | 0.29 | | 0.18 | 0.02 | 0.06 |
| BDL48 | 10271.1 | Av | | | 1.13 | 1.21 | 1.24 | 1.11 | | 1.22 | 1.02 | 1.02 |
| BDL48 | 10271.5 | P | | | | | | 0.51 | | | | |
| BDL48 | 10271.5 | Av | | | | | | 1.1 | | | | |
| BDL48 | 10274.3 | P | | | 0.01 | <0.01 | <0.0 1 | <0.01 | <0.01 | <0.0 1 | | |
| BDL48 | 10274.3 | Av | | | 1.24 | 1.33 | 1.16 | 1.44 | 1.32 | 1.17 | | |
| BDL48 | 10274.4 | P | | | 0.11 | 0.02 | 0.15 | 0.53 | 0.15 | 0.3 | | |
| BDL48 | 10274.4 | Av | | | 1.21 | 1.23 | 1.2 | 1.18 | 1.25 | 1.21 | | |
| BDL48 | 10274.5 | P | | | 0.41 | 0.48 | 0.59 | 0.27 | 0.02 | 0.21 | | |
| BDL48 | 10274.5 | Av | | | 1.12 | 1.23 | 1.12 | 1.24 | 1.2 | 1.23 | | |
| BDL63 | 10381.2 | P | | | | | | 0.48 | | | | |
| BDL63 | 10381.2 | Av | | | | | | 1.29 | | | | |
| BDL63 | 10381.1 | P | 0.04 | 0.1 | 0.21 | 0.23 | 0.04 | 0.19 | 0.01 | <0.0 1 | | |
| BDL63 | 10381.1 | Av | 1.1 | 1.05 | 1.22 | 1.34 | 1.29 | 1.34 | 1.26 | 1.25 | | |
| BDL63 | 10381.2 | P | | | 0.21 | 0.5 | 0.48 | 0.17 | 0.01 | 0.23 | | |
| BDL63 | 10381.2 | Av | | | 1.21 | 1.28 | 1.25 | 1.26 | 1.22 | 1.21 | | |
| BDL63 | 10384.8 | P | | 0.1 | | 0.04 | <0.0 1 | 0.33 | 0.14 | <0.0 1 | | |
| BDL63 | 10384.8 | Av | | 1.05 | | 1.2 | 1.2 | 1.15 | 1.1 | 1.25 | | |
| BDL79 | 11042.1 | P | <0.01 | | | 0.12 | | 0.2 | 0.03 | | | |
| BDL79 | 11042.1 | Av | 1.08 | | | 1.1 | | 1.14 | 1.11 | | | |
| BDL79 | 11044.3 | P | | | | 0.12 | | <0.01 | 0.01 | 0.41 | | |
| BDL79 | 11044.3 | Av | | | | 1.12 | | 1.24 | 1.15 | 1.18 | | |
| BDL81 | 10371.8 | P | | | 0.18 | | | | | | | |
| BDL81 | 10371.8 | Av | | | 1.15 | | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>11</i> | <i>12</i> | <i>13</i> | <i>14</i> | <i>15</i> | <i>16</i> | <i>17</i> | <i>18</i> | <i>19</i> | <i>20</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL81 | 10374.1 | P | | | 0.24 | | | | | | | |
| BDL81 | 10374.1 | Av | | | 1.13 | | | | | | | |
| BDL81 | 10371.5 | P | | | | 0.2 | 0.32 | 0.06 | | 0.02 | | |
| BDL81 | 10371.5 | Av | | | | 1.15 | 1.15 | 1.18 | | 1.1 | | |
| BDL81 | 10371.8 | P | | | | 0.72 | 0.62 | 0.68 | 0.57 | 0.49 | | |
| BDL81 | 10371.8 | Av | | | | 1.16 | 1.19 | 1.15 | 1.11 | 1.23 | | |
| BDL81 | 10374.1 | P | | | 0.18 | 0.17 | 0.35 | 0.1 | 0.15 | 0.41 | | |
| BDL81 | 10374.1 | Av | | | 1.41 | 1.41 | 1.35 | 1.3 | 1.35 | 1.26 | | |
| BDL85 | 10411.1 | P | | | 0.16 | 0.34 | 0.26 | 0.23 | 0.62 | <0.01 | | |
| BDL85 | 10411.1 | Av | | | 1.29 | 1.3 | 1.28 | 1.32 | 1.12 | 1.1 | | |
| BDL85 | 10414.1 | P | | | | | | | | | | 0.07 |
| BDL85 | 10414.1 | Av | | | | | | | | | | 1.02 |
| BDL85 | 10414.2 | P | | | 0.71 | | | | | | | |
| BDL85 | 10414.2 | Av | | | 1.1 | | | | | | | |

Table 25. Results of the greenhouse experiments. Provided are the measured values of each parameter [parameters (Par.) 11-20 according to the parameters described in Table 23 above] in plants expressing the indicated polynucleotides. “Ev” = event; “P” = P-value; “Av” = ratio between the averages of event and control. Note that when the average ratio is higher than “1” the effect of exogenous expression of the gene is an increase of the desired trait;

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Table 26
Results from greenhouse experiments

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL102 | 10471.1 | P | | 0.18 | 0.42 | | 0.39 | | 0.46 | | 0.46 | |
| BDL102 | 10471.1 | Av | | 1.15 | 1.82 | | 1.16 | | 1.13 | | 1.13 | |
| BDL102 | 10471.3 | P | | | 0.48 | | | | | | | |
| BDL102 | 10471.3 | Av | | | 1.38 | | | | | | | |
| BDL102 | 10472.1 | P | | 0.01 | 0.54 | | 0.17 | | 0.22 | | 0.22 | 0.43 |
| BDL102 | 10472.1 | Av | | 1.26 | 2.05 | | 1.28 | | 1.24 | | 1.24 | 1.11 |
| BDL102 | 10474.1 | P | | 0.06 | | 0.29 | 0.01 | | 0.02 | 0.17 | 0.02 | 0.1 |
| BDL102 | 10474.1 | Av | | 1.15 | | 1.43 | 1.54 | | 1.48 | 1.14 | 1.48 | 1.29 |
| BDL102 | 10474.2 | P | | 0.03 | | | 0.1 | | 0.18 | | 0.18 | |
| BDL102 | 10474.2 | Av | | 1.14 | | | 1.32 | | 1.25 | | 1.25 | |
| BDL102 | 10474.6 | P | 0.02 | | 0.55 | | | | | | | |
| BDL102 | 10474.6 | Av | 1.02 | | 1.76 | | | | | | | |
| BDL117 | 10071.2 | P | | | | | | 0.24 | | | | |
| BDL117 | 10071.2 | Av | | | | | | 1.15 | | | | |
| BDL117 | 10073.2 | P | | 0.46 | 0.01 | 0.01 | | | | | | |
| BDL117 | 10073.2 | Av | | 1.19 | 1.2 | 1.14 | | | | | | |
| BDL117 | 10074.1 | P | | | 0.53 | | 0.08 | 0.08 | 0.03 | 0.11 | 0.02 | |
| BDL117 | 10074.1 | Av | | | 1.13 | | 1.28 | 1.22 | 1.42 | 1.18 | 1.44 | |
| BDL117 | 10074.4 | P | | | | | 0.33 | | 0.19 | | 0.14 | |
| BDL117 | 10074.4 | Av | | | | | 1.16 | | 1.24 | | 1.26 | |
| BDL117 | 10071.2 | P | | | | | | 0.21 | | | | |
| BDL117 | 10071.2 | Av | | | | | | 1.16 | | | | |
| BDL117 | 10073.1 | P | | | | | 0.35 | | 0.43 | | | 0.47 |
| BDL117 | 10073.1 | Av | | | | | 1.17 | | 1.14 | | | 1.16 |
| BDL117 | 10073.2 | P | | | | | 0.09 | | 0.16 | 0.08 | 0.16 | |
| BDL117 | 10073.2 | Av | | | | | 1.3 | | 1.25 | 1.2 | 1.25 | |
| BDL117 | 10074.1 | P | | | | | 0.16 | 0.29 | 0.08 | 0.1 | 0.08 | |

