



(86) Date de dépôt PCT/PCT Filing Date: 2010/12/22
(87) Date publication PCT/PCT Publication Date: 2011/07/07
(85) Entrée phase nationale/National Entry: 2012/06/13
(86) N° demande PCT/PCT Application No.: IB 2010/056023
(87) N° publication PCT/PCT Publication No.: 2011/080674
(30) Priorités/Priorities: 2009/12/28 (US61/282,183);
2010/05/17 (US61/345,205)

(51) Cl.Int./Int.Cl. *C12N 15/29* (2006.01),
A01H 5/00 (2006.01), *C07K 14/415* (2006.01),
C12N 15/00 (2006.01), *C12N 15/82* (2006.01),
C12N 5/10 (2006.01), *C12P 7/64* (2006.01)
(71) Demandeur/Applicant:
EVOGENE LTD., IL
(72) Inventeurs/Inventors:
GRANEVITZE, ZUR, IL;
KARCHI, HAGAI, IL
(74) Agent: INTEGRAL IP

(54) Titre : POLYNUCLEOTIDES ISOLES ET POLYPEPTIDES ET PROCEDES POUR LES UTILISER AFIN
D'AUGMENTER LE RENDEMENT DES CULTURES, LA BIOMASSE, LA VITESSE DE CROISSANCE, LA
VIGUEUR, LA TENEUR EN HUILE, LA TOLERANCE AU STRESS ABIOTIQUE DES PLANTES ET L'EFFICACITE
D'UTILISATION DE L'AZOTE
(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) **Abrégé/Abstract:**

Provided are isolated polynucleotides encoding a polypeptide at least 80% homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091; and isolated polynucleotide comprising nucleic acid sequences at least 80 % identical to SEQ ID NO: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632- 1642, 1645-4850 or 4851. Also provided are nucleic acid constructs comprising same, isolated polypeptides encoded thereby, transgenic cells and transgenic plants comprising same and methods of using same for increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant. Also provided are isolated polynucleotides comprising the nucleic acid sequence set forth by SEQ ID NO: 8096, wherein the isolated polynucleotide is capable of regulating expression of at least one polynucleotide sequence operably linked thereto.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 July 2011 (07.07.2011)



(10) International Publication Number
WO 2011/080674 A3

(51) International Patent Classification:
C12N 15/82 (2006.01)

(21) International Application Number:
PCT/IB2010/056023

(22) International Filing Date:
22 December 2010 (22.12.2010)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/282,183 28 December 2009 (28.12.2009) US
61/345,205 17 May 2010 (17.05.2010) US

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

(72) Inventors; and

(75) Inventors/Applicants (for US only): **GRANEVITZE, Zur** [IL/IL]; 74 Menachem Begin Street, 49732 Petach-Tikva (IL). **KARCHI, Hagai** [IL/IL]; 249 Sapir Street, 76834 Moshav Sitriya (IL).

(74) Agents: **G.E. EHRLICH (1995) LTD.** et al.; 11 Menachem Begin Road, 52681 Ramat Gan (IL).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ,

CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

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

Declarations under Rule 4.17:

— of inventorship (Rule 4.17(iv))

Published:

— with international search report (Art. 21(3))

— with sequence listing part of description (Rule 5.2(a))

(88) Date of publication of the international search report:
17 November 2011

(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

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WO 2011/080674 A3

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NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

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 isolated polypeptides and polynucleotides, nucleic acid constructs comprising same, transgenic cells comprising same, transgenic plants exogenously expressing same and more particularly, but not exclusively, to methods of using same for increasing yield (e.g., seed yield, oil yield), biomass, growth rate, vigor, oil content, fiber yield, fiber quality abiotic stress tolerance, and/or fertilizer use efficiency (e.g., nitrogen use efficiency) of a plant.

Abiotic stress (ABS; also referred to as “environmental 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 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. Water deficit is a common component of many plant stresses and occurs in plant cells when the whole plant transpiration rate exceeds the water uptake. In addition to drought, other stresses, such as salinity and low temperature, produce cellular dehydration.

Drought is a gradual phenomenon, which involves periods of abnormally dry weather that persists long enough to produce serious hydrologic imbalances such as crop damage and water supply shortage. In severe cases, drought can last many years

and results in devastating effects on agriculture and water supplies. Furthermore, drought is associated with increase susceptibility to various diseases.

For most crop plants, the land regions of the world are too arid. In addition, overuse of available water results in increased loss of agriculturally-usable land (desertification), and increase of salt accumulation in soils adds to the loss of available water in soils.

Salinity, high salt levels, affects one in five hectares of irrigated land. This condition is only expected to worsen, further reducing the availability of arable land and crop production, since none of the top five food crops, *i.e.*, wheat, corn, rice, potatoes, and soybean, can tolerate excessive salt. Detrimental effects of salt on plants result from both water deficit which leads to osmotic stress (similar to drought stress) and the effect of excess sodium ions on critical biochemical processes. As with freezing and drought, high salt causes water deficit; and the presence of high salt makes it difficult for plant roots to extract water from their environment. Soil salinity is thus one of the more important variables that determine whether a plant may thrive. In many parts of the world, sizable land areas are uncultivable due to naturally high soil salinity. Thus, salination of soils that are used for agricultural production is a significant and increasing problem in regions that rely heavily on agriculture, and is worsen by over-utilization, over-fertilization and water shortage, typically caused by climatic change and the demands of increasing population. Salt tolerance is of particular importance early in a plant's lifecycle, since evaporation from the soil surface causes upward water movement, and salt accumulates in the upper soil layer where the seeds are placed. On the other hand, germination normally takes place at a salt concentration which is higher than the mean salt level in the whole soil profile.

Germination of many crops is sensitive to temperature. A gene that would enhance germination in hot conditions would be useful for crops that are planted late in the season or in hot climates. In addition, seedlings and mature plants that are exposed to excess heat may experience heat shock, which may arise in various organs, including leaves and particularly fruit, when transpiration is insufficient to overcome heat stress. Heat also damages cellular structures, including organelles and cytoskeleton, and impairs membrane function. Heat shock may produce a decrease in overall protein

synthesis, accompanied by expression of heat shock proteins, e.g., chaperones, which are involved in refolding proteins denatured by heat.

Heat stress often accompanies conditions of low water availability. Heat itself is seen as an interacting stress and adds to the detrimental effects caused by water deficit conditions. Water evaporation increases along with the rise in daytime temperatures and can result in high transpiration rates and low plant water potentials. High-temperature damage to pollen almost always occurs in conjunction with drought stress, and rarely occurs under well-watered conditions. Combined stress can alter plant metabolism in various ways; therefore understanding the interaction between different stresses may be important for the development of strategies to enhance stress tolerance by genetic manipulation.

Excessive chilling conditions, e.g., low, but above freezing, temperatures affect crops of tropical origins, such as soybean, rice, maize, and cotton. Typical chilling damage includes wilting, necrosis, chlorosis or leakage of ions from cell membranes. The underlying mechanisms of chilling sensitivity are not completely understood yet, but probably involve the level of membrane saturation and other physiological deficiencies. For example, photoinhibition of photosynthesis (disruption of photosynthesis due to high light intensities) often occurs under clear atmospheric conditions subsequent to cold late summer/autumn nights. In addition, chilling may lead to yield losses and lower product quality through the delayed ripening of maize.

Salt and drought stress signal transduction consist of ionic and osmotic homeostasis signaling pathways. The ionic aspect of salt stress is signaled via the SOS pathway where a calcium-responsive SOS3-SOS2 protein kinase complex controls the expression and activity of ion transporters such as SOS1. The osmotic component of salt stress involves complex plant reactions that overlap with drought and/or cold stress responses.

Common aspects of drought, cold and salt stress response [Reviewed in Xiong and Zhu (2002) *Plant Cell Environ.* 25: 131-139] include: (a) transient changes in the cytoplasmic calcium levels early in the signaling event; (b) signal transduction via mitogen-activated and/or calcium dependent protein kinases (CDPKs) and protein phosphatases; (c) increases in abscisic acid levels in response to stress triggering a subset of responses; (d) inositol phosphates as signal molecules (at least for a subset of

the stress responsive transcriptional changes; (e) activation of phospholipases which in turn generates a diverse array of second messenger molecules, some of which might regulate the activity of stress responsive kinases; (f) induction of late embryogenesis abundant (LEA) type genes including the CRT/DRE responsive COR/RD genes; (g) increased levels of antioxidants and compatible osmolytes such as proline and soluble sugars; and (h) accumulation of reactive oxygen species such as superoxide, hydrogen peroxide, and hydroxyl radicals. Absciscic acid biosynthesis is regulated by osmotic stress at multiple steps. Both ABA-dependent and -independent osmotic stress signaling first modify constitutively expressed transcription factors, leading to the expression of early response transcriptional activators, which then activate downstream stress tolerance effector genes.

Several genes which increase tolerance to cold or salt stress can also improve drought stress protection, these include for example, the transcription factor AtCBF/DREB1, OsCDPK7 (Saijo et al. 2000, Plant J. 23: 319-327) or AVP1 (a vacuolar pyrophosphatase-proton pump, Gaxiola et al. 2001, Proc. Natl. Acad. Sci. USA 98: 11444-11449).

Developing stress-tolerant plants is a strategy that has the potential to solve or mediate at least some of these problems. However, traditional plant breeding strategies used to develop new lines of plants that exhibit tolerance to ABS are relatively inefficient since they are tedious, time consuming and of unpredictable outcome. Furthermore, limited germplasm resources for stress tolerance and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Additionally, the cellular processes leading to ABS tolerance are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways.

Genetic engineering efforts, aimed at conferring abiotic stress tolerance to transgenic crops, have been described in various publications [Apse and Blumwald (Curr Opin Biotechnol. 13:146-150, 2002), Quesada *et al.* (Plant Physiol. 130:951-963, 2002), Holmström *et al.* (Nature 379: 683-684, 1996), Xu *et al.* (Plant Physiol 110: 249-257, 1996), Pilon-Smits and Ebskamp (Plant Physiol 107: 125-130, 1995) and Tarczynski *et al.* (Science 259: 508-510, 1993)].

Various patents and patent applications disclose genes and proteins which can be used for increasing tolerance of plants to abiotic stresses. These include for example, U.S. Pat. Nos. 5,296,462 and 5,356,816 (for increasing tolerance to cold stress); U.S. Pat. No. 6,670,528 (for increasing ABST); U.S. Pat. No. 6,720,477 (for increasing ABST); U.S. Application Ser. Nos. 09/938842 and 10/342224 (for increasing ABST); U.S. Application Ser. No. 10/231035 (for increasing ABST); WO2004/104162 (for increasing ABST and biomass); WO2007/020638 (for increasing ABST, biomass, vigor and/or yield); WO2007/049275 (for increasing ABST, biomass, vigor and/or yield); WO2010/076756 (for increasing ABST, biomass and/or yield);. WO2009/083958 (for increasing water use efficiency, fertilizer use efficiency, biotic/abiotic stress tolerance, yield and/or biomass); WO2010/020941 (for increasing nitrogen use efficiency, abiotic stress tolerance, yield and/or biomass); WO2009/141824 (for increasing plant utility); WO2010/049897 (for increasing plant yield).

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. 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].

Genetic engineering efforts aiming at increasing oil content in plants (e.g., in seeds) include upregulating endoplasmic reticulum (FAD3) and plastidal (FAD7) fatty acid desaturases in potato (Zabrouskov V., *et al.*, 2002; *Physiol Plant.* 116:172-185); over-expressing the GmDof4 and GmDof11 transcription factors (Wang HW *et al.*, 2007; *Plant J.* 52:716-29); over-expressing a yeast glycerol-3-phosphate dehydrogenase under the control of a seed-specific promoter (Vigeolas H, *et al.* 2007, *Plant Biotechnol J.* 5:431-41; U.S. Pat. Appl. No. 20060168684); using Arabidopsis FAE1 and yeast SLC1-1 genes for improvements in erucic acid and oil content in rapeseed (Katavic V, *et al.*, 2000, *Biochem Soc Trans.* 28:935-7).

Various patent applications disclose genes and proteins which can increase oil content in plants. These include for example, U.S. Pat. Appl. No. 20080076179 (lipid metabolism protein); U.S. Pat. Appl. No. 20060206961 (the Ypr140w polypeptide); U.S. Pat. Appl. No. 20060174373 [triacylglycerols synthesis enhancing protein (TEP)]; 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); WO2008/122980 (polynucleotides for increasing oil content, growth rate, biomass, yield and/or vigor of a plant).

Cotton and cotton by-products provide raw materials that are used to produce a wealth of consumer-based products in addition to textiles including cotton foodstuffs, livestock feed, fertilizer and paper. The production, marketing, consumption and trade of cotton-based products generate an excess of \$100 billion annually in the U.S. alone, making cotton the number one value-added crop.

Even though 90 % of cotton's value as a crop resides in the fiber (lint), yield and fiber quality has declined due to general erosion in genetic diversity of cotton varieties, and an increased vulnerability of the crop to environmental conditions.

There are many varieties of cotton plant, from which cotton fibers with a range of characteristics can be obtained and used for various applications. Cotton fibers may be characterized according to a variety of properties, some of which are considered highly desirable within the textile industry for the production of increasingly high quality products and optimal exploitation of modern spinning technologies. Commercially desirable properties include length, length uniformity, fineness, maturity ratio, decreased fuzz fiber production, micronaire, bundle strength, and single fiber strength. Much effort has been put into the improvement of the characteristics of cotton fibers mainly focusing on fiber length and fiber fineness. In particular, there is a great demand for cotton fibers of specific lengths.

A cotton fiber is composed of a single cell that has differentiated from an epidermal cell of the seed coat, developing through four stages, i.e., initiation, elongation, secondary cell wall thickening and maturation stages. More specifically, the elongation of a cotton fiber commences in the epidermal cell of the ovule immediately following flowering, after which the cotton fiber rapidly elongates for approximately 21 days. Fiber elongation is then terminated, and a secondary cell wall is formed and grown through maturation to become a mature cotton fiber.

Several candidate genes which are associated with the elongation, formation, quality and yield of cotton fibers were disclosed in various patent applications such as U.S. Pat. No. 5,880,100 and U.S. patent applications Ser. Nos. 08/580,545, 08/867,484 and 09/262,653 (describing genes involved in cotton fiber elongation stage); WO0245485 (improving fiber quality by modulating sucrose synthase); U.S. Pat. No. 6,472,588 and WO0117333 (increasing fiber quality by transformation with a DNA encoding sucrose phosphate synthase); WO9508914 (using a fiber-specific promoter

and a coding sequence encoding cotton peroxidase); WO9626639 (using an ovary specific promoter sequence to express plant growth modifying hormones in cotton ovule tissue, for altering fiber quality characteristics such as fiber dimension and strength); U.S. Pat. No. 5,981,834, U.S. Pat. No. 5,597,718, U.S. Pat. No. 5,620,882, U.S. Pat. No. 5,521,708 and U.S. Pat. No. 5,495,070 (coding sequences to alter the fiber characteristics of transgenic fiber producing plants); U.S. patent applications U.S. 2002049999 and U.S. 2003074697 (expressing a gene coding for endoxyloglucan transferase, catalase or peroxidase for improving cotton fiber characteristics); WO 01/40250 (improving cotton fiber quality by modulating transcription factor gene expression); WO 96/40924 (a cotton fiber transcriptional initiation regulatory region associated which is expressed in cotton fiber); EP0834566 (a gene which controls the fiber formation mechanism in cotton plant); WO2005/121364 (improving cotton fiber quality by modulating gene expression); WO2008/075364 (improving fiber quality, yield/biomass/vigor and/or abiotic stress tolerance of plants).

A promoter is a nucleic acid sequence approximately 200-1500 base pairs (bp) in length which is typically located upstream of coding sequences. A promoter functions in directing transcription of an adjacent coding sequence and thus acts as a switch for gene expression in an organism. Thus, all cellular processes are ultimately governed by the activity of promoters, making such regulatory elements important research and commercial tools.

Promoters are routinely utilized for heterologous gene expression in commercial expression systems, gene therapy and a variety of research applications.

The choice of the promoter sequence determines when, where and how strongly the heterologous gene of choice is expressed. Accordingly, when a constitutive expression throughout an organism is desired, a constitutive promoter is preferably utilized. On the other hand, when triggered gene expression is desired, an inductive promoter is preferred. Likewise, when an expression is to be confined to a particular tissue, or a particular physiological or developmental stage, a tissue specific or a stage specific promoter is respectively preferred.

Constitutive promoters are active throughout the cell cycle and have been utilized to express heterologous genes in transgenic plants so as to enable expression of traits encoded by the heterologous genes throughout the plant at all times. Examples of

known constitutive promoters often used for plant transformation include the cauliflower heat shock protein 80 (hsp80) promoter, 35S cauliflower mosaic virus promoter, nopaline synthase (nos) promoter, octopine (ocs) *Agrobacterium* promoter and the mannopine synthase (mas) *Agrobacterium* promoter.

5 Inducible promoters can be switched on by an inducing agent and are typically active as long as they are exposed to the inducing agent. The inducing agent can be a chemical agent, such as a metabolite, growth regulator, herbicide, or phenolic compound, or a physiological stress directly imposed upon the plant such as cold, heat, salt, toxins, or through the action of a microbial pathogen or an insecticidal pest.
10 Accordingly, inducible promoters can be utilized to regulate expression of desired traits, such as genes that control insect pests or microbial pathogens, whereby the protein is only produced shortly upon infection or first bites of the insect and transiently so as to decrease selective pressure for resistant insects. For example, plants can be transformed to express insecticidal or fungicidal traits such as the *Bacillus thuringiensis* (Bt) toxins,
15 viruses coat proteins, glucanases, chitinases or phytoalexins. In another example, plants can be transformed to tolerate herbicides by overexpressing, upon exposure to a herbicide, the acetohydroxy acid synthase enzyme, which neutralizes multiple types of herbicides [Hattori, J. *et al.*, Mol. General. Genet. 246: 419 (1995)].

Several fruit-specific promoters have been described, including an apple-isolated
20 Thi promoter (U.S. Pat. No. 6,392,122); a strawberry-isolated promoter (U.S. Pat. No. 6,080,914); tomato-isolated E4 and E8 promoters (U.S. Pat. No. 5,859,330); a polygalacturonase promoter (U.S. Pat. No. 4,943,674); and the 2AII tomato gene promoter [Van Haaren *et al.*, Plant Mol. Biol. 21: 625-640 (1993)]. Such fruit specific promoters can be utilized, for example, to modify fruit ripening by regulating
25 expression of ACC deaminase which inhibits biosynthesis of ethylene. Other gene products which may be desired to express in fruit tissue include genes encoding flavor or color traits, such as thaumatin, cyclase or sucrose phosphate synthase.

Seed specific promoters have been described in U.S. Pat. Nos. 6,403,862, 5,608,152 and 5,504,200; and in U.S. Patent Application Ser. Nos. 09/998059 and
30 10/137964. Such seed specific promoters can be utilized, for example, to alter the levels of saturated or unsaturated fatty acids; to increase levels of lysine- or sulfur-containing amino acids, or to modify the amount of starch contained in seeds.

Several promoters which regulate gene expression specifically during germination stage have been described, including the α -glucoronidase and the cystatin-1 barely-isolated promoters (U.S. Pat. No. 6,359,196), and the hydrolase promoter [Skriver *et al.*, Proc. Natl. Acad. Sci. USA, 88:7266-7270 (1991)].

5 WO2004/081173 discloses novel plant derived regulatory sequences and constructs and methods of using same for directing expression of exogenous polynucleotide sequences in plants.

SUMMARY OF THE INVENTION

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, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least 80 % identical to SEQ ID NO:
15 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8090 or 8091, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing yield, biomass, growth rate, vigor, oil content, fiber
20 yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-
25 5557, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing oil content, fiber yield and/or fiber quality of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a
30 nucleic acid sequence encoding a polypeptide at least 80 % identical to SEQ ID NO: 5470, 5476, or 5481, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4850 or 4851, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the present invention there is provided a method of increasing oil content, fiber yield and/or fiber quality of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 1627, 1629, or 1631, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises an amino acid sequence at least 80 % homologous to the amino acid sequence set forth in SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8090 or 8091, wherein the amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553,

5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4850 or 4851, wherein the nucleic acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

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

According to an aspect of some embodiments of the present invention there is provided an isolated polypeptide comprising an amino acid sequence at least 80 % homologous to SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8090 or 8091, wherein the amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

According to an aspect of some embodiments of the present invention there is provided an isolated polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

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

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

According to an aspect of some embodiments of the present invention there is provided a transgenic plant exogenously expressing the isolated polynucleotide of some
5 embodiments of the invention.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant comprising the nucleic acid construct of some embodiments of the invention.

According to an aspect of some embodiments of the present invention there is provided an isolated polynucleotide comprising the nucleic acid sequence set forth by
10 SEQ ID NO: 8096.

According to an aspect of some embodiments of the present invention there is provided a nucleic acid construct comprising the isolated polynucleotide of some
15 embodiments of the invention.

According to an aspect of some embodiments of the present invention there is provided a transgenic cell comprising the nucleic acid construct of some embodiments of the invention.

According to an aspect of some embodiments of the present invention there is provided a transgenic plant comprising the nucleic acid construct of some embodiments
20 of the invention.

According to an aspect of some embodiments of the present invention there is provided a method of producing a transgenic plant, comprising transforming a plant with the isolated polynucleotide of some embodiments of the invention or with the
25 nucleic acid construct of some embodiments of the invention.

According to an aspect of some embodiments of the present invention there is provided a method of expressing a polypeptide of interest in a cell comprising transforming the cell with a nucleic acid construct which comprises a polynucleotide sequence encoding the polypeptide of interest operably linked to the isolated
30 polynucleotide of some embodiments of the invention, thereby expressing the polypeptide of interest in the cell.

According to some embodiments of the invention, the nucleic acid sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

5 According to some embodiments of the invention, the nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to some embodiments of the invention, the polynucleotide consists of the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487,
10 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

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: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459,
15 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

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

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

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

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

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

According to some embodiments of the invention, the promoter is set forth by
30 SEQ ID NO: 8096.

According to some embodiments of the invention, the nucleic acid construct further comprising at least one heterologous polynucleotide operably linked to the isolated polynucleotide.

According to some embodiments of the invention, the at least one heterologous polynucleotide is a reporter gene.

According to some embodiments of the invention, the nucleic acid construct further comprising a heterologous polynucleotide operably linked to the isolated polynucleotide.

According to some embodiments of the invention, the heterologous polynucleotide comprises the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to some embodiments of the invention, the transgenic cell of some embodiments of the invention, being a plant cell.

According to some embodiments of the invention, the polypeptide of interest comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

According to some embodiments of the invention, the polynucleotide encoding the polypeptide of interest comprises the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

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

BRIEF DESCRIPTION OF THE DRAWINGS

Some embodiments of the invention are herein described, by way of example only, with reference to the accompanying drawings. With specific reference now to the drawings in detail, it is stressed that the particulars shown are by way of example and for purposes of illustrative discussion of embodiments of the invention. In this regard, the description taken with the drawings makes apparent to those skilled in the art how embodiments of the invention may be practiced.