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| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL117 | 10074.1 | Av | | | | | 1.24 | 1.12 | 1.31 | 1.17 | 1.31 | |
| BDL117 | 10074.4 | P | | 0.71 | | | 0.54 | | 0.43 | 0.27 | 0.43 | |
| BDL117 | 10074.4 | Av | | 1.14 | | | 1.1 | | 1.13 | 1.1 | 1.13 | |
| BDL138 | 9811.1 | P | | | | 0.15 | | | | | | |
| BDL138 | 9811.1 | Av | | | | 1.13 | | | | | | |
| BDL138 | 9811.4 | P | | 0.41 | 0.03 | <0.01 | | | | | | |
| BDL138 | 9811.4 | Av | | 1.21 | 1.07 | 1.26 | | | | | | |
| BDL138 | 9812.1 | P | | <0.01 | 0.42 | <0.01 | | | | | | |
| BDL138 | 9812.1 | Av | | 1.14 | 1.16 | 1.2 | | | | | | |
| BDL138 | 9812.3 | P | 0.07 | | | | | | | | | |
| BDL138 | 9812.3 | Av | 1.02 | | | | | | | | | |
| BDL138 | 9813.1 | P | | | | | | 0.28 | | | | |
| BDL138 | 9813.1 | Av | | | | | | 1.13 | | | | |
| BDL138 | 9813.3 | P | | 0.06 | 0.55 | | | | | | | |
| BDL138 | 9813.3 | Av | | 1.3 | 1.12 | | | | | | | |
| BDL138 | 9811.1 | P | 0.04 | | | | | | | | | |
| BDL138 | 9811.1 | Av | 1.02 | | | | | | | | | |
| BDL138 | 9813.1 | P | | 0.56 | | | | 0.1 | | | | |
| BDL138 | 9813.1 | Av | | 1.19 | | | | 1.18 | | | | |
| BDL138 | 9813.4 | P | | 0.75 | | | | | | | | |
| BDL138 | 9813.4 | Av | | 1.14 | | | | | | | | |
| BDL138 | 9811.4 | P | | 0.29 | | | | | | | | |
| BDL138 | 9811.4 | Av | | 1.1 | | | | | | | | |
| BDL138 | 9812.1 | P | | 0.39 | | | | | | | | |
| BDL138 | 9812.1 | Av | | 1.61 | | | | | | | | |
| BDL138 | 9813.1 | P | | 0.14 | | | | 0.29 | | | | |
| BDL138 | 9813.1 | Av | | 1.33 | | | | 1.12 | | | | |
| BDL138 | 9813.3 | P | | 0.36 | 0.09 | | | | | | | |
| BDL138 | 9813.3 | Av | | 1.87 | 1.07 | | | | | | | |
| BDL140 | 10421.3 | P | | 0.84 | | 0.37 | | | | | | |
| BDL140 | 10421.3 | Av | | 1.16 | | 1.18 | | | | | | |
| BDL140 | 10424.3 | P | | | 0.47 | | | | | | | |
| BDL140 | 10424.3 | Av | | | 1.18 | | | | | | | |
| BDL140 | 10421.2 | P | | 0.02 | 0.22 | | | | | | | |
| BDL140 | 10421.2 | Av | | 1.14 | 1.12 | | | | | | | |
| BDL140 | 10423.1 | P | 0.08 | | | | | | | | | |
| BDL140 | 10423.1 | Av | 1.03 | | | | | | | | | |
| BDL147 | 10301.3 | P | | 0.54 | | | | | | | | |
| BDL147 | 10301.3 | Av | | 1.17 | | | | | | | | |
| BDL147 | 10303.1 | P | 0.01 | | | | 0.53 | | 0.32 | | 0.32 | |
| BDL147 | 10303.1 | Av | 1.02 | | | | 1.11 | | 1.18 | | 1.18 | |
| BDL147 | 10303.6 | P | 0.07 | | | | | | | | | |
| BDL147 | 10303.6 | Av | 1.02 | | | | | | | | | |
| BDL147 | 10304.2 | P | <0.01 | | | | | 0.55 | | | | |
| BDL147 | 10304.2 | Av | 1.04 | | | | | 1.1 | | | | |
| BDL147 | 10301.5 | P | | 0.36 | | | | | | | | |
| BDL147 | 10301.5 | Av | | 1.15 | | | | | | | | |
| BDL147 | 10301.6 | P | | 0.02 | | | | | | | | |
| BDL147 | 10301.6 | Av | | 1.14 | | | | | | | | |
| BDL147 | 10303.1 | P | | 0.01 | | | | | | | | |
| BDL147 | 10303.1 | Av | | 1.29 | | | | | | | | |
| BDL147 | 10303.5 | P | | 0.02 | | 0.43 | | 0.31 | | | | 0.08 |
| BDL147 | 10303.5 | Av | | 1.17 | | 1.17 | | 1.12 | | | | 1.09 |
| BDL147 | 10304.2 | P | | | | | | 0.04 | 0.36 | | 0.36 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL147 | 10304.2 | Av | | | | | | 1.23 | 1.14 | | 1.14 | |
| BDL149 | 9823.1 | P | | 0.04 | 0.05 | 0.11 | | | | | | |
| BDL149 | 9823.1 | Av | | 1.17 | 1.19 | 1.17 | | | | | | |
| BDL149 | 9823.3 | P | | <0.01 | <0.01 | 0.23 | | 0.34 | 0.42 | | | |
| BDL149 | 9823.3 | Av | | 1.17 | 1.14 | 1.12 | | 1.12 | 1.14 | | | |
| BDL149 | 9824.3 | P | | | | | | 0.34 | | | | |
| BDL149 | 9824.3 | Av | | | | | | 1.11 | | | | |
| BDL149 | 9824.4 | P | | | | | 0.28 | | 0.11 | | 0.08 | <0.01 |
| BDL149 | 9824.4 | Av | | | | | 1.17 | | 1.28 | | 1.3 | 1.15 |
| BDL149 | 9823.3 | P | | | | | 0.48 | | 0.48 | | 0.48 | 0.1 |
| BDL149 | 9823.3 | Av | | | | | 1.12 | | 1.12 | | 1.12 | 1.08 |
| BDL149 | 9824.3 | P | | | | | | 0.27 | | | | |
| BDL149 | 9824.3 | Av | | | | | | 1.14 | | | | |
| BDL152 | 10431.1 | P | 0.01 | | | | | | | | | |
| BDL152 | 10431.1 | Av | 1.02 | | | | | | | | | |
| BDL152 | 10432.5 | P | | | | | 0.37 | | | | | |
| BDL152 | 10432.5 | Av | | | | | 1.17 | | | | | |
| BDL152 | 10434.1 | P | | | 0.05 | | | | | | | |
| BDL152 | 10434.1 | Av | | | 1.16 | | | | | | | |
| BDL152 | 10434.4 | P | | 0.58 | 0.27 | | 0.3 | | 0.32 | 0.31 | 0.32 | 0.56 |
| BDL152 | 10434.4 | Av | | 1.14 | 1.17 | | 1.19 | | 1.19 | 1.15 | 1.19 | 1.1 |
| BDL152 | 10431.1 | P | | 0.43 | 0.58 | | | | | | | |
| BDL152 | 10431.1 | Av | | 1.18 | 1.1 | | | | | | | |
| BDL152 | 10431.3 | P | | | | 0.02 | | | | | | |
| BDL152 | 10431.3 | Av | | | | 1.18 | | | | | | |
| BDL152 | 10434.1 | P | | | 0.42 | | | | | | | |
| BDL152 | 10434.1 | Av | | | 1.1 | | | | | | | |
| BDL152 | 10434.4 | P | 0.09 | | | | | | | | | |
| BDL152 | 10434.4 | Av | 1.03 | | | | | | | | | |
| BDL153 | 10141.3 | P | 0.09 | | | | 0.12 | | 0.07 | 0.23 | 0.05 | |
| BDL153 | 10141.3 | Av | 1.02 | | | | 1.25 | | 1.33 | 1.13 | 1.35 | |
| BDL153 | 10142.2 | P | | | | | 0.04 | 0.09 | 0.01 | 0.11 | <0.01 | |
| BDL153 | 10142.2 | Av | | | | | 1.37 | 1.22 | 1.56 | 1.2 | 1.58 | |
| BDL153 | 10143.1 | P | | | | | 0.45 | | 0.48 | | 0.4 | |
| BDL153 | 10143.1 | Av | | | | | 1.12 | | 1.12 | | 1.14 | |
| BDL153 | 10144.1 | P | | | | | 0.52 | 0.25 | 0.53 | | 0.45 | |
| BDL153 | 10144.1 | Av | | | | | 1.1 | 1.13 | 1.11 | | 1.12 | |
| BDL153 | 10141.3 | P | | 0.22 | 0.67 | | 0.48 | | 0.39 | | 0.39 | |
| BDL153 | 10141.3 | Av | | 1.28 | 1.12 | | 1.11 | | 1.14 | | 1.14 | |
| BDL153 | 10142.2 | P | | 0.05 | <0.01 | 0.63 | 0.11 | | 0.06 | 0.04 | 0.06 | |
| BDL153 | 10142.2 | Av | | 1.36 | 1.2 | 1.1 | 1.26 | | 1.33 | 1.18 | 1.33 | |
| BDL153 | 10142.3 | P | | | | | 0.26 | | 0.29 | 0.2 | 0.29 | |
| BDL153 | 10142.3 | Av | | | | | 1.19 | | 1.18 | 1.12 | 1.18 | |
| BDL153 | 10143.1 | P | | 0.09 | | | | | | | | 0.25 |
| BDL153 | 10143.1 | Av | | 1.09 | | | | | | | | 1.11 |
| BDL153 | 10143.2 | P | | 0.05 | | | 0.47 | 0.22 | 0.36 | 0.23 | 0.36 | 0.23 |
| BDL153 | 10143.2 | Av | | 1.11 | | | 1.11 | 1.15 | 1.15 | 1.1 | 1.15 | 1.13 |
| BDL153 | 10144.1 | P | | | | | 0.28 | | 0.26 | 0.06 | 0.26 | |
| BDL153 | 10144.1 | Av | | | | | 1.17 | | 1.18 | 1.17 | 1.18 | |
| BDL154 | 10703.1 | P | | 0.11 | 0.64 | 0.67 | | | | | | |
| BDL154 | 10703.1 | Av | | 1.1 | 1.2 | 1.27 | | | | | | |
| BDL154 | 10703.5 | P | | 0.37 | 0.44 | 0.66 | | | | | | |
| BDL154 | 10703.5 | Av | | 1.18 | 1.26 | 1.13 | | | | | | |
| BDL154 | 10703.6 | P | | 0.25 | 0.59 | 0.59 | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL154 | 10703.6 | Av | | 1.28 | 1.47 | 1.29 | | | | | | |
| BDL154 | 10703.8 | P | | 0.29 | | | 0.58 | | 0.58 | | 0.58 | |
| BDL154 | 10703.8 | Av | | 1.17 | | | 1.1 | | 1.1 | | 1.1 | |
| BDL155 | 9991.3 | P | | | | 0.65 | | | | | | |
| BDL155 | 9991.3 | Av | | | | 1.11 | | | | | | |
| BDL155 | 9991.5 | P | | | 0.5 | | 0.34 | | 0.57 | 0.4 | 0.57 | 0.32 |
| BDL155 | 9991.5 | Av | | | 1.23 | | 1.17 | | 1.11 | 1.12 | 1.11 | 1.22 |
| BDL155 | 9991.9 | P | | | 0.39 | | | | | | | |
| BDL155 | 9991.9 | Av | | | 1.22 | | | | | | | |
| BDL155 | 9994.3 | P | | | 0.49 | 0.56 | 0.4 | | 0.31 | 0.49 | 0.31 | |
| BDL155 | 9994.3 | Av | | | 1.1 | 1.14 | 1.15 | | 1.19 | 1.1 | 1.19 | |
| BDL155 | 9994.5 | P | | | | | | 0.41 | | | | |
| BDL155 | 9994.5 | Av | | | | | | 1.14 | | | | |
| BDL157 | 9911.3 | P | | 0.25 | 0.14 | | | | | | | |
| BDL157 | 9911.3 | Av | | 1.54 | 1.11 | | | | | | | |
| BDL157 | 9911.4 | P | | <0.01 | | | | | | | | |
| BDL157 | 9911.4 | Av | | 1.26 | | | | | | | | |
| BDL157 | 9914.2 | P | | 0.37 | | | | | | | | |
| BDL157 | 9914.2 | Av | | 1.23 | | | | | | | | |
| BDL157 | 9911.3 | P | | 0.08 | 0.28 | | | | | | | |
| BDL157 | 9911.3 | Av | | 1.15 | 1.25 | | | | | | | |
| BDL157 | 9911.4 | P | | 0.46 | | | | | | | | |
| BDL157 | 9911.4 | Av | | 1.23 | | | | | | | | |
| BDL157 | 9913.3 | P | | 0.37 | | | | | | | | |
| BDL157 | 9913.3 | Av | | 1.21 | | | | | | | | |
| BDL157 | 9914.2 | P | | | | | | | | | | 0.45 |
| BDL157 | 9914.2 | Av | | | | | | | | | | 1.16 |
| BDL160 | 10011.5 | P | | 0.34 | | 0.54 | | 0.35 | | | | |
| BDL160 | 10011.5 | Av | | 1.59 | | 1.26 | | 1.15 | | | | |
| BDL160 | 10011.6 | P | | 0.03 | 0.61 | 0.67 | | | | | | |
| BDL160 | 10011.6 | Av | | 1.15 | 1.23 | 1.16 | | | | | | |
| BDL160 | 10011.7 | P | | 0.02 | | | | | | | | |
| BDL160 | 10011.7 | Av | | 1.16 | | | | | | | | |
| BDL160 | 10013.1 | P | | 0.01 | | 0.41 | | | | | | |
| BDL160 | 10013.1 | Av | | 1.32 | | 1.27 | | | | | | |
| BDL160 | 10015.1 | P | | 0.09 | | 0.09 | | | | | | |
| BDL160 | 10015.1 | Av | | 1.1 | | 1.14 | | | | | | |
| BDL162 | 10491.1 | P | | 0.42 | | | | | | | | |
| BDL162 | 10491.1 | Av | | 1.44 | | | | | | | | |
| BDL162 | 10492.2 | P | | | | | 0.04 | | 0.09 | 0.27 | 0.09 | 0.05 |
| BDL162 | 10492.2 | Av | | | | | 1.4 | | 1.34 | 1.17 | 1.34 | 1.44 |
| BDL162 | 10492.4 | P | | 0.37 | 0.39 | | | 0.55 | | | | |
| BDL162 | 10492.4 | Av | | 1.83 | 1.25 | | | 1.11 | | | | |
| BDL162 | 10494.1 | P | | | 0.63 | | | | | | | |
| BDL162 | 10494.1 | Av | | | 1.13 | | | | | | | |
| BDL167 | 10042.3 | P | | 0.19 | | | | | | | | |
| BDL167 | 10042.3 | Av | | 1.21 | | | | | | | | |
| BDL167 | 10042.3 | P | | | | | | 0.24 | | | | |
| BDL167 | 10042.3 | Av | | | | | | 1.15 | | | | |
| BDL167 | 10043.2 | P | | 0.13 | | | | | | | | 0.6 |
| BDL167 | 10043.2 | Av | | 1.13 | | | | | | | | 1.14 |
| BDL167 | 10043.3 | P | | | | | 0.44 | | | | | 0.27 |
| BDL167 | 10043.3 | Av | | | | | 1.12 | | | | | 1.12 |
| BDL167 | 10043.4 | P | | 0.05 | | 0.33 | | | | | | 0.14 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL167 | 10043.4 | Av | | 1.16 | | 1.12 | | | | | | 1.46 |
| BDL167 | 10044.2 | P | | 0.2 | | | 0.27 | | 0.2 | | 0.2 | 0.24 |
| BDL167 | 10044.2 | Av | | 1.18 | | | 1.18 | | 1.21 | | 1.21 | 1.19 |
| BDL168 | 9881.3 | P | | | | | 0.01 | | 0.01 | 0.04 | 0.01 | |
| BDL168 | 9881.3 | Av | | | | | 1.44 | | 1.48 | 1.23 | 1.5 | |
| BDL168 | 9881.4 | P | | | 0.36 | | 0.06 | 0.05 | 0.07 | 0.11 | 0.05 | |
| BDL168 | 9881.4 | Av | | | 1.14 | | 1.31 | 1.24 | 1.33 | 1.18 | 1.35 | |
| BDL168 | 9882.1 | P | | | | | | | | | 0.51 | |
| BDL168 | 9882.1 | Av | | | | | | | | | 1.11 | |
| BDL168 | 9882.3 | P | | | | | 0.08 | | 0.09 | 0.16 | 0.07 | |
| BDL168 | 9882.3 | Av | | | | | 1.31 | | 1.33 | 1.17 | 1.35 | |
| BDL168 | 9884.4 | P | <0.01 | | | | 0.32 | | 0.46 | 0.2 | 0.39 | |
| BDL168 | 9884.4 | Av | 1.03 | | | | 1.17 | | 1.14 | 1.16 | 1.16 | |
| BDL168 | 9881.3 | P | | | 0.66 | | | | | | | <0.01 |
| BDL168 | 9881.3 | Av | | | 1.1 | | | | | | | 1.19 |
| BDL168 | 9881.4 | P | | 0.12 | | | 0.44 | | 0.34 | 0.14 | 0.34 | |
| BDL168 | 9881.4 | Av | | 1.17 | | | 1.13 | | 1.16 | 1.13 | 1.16 | |
| BDL168 | 9882.1 | P | | | | | 0.53 | | 0.39 | | | 0.58 |
| BDL168 | 9882.1 | Av | | | | | 1.1 | | 1.14 | | | 1.13 |
| BDL168 | 9882.3 | P | | 0.01 | 0.42 | | | 0.35 | | | | 0.18 |
| BDL168 | 9882.3 | Av | | 1.19 | 1.1 | | | 1.12 | | | | 1.2 |
| BDL168 | 9883.3 | P | | | 0.06 | | | | | | | |
| BDL168 | 9883.3 | Av | | | 1.09 | | | | | | | |
| BDL168 | 9884.1 | P | | | | | | | | 0.07 | | |
| BDL168 | 9884.1 | Av | | | | | | | | 1.17 | | |
| BDL169 | 10743.4 | P | | | | | 0.54 | | 0.37 | | 0.65 | |
| BDL169 | 10743.4 | Av | | | | | 1.11 | | 1.18 | | 1.1 | |
| BDL169 | 10744.1 | P | | | 0.28 | | | 0.3 | | | | |
| BDL169 | 10744.1 | Av | | | 1.12 | | | 1.13 | | | | |
| BDL169 | 10747.1 | P | | 0.6 | 0.53 | | | | | | | |
| BDL169 | 10747.1 | Av | | 1.12 | 1.17 | | | | | | | |
| BDL169 | 10747.5 | P | | | | | | | 0.61 | | 0.44 | |
| BDL169 | 10747.5 | Av | | | | | | | 1.1 | | 1.16 | |
| BDL169 | 10741.3 | P | | 0.73 | | | | | | | | |
| BDL169 | 10741.3 | Av | | 1.1 | | | | | | | | |
| BDL169 | 10744.2 | P | | | | | 0.04 | | 0.05 | 0.07 | 0.05 | 0.84 |
| BDL169 | 10744.2 | Av | | | | | 1.43 | | 1.41 | 1.19 | 1.41 | 1.1 |
| BDL169 | 10747.1 | P | | | 0.65 | 0.43 | 0.35 | | 0.43 | | 0.43 | |
| BDL169 | 10747.1 | Av | | | 1.21 | 1.24 | 1.18 | | 1.15 | | 1.15 | |
| BDL169 | 10747.3 | P | | | | 0.4 | | | | | | |
| BDL169 | 10747.3 | Av | | | | 2.16 | | | | | | |
| BDL169 | 10747.5 | P | | | | | 0.16 | | 0.53 | | 0.53 | |
| BDL169 | 10747.5 | Av | | | | | 1.27 | | 1.11 | | 1.11 | |
| BDL171 | 10661.2 | P | | | | | 0.3 | | 0.31 | 0.54 | 0.31 | 0.34 |
| BDL171 | 10661.2 | Av | | | | | 1.19 | | 1.21 | 1.1 | 1.21 | 1.3 |
| BDL171 | 10661.5 | P | | | 0.36 | | | | | | | |
| BDL171 | 10661.5 | Av | | | 1.13 | | | | | | | |
| BDL171 | 10664.1 | P | | | 0.02 | | 0.07 | | 0.03 | 0.28 | 0.03 | 0.67 |
| BDL171 | 10664.1 | Av | | | 1.19 | | 1.39 | | 1.48 | 1.17 | 1.48 | 1.22 |
| BDL171 | 10664.3 | P | | | | | 0.34 | | 0.08 | 0.46 | 0.08 | 0.61 |
| BDL171 | 10664.3 | Av | | | | | 1.17 | | 1.36 | 1.11 | 1.36 | 1.25 |
| BDL171 | 10662.2 | P | | 0.09 | 0.07 | | | | | | | |
| BDL171 | 10662.2 | Av | | 1.45 | 1.45 | | | | | | | |
| BDL171 | 10662.3 | P | | | 0.42 | | 0.07 | | 0.11 | 0.21 | 0.07 | 0.6 |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL171 | 10662.3 | Av | | | 1.2 | | 1.33 | | 1.32 | 1.16 | 1.4 | 1.15 |
| BDL171 | 10663.3 | P | | 0.22 | 0.01 | 0.56 | | | | | | |
| BDL171 | 10663.3 | Av | | 1.19 | 1.51 | 1.14 | | | | | | |
| BDL171 | 10664.1 | P | | | | | | | | | 0.68 | |
| BDL171 | 10664.1 | Av | | | | | | | | | 1.1 | |
| BDL171 | 10664.3 | P | 0.09 | | 0.07 | | | | 0.48 | | 0.34 | |
| BDL171 | 10664.3 | Av | 1.02 | | 1.22 | | | | 1.14 | | 1.21 | |
| BDL173 | 9952.1 | P | | | 0.18 | | 0.39 | 0.22 | 0.51 | | 0.44 | |
| BDL173 | 9952.1 | Av | | | 1.13 | | 1.14 | 1.15 | 1.12 | | 1.13 | |
| BDL173 | 9954.2 | P | | | | 0.09 | | 0.35 | | | | |
| BDL173 | 9954.2 | Av | | | | 1.08 | | 1.11 | | | | |
| BDL173 | 9953.4 | P | 0.03 | | | | | | | | | 0.23 |
| BDL173 | 9953.4 | Av | 1.02 | | | | | | | | | 1.3 |
| BDL173 | 9954.2 | P | 0.02 | | | | | | | | | 0.1 |
| BDL173 | 9954.2 | Av | 1.02 | | | | | | | | | 1.11 |
| BDL176 | 9891.2 | P | | 0.6 | 0.58 | | | | | | | |
| BDL176 | 9891.2 | Av | | 1.24 | 1.19 | | | | | | | |
| BDL176 | 9892.3 | P | | 0.38 | | | | | | | | |
| BDL176 | 9892.3 | Av | | 1.89 | | | | | | | | |
| BDL176 | 9893.2 | P | | 0.73 | | | | | | | | |
| BDL176 | 9893.2 | Av | | 1.11 | | | | | | | | |
| BDL176 | 9893.3 | P | 0.01 | | | | | | | | | 0.37 |
| BDL176 | 9893.3 | Av | 1.02 | | | | | | | | | 1.12 |
| BDL177 | 10521.3 | P | | | | | 0.41 | | | 0.53 | | |
| BDL177 | 10521.3 | Av | | | | | 1.15 | | | 1.1 | | |
| BDL177 | 10522.2 | P | | 0.44 | | | | | | | | |
| BDL177 | 10522.2 | Av | | 1.19 | | | | | | | | |
| BDL182 | 10691.2 | P | | | 0.45 | | 0.35 | | 0.57 | 0.52 | 0.57 | |
| BDL182 | 10691.2 | Av | | | 1.11 | | 1.17 | | 1.11 | 1.1 | 1.11 | |
| BDL182 | 10693.2 | P | | 0.12 | | | | | | | | |
| BDL182 | 10693.2 | Av | | 1.28 | | | | | | | | |
| BDL182 | 10693.3 | P | | | | | | | 0.55 | | 0.55 | |
| BDL182 | 10693.3 | Av | | | | | | | 1.11 | | 1.11 | |
| BDL182 | 10693.5 | P | | | 0.01 | 0.07 | | | | | | |
| BDL182 | 10693.5 | Av | | | 1.28 | 1.08 | | | | | | |
| BDL182 | 10691.2 | P | | | | 0.58 | | | | | | |
| BDL182 | 10691.2 | Av | | | | 1.12 | | | | | | |
| BDL182 | 10691.4 | P | 0.09 | | 0.29 | | | 0.11 | | | | |
| BDL182 | 10691.4 | Av | 1.02 | | 1.27 | | | 1.2 | | | | |
| BDL182 | 10691.8 | P | | | 0.61 | | | | | | | |
| BDL182 | 10691.8 | Av | | | 1.11 | | | | | | | |
| BDL182 | 10693.2 | P | | | 0.38 | 0.57 | | 0.37 | | | | |
| BDL182 | 10693.2 | Av | | | 1.1 | 1.13 | | 1.12 | | | | |
| BDL182 | 10693.3 | P | | 0.69 | 0.43 | 0.46 | | | | | | |
| BDL182 | 10693.3 | Av | | 1.25 | 1.59 | 1.25 | | | | | | |
| BDL183 | 9941.1 | P | | | | | 0.37 | 0.25 | 0.5 | | 0.42 | |
| BDL183 | 9941.1 | Av | | | | | 1.14 | 1.14 | 1.12 | | 1.13 | |
| BDL183 | 9942.1 | P | | | | | | | | | | 0.55 |