In the drawings:

FIG. 1 is a schematic illustration of the modified pGI binary plasmid containing the new At6669 promoter (SEQ ID NO:8096) and the GUSintron (pQYN_6669) used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; MCS - Multiple cloning site; RE - any restriction enzyme; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); GUSintron - the GUS reporter gene (coding sequence and intron). The isolated polynucleotide sequences of the invention were cloned into the vector while replacing the GUSintron reporter gene.

FIG. 2 is a schematic illustration of the modified pGI binary plasmid containing the new At6669 promoter (SEQ ID NO:8096) (pQFN or pQFNc) used for expressing the isolated polynucleotide sequences of the invention. RB - T-DNA right border; LB - T-DNA left border; MCS - Multiple cloning site; RE - any restriction enzyme; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; Poly-A signal (polyadenylation signal); GUSintron - the GUS reporter gene (coding sequence and intron). The isolated polynucleotide sequences of the invention were cloned into the MCS of the vector.

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

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

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

FIG. 5 depicts sequence alignment between the novel promoter sequence (SEQ ID NO:8096) identified herein from *Arabidopsis thaliana* and the previously disclosed *Arabidopsis* At6669 promoter (WO2004/081173; set forth by SEQ ID NO:8093 herein). Mismatched nucleotides are underlined in positions 270; 484; 867-868; 967; 2295 and 2316-2318 of SEQ ID NO: 8096. New Domains are marked with an empty box in positions 862-865; 2392-2395 and 2314-2317 of SEQ ID NO:8096. Note that the YACT regulatory element at position 862-865 and the AAAG regulatory element at positions 2392-2395 and 2314-2317 of the novel promoter sequence (SEQ ID NO:8096) are absent in the previously disclosed At6669 promoter (SEQ ID NO:8093).

FIG. 6 is a schematic illustration of the pQYN plasmid.

FIG. 7 is a schematic illustration of the pQFN plasmid.

FIG. 8 is a schematic illustration of the pQFYN plasmid.

FIGs. 9A-D are images depicting GUS staining in 11 day-old *A. thaliana* seedlings which were transformed with the GUS intron expression cassette under the novel At6669 promoter (SEQ ID NO:8096). Note that the novel promoter sequence

p6669 induces GUS expression (blue staining) in 11 day-old seedling of *A. thaliana*, especially in roots, cotyledons and leaves. GUS expression is demonstrated for 4 independent events (event numbers 12516, 12515, 12512, 12511).

FIGs. 10A-D are images depicting GUS staining in 20-day-old *A. thaliana* seedlings which were transformed with the GUS intron expression cassette under the novel At6669 promoter (SEQ ID NO:8096). Note that the novel promoter sequence p6669 induces GUS expression (blue staining) in 20 day-old *A. thaliana*, especially in roots mainly root tip and leaves. GUS expression is demonstrated for 4 independent events (event numbers 12516, 12515, 12512, 12511).

FIGs. 11A-L are images depicting GUS staining in 41-day-old *A. thaliana* seedlings which were transformed with the GUS intron expression cassette under the novel At6669 promoter (SEQ ID NO:8096). Note that the novel promoter sequence p6669 induces GUS expression (blue staining) in 41 day old *A. thaliana*, especially in the stem, roots mainly root tip. Strong expression was detected in flower, leaves and cauline leaves. GUS expression is demonstrated for 4 independent events: Figures 11A-C - event 12511; Figures 11D-F - event 12516; Figures 11G-I - event 12515; Figures 11J-L - event 12512.

FIG. 12 is a schematic illustration of the modified 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; NOS pro = nopaline synthase promoter; NPT-II = neomycin phosphotransferase gene; NOS ter = nopaline synthase terminator; RE = any restriction enzyme; Poly-A signal (polyadenylation signal); 35S - the 35S promoter (SEQ ID NO:8094). The isolated polynucleotide sequences of some embodiments of the invention were cloned into the MCS (Multiple cloning site) of the vector.

DESCRIPTION OF SPECIFIC EMBODIMENTS OF THE INVENTION

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

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

5 The present inventors have identified novel polypeptides and polynucleotides which can be used to increase yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality abiotic stress tolerance, and/or fertilizer use efficiency (e.g., nitrogen use efficiency) of a plant, and a novel regulatory sequence which can be used to express heterologous genes in host cells such as in plants.

10 Thus, as shown in the Examples section which follows, the present inventors have utilized bioinformatics tools to identify polynucleotides which enhance yield (e.g., seed yield, oil yield, oil content), growth rate, biomass, vigor, fiber yield, fiber quality, abiotic stress tolerance and/or nitrogen use efficiency) of a plant. Genes which affect the trait-of-interest were identified (Table 27, Example 10) based on correlation analyses
15 performed using Arabidopsis ecotypes (Examples 2 and 3), tomato varieties (Example 4), *b. Juncea* ecotypes (Examples 5 and 6), Sorghum varieties (Example 7), Maize hybrids (Example 8) and the expression profiles of the genes according to selected expression sets (e.g., tissues, developmental stages and stress conditions) (Tables 1-26, Examples 1-9). Homologous polypeptides and polynucleotides having the same
20 function were also identified (Table 28, Example 11). The identified polynucleotides were cloned into binary vectors (Example 12, Table 29) and transgenic plants over-expressing the identified polynucleotides and polypeptides were generated (Example 13) and further tested for the effect of the exogenous gene on the trait of interest (e.g., increased fresh and dry weight, leaf area, root coverage and length, relative growth rate
25 (RGR) of leaf area, RGR of root coverage, RGR of root length, seed yield, oil yield, dry matter, harvest index, growth rate, rosette area, rosette diameter, RGR leaf number, RGR plot coverage, RGR rosette diameter, leaf blade area, oil percentage in seed and weight of 1000 seeds, plot coverage, tolerance to abiotic stress conditions and to fertilizer limiting conditions; Examples 14-16; Tables 30-48). In addition, as is further
30 shown in the Examples section which follows, the present inventors have uncovered a novel promoter sequence which can be used to express the gene-of-interest in a host cell (Example 17, Figures 5, 8-11). Altogether, 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, fiber yield, fiber quality, abiotic stress tolerance and/or nitrogen use efficiency of a plant.

Thus, according to an aspect of some embodiments of the invention, there is provided method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4850 or 4851, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

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

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

As used herein the phrase "seed yield" refers to the number or weight of the seeds per plant, seeds per pod, or per growing area or to the weight of a single seed, or to the oil extracted per seed. Hence seed yield can be affected by seed dimensions (e.g., length, width, perimeter, area and/or volume), number of (filled) seeds and seed filling rate and by seed oil content. Hence increase seed yield per plant could affect the

economic benefit one can obtain from the plant in a certain growing area and/or growing time; and increase seed yield per growing area could be achieved by increasing seed yield per plant, and/or by increasing number of plants grown on the same given area.

5 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.

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

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

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

20 As used herein the phrase "plant biomass" refers to the amount (e.g., measured in grams of air-dry tissue) of a tissue produced from the plant in a growing season, which could also determine or affect the plant yield or the yield per growing area. An increase in plant biomass can be in the whole plant or in parts thereof such as aboveground (harvestable) parts, vegetative biomass, roots and seeds.

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

 As used herein the phrase "plant vigor" refers to the amount (measured by weight) of tissue produced by the plant in a given time. Hence increased vigor could determine or affect the plant yield or the yield per growing time or growing area. In addition, early vigor (seed and/or seedling) results in improved field stand.

30 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.

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

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

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

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

Plants are subject to a range of environmental challenges. Several of these, including salt stress, general osmotic stress, drought stress and freezing stress, have the

ability to impact whole plant and cellular water availability. Not surprisingly, then, plant responses to this collection of stresses are related. Zhu (2002) *Ann. Rev. Plant Biol.* 53: 247-273 et al. note that "most studies on water stress signaling have focused on salt stress primarily because plant responses to salt and drought are closely related and the mechanisms overlap". Many examples of similar responses and pathways to this set of stresses have been documented. For example, the CBF transcription factors have been shown to condition resistance to salt, freezing and drought (Kasuga et al. (1999) *Nature Biotech.* 17: 287-291). The *Arabidopsis* rd29B gene is induced in response to both salt and dehydration stress, a process that is mediated largely through an ABA signal transduction process (Uno et al. (2000) *Proc. Natl. Acad. Sci. USA* 97: 11632-11637), resulting in altered activity of transcription factors that bind to an upstream element within the rd29B promoter. In *Mesembryanthemum crystallinum* (ice plant), Patharker and Cushman have shown that a calcium-dependent protein kinase (McCDPK1) is induced by exposure to both drought and salt stresses (Patharker and Cushman (2000) *Plant J.* 24: 679-691). The stress-induced kinase was also shown to phosphorylate a transcription factor, presumably altering its activity, although transcript levels of the target transcription factor are not altered in response to salt or drought stress. Similarly, Saijo et al. demonstrated that a rice salt/drought-induced calmodulin-dependent protein kinase (OsCDPK7) conferred increased salt and drought tolerance to rice when overexpressed (Saijo et al. (2000) *Plant J.* 23: 319-327).

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

It will be appreciated that some pathways involved in resistance to one stress (as described above), will also be involved in resistance to other stresses, regulated by the same or homologous genes. Of course, the overall resistance pathways are related, not

identical, and therefore not all genes controlling resistance to one stress will control resistance to the other stresses. Nonetheless, if a gene conditions resistance to one of these stresses, it would be apparent to one skilled in the art to test for resistance to these related stresses. Methods of assessing stress resistance are further provided in the Examples section which follows.

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

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

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

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

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

Improved plant NUE and FUE is translated in the field into either harvesting similar quantities of yield, while implementing less fertilizers, or increased yields gained by implementing the same levels of fertilizers. Thus, improved NUE or FUE has a direct effect on plant yield in the field. Thus, the polynucleotides and polypeptides of

some embodiments of the invention positively affect plant yield, seed yield, and plant biomass. In addition, the benefit of improved plant NUE will certainly improve crop quality and biochemical constituents of the seed such as protein yield and oil yield.

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

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

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

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

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

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

As used herein the term "increasing" refers to at least about 2 %, at least about 3 %, at least about 4 %, at least about 5 %, at least about 10 %, at least about 15 %, at
30 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, seed yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, 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).

5 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 a plant and expressing by recombinant means, as further described herein below.

10 As used herein “expressing” refers to expression at the mRNA and optionally polypeptide level.

15 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.

20 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.

25 According to some embodiments of the invention the exogenous polynucleotide comprises a nucleic acid sequence which is at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851.

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

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

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

According to some embodiments of the invention the exogenous polynucleotide is at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID NOs:1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851.

According to some embodiments of the invention the exogenous polynucleotide is set forth by SEQ ID NO: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, or 1644.

According to an aspect of some embodiments of the invention, there is provided a method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to some embodiments of the invention the exogenous polynucleotide is set forth by the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to an aspect of some embodiments of the invention, there is provided a method of increasing oil content, fiber yield and/or fiber quality of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid

sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID NOs:1627, 1629 and 1631, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.

According to an aspect of some embodiments of the invention, there is provided a method of increasing oil content, fiber yield and/or fiber quality 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: 1627, 1629, and 1631, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.

According to some embodiments of the invention the exogenous polynucleotide is set forth by the nucleic acid sequence selected from the group consisting of SEQ ID NOs:1627, 1629, and 1631.

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

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

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

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

As used herein the phrase "composite polynucleotide sequence" refers to a sequence, which is at least partially complementary and at least partially genomic. A composite sequence can include some exonal sequences required to encode the

polypeptide of the present invention, as well as some intronic sequences interposing therebetween. The intronic sequences can be of any source, including of other genes, and typically will include conserved splicing signal sequences. Such intronic sequences may further include cis acting expression regulatory elements.

5 According to some embodiments of the invention, the exogenous polynucleotide of the invention encodes a polypeptide having an amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs:488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091.

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

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

25 One option to identify orthologues in monocot plant species is by performing a reciprocal blast search. This may be done by a first blast involving blasting the sequence-of-interest against any sequence database, such as the publicly available NCBI database which may be found at: Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov. If orthologues in rice were sought, the sequence-of-interest would be blasted against, for example, the 28,469 full-length cDNA clones from *Oryza sativa* Nipponbare available at NCBI. The blast results may be filtered. The full-length sequences of either the filtered results or the non-filtered results are then blasted

back (second blast) against the sequences of the organism from which the sequence-of-interest is derived. The results of the first and second blasts are then compared. An orthologue is identified when the sequence resulting in the highest score (best hit) in the first blast identifies in the second blast the query sequence (the original sequence-of-interest) as the best hit. Using the same rational a paralogue (homolog to a gene in the same organism) is found. In case of large sequence families, the ClustalW program may be used [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 of the invention encodes a polypeptide having an amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % identical to the amino acid sequence selected from the group consisting of SEQ ID NOs:488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091.

According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide consisting of the amino acid sequence set forth by SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, 5554-5556 or 5557.

According to an aspect of some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, is effected by expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least

about 99 %, or more say 100 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs:488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, is effected by expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % identical to the amino acid sequence selected from the group consisting of SEQ ID NOs:488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to an aspect of some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, is effected by expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

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

expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557, thereby
5 increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide consisting of the amino acid sequence set forth by SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-
10 5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, 5554-5556 or 5557.

According to an aspect of some embodiments of the invention, there is provided a method of increasing oil content, fiber yield and/or fiber quality of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least about 80 %, at least about 81 %, at least about
15 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to the amino acid sequence selected from the group
20 consisting of SEQ ID NOs: 5470, 5476, and 5481, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.

According to an aspect of some embodiments of the invention, the method of increasing oil content, fiber yield and/or fiber quality of a plant is effected by expressing within the plant an exogenous polynucleotide comprising a nucleic acid
25 sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 5470, 5476, and 5481, thereby increasing the oil content, fiber yield and/or fiber quality of a plant.

According to some embodiments of the invention, the exogenous polynucleotide encodes a polypeptide consisting of the amino acid sequence set forth by SEQ ID NO:
30 5470, 5476, or 5481.

Nucleic acid sequences encoding the polypeptides of the present invention may be optimized for expression. Examples of such sequence modifications include, but are

not limited to, an altered G/C content to more closely approach that typically found in the plant species of interest, and the removal of codons atypically found in the plant species commonly referred to as codon optimization.

The phrase "codon optimization" refers to the selection of appropriate DNA
5 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
10 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
15 of highly expressed plant genes, followed by a calculation of the average squared deviation. The formula used is: $1 \text{ SDCU} = n = 1/N \sum [(X_n - Y_n) / Y_n]^2 / N$, 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
20 expressed genes of dicotyledonous plants is compiled using the data of Murray et al. (1989, Nuc Acids Res. 17:477-498).

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

30 By using the above Tables to determine the most preferred or most favored codons for each amino acid in a particular species (for example, rice), a naturally-occurring nucleotide sequence encoding a protein of interest can be codon optimized for

that particular plant species. This is effected by replacing codons that may have a low statistical incidence in the particular species genome with corresponding codons, in regard to an amino acid, that are statistically more favored. However, one or more less-favored codons may be selected to delete existing restriction sites, to create new ones at potentially useful junctions (5' and 3' ends to add signal peptide or termination cassettes, internal sites that might be used to cut and splice segments together to produce a correct full-length sequence), or to eliminate nucleotide sequences that may negatively effect mRNA stability or expression.

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

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

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

Non-limiting examples of non-coding RNA polynucleotides are provided in SEQ ID NOs: 211-217, 278-284, 486 and 487.

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

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

The invention provides an isolated polynucleotide comprising a nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID NOs:1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851.

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

According to some embodiments of the invention the isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to some embodiments of the invention the isolated polynucleotide is set forth by SEQ ID NO: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, or 1644.

The invention provides an isolated polynucleotide comprising a nucleic acid sequence encoding a polypeptide which comprises an amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to the amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091.

According to some embodiments of the invention the amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, 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: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

The invention provides an isolated polypeptide comprising an amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, or more say 100 % homologous to an amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, and 5558-8091.

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

According to some embodiments of the invention, the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

According to some embodiments of the invention, the polypeptide is set forth by SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, 5554-5556 or 5557.

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

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

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

Acacia spp., Acer spp., Actinidia spp., Aesculus spp., Agathis australis, Albizia amara, Alsophila tricolor, Andropogon spp., Arachis spp, Areca catechu, Astelia fragrans, Astragalus cicer, Baikiaea plurijuga, Betula spp., Brassica spp., Bruguiera gymnorhiza, Burkea africana, Butea frondosa, Cadaba farinosa, Calliandra spp, Camellia sinensis, Canna indica, Capsicum spp., Cassia spp., Centroema pubescens, Chacoomeles spp., Cinnamomum cassia, Coffea arabica, Colophospermum mopane, Coronillia varia, Cotoneaster serotina, Crataegus spp., Cucumis spp., Cupressus spp., Cyathea dealbata, Cydonia oblonga, Cryptomeria japonica, Cymbopogon spp., Cynthea dealbata, Cydonia oblonga, Dalbergia monetaria, Davallia divaricata, Desmodium spp., Dicksonia squarosa, Dibeteropogon amplexans, Dioclea spp, Dolichos spp., Dorycnium rectum, Echinochloa pyramidalis, Ehraffia spp., Eleusine coracana, Eragrestis spp., Erythrina spp., Eucalyptus spp., Euclea schimperi, Eulalia villosa, Pagopyrum spp., Feijoa sellowiana, Fragaria spp., Flemingia spp, Freycinetia banksii, Geranium thunbergii, GinAgo biloba, Glycine javanica, Gliricidia spp, Gossypium hirsutum, Grevillea spp., Guibourtia coleosperma, Hedysarum spp., Hemaphysalis altissima, Heteropogon contortus, Hordeum vulgare, Hyparrhenia rufa, Hypericum erectum, Hypochoeris glabra, Indigo incamata, Iris spp., Leptarrhena pyrolifolia, Lespedeza spp., Lettuce spp., Leucaena leucocephala, Loudetia simplex, Lotonus bainesii, Lotus spp., Macrotyloma axillare, Malus spp., Manihot esculenta, Medicago sativa, Metasequoia glyptostroboides, Musa sapientum, Nicotiana 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 sativum, Podocarpus totara, Pogonarthria fleckii, Pogonaffhria squarrosa, Populus spp., Prosopis cineraria, Pseudotsuga menziesii, Pterolobium stellatum, Pyrus

communis, *Quercus* spp., *Rhaphiolepis* 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, 5 *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, 10 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.

15 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.

20 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.

25 According to some embodiments of the invention, expressing the exogenous polynucleotide of the invention within the plant is effected by transforming one or more cells of the plant with the exogenous polynucleotide, followed by generating a mature plant from the transformed cells and cultivating the mature plant under conditions suitable for expressing the exogenous polynucleotide within the mature plant.

30 According to some embodiments of the invention, the transformation is effected by introducing to the plant cell a nucleic acid construct which includes the exogenous polynucleotide of some embodiments of the invention and at least one promoter for directing transcription of the exogenous polynucleotide in a host cell (a plant cell). Further details of suitable transformation approaches are provided hereinbelow.

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

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

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

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

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

According to some embodiments of the invention, the promoter is a plant promoter, which is suitable for expression of the exogenous polynucleotide in a plant cell.

Suitable constitutive promoters include, for example, CaMV 35S promoter (SEQ ID NO:8094; Odell et al., Nature 313:810-812, 1985); Arabidopsis At6669 promoter (SEQ ID NO:8093; see PCT Publication No. WO04081173A2) or the novel At6669 promoter (SEQ ID NO:8096); maize Ubi 1 (Christensen et al., Plant Sol. Biol. 18:675-689, 1992); rice actin (McElroy et al., Plant Cell 2:163-171, 1990); pEMU (Last et al., Theor. Appl. Genet. 81:581-588, 1991); CaMV 19S (Nilsson et al., Physiol. Plant 100:456-462, 1997); GOS2 (de Pater et al, Plant J Nov;2(6):837-44, 1992); ubiquitin (Christensen et al, Plant Mol. Biol. 18: 675-689, 1992); Rice cyclophilin (Bucholz et al, Plant Mol Biol. 25(5):837-43, 1994); Maize H3 histone (Lepetit et al, Mol. Gen. Genet. 231: 276-285, 1992); Actin 2 (An et al, Plant J. 10(1):107-121, 1996) and Synthetic Super MAS (Ni et al., The Plant Journal 7: 661-76, 1995). Other constitutive promoters include those in U.S. Pat. Nos. 5,659,026, 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; and 5,608,142.

Suitable tissue-specific promoters include, but not limited to, leaf-specific promoters [such as described, for example, by Yamamoto et al., *Plant J.* 12:255-265, 1997; Kwon et al., *Plant Physiol.* 105:357-67, 1994; Yamamoto et al., *Plant Cell Physiol.* 35:773-778, 1994; Gotor et al., *Plant J.* 3:509-18, 1993; Orozco et al., *Plant Mol. Biol.* 23:1129-1138, 1993; and Matsuoka et al., *Proc. Natl. Acad. Sci. USA* 90:9586-9590, 1993], seed-preferred promoters [e.g., Napin (originated from *Brassica napus* which is characterized by a seed specific promoter activity; Stuitje A. R. et al. *Plant Biotechnology Journal* 1 (4): 301-309; SEQ ID NO:8095), 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, et al., *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 (*EMBO*3:1409-15, 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 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*] and root promoters such as the ROOTP promoter [SEQ ID NO: 8097].

Suitable abiotic stress-inducible promoters include, but not limited to, salt-inducible promoters such as RD29A (Yamaguchi-Shinozaki et al., Mol. Gen. Genet. 236:331-340, 1993); drought-inducible promoters such as maize rab17 gene promoter (Pla et. al., Plant Mol. Biol. 21:259-266, 1993), maize rab28 gene promoter (Busk et. 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).

As mentioned above, and further described in Example 15 of the Examples section which follows, the present inventors have uncovered a novel promoter sequences (regulatory nucleic acid sequences) which can be used to express a polynucleotide-of-interest in a plant.

Thus, according to an aspect of some embodiments of the invention, there is provided an isolated polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO:8096.

According to some embodiments of the invention the isolated polynucleotide is capable of regulating expression of the heterologous polynucleotide in a host cell.

According to some embodiments of the invention the heterologous polynucleotide is operably linked to the regulatory nucleic acid sequence set forth by SEQ ID NO: 8096.

According to an aspect of some embodiments of the invention, there is provided a nucleic acid construct comprising the isolated polynucleotide set forth by SEQ ID NO:8096.

According to some embodiments of the invention the nucleic acid construct further comprising at least one heterologous polynucleotide operably linked to the isolated polynucleotide.

According to some embodiments of the invention, the regulatory nucleic acid sequence of the invention ranges in length from about 500 nucleotides to about 4000 nucleotides and includes one or more sequence regions which are capable of recognizing and binding RNA polymerase II and other proteins (trans-acting transcription factors) involved in transcription.