| BDL183 | 9942.1 | Av | | | | | | | | | | 1.12 |
| BDL183 | 9942.4 | P | | 0.22 | 0.09 | 0.01 | | 0.07 | | | 0.53 | |
| BDL183 | 9942.4 | Av | | 1.24 | 1.17 | 1.13 | | 1.21 | | | 1.11 | |
| BDL183 | 9943.4 | P | | | | | 0.31 | | 0.53 | 0.37 | | |
| BDL183 | 9943.4 | Av | | | | | 1.16 | | 1.11 | 1.1 | | |
| BDL183 | 9944.1 | P | | | | | 0.46 | | 0.23 | | 0.18 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL183 | 9944.1 | Av | | | | | 1.12 | | 1.21 | | 1.23 | |
| BDL183 | 9944.4 | P | <0.01 | | | | | | | | | |
| BDL183 | 9944.4 | Av | 1.03 | | | | | | | | | |
| BDL183 | 9941.1 | P | | | | | 0.38 | | 0.42 | 0.21 | 0.42 | |
| BDL183 | 9941.1 | Av | | | | | 1.15 | | 1.13 | 1.13 | 1.13 | |
| BDL183 | 9942.1 | P | | 0.17 | | | 0.48 | | 0.42 | | 0.42 | |
| BDL183 | 9942.1 | Av | | 1.15 | | | 1.11 | | 1.13 | | 1.13 | |
| BDL183 | 9942.4 | P | | 0.02 | 0.21 | | | | | | | |
| BDL183 | 9942.4 | Av | | 1.16 | 1.13 | | | | | | | |
| BDL183 | 9943.4 | P | | 0.35 | | | | 0.33 | | | | 0.12 |
| BDL183 | 9943.4 | Av | | 1.24 | | | | 1.13 | | | | 1.16 |
| BDL183 | 9944.2 | P | | 0.59 | 0.5 | | | | | | | |
| BDL183 | 9944.2 | Av | | 1.12 | 1.14 | | | | | | | |
| BDL186 | 10002.2 | P | | | | | 0.15 | 0.23 | 0.14 | 0.24 | 0.1 | |
| BDL186 | 10002.2 | Av | | | | | 1.23 | 1.14 | 1.26 | 1.13 | 1.28 | |
| BDL186 | 10004.3 | P | | | | | 0.32 | | 0.39 | 0.2 | 0.33 | |
| BDL186 | 10004.3 | Av | | | | | 1.16 | | 1.16 | 1.16 | 1.18 | |
| BDL186 | 10001.3 | P | | | 0.46 | | | | | | | |
| BDL186 | 10001.3 | Av | | | 1.1 | | | | | | | |
| BDL186 | 10004.3 | P | | 0.55 | | | | | | | | |
| BDL186 | 10004.3 | Av | | 1.15 | | | | | | | | |
| BDL187 | 10502.2 | P | | 0.43 | | | | | | | | |
| BDL187 | 10502.2 | Av | | 1.21 | | | | | | | | |
| BDL187 | 10501.2 | P | 0.01 | 0.58 | | | | | | | | |
| BDL187 | 10501.2 | Av | 1.02 | 1.38 | | | | | | | | |
| BDL187 | 10502.4 | P | | 0.66 | | | | | | | | |
| BDL187 | 10502.4 | Av | | 1.1 | | | | | | | | |
| BDL187 | 10503.5 | P | | 0.38 | 0.2 | 0.34 | | | | | | |
| BDL187 | 10503.5 | Av | | 1.13 | 1.24 | 1.12 | | | | | | |
| BDL188 | 10462.1 | P | | 0.46 | | | | | | | | |
| BDL188 | 10462.1 | Av | | 1.41 | | | | | | | | |
| BDL188 | 10464.5 | P | | | | | | 0.33 | | | | |
| BDL188 | 10464.5 | Av | | | | | | 1.12 | | | | |
| BDL188 | 10462.1 | P | | | | | 0.38 | | 0.35 | | 0.35 | |
| BDL188 | 10462.1 | Av | | | | | 1.16 | | 1.18 | | 1.18 | |
| BDL188 | 10462.4 | P | 0.02 | 0.41 | | | 0.26 | | 0.24 | | 0.24 | |
| BDL188 | 10462.4 | Av | 1.02 | 1.32 | | | 1.2 | | 1.22 | | 1.22 | |
| BDL188 | 10464.3 | P | | 0.66 | | | | | | | | |
| BDL188 | 10464.3 | Av | | 1.24 | | | | | | | | |
| BDL188 | 10464.5 | P | | 0.29 | 0.1 | | | | | | | |
| BDL188 | 10464.5 | Av | | 1.38 | 1.12 | | | | | | | |
| BDL190 | 10232.2 | P | | | | | | | | | | 0.6 |
| BDL190 | 10232.2 | Av | | | | | | | | | | 1.1 |
| BDL190 | 10233.4 | P | | | | | | | | | | 0.01 |
| BDL190 | 10233.4 | Av | | | | | | | | | | 1.2 |
| BDL190 | 10234.1 | P | 0.01 | | | | | | | | | 0.4 |
| BDL190 | 10234.1 | Av | 1.02 | | | | | | | | | 1.14 |
| BDL190 | 10231.1 | P | | 0.42 | 0.24 | | | | | | | |
| BDL190 | 10231.1 | Av | | 1.18 | 1.21 | | | | | | | |
| BDL190 | 10231.2 | P | | 0.64 | | | | | | | | 0.5 |
| BDL190 | 10231.2 | Av | | 1.14 | | | | | | | | 1.2 |
| BDL190 | 10232.2 | P | | <0.01 | | | 0.26 | | 0.14 | | 0.14 | |
| BDL190 | 10232.2 | Av | | 1.29 | | | 1.18 | | 1.25 | | 1.25 | |
| BDL190 | 10233.2 | P | | | | | 0.1 | 0.29 | 0.05 | 0.01 | 0.05 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL190 | 10233.2 | Av | | | | | 1.25 | 1.13 | 1.32 | 1.24 | 1.32 | |
| BDL190 | 10233.4 | P | | | | | 0.16 | | 0.29 | 0.29 | 0.29 | |
| BDL190 | 10233.4 | Av | | | | | 1.23 | | 1.17 | 1.1 | 1.17 | |
| BDL190 | 10234.2 | P | | 0.04 | | | | | | | | 0.02 |
| BDL190 | 10234.2 | Av | | 1.11 | | | | | | | | 1.09 |
| BDL192 | 9921.3 | P | | 0.54 | 0.56 | | | 0.16 | | | | |
| BDL192 | 9921.3 | Av | | 1.19 | 1.11 | | | 1.16 | | | | |
| BDL192 | 9921.6 | P | | | | | 0.51 | | 0.47 | | 0.4 | |
| BDL192 | 9921.6 | Av | | | | | 1.1 | | 1.12 | | 1.14 | |
| BDL192 | 9922.1 | P | | | | | | | | | 0.52 | |
| BDL192 | 9922.1 | Av | | | | | | | | | 1.11 | |
| BDL192 | 9922.2 | P | <0.01 | | | | | | | | | |
| BDL192 | 9922.2 | Av | 1.02 | | | | | | | | | |
| BDL192 | 9921.6 | P | | | | | 0.49 | 0.03 | 0.45 | | 0.45 | |
| BDL192 | 9921.6 | Av | | | | | 1.15 | 1.25 | 1.16 | | 1.16 | |
| BDL192 | 9922.5 | P | | | | | | | 0.54 | | | 0.51 |
| BDL192 | 9922.5 | Av | | | | | | | 1.13 | | | 1.15 |
| BDL193 | 10152.2 | P | | | | | | 0.15 | | | | |
| BDL193 | 10152.2 | Av | | | | | | 1.17 | | | | |
| BDL193 | 10152.3 | P | | | | 0.3 | | 0.1 | | | | |
| BDL193 | 10152.3 | Av | | | | 1.11 | | 1.2 | | | | |
| BDL193 | 10153.2 | P | | | | | | 0.24 | | | | |
| BDL193 | 10153.2 | Av | | | | | | 1.14 | | | | |
| BDL193 | 10153.4 | P | 0.04 | | | | 0.39 | | 0.4 | | 0.33 | |
| BDL193 | 10153.4 | Av | 1.02 | | | | 1.14 | | 1.14 | | 1.16 | |
| BDL193 | 10152.2 | P | | | 0.7 | | | | | | | |
| BDL193 | 10152.2 | Av | | | 1.12 | | | | | | | |
| BDL193 | 10152.3 | P | | | | | | 0.14 | | | | |
| BDL193 | 10152.3 | Av | | | | | | 1.16 | | | | |
| BDL193 | 10153.2 | P | 0.01 | | | | | | | | | |
| BDL193 | 10153.2 | Av | 1.02 | | | | | | | | | |
| BDL193 | 10153.3 | P | | 0.35 | | | | 0.4 | 0.48 | | 0.48 | |
| BDL193 | 10153.3 | Av | | 1.22 | | | | 1.1 | 1.14 | | 1.14 | |
| BDL193 | 10153.4 | P | | | | | 0.63 | | 0.5 | | 0.5 | |
| BDL193 | 10153.4 | Av | | | | | 1.1 | | 1.14 | | 1.14 | |
| BDL196 | 10241.3 | P | | 0.5 | | | | | | | | |
| BDL196 | 10241.3 | Av | | 1.1 | | | | | | | | |
| BDL196 | 10243.1 | P | | | 0.01 | | | | 0.56 | | 0.56 | |
| BDL196 | 10243.1 | Av | | | 1.08 | | | | 1.14 | | 1.14 | |
| BDL196 | 10243.2 | P | | 0.37 | | | | | | | | |
| BDL196 | 10243.2 | Av | | 1.29 | | | | | | | | |
| BDL196 | 10244.1 | P | | 0.02 | 0.22 | 0.82 | | | | | | 0.02 |
| BDL196 | 10244.1 | Av | | 1.21 | 1.11 | 1.1 | | | | | | 1.13 |
| BDL201 | 9961.3 | P | | | | | 0.12 | | 0.12 | 0.31 | 0.12 | |
| BDL201 | 9961.3 | Av | | | | | 1.31 | | 1.32 | 1.16 | 1.32 | |
| BDL201 | 9961.4 | P | | | 0.62 | | | | | | | |
| BDL201 | 9961.4 | Av | | | 1.14 | | | | | | | |
| BDL201 | 9961.6 | P | 0.01 | 0.01 | | | | | | | | |
| BDL201 | 9961.6 | Av | 1.02 | 1.54 | | | | | | | | |
| BDL201 | 9963.6 | P | | 0.46 | 0.37 | 0.21 | | | | | | |
| BDL201 | 9963.6 | Av | | 1.29 | 1.13 | 1.15 | | | | | | |
| BDL220 | 10331.5 | P | | 0.76 | | | | | | | | |
| BDL220 | 10331.5 | Av | | 1.13 | | | | | | | | |
| BDL220 | 10331.7 | P | | | 0.62 | 0.42 | | 0.29 | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL220 | 10331.7 | Av | | | 1.21 | 1.17 | | 1.18 | | | | |
| BDL220 | 10333.2 | P | | 0.62 | | | | | | | | |
| BDL220 | 10333.2 | Av | | 1.49 | | | | | | | | |
| BDL220 | 10333.5 | P | | | | 0.01 | 0.25 | | | 0.26 | | 0.65 |
| BDL220 | 10333.5 | Av | | | | 1.13 | 1.22 | | | 1.18 | | 1.14 |
| BDL220 | 10334.1 | P | <0.01 | | 0.36 | 0.64 | | | | | | |
| BDL220 | 10334.1 | Av | 1.04 | | 1.31 | 1.11 | | | | | | |
| BDL223 | 10791.1 | P | | | | 0.51 | | | | | | |
| BDL223 | 10791.1 | Av | | | | 1.78 | | | | | | |
| BDL223 | 10793.1 | P | | 0.02 | 0.58 | | | | | | | |
| BDL223 | 10793.1 | Av | | 1.16 | 1.34 | | | | | | | |
| BDL223 | 10793.3 | P | | | | 0.7 | | | | | | |
| BDL223 | 10793.3 | Av | | | | 1.1 | | | | | | |
| BDL223 | 10793.5 | P | | 0.01 | | <0.01 | 0.42 | | 0.48 | | 0.48 | 0.18 |
| BDL223 | 10793.5 | Av | | 1.18 | | 1.41 | 1.15 | | 1.13 | | 1.13 | 1.17 |
| BDL223 | 10793.8 | P | | | 0.6 | | | | | | | |
| BDL223 | 10793.8 | Av | | | 1.36 | | | | | | | |
| BDL224 | 10451.3 | P | | | | | | | 0.61 | 0.5 | 0.61 | |
| BDL224 | 10451.3 | Av | | | | | | | 1.1 | 1.11 | 1.1 | |
| BDL224 | 10451.7 | P | | | | | | | | | | 0.78 |