According to some embodiments of the invention, the regulatory sequence is positioned 1-500 bp upstream of the ATG codon of the coding nucleic acid sequence,

although it will be appreciated that regulatory sequences can also exert their effect when positioned elsewhere with respect to the coding nucleic acid sequence (e.g., within an intron).

As is clearly illustrated in the Examples section which follows, the novel At6669 promoter sequence of some embodiments of the invention is capable of regulating expression of a coding nucleic acid sequence (e.g., a reporter gene such as GUS, luciferase) operably linked thereto (see Example 17 of the Examples section which follows).

According to some embodiments of the invention, the regulatory nucleic acid sequences of the invention are modified to create variations in the molecule sequences such as to enhance their promoting activities, using methods known in the art, such as PCR-based DNA modification, or standard DNA mutagenesis techniques, or by chemically synthesizing the modified polynucleotides.

Accordingly, the regulatory nucleic acid sequence of the invention (e.g., SEQ ID NO: 8096) may be truncated or deleted and still retain the capacity of directing the transcription of an operably linked heterologous DNA sequence. The minimal length of a promoter region can be determined by systematically removing sequences from the 5' and 3'-ends of the isolated polynucleotide by standard techniques known in the art, including but not limited to removal of restriction enzyme fragments or digestion with nucleases. Consequently, any sequence fragments, portions, or regions of the disclosed promoter polynucleotide sequences of the invention can be used as regulatory sequences. It will be appreciated that modified sequences (mutated, truncated and the like) can acquire different transcriptional properties such as the direction of different pattern of gene expression as compared to the unmodified element.

Optionally, the sequences set forth in SEQ ID NO:8096 may be modified, for example for expression in a range of plant systems. In another approach, novel hybrid promoters can be designed or engineered by a number of methods. Many promoters contain upstream sequences which activate, enhance or define the strength and/or specificity of the promoter, such as described, for example, by Atchison [Ann. Rev. Cell Biol. 4:127 (1988)]. T-DNA genes, for example contain "TATA" boxes defining the site of transcription initiation and other upstream elements located upstream of the transcription initiation site modulate transcription levels [Gelvin In: Transgenic Plants

(Kung, S.-D. and Us, R., eds, San Diego: Academic Press, pp.49-87, (1988)]. Another chimeric promoter combined a trimer of the octopine synthase (ocs) activator to the mannopine synthase (mas) activator plus promoter and reported an increase in expression of a reporter gene [Min Ni *et al.*, The Plant Journal 7:661 (1995)]. The
5 upstream regulatory sequences of the promoter polynucleotide sequences of the invention can be used for the construction of such chimeric or hybrid promoters. Methods for construction of variant promoters include, but are not limited to, combining control elements of different promoters or duplicating portions or regions of a promoter (see for example, U.S. Pat. Nos. 5,110,732 and 5,097,025). Those of skill in the art are
10 familiar with the specific conditions and procedures for the construction, manipulation and isolation of macromolecules (e.g., DNA molecules, plasmids, etc.), generation of recombinant organisms and the screening and isolation of genes, [see for example Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, (1989); Mailga *et al.*, Methods in Plant Molecular Biology, Cold Spring Harbor Press,
15 (1995); Birren *et al.*, Genome Analysis: volume 1, Analyzing DNA, (1997); volume 2, Detecting Genes, (1998); volume 3, Cloning Systems, (1999); and volume 4, Mapping Genomes, (1999), Cold Spring Harbor, N.Y].

According to some embodiments of the invention the heterologous polynucleotide, which is regulated by the regulatory nucleic acid sequence set forth by
20 SEQ ID NO:8096, comprises a nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide
25 selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to some embodiments of the invention the heterologous polynucleotide, which is regulated by the regulatory nucleic acid sequence set forth by
30 SEQ ID NO:8096, encodes an amino acid sequence at least at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the amino acid sequence

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 % homologous to SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, 5554-5556 or 5557.

According to some embodiments of the invention the heterologous polynucleotide, which is regulated by the regulatory nucleic acid sequence set forth by SEQ ID NO:8096, comprises a nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, 10 at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID NOs: 1627, 1629 and 1631.

15 According to some embodiments of the invention the heterologous polynucleotide, which is regulated by the regulatory nucleic acid sequence set forth by SEQ ID NO:8096, encodes an amino acid sequence at least 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 %, 20 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 % homologous to SEQ ID NO: 5470, 5476 and 5481.

According to some embodiments of the invention, the method of increasing 25 yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant is effected by expressing within the plant a nucleic acid construct which comprises the nucleic acid sequence set forth by SEQ ID NO: 8096 and a heterologous polynucleotide sequence which comprises a nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at 30 least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % homologous to SEQ ID NO: 5470, 5476 and 5481.

at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to SEQ ID NO: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644, wherein the nucleic acid sequence is capable of regulating expression of the heterologous polynucleotide in a host cell.

According to some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant is effected by expressing within the plant a nucleic acid construct which comprises the nucleic acid sequence set forth by SEQ ID NO: 8096 and a heterologous polynucleotide sequence which encodes an amino acid sequence at least at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % homologous to SEQ ID NO: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, 5554-5556 or 5557, wherein the nucleic acid sequence is capable of regulating expression of the heterologous polynucleotide in a host cell.

According to some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant is effected by expressing within the plant a nucleic acid construct which comprises the nucleic acid sequence set forth by SEQ ID NO: 8096 and a heterologous polynucleotide sequence which comprises a nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to SEQ ID NO: 1627, 1629 or 1631, wherein the

nucleic acid sequence is capable of regulating expression of the heterologous polynucleotide in a host cell.

According to some embodiments of the invention, the method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant is effected by expressing within the
5 plant a nucleic acid construct which comprises the nucleic acid sequence set forth by SEQ ID NO: 8096 and a heterologous polynucleotide sequence which encodes an amino acid sequence at least 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
10 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 % homologous to SEQ ID NO: 5470, 5476 or 5481, wherein the nucleic acid sequence is capable of regulating expression of the
15 heterologous polynucleotide in a host cell.

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
20 appropriate selectable marker and origin of replication) and be compatible with propagation in cells. The construct according to the present invention can be, for example, a plasmid, a bacmid, a phagemid, a cosmid, a phage, a virus or an artificial chromosome.

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

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

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

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

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

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

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

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

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

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

Micropropagation is a multi-stage procedure that requires alteration of culture medium or growth conditions between stages. Thus, the micropropagation process involves four basic stages: Stage one, initial tissue culturing; stage two, tissue culture multiplication; stage three, differentiation and plant formation; and stage four, greenhouse culturing and hardening. During stage one, initial tissue culturing, the tissue

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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 chloroplasts per cell to
10 about one. Then, the exogenous polynucleotide is introduced via particle bombardment into the cells with the aim of introducing at least one exogenous polynucleotide molecule into the chloroplasts. The exogenous polynucleotides selected such that it is integratable into the chloroplast's genome via homologous recombination which is readily effected by enzymes inherent to the chloroplast. To this end, the exogenous
15 polynucleotide includes, in addition to a gene of interest, at least one polynucleotide stretch which is derived from the chloroplast's genome. In addition, the exogenous polynucleotide includes a selectable marker, which serves by sequential selection procedures to ascertain that all or substantially all of the copies of the chloroplast genomes following such selection will include the exogenous polynucleotide. Further
20 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 oil content, yield, growth rate, biomass, vigor,
25 nitrogen use efficiency and/or abiotic stress tolerance 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 oil content, yield, growth rate, biomass, vigor, nitrogen use efficiency and/or abiotic
30 stress tolerance.

Expressing a plurality of exogenous polynucleotides in a single host plant can be effected by co-introducing multiple nucleic acid constructs, each including a different

exogenous polynucleotide, into a single plant cell. The transformed cell can then be regenerated into a mature plant using the methods described hereinabove.

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

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

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

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

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

According to an aspect of some embodiments of the invention there is provided a method of expressing a polypeptide of interest in a cell, the method is effected by transforming the cell with a nucleic acid construct which comprises a polynucleotide sequence encoding the polypeptide of interest operably linked to the isolated
5 polynucleotide set forth by SEQ ID NO: 8096, thereby expressing the polypeptide of interest in the cell.

According to some embodiments of the invention, the polypeptide of interest comprises the 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
10 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 % homologous to the polypeptide selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550,
15 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

According to some embodiments of the invention, the polypeptide of interest comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 488-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459,
20 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

According to some embodiments of the invention, the polypeptide of interest comprises the amino acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % homologous to the polypeptide selected from the group consisting of SEQ ID NOs: 5470, 5476 and 5481.
25

According to some embodiments of the invention, the polypeptide of interest
30 comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 5470, 5476 and 5481.

According to some embodiments of the invention, the polynucleotide encoding the polypeptide of interest comprises the nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 94 %, at least about 95 %, at least about 96 %, at least about 97 %, at least about 98 %, at least about 99 %, e.g., 100 % identical to the polynucleotide selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to some embodiments of the invention, the polynucleotide encoding the polypeptide of interest comprises the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

According to some embodiments of the invention, the polynucleotide encoding the polypeptide of interest comprises the nucleic acid sequence at least about 80 %, at least about 81 %, at least about 82 %, at least about 83 %, at least about 84 %, at least about 85 %, at least about 86 %, at least about 87 %, at least about 88 %, at least about 89 %, at least about 90 %, at least about 91 %, at least about 92 %, at least about 93 %, at least about 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: 1627, 1629 and 1631.

According to some embodiments of the invention, the polynucleotide encoding the polypeptide of interest comprises the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1627, 1629 and 1631.

Thus, the invention encompasses transgenic cells (e.g., transgenic plant cells), plants exogenously expressing the polynucleotide(s) (e.g., transgenic plants), the nucleic acid constructs and/or polypeptide(s) of the invention, and methods of generating or producing same. Once expressed within the plant cell or the entire plant, the level of the polypeptide encoded by the exogenous polynucleotide can be determined by methods well known in the art such as, activity assays, Western blots using antibodies capable of specifically binding the polypeptide, Enzyme-Linked Immuno Sorbent Assay

(ELISA), radio-immuno-assays (RIA), immunohistochemistry, immunocytochemistry, immunofluorescence and the like.

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

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

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

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

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

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

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

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

For example, a salinity tolerance test can be performed by irrigating plants at different developmental stages with increasing concentrations of sodium chloride (for example 50 mM, 100 mM, 200 mM, 400 mM NaCl) applied from the bottom and from above to ensure even dispersal of salt. Following exposure to the stress condition the plants are frequently monitored until substantial physiological and/or morphological effects appear in wild type plants. Thus, the external phenotypic appearance, degree of wilting and overall success to reach maturity and yield progeny are compared between control and transgenic plants.

Quantitative parameters of tolerance measured include, but are not limited to, the average wet and dry weight, growth rate, leaf size, leaf coverage (overall leaf area), the weight of the seeds yielded, the average seed size and the number of seeds produced

per plant. Transformed plants not exhibiting substantial physiological and/or morphological effects, or exhibiting higher biomass than wild-type plants, are identified as abiotic stress tolerant plants.

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

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

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

Cold stress tolerance - To analyze cold stress, mature (25 day old) plants are transferred to 4 °C chambers for 1 or 2 weeks, with constitutive light. Later on plants are moved back to greenhouse. Two weeks later damages from chilling period, resulting in growth retardation and other phenotypes, are compared between both

control and transgenic plants, by measuring plant weight (wet and dry), and by comparing growth rates measured as time to flowering, plant size, yield, and the like.

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

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

Formula I

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

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

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

Nitrogen Use efficiency assay using plantlets – The assay is done according to Yanagisawa-S. et al. with minor modifications (“Metabolic engineering with Dof1 transcription factor in plants: Improved nitrogen assimilation and growth under low-nitrogen conditions” *Proc. Natl. Acad. Sci. USA* 101, 7833-7838). Briefly, transgenic plants which are grown for 7-10 days in 0.5 x MS [Murashige-Skoog] supplemented with a selection agent are transferred to two nitrogen-limiting conditions: MS media in which the combined nitrogen concentration (NH_4NO_3 and KNO_3) was 0.75 mM 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 20 seedlings (each one representing an independent transformation event) are carefully transferred to the nitrogen-limiting media. For constructs for which T2 seeds are available, different transformation events are analyzed. Usually, 20 randomly selected plants from each event are transferred to the nitrogen-limiting media allowed to grow for 3-4 additional weeks and individually weighed at the end of that period. Transgenic plants are compared to control plants grown in parallel under the same conditions. Mock-transgenic plants expressing the uidA reporter gene (GUS) under the same promoter or

transgenic plants carrying the same promoter but lacking a reporter gene are used as control.

Nitrogen determination – The procedure for N (nitrogen) concentration determination in the structural parts of the plants involves the potassium persulfate digestion method to convert organic N to NO_3^- (Purcell and King 1996 Argon. J. 88:111-113, the modified Cd^{2+} 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
10 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
15 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
20 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
25 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
30 be captured every 3 days and the rosette area can be calculated by digital analysis. Rosette area growth is calculated using the difference of rosette area between days of sampling divided by the difference in days between samples.

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

Relative growth area can be calculated using Formula II.

5 **Formula II:**

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

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

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

For example, the total seeds from 8-16 plants can be collected, weighted using e.g., an analytical balance and the total weight can be divided by the number of plants. Seed yield per growing area can be calculated in the same manner while taking into account the growing area given to a single plant. Increase seed yield per growing area could be achieved by increasing seed yield per plant, and/or by increasing number of plants capable of growing in a given area.

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

25 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 ($\text{g grain protein kg}^{-1}$ 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
5 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
10 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
15 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
20 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
25 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
30 in yield may also result in modified architecture, or may occur because of modified architecture.

Increased yield of cotton may be manifested by an increase in one or more of the following: number of plants per growing area, number of bolls per plant, number of seeds per boll, increase in the seed filling rate, increase in thousand seed weight (1000-weight), increase oil content per seed, improve fiber length, fiber strength, among
5 others. An increase in yield may also result in modified architecture, or may occur because of modified architecture.

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

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

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

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

The plant oil (including the seed oil and/or the vegetative portion oil) produced
30 according to the method of the invention may be combined with a variety of other ingredients. The specific ingredients included in a product are determined according to the intended use. Exemplary products include animal feed, raw material for chemical

modification, biodegradable plastic, blended food product, edible oil, biofuel, cooking oil, lubricant, biodiesel, snack food, cosmetics, and fermentation process raw material. Exemplary products to be incorporated to the plant oil include animal feeds, human food products such as extruded snack foods, breads, as a food binding agent, 5 aquaculture feeds, fermentable mixtures, food supplements, sport drinks, nutritional food bars, multi-vitamin supplements, diet drinks, and cereal foods.

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

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

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

15 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.

20 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 25 is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as 30 from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

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

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

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable subcombination or as suitable in any other described embodiment of the invention. Certain features described in the context of various embodiments are not to be considered essential features of those embodiments, unless the embodiment is inoperative without those elements.

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

EXAMPLES

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

Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et

al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980); available immunoassays are extensively described in the patent and scientific literature, see, for example, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 and 5,281,521; "Oligonucleotide Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., Eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference as if fully set forth herein. Other general references are provided throughout this document. The procedures therein are believed to be well known in the art and are provided for the convenience of the reader. All the information contained therein is incorporated herein by reference.

GENERAL EXPERIMENTAL AND BIOINFORMATICS METHODS

RNA extraction – Tissues growing at various growth conditions (as described below) were sampled and RNA was extracted using TRIzol Reagent from Invitrogen [Hypertext Transfer Protocol://World Wide Web (dot) invitrogen (dot) com/content

(dot)cfm?pageid=469]. 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.

5 The RNA was eluted in 30 µl of RNase-free water. RNA samples were cleaned up using Qiagen's RNeasy minikit clean-up protocol as per the manufacturer's protocol (QIAGEN Inc, CA USA). For convenience, each micro-array expression information tissue type has received an expression Set ID.

Correlation analysis – was performed for selected genes according to some
10 embodiments of the invention, in which the characterized parameters (measured parameters according to the correlation IDs) were used as “x axis” for correlation with the tissue transcriptom which was used as the “Y axis”. For each gene and measured parameter a correlation coefficient “R” was calculated [using Pearson correlation test
Hypertext Transfer Protocol://World Wide Web (dot) davidmlane (dot)
15 com/hyperstat/A34739 (dot) html] along with a p-value for the significance of the correlation. When the correlation coefficient (R) between the levels of a gene's expression in a certain tissue and a phenotypic performance across ecotypes/variety/hybrid is high in absolute value (between 0.5-1), there is an association between the gene (specifically the expression level of this gene) the phenotypic
20 characteristic (e.g., improved nitrogen use efficiency, abiotic stress tolerance, yield, growth rate and the like). 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
25 association (while the one is increasing the other is decreasing and vice versa). Genes which expression thereof in certain tissue significantly correlates with certain trait are presented in Table 26 along with their correlation coefficient (R, calculated using Pearson correlation) and the p-values under the category of the biodiesel ecotypes vector set.

EXAMPLE 1**IDENTIFICATION OF GENES AND PREDICTED ROLE USING
BIOINFORMATICS TOOLS**

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

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,
10 comprehensive database. Other information on gene expression, protein annotation,
enzymes and pathways were also incorporated. Major databases used include:

Genomes

Arabidopsis genome [TAIR genome version 8 (Hypertext Transfer
Protocol://World Wide Web (dot) arabidopsis (dot) org)];

15 Rice genome [build 6.0 (Hypertext Transfer Protocol:// http://rice (dot)
plantbiology(dot)msu(dot)edu/index.shtml];

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
20 Web (dot) brachpodium (dot) org)];

Soybean [DOE-JGI SCP, version Glyma1 (Hypertext Transfer Protocol://World
Wide Web (dot) phytozome (dot) net/)];

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

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

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

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

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

EST and RNA sequences from NCBI (Hypertext Transfer Protocol://World Wide Web (dot) ncbi (dot) nlm (dot) nih (dot) gov/dbEST/);

5 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/);

Protein and pathway databases

10 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].

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

15 ***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 Examples 2-9 below.

QTL and SNPs information

20 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].

25 ***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.

30 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.

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.

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.

A digital expression profile summary was compiled for each cluster according to all keywords included in the sequence records comprising the cluster. Digital expression, also known as electronic Northern Blot, is a tool that displays virtual expression profile based on the EST sequences forming the gene cluster. The tool provides the expression profile of a cluster in terms of plant anatomy (e.g., the tissue/organ in which the gene is expressed), developmental stage (e.g., the developmental stages at which a gene can be found/expressed) and profile of treatment (provides the physiological conditions under which a gene is expressed such as drought, cold, pathogen infection, etc). Given a random distribution of ESTs in the different clusters, the digital expression provides a probability value that describes the probability of a cluster having a total of N ESTs to contain X ESTs from a certain collection of libraries. For the probability calculations, the following is taken into consideration: a) the number of ESTs in the cluster, b) the number of ESTs of the implicated and related libraries, c) the overall number of ESTs available representing the species. Thereby clusters with low probability values are highly enriched with ESTs from the group of libraries of interest indicating a specialized expression.

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

data obtained against the Cucurbit Genomics Database [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.

5

EXAMPLE 2

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

10 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
15 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
20 levels and the characterized parameters was analyzed using Pearson correlation test.

Experimental procedures

RNA extraction – Five tissues at different developmental stages including root, leaf, flower at anthesis, seed at 5 days after flowering (DAF) and seed at 12 DAF, representing different plant characteristics, were sampled and RNA was extracted as
25 described above. The Expression sets (e.g., roots, leaf etc.) are included in Table 26 below.

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
30 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 assays - 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 assays - 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/](http://rsbweb.nih.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 2 days starting at day 7 in the photography room and the roots development was documented (Figures 3A-F). The growth rate of roots was calculated according to Formula V.

5 **Formula V:**

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.

10 **Formula VI**

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
15 with 8 leaves had been sampled twice (for example at day 10 and day 13), only the largest sample was chosen and added to the Anova comparison.

Seeds in siliques analysis - On day 70, 15-17 siliques were collected from each plot in blocks D and E. The chosen siliques were light brown color but still intact. The siliques from each plot were opened in the photography room, the seeds were scatter on
20 a glass tray and photographed using a high resolution digital camera. 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
25 digital analysis, the number of seeds in each sample was calculated.

Oil percentage in seeds - At the end of the experiment all seeds from plots of blocks A-C were collected. Columbia seeds from 3 plots were mixed grounded and then mounted onto the extraction chamber. 210 ml of n-Hexane (Cat No. 080951 Biolab Ltd.) were used as the solvent. The extraction was performed for 30 hours at medium
30 heat 50 °C. Once the extraction has ended the n-Hexane was evaporated using the evaporator at 35 °C and vacuum conditions. The process was repeated twice. The information gained from the Soxhlet extractor (Soxhlet, F. Die gewichtsanalytische

Bestimmung des Milchfettes, Polytechnisches J. (Dingler's) 1879, 232, 461) was used to create a calibration curve for the Low Resonance NMR. The content of oil of all seed samples was determined using the Low Resonance NMR (MARAN Ultra– Oxford Instrument) and its MultiQuant 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).

15 **Oil yield** - The oil yield was calculated using Formula VII.

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].

20 **Experimental Results**

Nine different *Arabidopsis* ecotypes were grown and characterized for 18 parameters (named as correlation vectors in Table 26). The measured parameters are provided in Tables 1 and 2 below. Correlations of gene's expression in various tissues with these phenotypic measurements are presented in Table 26, as "Arabidopsis 1" in
25 vector set column.

Table 1
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 (cm²)</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

<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 (cm²)</i>	<i>Seeds per silique</i>	<i>Silique length (cm)</i>
Col-0	0.44	138.73	31.19	0.0230	1.27	0.35	109.89	53.47	1.26
Ct-1	0.59	224.06	38.05	0.0252	1.05	0.56	58.36	58.47	1.31
Cvi (N8580)	0.42	116.26	27.76	0.0344	1.28	0.33	56.80	35.27	1.47
Gr-6	0.61	218.27	35.49	0.0202	1.69	0.37	114.66	48.56	1.24
Kondara	0.43	142.11	32.91	0.0263	1.34	0.32	110.82	37.00	1.09
Ler-1	0.36	114.15	31.56	0.0205	0.81	0.45	88.49	39.38	1.18
Mt-0	0.62	190.06	30.79	0.0226	1.21	0.51	121.79	40.53	1.18
Shakdara	0.55	187.62	34.02	0.0235	1.35	0.41	93.04	25.53	1.00

Table 1. 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 (cm²); seeds per silique; Silique length (cm). “gr.” = grams; “mg” = milligrams; “cm” = centimeters”.

5

Table 2
Additional measured parameters in Arabidopsis ecotypes

<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
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 2. 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.

10

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

Experimental procedures

RNA extraction – Two tissues of plants [leaves and stems] growing at two different nitrogen fertilization levels (1.5 mM Nitrogen or 6 mM Nitrogen) were sampled and RNA was extracted as described above. The Expression sets (e.g., roots, leaf etc.) are included in Table 26 below.