| BDL224 | 10451.7 | Av | | | | | | | | | | 1.11 |
| BDL224 | 10451.8 | P | | 0.03 | | | | | | | | 0.54 |
| BDL224 | 10451.8 | Av | | 1.78 | | | | | | | | 1.11 |
| BDL224 | 10453.1 | P | | | | | | | | | | 0.77 |
| BDL224 | 10453.1 | Av | | | | | | | | | | 1.11 |
| BDL224 | 10453.3 | P | | 0.62 | | | | 0.39 | | | | |
| BDL224 | 10453.3 | Av | | 1.82 | | | | 1.14 | | | | |
| BDL225 | 10401.4 | P | | | | | | 0.18 | | | | |
| BDL225 | 10401.4 | Av | | | | | | 1.17 | | | | |
| BDL225 | 10402.2 | P | | 0.29 | 0.74 | | | | | | | |
| BDL225 | 10402.2 | Av | | 1.28 | 1.1 | | | | | | | |
| BDL225 | 10402.5 | P | | | | 0.38 | | | | | | |
| BDL225 | 10402.5 | Av | | | | 1.13 | | | | | | |
| BDL225 | 10401.4 | P | | 0.5 | | | | | | | | 0.65 |
| BDL225 | 10401.4 | Av | | 1.12 | | | | | | | | 1.15 |
| BDL225 | 10402.2 | P | | | | 0.42 | | | | | | 0.38 |
| BDL225 | 10402.2 | Av | | | | 1.1 | | | | | | 1.15 |
| BDL225 | 10402.6 | P | | | | | | | | | | 0.38 |
| BDL225 | 10402.6 | Av | | | | | | | | | | 1.15 |
| BDL225 | 10402.9 | P | | | 0.07 | 0.01 | | | | | | |
| BDL225 | 10402.9 | Av | | | 1.14 | 1.15 | | | | | | |
| BDL226 | 10861.2 | P | | | 0.53 | 0.54 | | | | | | |
| BDL226 | 10861.2 | Av | | | 1.22 | 1.12 | | | | | | |
| BDL226 | 10862.2 | P | 0.03 | | | | | | | | | |
| BDL226 | 10862.2 | Av | 1.03 | | | | | | | | | |
| BDL226 | 10864.2 | P | | | 0.44 | | 0.58 | | 0.32 | | 0.21 | |
| BDL226 | 10864.2 | Av | | | 1.17 | | 1.1 | | 1.2 | | 1.27 | |
| BDL226 | 10861.1 | P | | | 0.68 | 0.72 | | | | | | |
| BDL226 | 10861.1 | Av | | | 1.27 | 1.21 | | | | | | |
| BDL226 | 10861.4 | P | | 0.04 | | 0.41 | | | | | | |
| BDL226 | 10861.4 | Av | | 1.13 | | 1.44 | | | | | | |
| BDL226 | 10862.2 | P | | | | 0.21 | | | | | | |
| BDL226 | 10862.2 | Av | | | | 1.51 | | | | | | |
| BDL226 | 10863.4 | P | | | 0.53 | | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL240 | 10806.2 | Av | | 1.1 | | | | | | | | 1.11 |
| BDL241 | 10873.1 | P | | | 0.55 | | 0.11 | | 0.09 | 0.17 | 0.09 | 0.34 |
| BDL241 | 10873.1 | Av | | | 1.86 | | 1.32 | | 1.33 | 1.13 | 1.33 | 1.25 |
| BDL241 | 10873.4 | P | | | | 0.44 | | | | | | |
| BDL241 | 10873.4 | Av | | | | 1.73 | | | | | | |
| BDL241 | 10874.2 | P | <0.01 | | | | | | | | | |
| BDL241 | 10874.2 | Av | 1.03 | | | | | | | | | |
| BDL241 | 10875.1 | P | | | | 0.33 | | | | | | |
| BDL241 | 10875.1 | Av | | | | 1.57 | | | | | | |
| BDL241 | 10875.2 | P | | | 0.58 | 0.09 | | | | | | |
| BDL241 | 10875.2 | Av | | | 1.48 | 1.19 | | | | | | |
| BDL242 | 10731.2 | P | | | | | 0.59 | | 0.46 | | 0.46 | |
| BDL242 | 10731.2 | Av | | | | | 1.1 | | 1.14 | | 1.14 | |
| BDL242 | 10731.3 | P | | | <0.01 | | | | | | | |
| BDL242 | 10731.3 | Av | | | 1.74 | | | | | | | |
| BDL242 | 10731.5 | P | | | 0.7 | | | | | | | |
| BDL242 | 10731.5 | Av | | | 1.18 | | | | | | | |
| BDL242 | 10731.6 | P | | | 0.63 | | 0.07 | | 0.07 | 0.09 | 0.07 | 0.04 |
| BDL242 | 10731.6 | Av | | | 1.48 | | 1.36 | | 1.35 | 1.17 | 1.35 | 1.16 |
| BDL242 | 10731.7 | P | | | 0.18 | | | | | | | |
| BDL242 | 10731.7 | Av | | | 2.28 | | | | | | | |
| BDL242 | 10737.2 | P | | | | 0.07 | | | | | | |
| BDL242 | 10737.2 | Av | | | | 1.22 | | | | | | |
| BDL245 | 10811.3 | P | | 0.22 | 0.05 | <0.01 | | 0.2 | | | | |
| BDL245 | 10811.3 | Av | | 1.47 | 1.25 | 1.25 | | 1.16 | | | | |
| BDL245 | 10813.3 | P | | | 0.28 | 0.02 | | 0.22 | | | | |
| BDL245 | 10813.3 | Av | | | 1.17 | 1.33 | | 1.15 | | | | |
| BDL245 | 10811.2 | P | | 0.37 | | 0.3 | | | | | | |
| BDL245 | 10811.2 | Av | | 1.22 | | 1.49 | | | | | | |
| BDL245 | 10811.3 | P | | 0.21 | 0.12 | 0.5 | | | | | | |
| BDL245 | 10811.3 | Av | | 1.18 | 1.44 | 1.79 | | | | | | |
| BDL245 | 10812.3 | P | | | 0.55 | 0.11 | | | | | | |
| BDL245 | 10812.3 | Av | | | 2.2 | 1.12 | | | | | | |
| BDL245 | 10813.3 | P | | 0.37 | | 0.45 | | 0.04 | | | | |
| BDL245 | 10813.3 | Av | | 1.19 | | 1.1 | | 1.26 | | | | |
| BDL245 | 10816.3 | P | | | 0.52 | 0.23 | | | | | | |
| BDL245 | 10816.3 | Av | | | 1.81 | 1.14 | | | | | | |
| BDL247 | 10911.4 | P | | 0.42 | | | | | | | | |
| BDL247 | 10911.4 | Av | | 1.1 | | | | | | | | |
| BDL247 | 10912.1 | P | | | 0.48 | 0.58 | | | | | | |
| BDL247 | 10912.1 | Av | | | 1.26 | 1.16 | | | | | | |
| BDL247 | 10912.6 | P | | | | 0.6 | | | | | | |
| BDL247 | 10912.6 | Av | | | | 1.33 | | | | | | |
| BDL248 | 11051.2 | P | | 0.45 | | | | | | | | |
| BDL248 | 11051.2 | Av | | 1.14 | | | | | | | | |
| BDL250 | 10841.3 | P | | 0.2 | | 0.13 | 0.58 | | 0.36 | | 0.36 | |
| BDL250 | 10841.3 | Av | | 1.14 | | 1.16 | 1.1 | | 1.17 | | 1.17 | |
| BDL250 | 10842.1 | P | | 0.45 | | 0.37 | | | | | | |
| BDL250 | 10842.1 | Av | | 1.12 | | 1.31 | | | | | | |
| BDL250 | 10842.3 | P | | 0.02 | | 0.46 | | | | | | |
| BDL250 | 10842.3 | Av | | 1.15 | | 1.14 | | | | | | |
| BDL250 | 10843.2 | P | | | | 0.42 | | | | | | |
| BDL250 | 10843.2 | Av | | | | 1.19 | | | | | | |
| BDL250 | 10846.2 | P | | 0.01 | | 0.06 | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>21</i> | <i>22</i> | <i>23</i> | <i>24</i> | <i>25</i> | <i>26</i> | <i>27</i> | <i>28</i> | <i>29</i> | <i>30</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL63 | 10384.3 | Av | | | | | | | | | | 1.14 |
| BDL63 | 10384.7 | P | | 0.04 | | | | | | | | <0.01 |
| BDL63 | 10384.7 | Av | | 1.12 | | | | | | | | 1.16 |
| BDL63 | 10384.8 | P | | | | | 0.12 | | 0.11 | 0.06 | 0.11 | 0.31 |
| BDL63 | 10384.8 | Av | | | | | 1.25 | | 1.26 | 1.17 | 1.26 | 1.12 |
| BDL79 | 11041.1 | P | | 0.13 | 0.49 | 0.77 | | | | | | |
| BDL79 | 11041.1 | Av | | 1.11 | 2.06 | 1.1 | | | | | | |
| BDL79 | 11042.1 | P | | 0.09 | | | | 0.2 | 0.54 | | 0.54 | |
| BDL79 | 11042.1 | Av | | 1.15 | | | | 1.16 | 1.11 | | 1.11 | |
| BDL79 | 11042.3 | P | | | 0.46 | | | | | | | |
| BDL79 | 11042.3 | Av | | | 1.37 | | | | | | | |
| BDL79 | 11043.1 | P | | | 0.47 | | | | | | | |
| BDL79 | 11043.1 | Av | | | 1.92 | | | | | | | |
| BDL79 | 11044.3 | P | | 0.01 | | 0.15 | | | | | | |
| BDL79 | 11044.3 | Av | | 1.21 | | 1.23 | | | | | | |
| BDL81 | 10371.5 | P | | | 0.6 | | | | | | | |
| BDL81 | 10371.5 | Av | | | 1.27 | | | | | | | |
| BDL81 | 10371.8 | P | | | 0.51 | | | | | | | |
| BDL81 | 10371.8 | Av | | | 2.2 | | | | | | | |
| BDL81 | 10372.1 | P | | | 0.54 | | | | | | | |
| BDL81 | 10372.1 | Av | | | 2.43 | | | | | | | |
| BDL81 | 10372.2 | P | | 0.06 | 0.66 | | | | | | | |
| BDL81 | 10372.2 | Av | | 1.12 | 1.28 | | | | | | | |
| BDL81 | 10374.1 | P | | | 0.42 | | | | | | | |
| BDL81 | 10374.1 | Av | | | 1.99 | | | | | | | |
| BDL81 | 10371.5 | P | | | | 0.01 | 0.25 | | 0.37 | 0.14 | 0.37 | 0.07 |
| BDL81 | 10371.5 | Av | | | | 1.13 | 1.18 | | 1.14 | 1.13 | 1.14 | 1.11 |
| BDL81 | 10371.8 | P | | 0.2 | 0.05 | 0.02 | 0.33 | | 0.23 | 0.19 | 0.23 | 0.04 |
| BDL81 | 10371.8 | Av | | 1.12 | 1.1 | 1.1 | 1.19 | | 1.24 | 1.18 | 1.24 | 1.07 |
| BDL81 | 10372.1 | P | | 0.05 | | | | | | | | |
| BDL81 | 10372.1 | Av | | 1.1 | | | | | | | | |
| BDL81 | 10372.2 | P | | 0.33 | 0.4 | | | | | | | 0.59 |
| BDL81 | 10372.2 | Av | | 1.13 | 1.29 | | | | | | | 1.18 |
| BDL81 | 10373.2 | P | | 0.01 | | | | | | | | |
| BDL81 | 10373.2 | Av | | 1.19 | | | | | | | | |
| BDL81 | 10374.1 | P | | | | | 0.06 | | 0.02 | 0.23 | 0.02 | 0.04 |
| BDL81 | 10374.1 | Av | | | | | 1.35 | | 1.48 | 1.14 | 1.48 | 1.15 |
| BDL85 | 10411.1 | P | | | | 0.01 | 0.12 | | 0.12 | 0.26 | 0.12 | 0.07 |
| BDL85 | 10411.1 | Av | | | | 1.09 | 1.29 | | 1.28 | 1.12 | 1.28 | 1.16 |
| BDL85 | 10411.3 | P | | 0.59 | | | | | | | | |
| BDL85 | 10411.3 | Av | | 1.51 | | | | | | | | |
| BDL85 | 10412.2 | P | | 0.62 | | | | | | | | |
| BDL85 | 10412.2 | Av | | 1.6 | | | | | | | | |
| BDL85 | 10414.1 | P | 0.1 | | | | | | | | | |
| BDL85 | 10414.1 | Av | 1.03 | | | | | | | | | |
| BDL85 | 10414.2 | P | | | | | | | | | | 0.62 |
| BDL85 | 10414.2 | Av | | | | | | | | | | 1.19 |

Table 26. Results of the greenhouse experiments. Provided are the measured values of each parameter [parameters (Par.) 21-30 according to the parameters described in Table 23 above] in plants expressing the indicated polynucleotides. "Ev" = event; "P" = P-value; "Av" = ratio between the averages of event and control. Note that when the average ratio is higher than "1" the effect of exogenous expression of the gene is an increase of the desired trait;

Table 27
Results from greenhouse experiments

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>31</i> | <i>32</i> | <i>33</i> | <i>34</i> | <i>35</i> | <i>36</i> | <i>37</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL102 | 10471.1 | P | 0.12 | | | | | | |
| BDL102 | 10471.1 | Av | 1.12 | | | | | | |
| BDL102 | 10474.1 | P | 0.26 | | | | | | |
| BDL102 | 10474.1 | Av | 1.35 | | | | | | |
| BDL117 | 10074.1 | P | | | | 0.69 | | | |
| BDL117 | 10074.1 | Av | | | | 1.1 | | | |
| BDL117 | 10074.4 | P | | | | 0.45 | | | |
| BDL117 | 10074.4 | Av | | | | 1.14 | | | |
| BDL138 | 9811.1 | P | | 0.06 | 0.11 | | 0.22 | | |
| BDL138 | 9811.1 | Av | | 1.18 | 1.11 | | 1.1 | | |
| BDL138 | 9811.4 | P | | <0.01 | 0.19 | | 0.48 | | |
| BDL138 | 9811.4 | Av | | 1.21 | 1.11 | | 1.2 | | |
| BDL138 | 9813.1 | P | | 0.1 | | | 0.02 | | |
| BDL138 | 9813.1 | Av | | 1.17 | | | 1.05 | | |
| BDL138 | 9813.4 | P | | | | | | 0.01 | |
| BDL138 | 9813.4 | Av | | | | | | 1.08 | |
| BDL138 | 9811.1 | P | | | | | 0.26 | 0.58 | |
| BDL138 | 9811.1 | Av | | | | | 1.15 | 1.13 | |
| BDL138 | 9811.4 | P | | <0.01 | 0.02 | | | | |
| BDL138 | 9811.4 | Av | | 1.18 | 1.18 | | | | |
| BDL138 | 9812.1 | P | | 0.01 | 0.03 | | 0.1 | | |
| BDL138 | 9812.1 | Av | | 1.13 | 1.1 | | 1.07 | | |
| BDL138 | 9813.1 | P | | 0.02 | 0.09 | | | | |
| BDL138 | 9813.1 | Av | | 1.09 | 1.08 | | | | |
| BDL138 | 9813.3 | P | | 0.09 | 0.03 | | | | |
| BDL138 | 9813.3 | Av | | 1.17 | 1.16 | | | | |
| BDL140 | 10423.1 | P | 0.71 | | | | | | |
| BDL140 | 10423.1 | Av | 1.11 | | | | | | |
| BDL147 | 10301.5 | P | | 0.01 | | | | | |
| BDL147 | 10301.5 | Av | | 1.1 | | | | | |
| BDL147 | 10301.6 | P | | 0.06 | 0.02 | | | | |
| BDL147 | 10301.6 | Av | | 1.14 | 1.09 | | | | |
| BDL147 | 10303.1 | P | | 0.16 | | | | 0.66 | |
| BDL147 | 10303.1 | Av | | 1.11 | | | | 1.14 | |
| BDL147 | 10303.5 | P | | 0.01 | 0.01 | | | | |
| BDL147 | 10303.5 | Av | | 1.13 | 1.11 | | | | |
| BDL147 | 10303.6 | P | | | | | | 0.1 | |
| BDL147 | 10303.6 | Av | | | | | | 1.13 | |
| BDL149 | 9824.4 | P | 0.01 | | | | | | |
| BDL149 | 9824.4 | Av | 1.19 | | | | | | |
| BDL152 | 10434.4 | P | 0.8 | | | | | | |
| BDL152 | 10434.4 | Av | 1.13 | | | | | | |
| BDL153 | 10143.1 | P | | | | 0.65 | | 0.52 | |
| BDL153 | 10143.1 | Av | | | | 1.1 | | 1.19 | |
| BDL153 | 10143.2 | P | | | | 0.26 | | | 0.05 |
| BDL153 | 10143.2 | Av | | | | 1.1 | | | 1.02 |
| BDL155 | 9991.5 | P | 0.56 | | | | | | |
| BDL155 | 9991.5 | Av | 1.23 | | | | | | |
| BDL155 | 9991.9 | P | 0.1 | | | | | | |
| BDL155 | 9991.9 | Av | 1.31 | | | | | | |
| BDL155 | 9993.2 | P | 0.62 | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>31</i> | <i>32</i> | <i>33</i> | <i>34</i> | <i>35</i> | <i>36</i> | <i>37</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL155 | 9993.2 | Av | 1.1 | | | | | | |
| BDL155 | 9994.3 | P | 0.47 | | | | | | |
| BDL155 | 9994.3 | Av | 1.14 | | | | | | |
| BDL157 | 9911.3 | P | | 0.02 | 0.33 | | | | |
| BDL157 | 9911.3 | Av | | 1.32 | 1.19 | | | | |
| BDL157 | 9911.4 | P | | | | 0.64 | | | |
| BDL157 | 9911.4 | Av | | | | 1.14 | | | |
| BDL157 | 9913.1 | P | | 0.01 | <0.01 | | | | |
| BDL157 | 9913.1 | Av | | 1.19 | 1.08 | | | | |
| BDL157 | 9913.3 | P | | 0.11 | | | | | |
| BDL157 | 9913.3 | Av | | 1.17 | | | | | |
| BDL157 | 9914.2 | P | | 0.13 | | | 0.4 | | |
| BDL157 | 9914.2 | Av | | 1.18 | | | 1.1 | | |
| BDL157 | 9911.3 | P | | 0.15 | | | | | |
| BDL157 | 9911.3 | Av | | 1.13 | | | | | |
| BDL157 | 9913.1 | P | | | | | | 0.36 | |
| BDL157 | 9913.1 | Av | | | | | | 1.15 | |
| BDL157 | 9913.3 | P | | | | | | 0.03 | |
| BDL157 | 9913.3 | Av | | | | | | 1.06 | |
| BDL157 | 9914.2 | P | | | | 0.22 | | | |
| BDL157 | 9914.2 | Av | | | | 1.18 | | | |
| BDL162 | 10492.2 | P | 0.1 | | | | | | |
| BDL162 | 10492.2 | Av | 1.8 | | | | | | |
| BDL167 | 10042.3 | P | | 0.14 | | | | | |
| BDL167 | 10042.3 | Av | | 1.15 | | | | | |
| BDL167 | 10042.4 | P | | 0.01 | 0.01 | 0.19 | 0.01 | | |
| BDL167 | 10042.4 | Av | | 1.15 | 1.05 | 1.1 | 1.06 | | |
| BDL167 | 10043.1 | P | | 0.01 | 0.04 | | <0.01 | | |
| BDL167 | 10043.1 | Av | | 1.16 | 1.06 | | 1.1 | | |
| BDL167 | 10043.3 | P | | 0.04 | 0.08 | | 0.01 | | |
| BDL167 | 10043.3 | Av | | 1.15 | 1.05 | | 1.06 | | |
| BDL167 | 10044.2 | P | | | | | 0.52 | | |
| BDL167 | 10044.2 | Av | | | | | 1.11 | | |
| BDL167 | 10043.2 | P | | | | 0.44 | 0.07 | | |
| BDL167 | 10043.2 | Av | | | | 1.22 | 1.08 | | |
| BDL167 | 10043.3 | P | | | | <0.01 | | | |
| BDL167 | 10043.3 | Av | | | | 1.2 | | | |
| BDL167 | 10043.4 | P | | | | 0.22 | | 0.2 | |
| BDL167 | 10043.4 | Av | | | | 1.21 | | 1.2 | |
| BDL167 | 10044.2 | P | | | | 0.1 | | | 0.05 |
| BDL167 | 10044.2 | Av | | | | 1.22 | | | 1.03 |
| BDL168 | 9881.3 | P | | | | <0.01 | | | |
| BDL168 | 9881.3 | Av | | | | 1.27 | | | |
| BDL168 | 9881.4 | P | | | | | 0.4 | 0.42 | |
| BDL168 | 9881.4 | Av | | | | | 1.21 | 1.2 | |
| BDL168 | 9882.1 | P | | | | | | 0.11 | |
| BDL168 | 9882.1 | Av | | | | | | 1.39 | |
| BDL168 | 9882.3 | P | | | | | | 0.18 | |
| BDL168 | 9882.3 | Av | | | | | | 1.32 | |
| BDL169 | 10744.2 | P | 0.57 | | | | | | |
| BDL169 | 10744.2 | Av | 1.16 | | | | | | |
| BDL169 | 10747.1 | P | 0.46 | | | | | | |
| BDL169 | 10747.1 | Av | 1.11 | | | | | | |
| BDL169 | 10747.5 | P | 0.28 | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>31</i> | <i>32</i> | <i>33</i> | <i>34</i> | <i>35</i> | <i>36</i> | <i>37</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL169 | 10747.5 | Av | 1.16 | | | | | | |
| BDL171 | 10661.2 | P | 0.7 | | | | | | |
| BDL171 | 10661.2 | Av | 1.23 | | | | | | |
| BDL171 | 10664.1 | P | 0.6 | | | | | | |
| BDL171 | 10664.1 | Av | 1.39 | | | | | | |
| BDL173 | 9951.2 | P | 0.66 | | | | | | |
| BDL173 | 9951.2 | Av | 1.13 | | | | | | |
| BDL173 | 9952.1 | P | | | | 0.21 | 0.12 | | |
| BDL173 | 9952.1 | Av | | | | 1.23 | 1.14 | | |
| BDL173 | 9952.2 | P | | 0.14 | | 0.64 | 0.34 | | 0.04 |
| BDL173 | 9952.2 | Av | | 1.1 | | 1.15 | 1.11 | | 1.04 |
| BDL173 | 9953.4 | P | | 0.58 | | <0.01 | 0.47 | 0.06 | |
| BDL173 | 9953.4 | Av | | 1.13 | | 1.41 | 1.1 | 1.1 | |
| BDL173 | 9954.2 | P | | 0.12 | 0.05 | 0.22 | | | |
| BDL173 | 9954.2 | Av | | 1.17 | 1.08 | 1.1 | | | |
| BDL173 | 9954.5 | P | | <0.01 | 0.04 | 0.57 | | | 0.07 |
| BDL173 | 9954.5 | Av | | 1.21 | 1.09 | 1.13 | | | 1.03 |
| BDL176 | 9891.2 | P | | 0.01 | <0.01 | 0.31 | 0.01 | | <0.01 |
| BDL176 | 9891.2 | Av | | 1.17 | 1.06 | 1.22 | 1.14 | | 1.06 |
| BDL176 | 9891.4 | P | | <0.01 | 0.05 | | | | |
| BDL176 | 9891.4 | Av | | 1.23 | 1.11 | | | | |
| BDL176 | 9892.3 | P | | <0.01 | <0.01 | | | | 0.09 |
| BDL176 | 9892.3 | Av | | 1.34 | 1.17 | | | | 1.03 |
| BDL176 | 9893.2 | P | | 0.08 | 0.16 | 0.25 | | | |
| BDL176 | 9893.2 | Av | | 1.23 | 1.15 | 1.13 | | | |
| BDL176 | 9893.3 | P | | <0.01 | | 0.01 | 0.12 | | |
| BDL176 | 9893.3 | Av | | 1.2 | | 1.36 | 1.22 | | |
| BDL177 | 10521.3 | P | 0.03 | | | | | | |
| BDL177 | 10521.3 | Av | 1.43 | | | | | | |
| BDL177 | 10524.2 | P | 0.22 | | | | | | |
| BDL177 | 10524.2 | Av | 1.28 | | | | | | |
| BDL183 | 9941.1 | P | | | | | 0.58 | | |
| BDL183 | 9941.1 | Av | | | | | 1.1 | | |
| BDL183 | 9942.1 | P | | | | | 0.08 | | |
| BDL183 | 9942.1 | Av | | | | | 1.11 | | |
| BDL183 | 9943.4 | P | | | | <0.01 | | | |
| BDL183 | 9943.4 | Av | | | | 1.25 | | | |
| BDL183 | 9944.2 | P | | | | | | 0.29 | |
| BDL183 | 9944.2 | Av | | | | | | 1.24 | |
| BDL190 | 10232.2 | P | | 0.27 | | 0.54 | | | |
| BDL190 | 10232.2 | Av | | 1.14 | | 1.13 | | | |
| BDL190 | 10233.2 | P | | 0.38 | | | | | 0.03 |
| BDL190 | 10233.2 | Av | | 1.13 | | | | | 1.04 |
| BDL190 | 10233.4 | P | | 0.03 | | <0.01 | 0.05 | | |
| BDL190 | 10233.4 | Av | | 1.13 | | 1.34 | 1.12 | | |
| BDL190 | 10234.1 | P | | 0.21 | 0.03 | 0.53 | | | |
| BDL190 | 10234.1 | Av | | 1.16 | 1.03 | 1.19 | | | |
| BDL190 | 10231.1 | P | | | | 0.07 | 0.07 | 0.01 | |
| BDL190 | 10231.1 | Av | | | | 1.06 | 1.09 | 1.15 | |
| BDL190 | 10231.2 | P | | | | | | 0.33 | |
| BDL190 | 10231.2 | Av | | | | | | 1.4 | |
| BDL190 | 10232.2 | P | | | | 0.04 | | | |
| BDL190 | 10232.2 | Av | | | | 1.08 | | | |
| BDL190 | 10233.2 | P | | | | | | 0.25 | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>31</i> | <i>32</i> | <i>33</i> | <i>34</i> | <i>35</i> | <i>36</i> | <i>37</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL190 | 10233.2 | Av | | | | | | 1.25 | |
| BDL192 | 9921.1 | P | | 0.22 | 0.11 | | | | 0.07 |
| BDL192 | 9921.1 | Av | | 1.18 | 1.1 | | | | 1.03 |
| BDL192 | 9922.1 | P | | 0.01 | 0.04 | | | | |
| BDL192 | 9922.1 | Av | | 1.15 | 1.06 | | | | |
| BDL192 | 9922.2 | P | | 0.02 | 0.04 | | | <0.01 | |
| BDL192 | 9922.2 | Av | | 1.21 | 1.09 | | | 1.12 | |
| BDL192 | 9922.5 | P | | | | 0.68 | | | |
| BDL192 | 9922.5 | Av | | | | 1.1 | | | |
| BDL193 | 10152.2 | P | | | | | | | 0.08 |
| BDL193 | 10152.2 | Av | | | | | | | 1.04 |
| BDL196 | 10243.2 | P | | | | | | 0.01 | |
| BDL196 | 10243.2 | Av | | | | | | 1.14 | |
| BDL201 | 9963.6 | P | 0.15 | | | | | | |
| BDL201 | 9963.6 | Av | 1.28 | | | | | | |
| BDL201 | 9964.3 | P | 0.15 | | | | | | |
| BDL201 | 9964.3 | Av | 1.36 | | | | | | |
| BDL220 | 10333.5 | P | 0.35 | | | | | | |
| BDL220 | 10333.5 | Av | 1.19 | | | | | | |
| BDL223 | 10793.5 | P | 0.05 | | | | | | |
| BDL223 | 10793.5 | Av | 1.15 | | | | | | |
| BDL224 | 10451.8 | P | 0.02 | | | | | | |
| BDL224 | 10451.8 | Av | 1.5 | | | | | | |
| BDL225 | 10401.1 | P | 0.08 | | | | | | |
| BDL225 | 10401.1 | Av | 1.32 | | | | | | |
| BDL225 | 10401.4 | P | 0.01 | | | | | | |
| BDL225 | 10401.4 | Av | 1.52 | | | | | | |
| BDL225 | 10402.2 | P | 0.03 | | | | | | |
| BDL225 | 10402.2 | Av | 1.43 | | | | | | |
| BDL225 | 10402.5 | P | 0.26 | | | | | | |
| BDL225 | 10402.5 | Av | 1.39 | | | | | | |
| BDL225 | 10402.6 | P | 0.08 | | | | | | |
| BDL225 | 10402.6 | Av | 1.57 | | | | | | |
| BDL225 | 10402.9 | P | 0.12 | | | | | | |
| BDL225 | 10402.9 | Av | 1.36 | | | | | | |
| BDL226 | 10861.2 | P | 0.35 | | | | | | |
| BDL226 | 10861.2 | Av | 1.1 | | | | | | |
| BDL227 | 11492.3 | P | 0.05 | | | | | | |
| BDL227 | 11492.3 | Av | 1.15 | | | | | | |
| BDL233 | 10825.4 | P | 0.53 | | | | | | |
| BDL233 | 10825.4 | Av | 1.13 | | | | | | |
| BDL238 | 10954.2 | P | <0.01 | | | | | | |
| BDL238 | 10954.2 | Av | 1.34 | | | | | | |
| BDL240 | 10802.2 | P | 0.23 | | | | | | |
| BDL240 | 10802.2 | Av | 1.3 | | | | | | |
| BDL241 | 10873.1 | P | 0.07 | | | | | | |
| BDL241 | 10873.1 | Av | 1.29 | | | | | | |
| BDL242 | 10731.2 | P | 0.62 | | | | | | |
| BDL242 | 10731.2 | Av | 1.1 | | | | | | |
| BDL242 | 10731.6 | P | 0.04 | | | | | | |
| BDL242 | 10731.6 | Av | 1.21 | | | | | | |
| BDL250 | 10846.3 | P | 0.53 | | | | | | |
| BDL250 | 10846.3 | Av | 1.15 | | | | | | |
| BDL48 | 10271.1 | P | 0.2 | | | | | | |