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
5 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
10 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 26 below.

15 ***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.
20 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
25 containers within an environmental controlled greenhouse. The image capturing process was 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,
30 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.

Relative growth rate area: The growth rate and the relative growth rate of the rosette and the leaves were calculated according to the following Formulas VIII and IX:

Formula VIII:

$$\text{Growth rate} = \frac{\Delta \text{Area}}{\Delta t}$$

Formula IX:
$$\text{Relative growth rate} = \frac{\Delta \text{Area}}{\Delta t} * \frac{1}{\Delta \text{Area}_{t0}}$$

* Δt is the current analyzed image day subtracted from the initial day (Meaning that area growth rate is in units of cm²/day and length growth rate is in units of cm/day).

* Though the examples shown here are for Area growth rate parameters, the Length growth rate parameters are calculated using similar formulas.

Seed yield and 1000 seeds weight - At the end of the experiment all seeds from all plots were collected and weighed in order to measure seed yield per plant in terms of total seed weight per plant (gr). For the calculation of 1000 seed weight, an average weight of 0.02 grams was measured from each sample, the seeds were scattered on a glass tray and a picture was taken. Using the digital analysis, the number of seeds in each sample was calculated.

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

Harvest Index - The harvest index was calculated using formula IV (Harvest Index = Average seed yield per plant/ Average dry weight).

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 meter and measurement was performed at time of flowering. SPAD meter readings were done on young fully developed leaf. Three measurements per leaf were taken per plot. Based on this measurement, parameters such as the ratio between seed yield per nitrogen unit [seed yield/N level = seed yield per plant [gr]/SPAD unit], plant DW per nitrogen unit [DW/ N level= plant biomass per plant [g]/SPAD unit], and nitrogen level per gram of biomass [N level/DW= SPAD unit/ plant biomass per plant (gr)] were calculated.

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

Table 3
Additional measured parameters in Arabidopsis ecotypes

<i>Arabidopsis</i> 2 NUE	<i>N 1.5</i> <i>mM</i> <i>Rosette</i> <i>Area</i> <i>8 day</i>	<i>N 1.5 mM</i> <i>Rosette</i> <i>Area 10</i> <i>day</i>	<i>N 1.5 mM</i> <i>Leaf</i> <i>Number 10</i> <i>day</i>	<i>N 1.5 mM</i> <i>Leaf Blade</i> <i>Area 10 day</i>	<i>N 1.5 mM</i> <i>RGR of</i> <i>Rosette</i> <i>Area 3 day</i>	<i>N 1.5 mM</i> <i>t50</i> <i>Flowering</i> <i>g</i>
Bay-0	0.760	1.430	6.875	0.335	0.631	15.967
Col-0	0.709	1.325	7.313	0.266	0.793	20.968
Ct-1	1.061	1.766	7.313	0.374	0.502	14.836
Gr-6	1.157	1.971	7.875	0.387	0.491	24.708
kondara	0.996	1.754	7.938	0.373	0.605	23.566
Mc-0	1.000	1.832	7.750	0.370	0.720	23.698
Mt-0	0.910	1.818	7.625	0.386	0.825	18.059
No-0	0.942	1.636	7.188	0.350	0.646	19.488
Oy-o	1.118	1.996	8.625	0.379	0.668	23.568
Shakadara	0.638	1.150	5.929	0.307	0.636	21.888

Table 3. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: N 1.5 mM Rosette Area 8 day (measured in cm²); N 1.5 mM Rosette Area 10 day (measured in cm²); N 1.5 mM Leaf Number 10 day; N 1.5 mM Leaf Blade Area 10 day (measured in cm²); N 1.5 mM RGR of Rosette Area 3 day; N 1.5 mM t50 Flowering (measured in days); “cm” = centimeters”.

Table 4
Additional measured parameters in Arabidopsis ecotypes

<i>Arabidopsis 2 NUE</i>	<i>N 1.5 mM Dry Weight</i>	<i>N 1.5 mM Seed Yield</i>	<i>N 1.5 mM Harvest Index</i>	<i>N 1.5 mM 1000 Seeds weight</i>	<i>N 1.5 mM seed yield per rosette area day 10</i>	<i>N 1.5 mM seed yield per leaf blade</i>
Bay-0	0.164	0.032	0.192	0.016	0.022	0.095
Col-0	0.124	0.025	0.203	0.016	0.019	0.095
Ct-1	0.082	0.023	0.295	0.018	0.014	0.063
Gr-6	0.113	0.010	0.085	0.014	0.005	0.026
kondara	0.184	0.006	0.031	0.018	0.003	0.015
Mc-0	0.124	0.009	0.071	0.022	0.005	0.024
Mt-0	0.134	0.032	0.241	0.015	0.018	0.084
No-0	0.106	0.019	0.179	0.014	0.013	0.059
Oy-o	0.148	0.012	0.081	0.022	0.007	0.034
Shakadara	0.171	0.014	0.079	0.019	0.012	0.044

Table 4. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: N 1.5 mM Dry Weight (measured in grams); N 1.5 mM Seed Yield (measured in gr/plant); N 1.5 mM Harvest Index; N 1.5 mM 1000 Seeds weight (measured in grams); N 1.5 mM seed yield per rosette area day 10 (measured in gr/plant*cm²); N 1.5 mM seed yield per leaf blade (measured in gr/plant*cm²);

Table 5

Additional measured parameters in Arabidopsis ecotypes

<i>Arabidopsis 2 NUE</i>	<i>N 6 mM Rosette Area 8 day</i>	<i>N 6 mM Rosette Area 10 day</i>	<i>N 6 mM Leaf Number 10 day</i>	<i>N 6 mM Leaf Blade Area 10 day</i>
Bay-0	0.759	1.406	6.250	0.342
Col-0	0.857	1.570	7.313	0.315
Ct-1	1.477	2.673	8.063	0.523
Gr-6	1.278	2.418	8.750	0.449
kondara	1.224	2.207	8.063	0.430
Mc-0	1.095	2.142	8.750	0.430
Mt-0	1.236	2.474	8.375	0.497
No-0	1.094	1.965	7.125	0.428
Oy-o	1.410	2.721	9.438	0.509
Shakadara	0.891	1.642	6.313	0.405

Table 5. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: N 6 mM Rosette Area 8 day; N 6 mM Rosette Area 10 day; N 6 mM Leaf Number 10 day; N 6 mM Leaf Blade Area 10 day.

Table 6

Additional measured parameters in Arabidopsis ecotypes

<i>Arabidopsis 2 NUE</i>	<i>N 6 mM RGR of Rosette Area 3 day</i>	<i>N 6 mM t50 Flowering</i>	<i>N 6 mM Dry Weight</i>	<i>N 6 mM Seed Yield</i>	<i>N 6 mM Harvest Index</i>	<i>N 6 mM 1000 Seeds weight</i>
Bay-0	0.689137	16.3714	0.41875	0.11575	0.279999	0.014743

<i>Arabidopsis 2 NUE</i>	<i>N 6 mM RGR of Rosette Area 3 day</i>	<i>N 6 mM t50 Flowering g</i>	<i>N 6 mM Dry Weight</i>	<i>N 6 mM Seed Yield</i>	<i>N 6 mM Harvest Index</i>	<i>N 6 mM 1000 Seeds weight</i>
Col-0	1.023853	20.5	0.53125	0.16516 3	0.308528	0.016869
Ct-1	0.614345	14.63465	0.38187 5	0.10846 9	0.283603	0.01777
Gr-6	0.600985	24	0.5175	0.08195	0.158357	0.012078
kondara	0.476947	23.378	0.49625	0.06754 4	0.136182	0.01601
Mc-0	0.650762	23.59507	0.57937 5	0.11918 1	0.205875	0.015535
Mt-0	0.675597	15.0327	0.50125	0.13876 9	0.276265	0.015434
No-0	0.584219	19.74969	0.6275	0.10695 6	0.170622	0.014038
Oy-o	0.612997	22.88714	0.64937 5	0.13808 8	0.21248	0.016601
Shakadara	0.515469	18.80415	0.57312 5	0.09481 3	0.165557	0.016081

Table 6. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: N 6 mM RGR of Rosette Area 3 day; N 6 mM t50 Flowering (measured in days); N 6 mM Dry Weight (measured in gr/plant); N 6 mM Seed Yield (measured in gr/plant); N 6 mM Harvest Index; N 6 mM 1000 Seeds weight (measured in gr); “gr.” = grams; “mg” = miligrams; “cm” = centimeters”.

Table 7
Additional measured parameters in Arabidopsis ecotypes

<i>Arabidopsis 2 NUE</i>	<i>N 6 mM seed yield/ rosette area day 10 day</i>	<i>N 6 mM seed yield/leaf blade</i>
Bay-0	0.082439	0.339198
Col-0	0.105792	0.52646
Ct-1	0.040511	0.207182
Gr-6	0.033897	0.182671
kondara	0.030718	0.157924
Mc-0	0.055634	0.277238
Mt-0	0.057027	0.281182
No-0	0.055374	0.252332
Oy-o	0.050715	0.271258
Shakadara	0.058181	0.235472

Table 7. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: N 6 mM seed yield/ rosette area day 10 day (measured in gr/plant*cm²); N 6 mM seed yield/leaf blade (measured in gr/plant*cm²);

Table 8
Additional measured parameters in Arabidopsis ecotypes

<i>Arabidopsis 2</i>	<i>N 6 mM Spad / FW</i>	<i>N 6 mM DW/SPAD (biomas/ Nunit)</i>	<i>N 6 mM spad/DW (gN/g plant)</i>	<i>N 6 mM Seed yield/N unit</i>	<i>N 1.5 mM Spad / FW</i>	<i>N 1.5 mM SPAD /DW</i>	<i>N 1.5 mM DW/S PAD</i>	<i>N 1.5 mM seed yield/spad</i>
Bay-0	22.49	0.01862	53.7055	0.004209	45.59	167.3004	0.005977	0.001155
Gr-6	28.27	0.018307	54.6248	0.002953	42.11	241.0608	0.004148	0.000361
kondara	17.64	0.028131	35.54803	0.002333	28.15	157.8231	0.006336	0.000191
Mt-0	33.32	0.015042	66.47908	0.005299	53.11	194.9767	0.005129	0.001234
Shakadara	39	0.014694	68.05368	0.003255	67	169.3431	0.005905	0.000466

Table 8. Provided are the values of each of the parameters measured in Arabidopsis ecotypes: N 6 mM Spad / FW; N 6 mM DW/SPAD (biomas/ Nunit); N 6 mM spad/DW (gN/g plant); N 6 mM Seed yield/N unit (measured in gr/N units); N 1.5 mM Spad / FW (measured in 1/gr); N 1.5 mM SPAD/DW (measured in 1/gr); N 1.5 mM DW/SPAD (measured in 1/gr); N 1.5 mM seed yield/spad (measured in gr);

Experimental Results

10 different Arabidopsis accessions (ecotypes) were grown and characterized for 33 parameters as described above (Tables 3-8). The average for each of the measured parameters was calculated using the JMP software. Subsequent correlation analysis was performed between the characterized parameters in the Arabidopsis ecotypes (which are used as x axis for correlation) and the tissue transcriptom, and genes exhibiting a significant correlation to selected traits (classified using the correlation vector) are presented in Table 26 below along with their correlation values (R, calculated using Pearson correlation) and the p-values under the category of the vector sets Arabidopsis 2 NUE vector and Arabidopsis 2.

EXAMPLE 4

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

In order to produce a high throughput correlation analysis, the present inventors utilized a Tomato oligonucleotide micro-array, produced by Agilent Technologies

[Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent (dot) com/Scripts/PDS (dot) asp?lPage=50879]. The array oligonucleotide represents about 44,000 Toamto genes and transcripts. In order to define correlations between the levels of RNA expression with ABST, yield components or vigor related parameters various plant characteristics of 18 different Tomato varieties were analyzed. Among them, 10 varieties encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

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

Experimental procedures

Growth procedure - Tomato variety was grown under normal conditions (4-6 Liters/m² per day) until flower stage. At this time, irrigation was reduced to 50 % compared to normal conditions.

RNA extraction – Two tissues at different developmental stages [flower and leaf], representing different plant characteristics, were sampled and RNA was extracted as described above. The Expression sets (e.g., flower and leaf) are included in Table 26 below.

Tomato yield components and vigor related parameters under 50 % water irrigation assessment – 10 Tomato varieties in 3 repetitive blocks (named A, B, and C), each containing 6 plants per plot were grown at net house. Plants were phenotyped on a daily basis following the standard descriptor of tomato (Table 11, below). Harvest was conducted while 50 % of the fruits were red (mature). Plants were separated to the vegetative part and fruits, of them, 2 nodes were analyzed for additional inflorescent parameters such as size, number of flowers, and inflorescent weight. Fresh weight of all vegetative material was measured. Fruits were separated to colors (red vs. green) and in accordance with the fruit size (small, medium and large). Next, analyzed data was saved to text files and processed using the JMP statistical analysis software (SAS institute).

Data parameters collected are summarized in Table 9, hereinbelow.

Table 9
Tomato correlated parameters (vectors)

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

Table 9. Provided are the tomato correlated parameters. “gr.” = grams; “SPAD” = chlorophyll levels;

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

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

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

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

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

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

15 **Experimental Results**

10 different Tomato varieties (accessions) were grown and characterized for 23 parameters as described above. The average for each of the measured parameter was calculated using the JMP software and values are summarized in Tables 10, 11 and 12 below. Subsequent correlation analysis between expression of selected genes in various
20 transcriptom expression sets and the measured parameters in tomato accessions (Tables 10-12) was conducted, and results were integrated to the database and provided in Table 26 below under the category of the vector sets Tomato vectors field Normal, Tomato vectors field Drought.

25

Table 10
Measured parameters in Tomato accessions

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

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

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

Table 11***Additional measured parameters in Tomato accessions***

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

Table 11: Provided are the measured yield components and vigor related parameters under 50 % water irrigation for the tomato accessions (Varieties) according to the Correlation (Corr.) ID numbers (described in Table 9 above) as follows: 22 [50 % Irrigation; Ripe fruit average weight (gr.)/ Normal Irrigation; Ripe fruit average weight (gr.)]; 8 [50 % Irrigation: SPAD]; 16 [Normal Irrigation; SPAD]; 5 [50 % Irrigation; relative Water use efficiency]; 13 [Normal Irrigation; relative Water use efficiency]; 23 [50 % Irrigation: SPAD/ Normal Irrigation; SPAD].

Table 12***Additional measured parameters in Tomato accessions***

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

Table 12: Provided are the measured yield components and vigor related parameters under 50 % water irrigation for the tomato accessions (Varieties) according to the Correlation (Corr.) ID numbers (described in Table 9 above) as follows: 21 [50 % Irrigation; relative Water use efficiency/ Normal Irrigation; Water use efficiency]; 4 [50 % Irrigation; number of flowers];

12 [Normal Irrigation; number of flowers]; 3 [50 % Irrigation; Inflorescence weight (gr.)]; 11 [Normal Irrigation; Inflorescence weight (gr.)]; 20 [50 % Irrigation; number of flowers/ Normal Irrigation; number of flowers]; 19 [50 % Irrigation; Inflorescence weight (gr.)/ Normal Irrigation; Inflorescence weight (gr.)].

5

II. Correlation of Tomato varieties under stress built under 50 % irrigation conditions

Experimental procedures

Growth procedure - Tomato varieties were grown under normal conditions (4-6
10 Liters/m² per day) until flower stage. At this time, irrigation was reduced to 50 % compared to normal conditions. Tissue sample were taken during the stress developed period every two days.

RNA extraction – All 10 selected Tomato varieties were sampled per each treatment. Two tissues [leaves and flowers] growing at 50% irrigation or under normal
15 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]. The Expression sets (e.g., flower and leaf) are included in Table 26 below. Extraction of RNA from tissues was performed as described in Example 2 above.

20 **Correlation of early vigor traits across collection of tomato ecotypes under high salinity concentration** – Ten tomato varieties were grown in 3 repetitive plots, each containing 17 plants, at a net house under semi-hydroponics conditions. Briefly, the growing protocol was as follows: Tomato seeds were sown in trays filled with a mix of vermiculite and peat in a 1:1 ratio. Following germination, the trays were
25 transferred to either high salinity growth conditions (100 mM NaCl solution) or to normal growth conditions [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
30 grams/liter; Co 1.5 grams/liter; and Mo 1.1 grams/liter), solution's pH should be 6.5 – 6.8].

Tomato vigor related parameters under 100 mM NaCl – Following 5 weeks of growing, plant were harvested and analyzed for leaf number, plant height, and plant weight (data parameters are summarized in Table 13). Next, analyzed data was saved to

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

Table 13
Tomato correlated parameters (vectors)

<i>Correlated parameter with</i>	<i>Correlation Id</i>
100 mM NaCl: leaf Number	1
100 mM NaCl: Plant height	2
100 mM NaCl: Plant biomass	3
Normal: leaf Number	4
Normal: Plant height	5
100 mM NaCl: leaf Number/Normal: leaf Number	6
100 mM NaCl: Plant height/Normal: Plant height	7

Table 13. Provided are the tomato correlated parameters (ID numbers 1-7).

Experimental Results

10 different Tomato varieties were grown and characterized for 7 parameters as described above (Table 13). The average for each of the measured parameters was calculated using the JMP software and values are summarized in Tables 14 below. Subsequent correlation analysis between expression of selected genes in various transcriptom expression sets and the average measured parameters was conducted and the results were integrated to the database and provided in Table 26 hereinbelow under the vector sets: Tomato vectors bath Normal, and Tomato vectors bath Salinity.

Table 14
Measured parameters in tomato accessions

<i>Corr. ID</i> <i>Variety</i>	<i>1</i>	<i>4</i>	<i>2</i>	<i>5</i>	<i>3</i>	<i>6</i>	<i>7</i>
1139	3.56	6.56	5.60	45.33	0.36	0.54	0.12
2078	3.94	6.89	6.46	47.78	0.44	0.57	0.14
2958	5.00	7.33	8.47	40.78	0.26	0.68	0.21
5077	4.00	6.22	8.56	55.33	0.71	0.64	0.15
5080	3.56	6.33	8.87	56.22	0.46	0.56	0.16
5084	4.39	6.44	7.56	48.67	0.54	0.68	0.16
5085	3.17	5.89	8.64	55.78	0.66	0.54	0.15
5088	3.72	5.56	5.57	37.44	0.40	0.67	0.15
5089	4.00	6.11	5.82	49.56	0.52	0.65	0.12
5092	4.28	5.67	9.36	46.33	0.45	0.75	0.20

Table 14. Provided are the measured vigor related parameters under 100 mM NaCl or normal conditions for the tomato accessions (Varieties) according to the Correlation (Corr.) ID numbers (described in Table 13 above) as follows: 1 [100 mM NaCl: leaf Number]; 4 [Normal: leaf Number]; 2 [100 mM NaCl: Plant height]; 5 [Normal: Plant height]; 3 [100 mM NaCl:

Plant biomass]; 6 [100 mM NaCl: leaf Number/Normal: leaf Number]; 7 [100 mM NaCl: Plant height/Normal: Plant height].

EXAMPLE 5

5 PRODUCTION OF *B. JUNCEA* TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS WITH YIELD PARAMETRERS USING 44K *B.* JUNCEA OLIGONUCLEOTIDE MICRO-ARRAYS

In order to produce a high throughput correlation analysis, the present inventors utilized a *B. juncea* oligonucleotide micro-array, produced by Agilent Technologies
10 [Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent (dot) com/Scripts/PDS (dot) asp?lPage=50879]. The array oligonucleotide represents about 60,000 *B. juncea* genes and transcripts. In order to define correlations between the levels of RNA expression with yield components or vigor related parameters, various plant characteristics of 11 different *B. juncea* varieties were analyzed and used for RNA
15 expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Correlation of *B. juncea* genes' expression levels with phenotypic characteristics across ecotype

Experimental procedures

20 11 *B. juncea* varieties were grown in three repetitive plots, in field. Briefly, the growing protocol was as follows: *B. juncea* seeds were sown in soil and grown under normal condition till harvest. In order to define correlations between the levels of RNA expression with yield components or vigor related parameters, the 11 different *B. juncea* varieties were analyzed and used for gene expression analyses.

25 ***RNA extraction*** – All 11 selected *B. juncea* varieties were sample per each treatment. Plant tissues [leaf, Pod, Lateral meristem and flower] growing under normal conditions were sampled and RNA was extracted as described above. The Expression sets (e.g., leaf, Pod, Lateral meristem and flower) are included in Table 26 below.

30 The collected data parameters were as follows:

Fresh weight (plot-harvest) [gr/plant] – total fresh weight per plot at harvest time normalized to the number of plants per plot.

Seed Weight [milligrams /plant] – total seeds from each plot was extracted, weighted and normalized for plant number in each plot.

Harvest index - The harvest index was calculated: seed weight / fresh weight

Days till bolting / flowering – number of days till 50% bolting / flowering for
5 each plot.

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 for each plot.

10 ***Main branch - average node length*** – total length / total number of nodes on main branch.

Lateral branch - average node length – total length / total number of nodes on lateral branch.

Main branch - 20th length – the length of the pod on the 20th node from the
15 apex of main branch.

Lateral branch - 20th length – the length of the pod on the 20th node from the apex of lateral branch.

Main branch - 20th seed No. – number of seeds in the pod on the 20th node from the apex of main branch.

20 ***Lateral branch - 20th seed number*** - number of seeds in the pod on the 20th node from the apex of lateral branch.

Number of lateral branches – total number of lateral branches, average of three plants per plot.

Main branch height [cm] – total length of main branch.

25 ***Min-lateral branch position*** – lowest node on the main branch that has developed lateral branch.

Max-lateral branch position [#node of main branch] – highest node on the main branch that has developed lateral branch.

Max-number of nodes in lateral branch – the highest number of node that a
30 lateral branch had per plant.

Max length of lateral branch [cm] – the highest length of lateral branch per plant.

Max diameter of lateral branch [mm] – the highest base diameter that a lateral branch had per plant.

Oil Content - Indirect oil content analysis was carried out using 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)];

Fresh weight (single plant) (gr/plant) – average fresh weight of three plants per plot taken at the middle of the season.

Main branch base diameter [mm] – the based diameter of main branch, average of three plants per plot.

1000 Seeds [gr] – weight of 1000 seeds per plot.

Experimental Results

Eleven different *B. juncea* varieties (i.e., seed ID 646, 648, 650, 657, 661, 662, 663, 664, 669, 670, 671) were grown and characterized for 23 parameters as specified above. The average for each of the measured parameters was calculated using the JMP software and values are summarized in Table 15 below. Subsequent correlation analysis between the various transcriptom expression sets and the average parameters, was conducted. Results were then integrated to the database and selected correlations are shown in Table 26, below, under the vector set Juncea ecotypes vector.