| <i>Gene</i> | <i>Ev.</i> | <i>Par</i> | <i>31</i> | <i>32</i> | <i>33</i> | <i>34</i> | <i>35</i> | <i>36</i> | <i>37</i> |
|-------------|------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| BDL48 | 10271.1 | Av | 1.23 | | | | | | |
| BDL48 | 10271.3 | P | 0.08 | | | | | | |
| BDL48 | 10271.3 | Av | 1.48 | | | | | | |
| BDL48 | 10273.2 | P | 0.58 | | | | | | |
| BDL48 | 10273.2 | Av | 1.12 | | | | | | |
| BDL48 | 10274.4 | P | 0.01 | | | | | | |
| BDL48 | 10274.4 | Av | 1.95 | | | | | | |
| BDL48 | 10271.3 | P | | 0.01 | 0.01 | | | | |
| BDL48 | 10271.3 | Av | | 1.12 | 1.1 | | | | |
| BDL48 | 10271.5 | P | | 0.06 | 0.1 | | | | |
| BDL48 | 10271.5 | Av | | 1.06 | 1.05 | | | | |
| BDL48 | 10274.3 | P | | | | | | <0.01 | |
| BDL48 | 10274.3 | Av | | | | | | 1.44 | |
| BDL48 | 10274.4 | P | | | | | | 0.08 | |
| BDL48 | 10274.4 | Av | | | | | | 1.05 | |
| BDL58 | 10282.3 | P | 0.63 | | | | | | |
| BDL58 | 10282.3 | Av | 1.19 | | | | | | |
| BDL63 | 10384.3 | P | 0.26 | | | | | | |
| BDL63 | 10384.3 | Av | 1.27 | | | | | | |
| BDL63 | 10381.1 | P | | | | <0.01 | 0.06 | | |
| BDL63 | 10381.1 | Av | | | | 1.26 | 1.08 | | |
| BDL63 | 10381.2 | P | | | | 0.56 | | | |
| BDL63 | 10381.2 | Av | | | | 1.14 | | | |
| BDL63 | 10384.2 | P | | | | <0.01 | 0.04 | | |
| BDL63 | 10384.2 | Av | | | | 1.27 | 1.08 | | |
| BDL63 | 10384.3 | P | | 0.01 | 0.02 | 0.3 | | | 0.01 |
| BDL63 | 10384.3 | Av | | 1.12 | 1.09 | 1.15 | | | 1.04 |
| BDL63 | 10384.7 | P | | 0.05 | 0.06 | 0.08 | | | |
| BDL63 | 10384.7 | Av | | 1.07 | 1.07 | 1.15 | | | |
| BDL63 | 10384.8 | P | | | | 0.51 | | | |
| BDL63 | 10384.8 | Av | | | | 1.13 | | | |
| BDL81 | 10371.5 | P | | <0.01 | 0.01 | <0.01 | | 0.23 | 0.04 |
| BDL81 | 10371.5 | Av | | 1.13 | 1.1 | 1.15 | | 1.14 | 1.02 |
| BDL81 | 10371.8 | P | | | | 0.03 | | | |
| BDL81 | 10371.8 | Av | | | | 1.08 | | | |
| BDL81 | 10372.1 | P | | <0.01 | 0.01 | | | | |
| BDL81 | 10372.1 | Av | | 1.17 | 1.1 | | | | |
| BDL81 | 10372.2 | P | | 0.22 | 0.1 | 0.59 | | | |
| BDL81 | 10372.2 | Av | | 1.11 | 1.11 | 1.14 | | | |
| BDL81 | 10373.2 | P | | 0.05 | | | | | |
| BDL81 | 10373.2 | Av | | 1.07 | | | | | |
| BDL81 | 10374.1 | P | | | | 0.05 | | | |
| BDL81 | 10374.1 | Av | | | | 1.2 | | | |
| BDL85 | 10411.1 | P | 0.1 | | | | | | |
| BDL85 | 10411.1 | Av | 1.21 | | | | | | |

Table 27. Results of the greenhouse experiments. Provided are the measured values of each parameter [parameters (Par.) 31-37 according to the parameters described in Table 23 above] in plants expressing the indicated polynucleotides. "Ev" = event; "P" = P-value; "Av" = ratio between the averages of event and control. Note that when the average ratio is higher than "1" the effect of exogenous expression of the gene is an increase of the desired trait;

EXAMPLE 10**PRODUCTION OF TOMATO TRANSCRIPTOM AND HIGH THROUGHPUT
CORRELATION ANALYSIS OF YIELD AND/OR VIGOR RELATED****5 PARAMETERS USING 44K TOMATO OLIGONUCLEOTIDE MICRO-ARRAY:
TOMATO FIELD EXPERIMENTS**

In order to produce a high throughput correlation analysis, the present inventors utilized a Tomato oligonucleotide micro-array, produced by Agilent Technologies [Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent
10 (dot) com/Scripts/PDS (dot) asp?lPage=50879]. The array oligonucleotide represents about 44,000 Tomato genes and transcripts. In order to define correlations between the levels of RNA expression with yield components, ABST or vigor related parameters various plant characteristics of 18 different Tomato varieties were analyzed. Among them, 10 varieties encompassing the observed variance were selected for RNA
15 expression analysis. The correlation between the RNA levels and the characterized parameters in field experiments was analyzed using Pearson correlation test [Hypertext Transfer Protocol://World Wide Web (dot) davidmlane (dot) com/hyperstat/A34739 (dot) html].

Experimental procedures

20 **Growth procedure in tomato field experiments** - Tomato varieties were grown under normal conditions (4-6 Liters/m² per day) until flower stage.

RNA extraction - Leaves at different developmental stages, representing different plant characteristics, were sampled and RNA was extracted using TRIzol Reagent from Invitrogen [Hypertext Transfer Protocol://World Wide Web (dot)
25 invitrogen (dot) com/content (dot) cfm?pageid=469].

Approximately 30-50 mg of tissue was taken from samples. The weighted 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
30 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).

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

5 **Experimental Results**

10 different Tomato varieties were grown and characterized for ripe fruit average weight (grams) as described above and the measured parameter [Ripe fruit average weight (gr.) at Normal Irrigation] is presented in Table 28 below.

10

Table 28
Measured parameters Tomato accessions

| <i>Variety</i> | <i>Normal Irrigation; Ripe fruit average weight (gr.)</i> |
|----------------|---|
| 612 | 0.05 |
| 613 | 0.01 |
| 617 | 0.01 |
| 618 | 0.05 |
| 622 | 0.01 |
| 623 | 0.01 |
| 626 | 0.03 |
| 629 | 0.00 |
| 630 | 0.00 |
| 631 | 0.01 |

Table 28: Provided are the measured yield components (Ripe fruit average weight under normal irrigation) for the tomato accessions (Varieties).

15

Subsequent correlation analysis between the leaf transcriptom set of BDL83_H74 Gene (SEQ ID NO:282) and the ripe fruit average weight under normal irrigation conditions was conducted and the correlation coefficient (R) was found to be 0.734.