Table 15
Measured parameters in *B. juncea* accessions

Seed ID Parameter	646	648	650	657	661	662	663	664	669	670	671
Fresh weight (plot-harvest) [gr/plant]	69.2	45.2	39.3	49.1	44.0	46.4	36.1	32.6	33.2	63.2	60.9
Seed Weight per plant	4.38	5.72	5.53	6.87	5.81	6.28	4.58	4.37	4.48	5.66	7.06
harvest index*10³	0.06	0.13	0.14	0.14	0.13	0.14	0.13	0.13	0.14	0.09	0.12
days till bolting	57.3	60.3	59.7	56.3	55.0	46.7	59.0	54.3	59.7	57.3	53.0
days till flowering	66.0	69.7	69.3	66.0	61.3	53.0	69.7	63.7	69.7	71.0	58.3
SPAD	33.0	30.0	32.8	37.5	41.4	35.4	33.2	32.9	34.8	31.8	41.5

Seed ID Parameter	646	648	650	657	661	662	663	664	669	670	671
Main branch - average node length	0.5	0.4	0.6	0.4	0.4	0.7	0.4	0.6	0.6	0.6	1.6
Lateral branch - average node length	0.7	0.4	0.7	0.6	0.6	0.8	0.6	0.8	1.0	0.8	0.9
Main branch - 20th length	4.3	3.7	3.6	3.5	2.7	5.2	3.9	4.0	3.5	3.7	4.0
Lateral branch - 20th length	4.3	3.7	4.1	3.4	3.1	4.0	4.3	4.2	4.1	4.0	3.9
Main branch - 20th seed No.	13.2	13.7	10.4	14.1	9.8	15.2	12.0	12.7	9.9	11.6	15.6
Lateral branch - 20th seed number	13.0	14.0	13.2	13.4	11.0	13.1	11.9	13.4	11.2	13.2	14.0
Number of lateral branches	15.2	14.9	13.6	14.9	14.0	9.8	16.4	14.3	14.6	14.1	16.8
Main branch height [cm]	140.7	125.2	112.4	133.4	142.0	101.5	145.4	131.6	129.9	131.6	116.4
Min-Lateral branch position	6.8	6.3	5.6	3.7	3.0	3.1	7.8	6.2	5.6	4.9	5.3
Max-Lateral branch position [#node of main branch]	15.2	14.9	13.6	14.9	14.0	10.9	16.4	14.3	14.6	14.1	16.8
Max-Number of nodes in lateral branch	5.2	7.0	5.2	7.0	6.6	9.4	6.1	5.2	5.7	6.6	6.0
Max Length of lateral branch [cm]	40.4	47.2	41.6	60.5	59.8	59.4	47.3	47.3	44.7	58.7	47.2
Max Diameter of lateral branch [mm]	4.2	4.9	4.3	5.7	5.9	5.7	4.5	4.9	4.7	5.6	5.5
Oil Content	40.2	40.7	40.9	38.6	40.1	42.6	41.3	40.8	40.8	38.1	37.2
Fresh Weight (single plant) (gr/plant)	197.8	142.2	147.2	243.3	192.3	163.8	164.4	181.1	176.2	217.9	261.1
Main branch base diameter [mm]	14.5	12.0	19.9	14.3	12.6	12.3	12.6	12.9	12.6	13.8	13.6
1000 Seeds [gr]	3.8	2.2	3.3	2.4	2.0	3.1	3.3	3.1	3.4	3.4	2.4

Table 15: Provided are the values of each of the parameters (as described above) measured in *B. juncea* accessions (Seed ID) under normal conditions.

EXAMPLE 6

***PRODUCTION OF B. JUNCEA TRANSCRIPTOM AND HIGH THROUGHPUT
CORRELATION ANALYSIS WITH YIELD PARAMETERS OF JUNCEA GROWN
UNDER VARIOUS POPULATION DENSITIES USING 44K B. JUNCEA
OLIGONUCLEOTIDE MICRO-ARRAYS***

In order to produce a high throughput correlation analysis, the present inventors utilized a *B. juncea* 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 60,000 *B. juncea* genes and transcripts. In order to define correlations between the levels of RNA expression with yield components or vigor related parameters, various plant characteristics of two different *B. juncea* varieties grown under seven different population densities were analyzed and used for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Correlation of B. juncea genes' expression levels with phenotypic characteristics across seven population densities for two ecotypes

Experimental procedures

Two *B. juncea* varieties (646 and 671) were grown in a field under seven population densities (10, 60, 120, 160, 200, 250 and 300 plants per m²) in two repetitive plots. Briefly, the growing protocol was as follows: *B. juncea* seeds were sown in soil and grown under normal condition till harvest. In order to define correlations between the levels of RNA expression with yield components or vigor related parameters, the two different *B. juncea* varieties grown under various population densities were analyzed and used for gene expression analyses. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test for each ecotype independently.

RNA extraction – the two *B. juncea* varieties grown under seven population densities were sample per each treatment. Plant tissues [Flower and Lateral meristem] growing under Normal conditions were sampled and RNA was extracted as described above. For convenience, each micro-array expression information tissue type has

received a Set ID. The Expression sets (e.g., Flower and Lateral meristem) are included in Table 26 below.

The collected data parameters were as follows:

Fresh weight (plot-harvest) [gr/plant] – total fresh weight per plot at harvest time normalized to the number of plants per plot.

Seed weight [gr/plant] – total seeds from each plot was extracted, weighted and normalized for plant number in each plot.

Harvest index - The harvest index was calculated: seed weight / fresh weight

Days till bolting / flowering – number of days till 50% bolting / flowering for each plot.

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 for each plot.

Main branch - average node length – total length / total number of nodes on main branch.

Lateral branch - average node length – total length / total number of nodes on lateral branch.

Main branch - 20th length – the length of the pod on the 20th node from the apex of main branch.

Lateral branch - 20th length – the length of the pod on the 20th node from the apex of lateral branch.

Main branch - 20th seed No. – number of seeds in the pod on the 20th node from the apex of main branch.

Lateral branch - 20th seed number - number of seeds in the pod on the 20th node from the apex of lateral branch.

Number of lateral branches – total number of lateral branches, average of three plants per plot.

Main branch height [cm] – total length of main branch.

Min-Lateral branch position – lowest node on the main branch that has developed lateral branch.

Max-Lateral branch position [#node of main branch] – highest node on the main branch that has developed lateral branch.

Max-number of nodes in lateral branch – the highest number of node that a lateral branch had per plant.

5 ***Max-length of lateral branch [cm]*** – the highest length of lateral branch per plant.

Max diameter of lateral branch [mm] – the highest base diameter that a lateral branch had per plant.

Oil content - Indirect oil content analysis was carried out using Nuclear
10 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)];

Fresh weight (single plant) (gr/plant) – average fresh weight of three plants per
15 plot taken at the middle of the season.

Main branch base diameter [mm] – the based diameter of main branch, average of three plants per plot.

1000 Seeds [gr] – weight of 1000 seeds per plot.

Main branch-total number of pods – total number of pods on the main branch,
20 average of three plants per plot.

Main branch-dist. 1-20 – the length between the youngest pod and pod number
20 on the main branch, average of three plants per plot.

Lateral branch-total number of pods - total number of pods on the lowest lateral branch, average of three plants per plot.

25 ***Lateral branch-dis. 1-20*** – the length between the youngest pod and pod number
20 on the lowest lateral branch, average of three plants per plot.

Dry weight/plant – weight of total plants per plot at harvest after three days at oven at 60°C normalized for the number of plants per plot.

Total leaf area – Total leaf area per plot was calculated based on random three
30 plants and normalized for number of plants per plot.

Total Perim. – total perimeter of leaves, was calculated based on random three plants and normalized for number of plants per plot.

Experimental Results

Two *B. juncea* varieties were grown under seven different population densities and characterized for 29 parameters as specified above. The average for each of the measured parameter was calculated using the JMP software and values are summarized in Table 16 below. Subsequent correlation analysis between the expression of selected genes in various transcriptom expression sets and the average parameters was conducted. Results were then integrated to the database and are provided in Table 26, below, under the vector sets Juncea population densities.

Table 16***Measured parameters in B. juncea accessions at various population densities***

<i>Popul. Density (plants per m²)</i>	<i>10</i>	<i>60</i>	<i>120</i>	<i>160</i>	<i>200</i>	<i>250</i>	<i>300</i>
Main branch base diameter [mm]	7.37	6.90	5.62	4.99	6.45	3.95	8.77
fresh Weight (single plant) [gr/plant]	0.07	0.04	0.03	0.02	0.04	0.02	0.07
Main branch height [cm]	116.0	115.5	111.3	106.0	117.5	108.0	157.3
Number of lateral branches	16.17	19.17	15.83	19.33	18.33	17.83	12.83
Min-Lateral branch position	5.00	11.00	7.00	11.00	9.00	9.00	3.00
Max-Lateral branch position	20.00	23.00	19.00	24.00	22.00	20.00	16.00
Max-Number of nodes in lateral branch	6.00	4.00	4.00	4.00	6.00	4.00	11.00
Max-Length of lateral branch [cm]	78.00	41.00	43.00	36.00	40.00	42.00	109.0
Max-Diameter of lateral branch [mm]	4.40	2.90	2.50	2.00	3.40	2.50	8.00
Main branch-total number of pods	15.17	15.33	17.67	16.50	23.17	16.83	33.83
Main branch-dist. 1-20	37.58	27.90	31.22	26.05	27.72	31.85	45.25
Main branch-20th length	5.10	4.63	4.60	4.67	4.73	4.68	4.43
Main branch-20th seed No.	17.67	17.67	18.00	18.50	17.67	17.50	13.17

<i>Popul. Density (plants per m²)</i>	<i>10</i>	<i>60</i>	<i>120</i>	<i>160</i>	<i>200</i>	<i>250</i>	<i>300</i>
Lateral branch- total number of pods	14.00	11.67	10.67	10.17	12.50	9.83	18.50
Lateral branch- dis. 1-20	28.25	17.53	19.08	15.65	15.23	17.73	21.58
Lateral branch- 20th length	4.95	4.48	4.37	4.33	4.35	4.40	4.72
Lateral branch- 20th seed number	14.55	19.33	17.00	18.83	15.67	17.17	11.17
Oil Content	26.78	29.62	29.57	30.59	29.87	25.22	37.55
SPAD	40.89	41.95	40.48	37.93	39.50	45.57	39.21
days till bolting	53.00	50.50	48.00	53.00	50.00	51.50	51.50
days till flowering	62.50	64.00	64.00	64.00	64.00	62.50	61.00
fresh weight (at harvest)/plant	0.05	0.02	0.01	0.01	0.01	0.01	0.04
dry weight/plant	0.01	0.01	0.00	0.00	0.00	0.00	0.01
Seed Weight/plant	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1000Seeds [gr]	1.56	1.75	1.62	1.99	1.92	1.54	2.77
Total Leaf Area	76.39	37.49	25.00	14.33	50.79	29.13	218.2
Total Perim.	219.1	100.5	68.0	37.9	97.5	61.2	329.0

Table 16: Provided are the values of each of the parameters (as described above) measured in *B. juncea* (Seed ID 671) grown in seven population densities (Populat. Density) under normal conditions. Param. = parameter.

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EXAMPLE 7

PRODUCTION OF SORGHUM TRANSCRIPTOM AND HIGH THROUGHPUT CORRELATION ANALYSIS WITH YIELD, NUE, AND ABST RELATED PARAMETERS MEASURED IN FIELDS USING 44K SORGHUM OLIGONUCLEOTIDE MICRO-ARRAYS

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In order to produce a high throughput correlation analysis between plant phenotype and gene expression level, the present inventors utilized a sorghum oligonucleotide micro-array, produced by Agilent Technologies [Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent (dot) com/Scripts/PDS (dot) asp?!Page=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, yield and NUE components or vigor related parameters, various plant characteristics of 17 different sorghum hybrids were analyzed. Among them, 10 hybrids encompassing the observed variance were selected for RNA expression

15

analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Correlation of Sorghum varieties across ecotypes grown under low nitrogen, regular growth and severe drought conditions

5 ***Experimental procedures***

17 Sorghum varieties were grown in 3 repetitive plots, in field. Briefly, the growing protocol was as follows:

1. Regular growth conditions: sorghum plants were grown in the field using commercial fertilization and irrigation protocols.

10 ***2. Low Nitrogen fertilization conditions:*** sorghum plants were fertilized with 50% less amount of nitrogen in the field than the amount of nitrogen applied in the regular growth treatment. All the fertilizer was applied before flowering.

3. Drought stress: sorghum seeds were sown in soil and grown under normal condition until around 35 days from sowing, around V8. At this point, irrigation was
15 stopped, and severe drought stress was developed. In order to define correlations between the levels of RNA expression with NUE, drought, and yield components or vigor related parameters, the 17 different sorghum varieties were analyzed. Among them, 10 varieties encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized
20 parameters was analyzed using Pearson correlation test.

Analyzed Sorghum tissues – All 10 selected Sorghum hybrids were sample per each treatment. Plant tissues [Flag leaf, Flower meristem and Flower] growing under low nitrogen, severe drought stress and plants grown under Normal conditions were sampled and RNA was extracted as described above.

25 The following parameters were collected using digital imaging system:

Average Grain Area (cm²) - At the end of the growing period the grains were separated from the Plant 'Head'. A sample of ~200 grains were weight, photographed and images were processed using the below described image processing system. The grain area was measured from those images and was divided by the number of grains.

30 ***Average Grain Length (cm)*** - At the end of the growing period the grains were separated from the Plant 'Head'. A sample of ~200 grains were weight, photographed and images were processed using the below described image processing system. The

sum of grain lengths (longest axis) was measured from those images and was divided by the number of grains.

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

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

The image processing system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.37, Java based image processing software, which was developed at the U.S. National Institutes of Health and is freely available on the internet 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 for seed area and seed length was saved to text files and analyzed using the JMP statistical analysis software (SAS institute).

Additional parameters were collected either by sampling 5 plants per plot or by measuring the parameter across all the plants within the plot.

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

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

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

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

Relative Growth Rate was calculated using Formulas X and XI as follows:

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

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

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

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

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

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

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

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

Experimental Results

17 different sorghum hybrids were grown and characterized for different parameters: The average for each of the measured parameter was calculated using the JMP software (Tables 17-21) and a subsequent correlation analysis was performed

(Table 26 below) under the vector sets “Vectors Sorghum Field Normal” or Vectors Sorghum Field NUE”.

Table 17
Sorghum correlated parameters (vectors)

<i>Correlation set</i>	<i>Correlation ID</i>
Total Seed Weight/Head gr based on plot-normal	1
Total Seed Weight /Head gr based on 5 heads-normal	2
Head Average Length cm-normal	3
Average Seed Area cm2-normal	4
Average Seed Length cm-normal	5
FW Head/Plant gr based on 5 plants-normal	6
FW Head/Plant gr based on plot-normal	7
Final Plant Height cm-normal	8
Total Seed Weight/Head gr based on plot-NUE	9
Total Seed Weight /Head gr based on 5 heads-NUE	10
Head Average Area cm2-NUE	11
Head Average Perimeter cm-NUE	12
Head Average Length cm-NUE	13
Average Seed Area cm2-NUE	14
Average Seed Perimeter cm-NUE	15
Average Seed Length cm-NUE	16
Average Seed Width cm-NUE	17
Upper Ratio Average Seed Area-NUE	18
Lower Ratio Average Seed Area-NUE	19
FW Head/Plant gr based on 5 plants-NUE	20
FW Head/Plant gr based on plot-NUE	21
FW/Plant gr based on plot-NUE	22
Leaf SPAD 64 Days Post Sowing-NUE	23
FW Heads/(FW Heads+ FW Plants) all plot-NUE	24
NUPE [biomass/SPAD](Low N)	25
NUE2 (total biomass/SPAD) (Low N)	26
NUE [yield /SPAD](Low N)	27
NUE [yield /SPAD](NORMAL)	28
NUE2 (total biomass/SPAD) (Normal)	29
NUPE [biomass/SPAD](NORMAL)	30
Total Seed Weight/Head gr based on plot-NUE	9
Total Seed Weight /Head gr based on 5 heads-NUE	10
Head Average Area cm2-NUE	11
Head Average Perimeter cm-NUE	12
Head Average Length cm-NUE	13
Average Seed Area cm2-NUE	14
Average Seed Perimeter cm-NUE	15
Average Seed Length cm-NUE	16
Average Seed Width cm-NUE	17
Upper Ratio Average Seed Area-NUE	18
Lower Ratio Average Seed Area-NUE	19
FW Head/Plant gr based on 5 plants-NUE	20
FW Head/Plant gr based on plot-NUE	21

<i>Correlation set</i>	<i>Correlation ID</i>
FW/Plant gr based on plot-NUE	22
Leaf SPAD 64 Days Post Sowing-NUE	23
FW Heads/(FW Heads+ FW Plants) all plot-NUE	24
NUpE [biomass/SPAD](Low N)	25
NUE2 (total biomass/SPAD) (Low N)	26
NUE [yield /SPAD](Low N)	27
NUE [yield /SPAD](NORMAL)	28
NUE2 (total biomass/SPAD) (Normal)	29
NUpE [biomass/SPAD](NORMAL)	30
Total Seed Weight/Head gr based on plot-Drought	31
Head Average Area cm2-Drought	32
Head Average Perimeter cm-Drought	33
Head Average Length cm-Drought	34
Head Average Width cm-Drought	35
RGR of Leaf Num-Drought	36
Final Plant Height cm-NUE	37
HI-normal	38

Table 17. Provided are the Sorghum correlated parameters (vectors). “gr.” = grams; “SPAD” = chlorophyll levels; “FW” = Plant Fresh weight; “DW”= Plant Dry weight; “normal” = standard growth conditions.

5

Table 18
Measured parameters in Sorghum accessions under normal conditions

<i>Ecotype/ parameter</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>38</i>
20	31.1	47.4	25.6	0.105	0.386	406	175	95.2	201
21	26.4	46.3	26.8	0.112	0.402	518	223	79.2	127
22	18.7	28.4	21	0.131	0.445	148	56.4	198	51.8
24	38.4	70.4	26.8	0.129	0.45	423	112	234	122
25								189	54.5
26								195	93.9
27	47.7	63.5	31.3	0.11	0.4	424	126	117	327
28	31	44.5	23.2	0.113	0.405	386	108	92.8	231
29	40	56.6	25.7	0.102	0.384	410	124	113	241
30	38.4	60	28.8	0.118	0.419	329	103	97.5	304
31	32.1	45.5	28.1	0.121	0.43	391	82.3	98	336
32	32.7	58.2	23	0.111	0.4	436	77.6	100	350
33	32.8	70.6	28.1	0.117	0.409	430	91.2	106	293
34	51.5	70.1	30	0.108	0.401	441	150	151	411
35	35.7	54	30.5	0.105	0.395	416	109	117	285
36	38.3	59.9	27.2	0.11	0.395	430	108	124	283
37	42.4	52.6	29.3	0.105	0.392	428	131	126	204

Table 18: Provided are the values of each of the parameters (as described above) measured in Sorghum accessions (Seed ID) under normal conditions. Growth conditions are specified in the experimental procedure section.

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Table 19
Measured parameters in Sorghum accessions under Low nitrogen conditions

<i>Ecotype/ parameter</i>	<i>9</i>	<i>10</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>
20	25.90	50.30	96.20	56.30	23.20	0.11	1.1 9	0.3 8	0.3 5	1.1 8	0.8 2
21	30.60	50.90	215.0 0	79.20	25.60	0.11	1.2 3	0.4 0	0.3 5	1.3 1	0.7 7
22	19.40	36.10	98.60	53.20	20.90	0.14	1.3 7	0.4 5	0.3 9	1.1 1	0.8 1
24	35.60	73.10	183.0 0	76.20	28.40	0.12	1.2 9	0.4 2	0.3 7	1.2 1	0.7 9
25	25.20	37.90	120.0 0	67.30	24.30	0.14	1.4 1	0.4 7	0.3 8	1.1 9	0.7 8
26	22.20	36.40	110.0 0	59.50	22.60	0.13	1.4 0	0.4 8	0.3 6	1.1 8	0.8 0
27	50.00	71.70	172.0 0	79.30	32.10	0.12	1.2 7	0.4 1	0.3 7	1.1 6	0.8 3
28	27.50	35.00	84.80	51.50	20.40	0.12	1.2 6	0.4 1	0.3 6	1.2 3	0.7 9
29	51.10	76.70	156.0 0	69.90	26.70	0.12	1.2 6	0.4 1	0.3 6	1.1 7	0.8 1
30	36.80	57.60	137.0 0	66.20	26.30	0.13	1.3 5	0.4 3	0.3 8	1.2 2	0.7 7
31	29.40	42.90	138.0 0	67.40	25.40	0.13	1.3 8	0.4 5	0.3 7	1.2 4	0.7 4
32	26.70	36.50	96.50	57.90	23.10	0.12	1.2 8	0.4 2	0.3 6	1.1 9	0.8 0
33	29.40	68.60	158.0 0	70.60	27.90	0.12	1.2 7	0.4 1	0.3 6	1.2 3	0.7 9
34	51.10	71.80	164.0 0	73.80	28.90	0.12	1.2 6	0.4 1	0.3 6	1.1 6	0.8 2
35	37.00	49.30	138.0 0	66.90	27.60	0.11	1.2 3	0.4 0	0.3 4	1.3 4	0.8 0
36	39.90	43.90	135.0 0	65.40	25.50	0.12	1.2 8	0.4 1	0.3 7	1.2 1	0.8 1
37	41.80	52.10	166.0 0	76.00	30.30	0.11	1.2 2	0.4 0	0.3 5	1.2 1	0.8 1

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

Table 20
Additional measured parameters in Sorghum accessions under low nitrogen growth conditions

<i>Ecotype/para meter</i>	<i>20</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>	<i>37</i>
20	388. 00	215. 00	205. 00	38. 30	0.5 1	5.3 4	6.0 2	0.6 8	0.7 2	4.5 0	3.7 8	10 4

<i>Ecotype/parameter</i>	20	21	22	23	24	25	26	27	28	29	30	37
21	429.00	205.00	200.00	39.00	0.51	5.12	5.91	0.78				80.9
22	298.00	73.50	341.00	42.30	0.17	8.05	8.50	0.46	0.43	8.17	7.74	205
24	280.00	123.00	241.00	40.90	0.39	5.88	6.75	0.87	0.86	7.86	7.01	125
25	208.00	153.00	538.00	43.10	0.21	12.50	13.00	0.58	0.58	10.70	10.10	225
26	304.00	93.20	359.00	39.90	0.19	9.02	9.58	0.56	0.69	8.34	7.65	208
27	436.00	134.00	149.00	42.70	0.48	3.50	4.67	1.17	1.05	4.40	3.34	121
28	376.00	77.40	129.00	43.30	0.38	2.98	3.61	0.63	0.69	3.74	3.05	100
29	475.00	130.00	179.00	39.00	0.42	4.58	5.89	1.31	0.93	4.83	3.90	121
30	438.00	99.80	124.00	42.70	0.44	2.91	3.77	0.86	0.84	3.67	2.83	94.5
31	383.00	76.90	101.00	40.10	0.43	2.53	3.26	0.74	0.72	2.89	2.18	110
32	375.00	84.20	132.00	44.00	0.39	3.00	3.61	0.61	0.72	2.91	2.19	115
33	425.00	92.20	118.00	45.40	0.44	2.59	3.24	0.65	0.71	3.12	2.41	105
34	434.00	139.00	177.00	44.80	0.44	3.95	5.10	1.14	1.17	4.75	3.58	174
35	409.00	113.00	144.00	42.60	0.44	3.37	4.24	0.87	0.79	3.69	2.90	116
36	378.00	95.50	127.00	43.80	0.43	2.90	3.81	0.91	0.85	3.85	3.01	139
37	432.00	129.00	180.00	46.70	0.42	3.86	4.76	0.89	0.98	5.84	4.85	144

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

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Table 21***Measured parameters in Sorghum accessions under drought conditions***

<i>Ecotype/parameter</i>	31	32	33	34	35	36
20	22.1	83.1	52.8	21.6	4.83	0.0971
21	16.8	108	64.5	21.9	6.31	0.178
22	9.19	88.7	56.6	21.6	5.16	0.162
24	104	136	64.4	22	7.78	0.212
						0.167
26	3.24	90.8	53.2	21	5.28	0.21
27	22	124	71.7	28.6	5.49	0.149
28	9.97	86.1	55.6	21.3	5.04	0.0808
29	18.6	85.2	53	20.8	5.07	0.138

<i>Ecotype/parameter</i>	<i>31</i>	<i>32</i>	<i>33</i>	<i>34</i>	<i>35</i>	<i>36</i>
30	29.3	113	69.8	24.7	5.77	
31	10.5	101	65.1	24.3	5.37	0.108
32	14.8	80.4	55.3	21.9	4.66	0.117
33	12.9	127	69.1	25	6.35	0.108
34	18.2	86.4	53.3	19.5	5.58	0.265
35	11.6	92.3	56.3	20.4	5.76	0.125
36	18.6	77.9	49.1	16.8	5.86	0.12
37	16.4	76.9	51.9	18.9	5.1	

Table 21: Provided are the values of each of the parameters (as described above) measured in Sorghum accessions (Seed ID) under drought conditions. Growth conditions are specified in the experimental procedure section.

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EXAMPLE 8

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

10 In order to produce a high throughput correlation analysis between plant phenotype and gene expression level, the present inventors utilized a maize oligonucleotide micro-array, produced by Agilent Technologies [Hypertext Transfer Protocol://World Wide Web (dot) chem. (dot) agilent (dot) com/Scripts/PDS (dot) asp?lPage=50879]. The array oligonucleotide represents about 44,000 maize genes and
15 transcripts. In order to define correlations between the levels of RNA expression with yield and NUE components or vigor related parameters, various plant characteristics of 12 different maize hybrids were analyzed. Among them, 10 hybrids encompassing the observed variance were selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson
20 correlation test.

Correlation of Maize hybrids across ecotypes grown under regular growth conditions

Experimental procedures

25 12 Maize hybrids were grown in 3 repetitive plots, in field. Maize seeds were planted and plants were grown in the field using commercial fertilization and irrigation protocols. In order to define correlations between the levels of RNA expression with NUE and yield components or vigor related parameters, the 12 different maize hybrids were analyzed. Among them, 10 hybrids encompassing the observed variance were

selected for RNA expression analysis. The correlation between the RNA levels and the characterized parameters was analyzed using Pearson correlation test.

Analyzed Sorghum tissues – All 10 selected maize hybrids were sample per each treatment. Plant tissues [Flag leaf, Flower meristem, Grain, Cobs, Internodes] growing under Normal conditions were sampled and RNA was extracted as described above.

The following parameters were collected using digital imaging system:

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

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

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

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

The image processing system was used, which consists of a personal desktop computer (Intel P4 3.0 GHz processor) and a public domain program - ImageJ 1.37, Java based image processing software, which was developed at the U.S. National Institutes of Health and is freely available on the internet 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 for seed area and seed length was saved to text files and analyzed using the JMP statistical analysis software (SAS institute).

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

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

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

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

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

Relative Growth Rate was calculated using Formulas X and XI (described above).

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

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

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

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

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

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

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

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

Experimental Results

10 12 different maize hybrids were grown and characterized for different parameters: The average for each of the measured parameter was calculated using the JMP software (Tables 22-25) and a subsequent correlation analysis was performed (Table 26) using the “Vectors Maize normal”.

15 **Table 22**
Maize correlated parameters (vectors)

Correlations	Correlation ID
Normal- Ear weight per plot (42 plants per plot) [0- RH]	1
Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	2
Normal- Seed yield per dunam [kg]	3
Normal- Plant Height 19.7.09	4
Normal- Plant Height 29.07.09	5
Normal- Plant Height 03.08.09	6
Normal- Plant Height 10.08.09	7
Normal- Final Plant Height	8
Normal- Final Main Ear Height	9
Normal- Leaf No 3.08.09	10
Normal- Final Leaf Number	11
Normal- Stalk width 20/08/09 close to TP5	12
Normal- Ear Length cm	13
Normal- Ear with mm	14
Normal- Ear length of filled area cm	15
Normal- No of rows per ear	16
Normal- SPAD 29.7.09	17
Normal- SPAD 3.8.09	18
Normal- SPAD 10.8.09	19
Normal- SPAD 1.9.09 R1-2	20
Normal- SPAD 6.9.09 R3-R4	21
Normal- NUE yield kg/N applied in soil kg	22
Normal- NUE at grain filling [R3-R4] yield Kg/ N in plant SPAD	23
Normal- NUE at early grain filling [R1-R2] yield Kg/ N in plant SPAD	24
Normal- Yield/stalk width	25

<i>Correlations</i>	<i>Correlation ID</i>
Normal- LAI	26
Normal- Yield/LAI	27

Table 22. SPAD 46DPS and SPAD 54DPS: Chlorophyll level after 46 and 54 days after sowing (DPS).

Table 23

Measured parameters in Maize accessions under normal conditions

<i>ecotype\parameter</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>
30G54	8.94	0.167	1340	27	19.8	74.3	101	273	130	9.39
32P75	7.02	0.136	1090	70.7	45.3	33.4	168	260	122	11.1
32W86	7.53	0.15	1200	70.2	48	75.8	183	288	128	11.8
32Y52	7.99	0.159	1270	67.5	45.7	55.9	160	238	113	11.3
3394	8.48	0.15	1200	23.8	16.9	72.3	102	287	135	9
Brasco	5.63	0.117	937	63.2	44.9	58.1	174	225	94.3	11.4
Oropesa	6.1	0.123	986	59.4	38.8	62.2	157	264	121	11.2
Pampero	6.66	0.131	1050	65.1	48.6	58.7	185	252	108	11.8
SC7201	8.21	0.153	1230	25.1	17.9	75.7	122	279	140	9.28
Simon	8.4	0.171	1370	58.7	45.4	51.6	178	278	112	12
SSC5007	1.88	0.0376	301	61.2	40.9	64.3	153	164	60.4	10.8

Table 23. Provided are the values of each of the parameters (as described above) measured in maize accessions (Seed ID) under regular growth conditions. Growth conditions are specified in the experimental procedure section.

Table 24

Additional measured parameters in Maize accessions under regular growth conditions

<i>ecotype\parameter</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>
30G54	11.8	2.91	19.9	51.1	16.2	16.1	49.6	50.9	60.3	56.9
32P75	11.1	2.64	20.2	46.3	17.5	14.7	48.4	46.7	55.8	57.2
32W86	13.3	2.71	18.1	45.9	17.7	15.4	45.7	43.7	60.3	59.3
32Y52	11.8	2.9	19.9	47.6	18.4	15.9	49.8	50.5	58.6	61.6
3394	11.9	2.7	19.5	51.4	15.7	16.2	48.3	51	60.4	58.6
Brasco	12.3	2.62	17.7	47.4	14.7	15.2	48.2	49	53.7	61.2
Oropesa	12.4	2.92	17.7	47.3	12.9	16	45.4	46.5	56.1	60.2
Pampero	12.2	2.72	17.3	46.8	14	14.8	47.9	46.7	55.2	61.1
SC7201	11.7	2.66	17.5	48.3	12.3	17.7	48.9	50.9	57.3	57.5
Simon	12.6	2.84	20.5	49.3	18.8	15.4	46.2	49.4	52.8	62.2
SSC5007	9.28	2.26	19.9	41.8	16.1	14.3	42.4	45.9	57.2	52

Table 24. Provided are the values of each of the parameters (as described above) measured in maize accessions (Seed ID) under regular growth conditions. Growth conditions are specified in the experimental procedure section.

Table 25

Additional measured parameters in Maize accessions under regular growth conditions

<i>ecotype\parameter</i>	<i>21</i>	<i>22</i>	<i>23</i>	<i>24</i>	<i>25</i>	<i>26</i>	<i>27</i>
30G54	59.9	4.45	25	23.4	457	3.21	426

<i>ecotype\parameter</i>	<i>21</i>	<i>22</i>	<i>23</i>	<i>24</i>	<i>25</i>	<i>26</i>	<i>27</i>
32P75	60.9	3.62	17.8	19.1	412	3.95	313
32W86	56.9	4.01	20.3	20.3	443	3.33	307
32Y52	58.7	4.24	20	20.7	439	4.01	362
3394	58.7	4.01	19	20.5	447	3.86	314
Brasco	63.2	3.12	13.9	15.4	357	4.19	225
Oropesa	59.8	3.29	16.2	16.4	337	3.97	266
Pampero	62.4	3.5	17.2	17.2	386	4.32	262
SC7201	57.2	4.09	21.5	21	472	4.31	
Simon	61.9	4.55	21	22	482	2.89	482
SSC5007	49.3	1	5.52	5.72	140		

Table 25. Provided are the values of each of the parameters (as described above) measured in maize accessions (Seed ID) under regular growth conditions. Growth conditions are specified in the experimental procedure section.

5

EXAMPLE 9

CORRELATION ANALYSES

Table 26 hereinbelow provides representative results of the correlation analyses described in Examples 2-8 above.

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Table 26

Correlation analyses

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD1	Arabidopsis 2 NUE	stem	N 1.5 mM seed yield per rossete area day 10	-0.90	1.09E-03
LYD1	Arabidopsis 2 NUE	stem	N 1.5 mM seed yield per leaf blead	-0.88	1.94E-03
LYD1	Arabidopsis 2 NUE	leaf	N 1.5 mM Leaf Blade Area 10 day	-0.81	4.87E-03
LYD10	Arabidopsis 1	seed5da f	Lamina width	-0.87	0.01
LYD10	Arabidopsis 1	seed5da f	Total Leaf Area per plant	-0.85	0.02
LYD10	Arabidopsis 2 NUE	leaf	N 1.5 mM t50 Flowering	-0.80	0.01
LYD101	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.89	0.04
LYD101	Arabidopsis 2	stem	N 6 mM Spad / FW	-0.89	0.04
LYD101	Arabidopsis 2	stem	N 6 mM spad/DW (gN/g plant)	-0.89	0.04
LYD102	Arabidopsis 2	stem	N 6 mM spad/DW (gN/g plant)	-0.95	0.01
LYD102	Arabidopsis 2	stem	N 1.5 mM Spad / FW	-0.85	0.07
LYD102	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.84	0.07

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD103	Arabidopsis 1	seed5daf	Harvest Index	-0.86	0.01
LYD103	Arabidopsis 2 NUE	leaf	N 6 mM Dry Weight	0.71	0.02
LYD103	Arabidopsis 1	root	fresh weight	0.71	0.05
LYD104	Arabidopsis 1	seed5daf	seed yield per plant	0.70	0.08
LYD104	Arabidopsis 2 NUE	leaf	N 6 mM RGR of Rosette Area 3 day	0.70	0.02
LYD104	Arabidopsis 2 NUE	stem	N 6 mM 1000 Seeds weight	0.71	0.03
LYD105	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.91	0.03
LYD105	Arabidopsis 2	stem	N 1.5 mM DW/SPAD	-0.86	0.06
LYD105	Arabidopsis 2 NUE	leaf	N 1.5 mM seed yield per rossete area day 10	-0.85	1.94E-03
LYD106	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.98	4.57E-03
LYD106	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.97	0.01
LYD106	Arabidopsis 2 NUE	stem	N 1.5 mM Leaf Blade Area 10 day	-0.79	0.01
LYD107	Arabidopsis 2	leaf	N 6 mMMSpad / FW	-0.97	0.01
LYD107	Arabidopsis 2	leaf	N 1.5 mM Spad / FW	-0.88	0.05
LYD107	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.82	0.09
LYD109	Juncea ecotypes vector	Mature flower	Min-Lateral branch position	-0.96	0.01
LYD109	Juncea ecotypes vector	Mature flower	Min-Lateral branch position	-0.96	0.01
LYD109	Juncea ecotypes vector	Mature flower	Min-Lateral branch position	-0.94	0.02
LYD111	Arabidopsis 2	stem	N 6 mMMSpad / FW	-0.94	0.02
LYD111	Arabidopsis 1	seed5daf	Lamina length	-0.90	0.01
LYD111	Arabidopsis 2	leaf	N 6 mMMSpad / FW	-0.88	0.05
LYD110	Juncea ecotypes vector	Mature flower	Lateral branch - average node length	-0.99	2.13E-03
LYD110	Juncea ecotypes vector	Mature flower	Lateral branch - average node length	-0.91	0.03
LYD110	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.89	0.04
LYD112	Juncea ecotypes vector	Mature flower	SPAD	-0.88	0.05
LYD112	Juncea ecotypes vector	Mature flower	Max-Length of lateral branch [cm]	-0.83	0.08
LYD112	Juncea ecotypes vector	Mature flower	Max-Diameter of lateral branch [mm]	-0.83	0.08

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD113	Juncea ecotypes vector	Flower	Days till flowering	-0.92	0.01
LYD113	Juncea ecotypes vector	Flower	Days till flowering	-0.92	0.01
LYD113	Juncea ecotypes vector	Flower	Days till flowering	-0.91	0.01
LYD114	Juncea population densities	flower	days till flowering	-0.93	0.02
LYD114	Juncea population densities	flower	Oil content	-0.91	0.03
LYD114	Juncea ecotypes vector	Mature flower	Lateral branch - 20th length	-0.88	0.05
LYD115	Juncea ecotypes vector	Flower	Fresh weight (plot-harvest) [gr/plant]	-0.82	0.05
LYD115	Juncea ecotypes vector	Mature flower	Lateral branch - 20th seed number	-0.80	0.10
LYD115	Juncea ecotypes vector	Mature flower	Lateral branch - 20th seed number	-0.80	0.10
LYD117	Juncea ecotypes vector	Mature flower	1000 Seeds [gr]	-0.92	0.03
LYD117	Juncea ecotypes vector	Mature flower	1000 Seeds [gr]	-0.91	0.03
LYD117	Juncea ecotypes vector	Mature flower	Lateral branch - 20th length	-0.88	0.05
LYD118	Juncea population densities	flower	Main branch-total number of pods	-0.92	0.03
LYD118	Juncea ecotypes vector	Mature flower	Lateral branch - 20th seed number	-0.83	0.09
LYD118	Juncea population densities	meristem	days till bolting	-0.79	0.03
LYD119	Juncea ecotypes vector	Flower	Main branch - 20th seed number	-0.97	1.05E-03
LYD119	Juncea ecotypes vector	Flower	Main branch - 20th seed number	-0.97	1.23E-03
LYD119	Juncea population densities	flower	Main branch-total number of pods	-0.96	0.01
LYD12	Arabidopsis 1	flower	Lamina width	-0.85	0.01
LYD12	Arabidopsis 1	flower	fresh weight	-0.78	0.02
LYD12	Arabidopsis 1	flower	Total Leaf Area per plant	-0.78	0.02
LYD120	Juncea ecotypes vector	Mature flower	Lateral branch - average node length	-0.98	2.56E-03
LYD120	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.95	0.01
LYD120	Juncea ecotypes vector	Mature flower	Lateral branch - average node length	-0.89	0.04
LYD122	Juncea ecotypes vector	Mature flower	Max-Lateral branch position [#node of main branch]	-0.99	1.78E-03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD122	Juncea ecotypes vector	Mature flower	Number of lateral branches	-0.99	1.91E-03
LYD122	Juncea ecotypes vector	Mature flower	Days till bolting	-0.98	3.54E-03
LYD123	Juncea ecotypes vector	Mature flower	Lateral branch - 20th seed number	-0.81	0.10
LYD123	Juncea ecotypes vector	Mature flower	Lateral branch - 20th seed number	-0.80	0.10
LYD123	Juncea ecotypes vector	Flower	Lateral branch - average node length	-0.78	0.07
LYD124	Juncea ecotypes vector	Mature flower	Lateral branch - average node length	-0.97	0.01
LYD124	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.94	0.02
LYD124	Juncea population densities	meristem	Main branch-dist. 1-20	-0.93	2.35E-03
LYD13	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.98	2.80E-03
LYD13	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.89	0.04
LYD13	Arabidopsis 2	stem	N 6 mM spad/DW (gN/g plant)	-0.89	0.05
LYD14	Arabidopsis 2 NUE	leaf	N 6 mM seed yield/leaf blade	0.70	0.02
LYD14	Arabidopsis 2 NUE	stem	N 1.5 mM Seed Yield	0.70	0.04
LYD14	Arabidopsis 2 NUE	stem	N 1.5 mM Harvest Index	0.71	0.02
LYD142	Tomato vectors bath Normal	leaf	SPAD Normal	-0.74	0.04
LYD142	Tomato vectors bath Normal	root	leaf No Normal	0.72	0.04
LYD142	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.97	2.66E-06
LYD144	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.75	0.01
LYD144	Tomato vectors bath Normal	root	leaf No Normal	0.72	0.05
LYD144	Tomato vectors bath Salinity	root	Plant biomass NaCl	0.74	0.01
LYD146	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.71	0.02
LYD146	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.75	0.01
LYD146	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.78	0.01
LYD149	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.99	1.18E-03
LYD149	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.98	4.29E-03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD149	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.94	0.02
LYD150	Arabidopsis 1	seed5daf	Lamina length	-0.99	2.07E-05
LYD150	Arabidopsis 1	seed5daf	fresh weight	-0.93	2.61E-03
LYD150	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.90	0.04
LYD152	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.94	0.02
LYD152	Arabidopsis 1	seed5daf	root length day 13	-0.89	0.01
LYD152	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.85	0.07
LYD153	Arabidopsis 2	stem	N 6 mM spad/DW (gN/g plant)	-0.86	0.06
LYD153	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.84	0.08
LYD153	Arabidopsis 2 NUE	leaf	N 1.5 mM Leaf Blade Area 10 day	-0.77	0.01
LYD156	Tomato vectors field Normal	leaf	RWC (Normal)	-0.73	0.02
LYD156	Tomato vectors field Normal	flower	SPAD 100% RWC (Normal)	-0.70	0.02
LYD156	Tomato vectors bath Normal	leaf	leaf No Normal	0.70	0.05
LYD157	Tomato vectors field Drought	flower	Num of flowers (Drought)	0.71	0.02
LYD157	Tomato vectors field Drought	flower	Num of Flower Drought/Normal	0.74	0.01
LYD157	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.75	0.01
LYD158	Tomato vectors bath Salinity	root	Plant height NaCl	-0.79	0.01
LYD158	Tomato vectors field Drought	leaf	FW drought/Normal	0.74	0.01
LYD158	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.78	0.01
LYD159	Juncea population densities	flower	Min-Lateral branch position	-0.93	0.02
LYD159	Juncea population densities	flower	Number of lateral branches	-0.90	0.04
LYD159	Juncea population densities	flower	Min-Lateral branch position	-0.90	0.04
LYD16	Arabidopsis 1	seed12daf	Lamina length	-0.83	0.01
LYD16	Arabidopsis 2 NUE	stem	N 1.5 mM t50 Flowering	-0.81	0.01
LYD16	Arabidopsis 2 NUE	stem	N 6 mM t50 Flowering	-0.78	0.01

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD166	Juncea population densities	flower	days till flowering	-0.96	0.01
LYD166	Juncea ecotypes vector	Meristem	Harvest index	-0.96	4.90E-05
LYD166	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.95	0.01
LYD167	Juncea ecotypes vector	Mature flower	Lateral branch - 20th length	-0.92	0.03
LYD167	Juncea ecotypes vector	Mature flower	1000 Seeds [gr]	-0.92	0.03
LYD167	Juncea ecotypes vector	Mature flower	1000 Seeds [gr]	-0.89	0.05
LYD172	Juncea ecotypes vector	Mature flower	Oil content	-0.96	0.01
LYD172	Juncea ecotypes vector	Mature flower	Oil content	-0.95	0.01
LYD172	Juncea population densities	meristem	Main branch-dist. 1-20	-0.92	3.48E-03
LYD173	Juncea ecotypes vector	Flower	Days till flowering	-0.96	2.00E-03
LYD173	Juncea ecotypes vector	Flower	Main branch - 20th seed number	-0.95	3.45E-03
LYD173	Juncea ecotypes vector	Flower	Main branch - average node length	-0.94	0.01
LYD174	Juncea ecotypes vector	Flower	Oil content	-0.95	3.82E-03
LYD174	Juncea ecotypes vector	Mature flower	Fresh weight (single plant) [gr/plant]	-0.90	0.04
LYD174	Juncea ecotypes vector	Mature flower	Main branch base diameter [mm]	-0.89	0.04
LYD176	Juncea population densities	meristem	Lateral branch-20th length	-0.97	3.50E-04
LYD176	Juncea population densities	meristem	Lateral branch-20th length	-0.95	8.42E-04
LYD176	Juncea ecotypes vector	Flower	Oil content	-0.95	3.65E-03
LYD177	Juncea ecotypes vector	Mature flower	Oil content	-0.98	2.20E-03
LYD177	Juncea population densities	meristem	Main branch-dist. 1-20	-0.97	2.64E-04
LYD177	Juncea ecotypes vector	Mature flower	Oil content	-0.95	0.01
LYD178	Juncea ecotypes vector	Flower	Oil content	-0.98	5.68E-04
LYD178	Juncea population densities	meristem	Max-Number of nodes in lateral branch	-0.93	2.41E-03
LYD178	Juncea population densities	meristem	Total leaf area	-0.91	4.77E-03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD18	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.94	0.02
LYD18	Arabidopsis 2 NUE	leaf	N 1.5 mM Harvest Index	-0.93	9.33E-05
LYD18	Arabidopsis 2 NUE	leaf	N 1.5 mM Seed Yield	-0.93	1.09E-04
LYD180	Juncea ecotypes vector	Mature flower	Oil content	-0.99	7.31E-04
LYD180	Juncea population densities	flower	Dry weight/hectare	-0.98	3.24E-03
LYD180	Juncea population densities	flower	Seed weight/hectare	-0.97	0.01
LYD184	Juncea population densities	meristem	Number of lateral branches	-0.88	0.01
LYD184	Juncea population densities	flower	Main branch-total number of pods	-0.85	0.07
LYD184	Juncea population densities	meristem	Max-Lateral branch position	-0.84	0.02
LYD185	Juncea population densities	flower	Main branch height [cm]	-0.96	0.01
LYD185	Juncea population densities	flower	Main branch height [cm]	-0.93	0.02
LYD185	Juncea population densities	meristem	Min-Lateral branch position	-0.93	2.59E-03
LYD186	Juncea ecotypes vector	Mature flower	SPAD	-0.99	1.20E-03
LYD186	Juncea population densities	meristem	days till bolting	-0.93	2.05E-03
LYD186	Juncea ecotypes vector	Mature flower	Main branch base diameter [mm]	-0.93	0.02
LYD187	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.98	2.49E-03
LYD187	Juncea population densities	meristem	Lateral branch-20th length	-0.98	1.34E-04
LYD187	Juncea ecotypes vector	Mature flower	Lateral branch - average node length	-0.97	0.01
LYD188	Juncea ecotypes vector	Mature flower	Oil content	-0.86	0.06
LYD188	Juncea ecotypes vector	Mature flower	Oil content	-0.85	0.07
LYD188	Juncea ecotypes vector	Flower	Max-Diameter of lateral branch [mm]	-0.74	0.09
LYD190	Juncea population densities	flower	Main branch-total number of pods	-0.98	3.93E-03
LYD190	Juncea population densities	flower	Main branch-total number of pods	-0.84	0.08
LYD190	Juncea ecotypes vector	Meristem	Oil content	-0.81	0.01
LYD192	Juncea ecotypes vector	Mature flower	Number of lateral branches	-0.96	0.01