20

25

EXAMPLE 11**PRODUCTION OF TOMATO TRANSCRIPTOM AND HIGH THROUGHPUT
CORRELATION ANALYSIS OF VIGOR RELATED PARAMETERS USING 44K
TOMATO OLIGONUCLEOTIDE MICRO-ARRAY**

5

Experimental procedures***Growth conditions for Tomato experiments******Correlation of early vigor traits across collection of Tomato ecotypes*** – Ten

Tomato varieties were grown in 3 repetitive plots, each containing 17 plants, at a net
house under semi-hydroponics conditions. Briefly, the growing protocol was as
follows: Tomato seeds were sown in trays filled with a mix of vermiculite and peat in a
1:1 ratio. Following germination, the trays were transferred to normal growth solution
[full Hogland; KNO₃ - 0.808 grams/liter, MgSO₄ - 0.12 grams/liter, KH₂ PO₄ - 0.172
grams/liter and 0.01 % (volume/volume) of 'Super coratin' micro elements (Iron-
EDDHA [ethylenediamine-N,N'-bis(2-hydroxyphenylacetic acid)]- 40.5 grams/liter; Mn
- 20.2 grams/liter; Zn 10.1 grams/liter; Co 1.5 grams/liter; and Mo 1.1 grams/liter),
solution's pH should be 6.5 – 6.8] at a temperature of 20-24 °C.

RNA extraction – All 10 selected Tomato varieties were sampled. Leaves
from plant under Normal conditions were sampled and RNA was extracted using
TRIzol Reagent from Invitrogen [Hypertext Transfer Protocol://World Wide Web (dot)
invitrogen (dot) com/content (dot) cfm?pageid=469].

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

25

Experimental Results

10 different Tomato varieties were grown and characterized for leaf number as
described above. The average leaf number was calculated using the JMP software and
values are summarized in Tables 29 below.

30

Table 29
Measured parameters Tomato accessions

| <i>Variety</i> | <i>Leaf number</i> |
|----------------|--------------------|
| 1139 | 6.56 |
| 2078 | 6.89 |
| 2958 | 7.33 |
| 5077 | 6.22 |
| 5080 | 6.33 |
| 5084 | 6.44 |
| 5085 | 5.89 |
| 5088 | 5.56 |
| 5089 | 6.11 |
| 5092 | 5.67 |

5 Table 29. Provided are the measured vigor related parameter (leaf number) for the tomato accessions (Varieties).

Subsequent correlation analysis between the leaf transcriptom set of BDL83_H73 gene (SEQ ID NO:281) with the average leaf number was conducted, the correlation coefficient (R) was -0.794.

10 The genes identified herein improve plant yield in general, and more specifically oil yield, seed yield, oil content, plant growth rate, plant biomass, root measurements, and plant vigor. The output of the bioinformatics method described herein is a set of genes highly predicted to improve yield (seed yield, oil yield and content, biomass) and/or other agronomic important yields by modifying their
15 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, plant growth rate, root measurements, plant vigor 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 plant
20 growth rate, root measurements, plant vigor and/or

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

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

WHAT IS CLAIMED IS:

1. A method of increasing yield, biomass, growth rate, vigor, oil content, 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: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 or 933, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

2. A method of increasing yield, biomass, growth rate, vigor, oil content, 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: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

3. A method of increasing yield, biomass, growth rate, vigor, oil content, 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932, thereby increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

4. A method of increasing yield, biomass, growth rate, vigor, oil content, 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932, thereby

increasing the yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of the plant.

5. An isolated polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 905, 882, 1-12, 15-105, 203-297, 299-523, 845-881, 883-904, 906-925 or 933, wherein said nucleic acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of a plant.

6. An isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933.

7. 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932, wherein said amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, abiotic stress tolerance and/or nitrogen use efficiency of a plant.

8. 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: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

9. A nucleic acid construct comprising the isolated polynucleotide of claim 5, 6, 7 or 8, and a promoter for directing transcription of said nucleic acid sequence in a host cell.

10. An isolated polypeptide comprising an amino acid sequence at least 80 % homologous to SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932, wherein said amino acid sequence is capable of

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

11. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

12. A plant cell exogenously expressing the polynucleotide of claim 5, 6, 7 or 8, or the nucleic acid construct of claim 9.

13. A plant cell exogenously expressing the polypeptide of claim 10 or 11.

14. The method of claim 1 or 3, the isolated polynucleotide of claim 5, the nucleic acid construct of claim 9 or the plant cell of claim 12, wherein said nucleic acid sequence is as set forth in SEQ ID NO: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 or 933.

15. The method of claim 1, 2, 3 or 4, the isolated polynucleotide of claim 5, 6, 7 or 8, the nucleic acid construct of claim 9 or the plant cell of claim 12, wherein said polynucleotide consists of the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 905, 882, 1-13, 15-105, 203-523, 845-881, 883-904, 906-925 and 933.

16. The method of claim 1, the isolated polynucleotide of claim 5 or the nucleic acid construct of claim 9, wherein said nucleic acid sequence encodes an amino acid sequence at least 80 % homologous to SEQ ID NO: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-616, 621-844, 926-931 or 932.

17. The method of claim 1, the isolated polynucleotide of claim 5 of the nucleic acid construct of claim 9, wherein said nucleic acid sequence encodes the amino

acid sequence selected from the group consisting of SEQ ID NOs: 172, 146, 106-117, 120-145, 147-171, 173-202, 524-844 and 926-932.

18. The plant cell of claim 12 or 13, wherein said plant cell forms part of a plant.

19. The method of claim 1, 2, 3 or 4, further comprising growing the plant expressing said exogenous polynucleotide under the abiotic stress.

20. The method of claim 1, 2, 3, 4 or 19, the isolated polynucleotide of claim 5 or 7, or the nucleic acid construct of claim 9, wherein said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature, high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

21. The method of claim 1, 2, 3 or 4, the isolated polynucleotide of claim 5 or 7, or the nucleic acid construct of claim 9, wherein the yield comprises seed yield or oil yield.

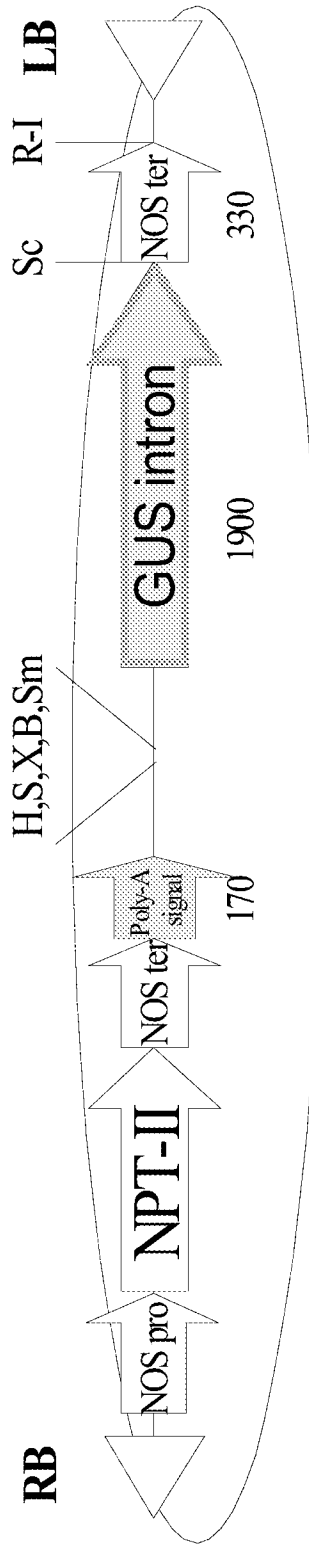


FIG. 1

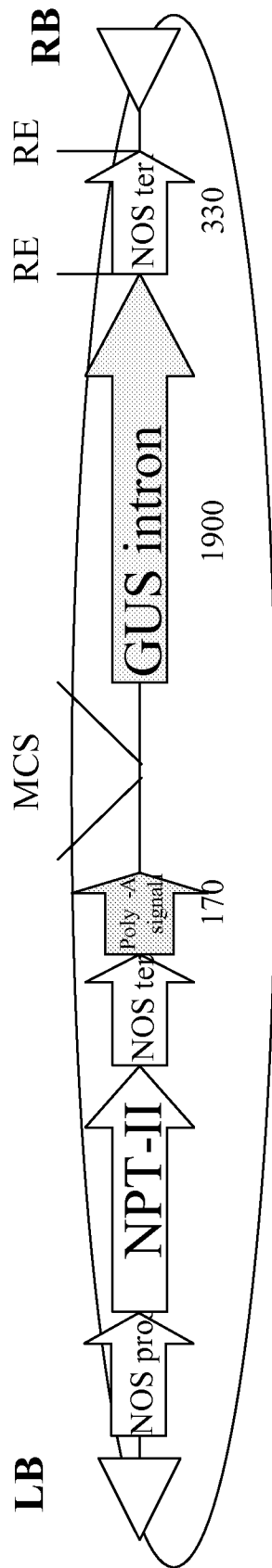


FIG. 2

Normal conditions

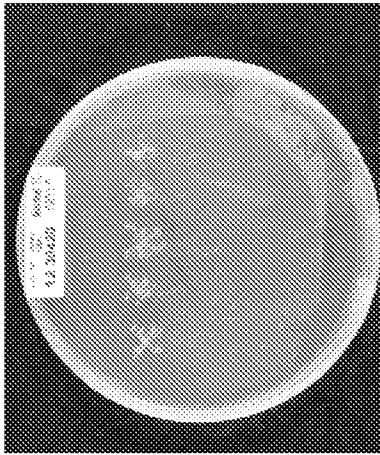


FIG. 3A

Osmotic stress
(15 % PEG)

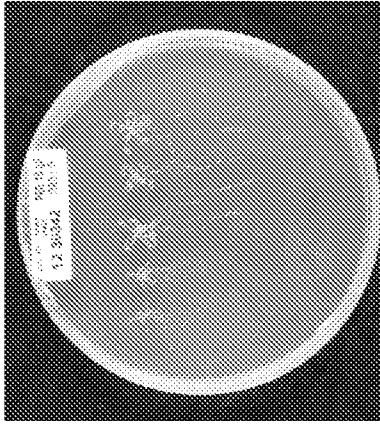


FIG. 3C

Nitrogen limiting
conditions

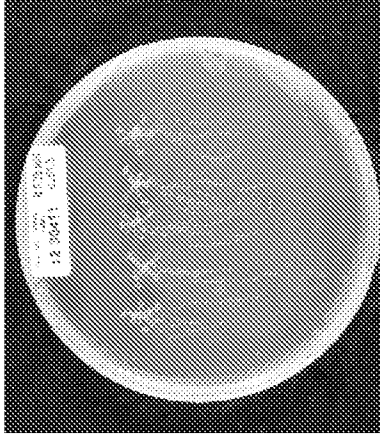


FIG. 3E

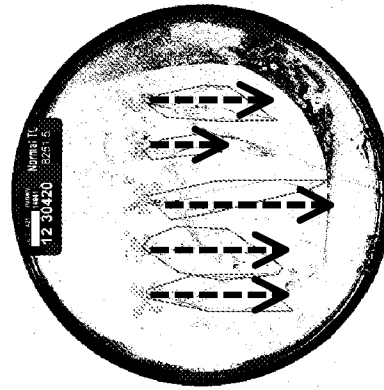


FIG. 3B

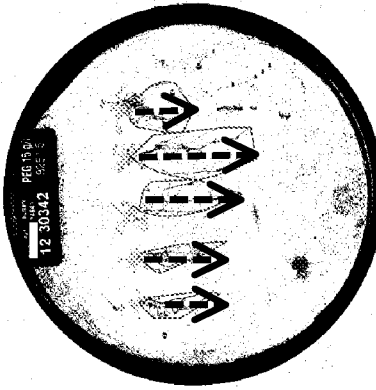


FIG. 3D

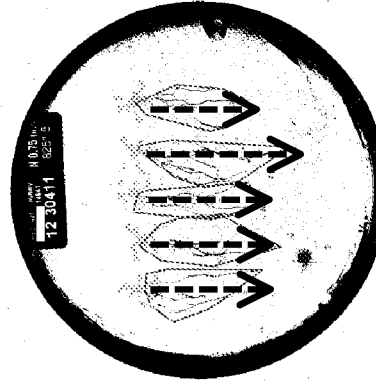


FIG. 3F