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD192	Juncea ecotypes vector	Mature flower	Days till flowering	-0.96	0.01
LYD192	Juncea ecotypes vector	Mature flower	Max-Lateral branch position [#node of main branch]	-0.95	0.01
LYD193	Juncea population densities	meristem	Lateral branch-20th length	-0.98	1.68E-04
LYD193	Juncea ecotypes vector	Flower	Oil content	-0.96	2.40E-03
LYD193	Juncea ecotypes vector	Flower	Oil content	-0.94	0.01
LYD194	Juncea population densities	meristem	Fresh weight (at harvest)/plant	-0.97	3.34E-04
LYD194	Juncea population densities	meristem	Seed weight/plant	-0.97	4.26E-04
LYD194	Juncea population densities	meristem	Fresh Weight (single plant) [gr/plant]	-0.96	4.67E-04
LYD195	Tomato vectors bath Normal	root	leaf No Normal	-0.74	0.04
LYD195	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.71	0.02
LYD195	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.85	1.98E-03
LYD197	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 8 day	-0.90	9.86E-04
LYD197	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 10 day	-0.85	3.86E-03
LYD197	Arabidopsis 2 NUE	stem	N 1.5 mM t50 Flowering	-0.83	2.68E-03
LYD2	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.92	0.03
LYD2	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.85	0.07
LYD2	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.85	0.07
LYD20	Arabidopsis 2	stem	N 6 mM Spad / FW	-0.92	0.03
LYD20	Arabidopsis 2	stem	N 6 mM spad/DW (gN/g plant)	-0.84	0.07
LYD20	Arabidopsis 1	seed5daf	Dry matter per plant	-0.81	0.03
LYD200	Juncea population densities	meristem	days till flowering	-0.93	2.17E-03
LYD200	Juncea population densities	meristem	Main branch-20th seed number	-0.90	0.01
LYD200	Juncea population densities	meristem	Main branch base diameter [mm]	-0.88	0.01
LYD201	Juncea population densities	flower	Main branch-20th length	-0.99	2.18E-03
LYD201	Juncea population densities	flower	SPAD	-0.98	3.77E-03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD201	Juncea ecotypes vector	Mature flower	Number of lateral branches	-0.98	4.51E-03
LYD202	Juncea ecotypes vector	Mature flower	Oil content	-0.98	3.86E-03
LYD202	Juncea ecotypes vector	Mature flower	Oil content	-0.97	0.01
LYD202	Juncea ecotypes vector	Mature flower	Main branch - 20th length	-0.92	0.03
LYD204	Juncea ecotypes vector	Flower	Oil content	-0.96	1.88E-03
LYD204	Juncea ecotypes vector	Flower	Oil content	-0.96	2.82E-03
LYD204	Juncea ecotypes vector	Mature flower	Main branch base diameter [mm]	-0.95	0.01
LYD206	Juncea population densities	meristem	Main branch-dist. 1-20	-0.93	2.14E-03
LYD206	Juncea population densities	meristem	Main branch-20th length	-0.91	4.19E-03
LYD206	Juncea population densities	meristem	Lateral branch-20th length	-0.90	0.01
LYD208	Juncea population densities	meristem	Min-Lateral branch position	-0.93	2.48E-03
LYD208	Juncea ecotypes vector	Meristem	Main branch - 20th seed number	-0.92	5.22E-04
LYD208	Juncea population densities	meristem	Min-Lateral branch position	-0.91	4.45E-03
LYD209	Juncea population densities	flower	Seed weight/plant	-0.99	1.23E-03
LYD209	Juncea population densities	flower	Dry weight/plant	-0.99	1.57E-03
LYD209	Juncea population densities	flower	Fresh weight (at harvest)/plant	-0.99	1.93E-03
LYD21	Arabidopsis 2 NUE	stem	N 1.5 mM RGR of Rosette Area 3 day	0.70	0.02
LYD21	Arabidopsis 2 NUE	leaf	N 1.5 mM RGR of Rosette Area 3 day	0.71	0.02
LYD21	Arabidopsis 1	seed12 daf	root length day 13	0.72	0.04
LYD212	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.94	0.02
LYD212	Arabidopsis 2 NUE	leaf	N 1.5 mM Harvest Index	-0.94	7.06E-05
LYD212	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.92	0.03
LYD213	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.93	0.02
LYD213	Arabidopsis 1	seed5daf	Oil % per seed	-0.92	3.48E-03
LYD213	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.89	0.04

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD214	Arabidopsis 2 NUE	leaf	N 1.5 mM Biomass reduction compared to 6 mM	-0.81	4.74E-03
LYD214	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.80	0.10
LYD214	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.76	0.14
LYD215	Arabidopsis 2	stem	N 1.5 mM DW/SPAD	-0.88	0.05
LYD215	Arabidopsis 1	seed5daf	Dry matter per plant	-0.80	0.03
LYD215	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.79	0.11
LYD216	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.97	0.01
LYD216	Arabidopsis 2	leaf	N 1.5 mM Spad / FW	-0.87	0.06
LYD216	Arabidopsis 2	leaf	N 6 mM Spad / FW	-0.85	0.07
LYD217	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.88	0.05
LYD217	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.87	0.06
LYD217	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.82	0.09
LYD219	Arabidopsis 2 NUE	stem	N 1.5 mM Leaf Blade Area 10 day	-0.86	3.09E-03
LYD219	Arabidopsis 2 NUE	stem	N 6 mM Leaf Blade Area 10 day	-0.82	0.01
LYD219	Arabidopsis 2 NUE	stem	N 6 mM Rosette Area 8 day	-0.82	0.01
LYD22	Arabidopsis 2	stem	N 1.5 mM DW/SPAD	-0.97	0.01
LYD22	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.94	0.02
LYD22	Arabidopsis 2	stem	N 1.5 mM DW/SPAD	-0.94	0.02
LYD220	Arabidopsis 2 NUE	stem	N 1.5 mM Leaf Blade Area 10 day	-0.90	1.06E-03
LYD220	Arabidopsis 2 NUE	leaf	N 1.5 mM Leaf Number 10 day	-0.73	0.02
LYD220	Arabidopsis 1	root	Oil % per seed	-0.72	0.05
LYD221	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.93	0.02
LYD221	Arabidopsis 2 NUE	leaf	N 1.5 mM seed yield per rosette area day 10	-0.85	2.02E-03
LYD221	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.84	0.08
LYD222	Arabidopsis 2	leaf	N 1.5 mM SPAD/DW	-0.96	0.01
LYD222	Arabidopsis 1	seed5daf	seed yield per plant	-0.86	0.01
LYD222	Arabidopsis 1	seed5daf	Oil yield per plant	-0.84	0.02
LYD223	Arabidopsis 1	leaf	root length day 13	-0.87	0.01
LYD223	Arabidopsis 1	leaf	Lamina width	-0.86	0.01

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD223	Arabidopsis 1	leaf	Total Leaf Area per plant	-0.84	0.01
LYD224	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 8 day	-0.86	2.64E-03
LYD224	Arabidopsis 1	seed12 daf	Vegetative growth rate	-0.85	0.01
LYD224	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 10 day	-0.82	0.01
LYD23	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.79	0.11
LYD23	Arabidopsis 1	leaf	Lamina length	-0.76	0.03
LYD23	Arabidopsis 1	flower	seed weight	-0.76	0.03
LYD232	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.81	4.44E-03
LYD232	Tomato vectors bath Normal	root	leaf No Normal	0.89	3.36E-03
LYD233	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.71	0.02
LYD233	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.88	7.54E-04
LYD233	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.90	4.31E-04
LYD234	Tomato vectors bath Salinity	leaf	leaf No NaCl	-0.78	0.01
LYD234	Tomato vectors field Drought	flower	Num of Flower Drought/NUE	0.70	0.02
LYD234	Tomato vectors field Drought	flower	flower cluster weight Drought/NUE	0.77	0.01
LYD235	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.76	0.01
LYD235	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.76	0.01
LYD235	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.94	5.12E-05
LYD236	Tomato vectors bath Salinity	leaf	Plant biomass NaCl	-0.72	0.02
LYD236	Tomato vectors field Normal	flower	Fruit yield /Plant (Normal)	0.71	0.02
LYD236	Tomato vectors field Drought	flower	Num of Flower Drought/Normal	0.72	0.02
LYD244	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.90	0.04
LYD244	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.89	0.04
LYD244	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 8 day	-0.86	2.96E-03
LYD245	Arabidopsis 1	root	Lamina length	-0.76	0.03
LYD245	Arabidopsis 2 NUE	leaf	N 1.5 mM 1000 Seeds weight	-0.74	0.01
LYD245	Arabidopsis 2 NUE	leaf	N 6 mM Seed Yield	0.71	0.02

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD246	Arabidopsis 1	leaf	Lamina length	-0.87	0.01
LYD246	Arabidopsis 1	seed5daf	fresh weight	-0.82	0.02
LYD246	Arabidopsis 1	seed5daf	Total Leaf Area per plant	-0.82	0.02
LYD248	Juncea ecotypes vector	Flower	Min-Lateral branch position	-0.95	4.36E-03
LYD248	Juncea ecotypes vector	Flower	Min-Lateral branch position	-0.94	0.01
LYD248	Juncea ecotypes vector	Flower	Min-Lateral branch position	-0.93	0.01
LYD250	Juncea ecotypes vector	Flower	Harvest index	-0.91	0.01
LYD250	Juncea population densities	meristem	days till bolting	-0.89	0.01
LYD250	Juncea ecotypes vector	Mature flower	Main branch base diameter [mm]	-0.86	0.06
LYD252	Juncea ecotypes vector	Flower	Seed weight per plant	-0.95	3.69E-03
LYD252	Juncea ecotypes vector	Flower	Main branch - average node length	-0.82	0.05
LYD252	Juncea population densities	meristem	Min-Lateral branch position	-0.80	0.03
LYD253	Juncea ecotypes vector	Mature flower	Max-Lateral branch position [#node of main branch]	-0.97	0.01
LYD253	Juncea ecotypes vector	Mature flower	Number of lateral branches	-0.96	0.01
LYD253	Juncea ecotypes vector	Mature flower	Days till bolting	-0.96	0.01
LYD256	Juncea ecotypes vector	Mature flower	Harvest index	-0.99	1.47E-03
LYD256	Juncea population densities	meristem	Max-Lateral branch position	-0.90	0.01
LYD256	Juncea ecotypes vector	Leaf	Harvest index	-0.90	3.57E-04
LYD257	Juncea ecotypes vector	Mature flower	Oil content	-0.94	0.02
LYD257	Juncea ecotypes vector	Flower	Main branch height [cm]	-0.92	0.01
LYD257	Juncea population densities	meristem	Main branch-dist. 1-20	-0.89	0.01
LYD259	Juncea ecotypes vector	Mature flower	Main branch - 20th seed number	-0.81	0.10
LYD259	Juncea ecotypes vector	Mature flower	Max-Number of nodes in lateral branch	-0.78	0.12
LYD259	Juncea ecotypes vector	Mature flower	Main branch - 20th length	-0.78	0.12

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD260	Juncea ecotypes vector	Flower	Main branch height [cm]	-0.89	0.02
LYD260	Juncea ecotypes vector	Mature flower	Oil content	-0.82	0.09
LYD260	Juncea ecotypes vector	Mature flower	Oil content	-0.79	0.11
LYD261	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.99	5.05E-04
LYD261	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.99	2.01E-03
LYD261	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.97	0.01
LYD262	Juncea ecotypes vector	Flower	Number of lateral branches	-0.94	0.01
LYD262	Juncea ecotypes vector	Flower	Max-Lateral branch position [#node of main branch]	-0.94	0.01
LYD262	Juncea ecotypes vector	Mature flower	Days till bolting	-0.78	0.12
LYD264	Juncea ecotypes vector	Flower	Lateral branch - average node length	-0.89	0.02
LYD264	Juncea population densities	meristem	Min-Lateral branch position	-0.81	0.03
LYD264	Juncea ecotypes vector	Flower	Main branch - average node length	-0.80	0.06
LYD265	Juncea population densities	meristem	Min-Lateral branch position	-0.85	0.02
LYD265	Juncea ecotypes vector	Mature flower	Oil content	-0.81	0.10
LYD265	Juncea ecotypes vector	Meristem	SPAD	-0.75	0.02
LYD266	Juncea ecotypes vector	Flower	Fresh weight (plot-harvest) [gr/plant]	-0.98	5.15E-04
LYD266	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.94	0.02
LYD266	Juncea ecotypes vector	Flower	Fresh weight (single plant) [gr/plant]	-0.93	0.01
LYD267	Juncea population densities	meristem	Seed weight/hectare	-0.86	0.01
LYD267	Juncea population densities	meristem	Dry weight/hectare	-0.85	0.02
LYD267	Juncea ecotypes vector	Flower	Main branch - 20th length	-0.82	0.05
LYD268	Juncea ecotypes vector	Mature flower	Lateral branch - 20th length	-0.98	4.50E-03
LYD268	Juncea ecotypes vector	Mature flower	1000 Seeds [gr]	-0.95	0.01
LYD268	Juncea population densities	meristem	Lateral branch-20th length	-0.89	0.01

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD269	Juncea ecotypes vector	Mature flower	Fresh weight (plot-harvest) [gr/plant]	-0.71	0.18
LYD269	Juncea population densities	meristem	Min-Lateral branch position	-0.71	0.07
LYD269	Juncea ecotypes vector	Leaf	Lateral branch - 20th length	0.70	0.02
LYD270	Juncea population densities	flower	Number of lateral branches	-0.92	0.03
LYD270	Juncea population densities	flower	Min-Lateral branch position	-0.91	0.03
LYD270	Juncea population densities	flower	Min-Lateral branch position	-0.85	0.07
LYD271	Juncea population densities	flower	Seed weight/hectare	-0.92	0.03
LYD271	Juncea ecotypes vector	Leaf	Min-Lateral branch position	-0.90	4.47E-04
LYD271	Juncea population densities	meristem	Main branch-dist. 1-20	-0.88	0.01
LYD273	Juncea ecotypes vector	Mature flower	Lateral branch - 20th length	-0.98	2.82E-03
LYD273	Juncea population densities	flower	Max-Number of nodes in lateral branch	-0.91	0.03
LYD273	Juncea population densities	flower	Lateral branch-total number of pods	-0.88	0.05
LYD275	Juncea population densities	flower	Fresh weight (at harvest)/plant	-0.96	0.01
LYD275	Juncea population densities	flower	Dry weight/plant	-0.96	0.01
LYD275	Juncea population densities	flower	Seed weight/plant	-0.95	0.01
LYD276	Juncea population densities	meristem	Main branch-dist. 1-20	-0.92	3.81E-03
LYD276	Juncea ecotypes vector	Mature flower	Lateral branch - 20th length	-0.92	0.03
LYD276	Juncea population densities	meristem	Lateral branch-20th length	-0.90	0.01
LYD278	Juncea ecotypes vector	Mature flower	Main branch - 20th length	-0.98	3.28E-03
LYD278	Juncea population densities	flower	Main branch base diameter [mm]	-0.98	4.41E-03
LYD278	Juncea population densities	flower	Main branch base diameter [mm]	-0.97	0.01
LYD279	Juncea population densities	meristem	Main branch-20th length	-0.98	1.19E-04
LYD279	Juncea population densities	flower	days till bolting	-0.94	0.02
LYD279	Juncea ecotypes vector	Mature flower	Oil content	-0.93	0.02

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD282	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.99	1.73E-03
LYD282	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.98	2.52E-03
LYD282	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.98	4.09E-03
LYD283	Juncea population densities	flower	Main branch-total number of pods	-0.99	9.63E-04
LYD283	Juncea ecotypes vector	Mature flower	Main branch - average node length	-0.94	0.02
LYD283	Juncea population densities	meristem	Main branch-20th length	-0.91	4.46E-03
LYD285	Juncea ecotypes vector	Mature flower	Main branch - 20th length	-1.00	3.85E-04
LYD285	Juncea population densities	flower	days till bolting	-0.97	0.01
LYD285	Juncea ecotypes vector	Mature flower	Main branch - 20th length	-0.93	0.02
LYD286	Juncea population densities	flower	1000Seeds [gr]	-1.00	1.73E-05
LYD286	Juncea ecotypes vector	Flower	Oil content	-0.95	3.31E-03
LYD286	Juncea population densities	flower	Max-Lateral branch position	-0.90	0.04
LYD287	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.99	1.85E-03
LYD287	Arabidopsis 2	leaf	N 6 mM Spad / FW	-0.98	4.23E-03
LYD287	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.96	0.01
LYD288	Juncea population densities	meristem	Min-Lateral branch position	-0.87	0.01
LYD288	Juncea ecotypes vector	Meristem	SPAD	-0.87	2.28E-03
LYD288	Juncea ecotypes vector	Leaf	Seed weight per plant	-0.85	1.74E-03
LYD3	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.98	4.15E-03
LYD3	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.93	0.02
LYD3	Arabidopsis 2	stem	N 1.5 mM SPAD/DW	-0.90	0.04
LYD33	Tomato vectors field Normal	flower	FW/Plant (Normal)	-0.79	0.01
LYD33	Tomato vectors field Normal	flower	FW/Plant (Normal)	-0.72	0.02
LYD33	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.70	0.02
LYD34	Tomato vectors bath Salinity	leaf	Plant biomass NaCl	-0.84	2.15E-03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD34	Tomato vectors bath Salinity	leaf	Plant biomass NaCl	-0.83	3.15E-03
LYD34	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.71	0.02
LYD35	Tomato vectors bath Salinity	leaf	Plant biomass NaCl	-0.82	3.39E-03
LYD35	Tomato vectors field Normal	leaf	Fruit yield /Plant (Normal)	0.71	0.02
LYD35	Tomato vectors field Normal	leaf	Fruit yield /Plant (Normal)	0.72	0.02
LYD36	Tomato vectors field Drought	flower	FW drought/Normal	0.71	0.02
LYD36	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.71	0.02
LYD36	Tomato vectors field Drought	flower	FW/Plant Drought	0.72	0.02
LYD37	Tomato vectors field Drought	flower	FW/Plant Drought	0.73	0.02
LYD37	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.73	0.02
LYD37	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.74	0.02
LYD38	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.70	0.02
LYD38	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.70	0.02
LYD38	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.72	0.02
LYD4	Arabidopsis 2 NUE	stem	N 6 mM t50 Flowering	-0.81	0.01
LYD4	Arabidopsis 2 NUE	stem	N 1.5 mM Seed yield reduction compared to 6 mM	-0.73	0.03
LYD4	Arabidopsis 2 NUE	stem	N 1.5 mM t50 Flowering	-0.73	0.03
LYD40	Tomato vectors bath Normal	leaf	leaf No Normal	0.70	0.05
LYD40	Tomato vectors field Drought	leaf	Num of Flower Drought/Normal	0.72	0.02
LYD40	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.80	0.01
LYD41	Tomato vectors field Drought	flower	FW/Plant Drought	0.77	0.01
LYD41	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.78	0.01
LYD41	Tomato vectors field Drought	flower	FW drought/Normal	0.83	2.70E-03
LYD42	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.80	0.01
LYD42	Tomato vectors field Drought	leaf	FW/Plant Drought	0.71	0.02

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD42	Tomato vectors field Drought	flower	Num of flowers (Drought)	0.72	0.02
LYD43	Tomato vectors field Drought	flower	FW drought/Normal	0.70	0.02
LYD43	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.73	0.02
LYD43	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.74	0.02
LYD44	Tomato vectors field Normal	leaf	Fruit yield /Plant (Normal)	0.72	0.02
LYD44	Tomato vectors field Drought	leaf	flower cluster weight Drought/NUE	0.83	2.79E-03
LYD44	Tomato vectors field Drought	leaf	Weight flower clusters (Drought)	0.84	2.55E-03
LYD45	Tomato vectors bath Normal	leaf	Plant height Normal	0.71	0.05
LYD45	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.74	0.01
LYD45	Tomato vectors bath Normal	root	leaf No Normal	0.76	0.03
LYD47	Tomato vectors bath Salinity	leaf	Plant Height NaCl/NUE	0.71	0.02
LYD47	Tomato vectors bath Salinity	leaf	Plant Height NaCl/NUE	0.72	0.02
LYD47	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.72	0.02
LYD48	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.75	0.01
LYD48	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.78	0.01
LYD48	Tomato vectors field Normal	leaf	Fruit yield /Plant (Normal)	0.84	2.27E-03
LYD49	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.79	0.01
LYD49	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.78	0.01
LYD49	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.71	0.02
LYD5	Arabidopsis 1	seed5daf	root length day 7	-0.96	7.18E-04
LYD5	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.95	0.01
LYD5	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.95	0.01
LYD50	Tomato vectors field Normal	flower	FW/Plant (Normal)	-0.71	0.02
LYD50	Tomato vectors field Drought	leaf	FW drought/Normal	0.71	0.02
LYD50	Tomato vectors field Drought	flower	FW/Plant Drought	0.71	0.02

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD51	Tomato vectors field Drought	leaf	FW drought/Normal	0.70	0.02
LYD51	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.71	0.02
LYD51	Tomato vectors bath Salinity	leaf	Plant Height NaCl/NUE	0.75	0.01
LYD52	Tomato vectors bath Normal	leaf	SPAD Normal	-0.78	0.02
LYD52	Tomato vectors field Drought	leaf	Num of Flower Drought/Normal	0.72	0.02
LYD52	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.73	0.02
LYD53	Tomato vectors field Drought	leaf	Fruit Yield Drought/Normal	-0.70	0.02
LYD53	Tomato vectors field Normal	leaf	Fruit yield /Plant (Normal)	0.71	0.02
LYD53	Tomato vectors field Drought	leaf	flower cluster weight Drought/NUE	0.72	0.02
LYD55	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.73	0.02
LYD55	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.78	0.01
LYD55	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.78	0.01
LYD57	Tomato vectors bath Salinity	root	Plant biomass NaCl	-0.74	0.01
LYD57	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.71	0.02
LYD57	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.73	0.02
LYD58	Tomato vectors field Normal	flower	Fruit yield /Plant (Normal)	0.74	0.02
LYD58	Tomato vectors field Drought	flower	Num of Flower Drought/Normal	0.77	0.01
LYD58	Tomato vectors field Drought	flower	Num of Flower Drought/Normal	0.78	0.01
LYD59	Tomato vectors bath Normal	leaf	Plant height Normal	-0.80	0.02
LYD59	Tomato vectors field Normal	flower	Fruit yield /Plant (Normal)	0.74	0.02
LYD59	Tomato vectors field Drought	flower	Num of Flower Drought/Normal	0.74	0.01
LYD6	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.97	0.01
LYD6	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.96	0.01
LYD6	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.91	0.03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD61	Tomato vectors field Drought	flower	FW/Plant Drought	0.70	0.02
LYD61	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.74	0.01
LYD61	Tomato vectors bath Normal	leaf	leaf No Normal	0.76	0.03
LYD62	Tomato vectors field Normal	flower	Fruit yield /Plant (Normal)	0.77	0.01
LYD62	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.80	0.01
LYD63	Tomato vectors field Normal	flower	Fruit yield /Plant (Normal)	0.70	0.02
LYD63	Tomato vectors field Normal	flower	Weight Flower clusters (Normal)	0.71	0.02
LYD63	Tomato vectors field Drought	leaf	Num of Flower Drought/NUE	0.72	0.02
LYD65	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.71	0.02
LYD65	Tomato vectors field Normal	leaf	Fruit yield /Plant (Normal)	0.73	0.02
LYD66	Tomato vectors bath Normal	root	leaf No Normal	-0.81	0.02
LYD66	Tomato vectors field Drought	leaf	FW/Plant Drought	0.70	0.02
LYD66	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.72	0.02
LYD67	Tomato vectors bath Normal	leaf	leaf No Normal	0.73	0.04
LYD67	Tomato vectors bath Normal	root	leaf No Normal	0.81	0.02
LYD67	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.84	2.62E-03
LYD69	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 10 day	-0.88	1.64E-03
LYD69	Arabidopsis 2 NUE	leaf	N 1.5 mM t50 Flowering	-0.88	8.38E-04
LYD69	Arabidopsis 2 NUE	leaf	N 1.5 mM Seed yield reduction compared to 6 mM	-0.85	1.64E-03
LYD7	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.88	0.05
LYD7	Arabidopsis 2	leaf	N 1.5 mM SPAD/DW	-0.79	0.11
LYD7	Arabidopsis 2 NUE	stem	N 1.5 mM Biomass reduction compared to 6 mM	-0.74	0.02
LYD73	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.84	2.20E-03
LYD73	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.79	0.01

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD73	Tomato vectors bath Salinity	leaf	leaf No NaCl	-0.75	0.01
LYD74	Tomato vectors bath Salinity	root	Plant height NaCl	-0.83	2.69E-03
LYD74	Tomato vectors field Normal	leaf	average red fruit weight (Normal)	0.72	0.02
LYD74	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.73	0.02
LYD75	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Normal	-0.72	0.02
LYD75	Tomato vectors bath Salinity	leaf	LeafNo NaCl/Nue	-0.70	0.02
LYD75	Tomato vectors field Normal	flower	Fruit yield /Plant (Normal)	0.71	0.02
LYD76	Tomato vectors bath Salinity	root	Plant biomass NaCl	-0.73	0.02
LYD76	Tomato vectors bath Salinity	leaf	Plant Height NaCl/NUE	0.71	0.02
LYD76	Tomato vectors field Drought	leaf	FW drought/Normal	0.75	0.01
LYD80	Arabidopsis 2	leaf	N 1.5 mM SPAD/DW	-0.85	0.07
LYD80	Arabidopsis 2	leaf	N 1.5 mM SPAD/DW	-0.83	0.08
LYD80	Arabidopsis 2 NUE	leaf	N 1.5 mM t50 Flowering	-0.82	3.45E-03
LYD82	Tomato vectors field Drought	leaf	Num of Flower Drought/NUE	-0.73	0.02
LYD82	Tomato vectors field Normal	flower	average red fruit weight (Normal)	0.71	0.02
LYD82	Tomato vectors bath Normal	leaf	leaf No Normal	0.73	0.04
LYD84	Arabidopsis 2 NUE	stem	N 1.5 mM Rosette Area 8 day	-0.82	0.01
LYD84	Arabidopsis 2 NUE	stem	N 1.5 mM Leaf Blade Area 10 day	-0.75	0.02
LYD84	Arabidopsis 2 NUE	stem	N 1.5 mM seed yield per leaf bleed	0.70	0.02
LYD85	Arabidopsis 2 NUE	stem	N 1.5 mM Seed yield reduction compared to 6 mM	-0.81	0.01
LYD85	Arabidopsis 2 NUE	stem	N 6 mM t50 Flowering	-0.78	0.01
LYD85	Arabidopsis 1	root	Lamina length	-0.78	0.02
LYD86	Arabidopsis 2	leaf	N 6 mM Spad / FW	-0.98	4.21E-03
LYD86	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.92	0.03
LYD86	Arabidopsis 2	leaf	N 1.5 mM Spad / FW	-0.88	0.05
LYD87	Tomato vectors bath Salinity	leaf	Plant Height NaCl/NUE	0.70	0.02
LYD87	Tomato vectors bath Normal	leaf	leaf No Normal	0.72	0.05

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD87	Tomato vectors field Drought	leaf	FW/Plant Drought	0.76	0.01
LYD88	Arabidopsis 2	leaf	N 1.5 mM seed yield/spad	-0.73	0.16
LYD88	Arabidopsis 1	seed5daf	Total Leaf Area per plant	-0.71	0.08
LYD88	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.71	0.18
LYD89	Arabidopsis 2 NUE	stem	N 6 mM Seed Yield	0.71	0.02
LYD89	Arabidopsis 2 NUE	leaf	N 6 mM Seed Yield	0.72	0.02
LYD89	Arabidopsis 2 NUE	stem	N 1.5 mM RGR of Rosette Area 3 day	0.72	0.03
LYD9	Arabidopsis 1	leaf	Harvest Index	-0.95	3.37E-04
LYD9	Arabidopsis 1	flower	Harvest Index	-0.91	1.68E-03
LYD9	Arabidopsis 1	root	Harvest Index	-0.90	2.07E-03
LYD90	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.91	0.03
LYD90	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.88	0.05
LYD90	Arabidopsis 2	leaf	N 1.5 mM Spad / FW	-0.85	0.07
LYD91	Tomato vectors bath Normal	root	SPAD Normal	-0.74	0.03
LYD91	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.87	1.11E-03
LYD91	Tomato vectors field Normal	leaf	Weight Flower clusters (Normal)	0.92	1.48E-04
LYD92	Arabidopsis 2	stem	N 6 mMDW/SPAD (biomas/ Nunit)	-0.91	0.03
LYD92	Arabidopsis 2	leaf	N 6 mMDW/SPAD (biomas/ Nunit)	-0.88	0.05
LYD92	Arabidopsis 1	flower	Vegetative growth rate	-0.80	0.02
LYD94	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.78	0.12
LYD94	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.73	0.16
LYD94	Arabidopsis 2	leaf	N 6 mM Seed yield/N unit	-0.72	0.17
LYD95	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.86	0.06
LYD95	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.86	0.06
LYD95	Arabidopsis 2	stem	N 1.5 mM DW/SPAD	-0.86	0.06
LYD96	Arabidopsis 2	stem	N 1.5 mM seed yield/spad	-0.87	0.05
LYD96	Arabidopsis 2	stem	N 6 mM Seed yield/N unit	-0.86	0.06
LYD96	Arabidopsis 2	leaf	N 1.5 mM DW/SPAD	-0.84	0.07
LYD97	Arabidopsis 2 NUE	leaf	N 1.5 mM Dry Weight	-0.83	2.85E-03
LYD97	Arabidopsis 2	stem	N 1.5 mM DW/SPAD	-0.82	0.09
LYD97	Arabidopsis 2 NUE	leaf	N 1.5 mM Dry Weight	-0.81	4.94E-03

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD99	Arabidopsis 2	leaf	N 1.5 mM Spad / FW	-0.92	0.03
LYD99	Arabidopsis 2	leaf	N 6 mM spad/DW (gN/g plant)	-0.77	0.13
LYD99	Arabidopsis 2	leaf	N 6 mM Spad / FW	-0.75	0.15
LYD119_H36	Vectors Sorghum Field Normal	flag leaf	Average Seed Area cm2-normal	0.872264	0.00216
LYD119_H36	Vectors Sorghum Field Normal	flag leaf	Average Seed Area cm2-normal	0.834752	0.005118
LYD119_H36	Vectors Sorghum Field Normal	flag leaf	Average Seed Length cm-normal	0.794902	0.010459
LYD119_H36	Vectors Sorghum Field Normal	flower	Average Seed Area cm2-normal	0.783305	0.012525
LYD119_H36	Vectors Sorghum Field Normal	flower	Average Seed Area cm2-normal	0.781653	0.01284
LYD119_H36	Vectors Sorghum Field Normal	Flag leaf	Average Seed Length cm-normal	0.760239	0.017416
LYD119_H36	Vectors Sorghum Field Normal	flower	Average Seed Length cm-normal	0.751083	0.019664
LYD119_H36	Vectors Sorghum Field Normal	flower	Average Seed Length cm-normal	0.750346	0.019853
LYD119_H36	Vectors Sorghum Field NUE	Flag leaf	FW/Plant gr based on plot-NUE	0.704512	0.022922
LYD148_H9	Vectors Sorghum Field Normal	flower	Average Seed Area cm2-normal	0.802856	0.009183
LYD148_H9	Vectors Sorghum Field Normal	flower	Average Seed Length cm-normal	0.7751	0.014142
LYD148_H9	Vectors Sorghum Field Normal	flower	Average Seed Area cm2-normal	0.752476	0.01931
LYD148_H9	Vectors Sorghum Field Normal	flower	Average Seed Length cm-normal	0.718216	0.0293
LYD196_H4	Vectors Sorghum Field NUE	flower meristem	FW/Plant gr based on plot-NUE	0.717177	0.019566
LYD196_H4	Vectors Sorghum Field Normal	flower meristem	Total Seed Weight /Head gr based on 5 heads-normal	0.715781	0.030116
LYD196_H4	Vectors Sorghum Field Normal	flower meristem	Total Seed Weight/Head gr based on plot-normal	0.71153	0.031578
LYD128_H9	Vectors Sorghum Field Normal	flower meristem	FW Head/Plant gr based on plot-normal	0.857557	0.003116
LYD128_H9	Vectors Sorghum Field NUE	flower meristem	FW/Plant gr based on plot-NUE	0.817108	0.0039
LYD128_H9	Vectors Sorghum Field NUE	flag leaf	Upper Ratio Average Seed Area-NUE	0.751105	0.012277

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD128_H9	Vectors Sorghum Field Normal	flower meristem	NUPE [biomass/SPAD](NORMAL)	0.745956	0.013234
LYD128_H9	Vectors Sorghum Field Normal	flower meristem	NUE2 (total biomass/SPAD) (Normal)	0.74293	0.013821
LYD128_H9	Vectors Sorghum Field NUE	flower meristem	Lower Ratio Average Seed Area-NUE	0.724484	0.017794
LYD128_H9	Vectors Sorghum Field NUE	flower meristem	NUE2 (total biomass/SPAD) (Low N)	0.719047	0.019102
LYD238_H8	Vectors Sorghum Field NUE	flower meristem	Leaf SPAD 64 Days Post Sowing-NUE	0.903146	0.000342
LYD238_H8	Vectors Sorghum Field Normal	flower meristem	Total Seed Weight/Head gr based on plot-normal	0.720223	0.028638
LYD238_H8	Vectors Sorghum Field Normal	flower meristem	NUPE [biomass/SPAD](NORMAL)	0.710718	0.021232
LYD238_H8	Vectors Sorghum Field Normal	flower meristem	NUE [yield /SPAD](NORMAL)	0.701844	0.023676
LYD238_H9	Vectors Sorghum Field NUE	flag leaf	Upper Ratio Average Seed Area-NUE	0.818415	0.003797
LYD238_H9	Vectors Sorghum Field Normal	flower meristem	FW Head/Plant gr based on plot-normal	0.817259	0.007148
LYD238_H9	Vectors Sorghum Field Normal	flower meristem	NUE2 (total biomass/SPAD) (Normal)	0.800525	0.005403
LYD238_H9	Vectors Sorghum Field Normal	flower meristem	NUPE [biomass/SPAD](NORMAL)	0.771903	0.008899
LYD238_H9	Vectors Sorghum Field Normal	flower meristem	Total Seed Weight/Head gr based on plot-normal	0.749855	0.01998
LYD238_H9	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.743576	0.013694
LYD238_H9	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.70978	0.021482
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.949658	2.64E-05
LYD194_H113	Vectors Sorghum Field NUE	flag leaf	Average Seed Area cm2-NUE	0.903812	0.000333

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.901429	0.000366
LYD194_H113	Vectors Sorghum Field NUE	flower	Average Seed Area cm2-NUE	0.898971	0.000403
LYD194_H113	Vectors Sorghum Field NUE	flower	Average Seed Perimeter cm-NUE	0.883792	0.000692
LYD194_H113	Vectors Sorghum Field NUE	flower	Average Seed Length cm-NUE	0.882948	0.000711
LYD194_H113	Vectors Sorghum Field NUE	flag leaf	Average Seed Perimeter cm-NUE	0.860641	0.00139
LYD194_H113	Vectors Sorghum Field NUE	flag leaf	Average Seed Length cm-NUE	0.851382	0.001777
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Length cm-NUE	0.849241	0.001876
LYD194_H113	Vectors Sorghum Field Normal	flower meristem	Average Seed Length cm-normal	0.819745	0.006831
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Width cm-NUE	0.808261	0.004658
LYD194_H113	Vectors Sorghum Field Normal	flower meristem	Average Seed Area cm2-normal	0.798585	0.009854
LYD194_H113	Vectors Sorghum Field Normal	flag leaf	Average Seed Area cm2-normal	0.768451	0.015551
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.766791	0.009659
LYD194_H113	Vectors Sorghum Field Normal	flag leaf	Average Seed Length cm-normal	0.759204	0.017661
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.724569	0.017774
LYD194_H113	Vectors Sorghum Field NUE	flower meristem	Average Seed Length cm-NUE	0.72005	0.018856
LYD194_H113	Vectors Sorghum Field NUE	flag leaf	Average Seed Width cm-NUE	0.715553	0.019976
LYD201_H233	Vectors Sorghum Field NUE	flag leaf	Upper Ratio Average Seed Area-NUE	0.731792	0.016136
LYD201_H235	Vectors Sorghum Field NUE	flower meristem	Average Seed Width cm-NUE	0.792292	0.006284
LYD201_H235	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.760077	0.010726

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD201_H235	Vectors Sorghum Field NUE	flower meriste m	Average Seed Perimeter cm-NUE	0.7357 88	0.015276
LYD216_H17	Vectors Sorghum Field Normal	flower	Total Seed Weight /Head gr based on 5 heads-normal	0.8401 28	0.004584
LYD216_H17	Vectors Sorghum Field Normal	flower meriste m	NUE [yield /SPAD](NORMAL)	0.7046 78	0.022876
LYD235_H20	Vectors Sorghum Field NUE	flower	FW Head/Plant gr based on plot-NUE	0.8427 82	0.002201
LYD235_H20	Vectors Sorghum Field NUE	flower meriste m	Average Seed Width cm-NUE	0.8341 42	0.002696
LYD235_H20	Vectors Sorghum Field Normal	flower meriste m	Average Seed Length cm-normal	0.7929 99	0.010781
LYD235_H20	Vectors Sorghum Field Normal	flower meriste m	Average Seed Length cm-normal	0.7926 81	0.010835
LYD235_H20	Vectors Sorghum Field Normal	flower meriste m	Average Seed Area cm2-normal	0.7882 56	0.011612
LYD235_H20	Vectors Sorghum Field NUE	flag leaf	Total Seed Weight/Head gr based on plot-NUE	0.7807 48	0.007686
LYD235_H20	Vectors Sorghum Field Normal	flower meriste m	Average Seed Area cm2-normal	0.7734 97	0.014474
LYD235_H20	Vectors Sorghum Field NUE	flag leaf	Total Seed Weight/Head gr based on plot-NUE	0.7597 81	0.010775
LYD235_H20	Vectors Sorghum Field NUE	flower meriste m	Average Seed Width cm-NUE	0.7507 37	0.012343
LYD235_H20	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on plot-normal	0.7499 56	0.019953
LYD235_H20	Vectors Sorghum Field NUE	flag leaf	FW Head/Plant gr based on plot-NUE	0.7333 17	0.015804
LYD235_H20	Vectors Sorghum Field NUE	flower	Total Seed Weight /Head gr based on 5 heads-NUE	0.7216 8	0.01846
LYD253_H83	Vectors Sorghum Field NUE	flower meriste m	NUpE [biomass/SPAD](Low N)	0.8254 15	0.003273
LYD253_H83	Vectors Sorghum Field NUE	flower meriste m	FW Head/Plant gr based on plot-NUE	0.8221 22	0.003513
LYD253_H83	Vectors Sorghum Field NUE	flower meriste m	NUE2 (total biomass/SPAD) (Low N)	0.7685 4	0.009394

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD253_H83	Vectors Sorghum Field NUE	flower meristem	FW/Plant gr based on plot-NUE	0.727157	0.017174
LYD253_H83	Vectors Sorghum Field NUE	flower meristem	FW/Plant gr based on plot-NUE	0.713731	0.020444
LYD253_H83	Vectors Sorghum Field Normal	flower meristem	NUE2 (total biomass/SPAD) (Normal)	0.71238	0.020794
LYD86_H90	Vectors Sorghum Field NUE	flag leaf	FW Heads/(FW Heads+ FW Plants) all plot-NUE	0.87859	0.000819
LYD86_H90	Vectors Sorghum Field NUE	flag leaf	FW Head/Plant gr based on plot-NUE	0.86986	0.001069
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	FW Heads/(FW Heads+ FW Plants) all plot-NUE	0.861399	0.001361
LYD86_H90	Vectors Sorghum Field Normal	flower meristem	Total Seed Weight/Head gr based on plot-normal	0.852872	0.003473
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Head Average Perimeter cm-NUE	0.844364	0.002118
LYD86_H90	Vectors Sorghum Field NUE	flag leaf	NUE2 (total biomass/SPAD) (Low N)	0.827284	0.003143
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Head Average Perimeter cm-NUE	0.820069	0.003668
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Head Average Length cm-NUE	0.819341	0.003724
LYD86_H90	Vectors Sorghum Field NUE	flag leaf	NUPE [biomass/SPAD](Low N)	0.815662	0.004018
LYD86_H90	Vectors Sorghum Field NUE	flower	FW Heads/(FW Heads+ FW Plants) all plot-NUE	0.805569	0.004908
LYD86_H90	Vectors Sorghum Field NUE	flower	NUE2 (total biomass/SPAD) (Low N)	0.800577	0.005397
LYD86_H90	Vectors Sorghum Field Normal	flower meristem	NUE [yield /SPAD](NORMAL)	0.794554	0.006032
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Head Average Area cm2-NUE	0.785066	0.007138
LYD86_H90	Vectors Sorghum Field NUE	flower	FW Head/Plant gr based on plot-NUE	0.784583	0.007198
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Head Average Length cm-NUE	0.781501	0.007588

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Total Seed Weight/Head gr based on plot-NUE	0.768858	0.009347
LYD86_H90	Vectors Sorghum Field NUE	flower	NUE2 (total biomass/SPAD) (Low N)	0.767357	0.009573
LYD86_H90	Vectors Sorghum Field NUE	flower	FW Head/Plant gr based on plot-NUE	0.76498	0.009939
LYD86_H90	Vectors Sorghum Field NUE	flower	NUPE [biomass/SPAD](Low N)	0.759768	0.010777
LYD86_H90	Vectors Sorghum Field NUE	flower	FW Heads/(FW Heads+ FW Plants) all plot-NUE	0.759184	0.010874
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	Head Average Area cm ² -NUE	0.756213	0.011376
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	FW Head/Plant gr based on 5 plants-NUE	0.747381	0.012964
LYD86_H90	Vectors Sorghum Field Normal	flower meristem	Head Average Length cm-normal	0.746972	0.020734
LYD86_H90	Vectors Sorghum Field Normal	flower meristem	NUE2 (total biomass/SPAD) (Normal)	0.745693	0.013284
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	NUE [yield /SPAD](Low N)	0.730988	0.016313
LYD86_H90	Vectors Sorghum Field NUE	flower meristem	FW Head/Plant gr based on plot-NUE	0.720473	0.018752
LYD86_H90	Vectors Sorghum Field NUE	flag leaf	FW Head/Plant gr based on plot-NUE	0.71657	0.019719
LYD86_H90	Vectors Sorghum Field Normal	flower meristem	FW Head/Plant gr based on plot-normal	0.710562	0.031916
LYD86_H90	Vectors Sorghum Field NUE	flag leaf	FW/Plant gr based on plot-NUE	0.706497	0.022372
LYD86_H91	Vectors Sorghum Field NUE	flower meristem	NUE2 (total biomass/SPAD) (Low N)	0.935567	6.97E-05
LYD86_H91	Vectors Sorghum Field NUE	flower meristem	NUPE [biomass/SPAD](Low N)	0.92457	0.000129
LYD86_H91	Vectors Sorghum Field NUE	flower meristem	FW Head/Plant gr based on plot-NUE	0.920916	0.000155
LYD86_H91	Vectors Sorghum Field NUE	flower meristem	FW/Plant gr based on plot-NUE	0.90971	0.00026

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD86_H91	Vectors Sorghum Field NUE	flower meristem	FW Heads/(FW Heads+ FW Plants) all plot-NUE	0.75019	0.012443
LYD86_H91	Vectors Sorghum Field NUE	flower	NUpE [biomass/SPAD](Low N)	0.732664	0.015946
LYD148	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on plot-normal	0.7631	0.01675
LYD148	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on 5 plants-normal	0.713855	0.030772
LYD148	Vectors Sorghum Field NUE	flag leaf	Leaf SPAD 64 Days Post Sowing-NUE	0.705262	0.022712
LYD148	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on plot-normal	0.7631	0.01675
LYD148	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on 5 plants-normal	0.713855	0.030772
LYD148	Vectors Sorghum Field NUE	flag leaf	Leaf SPAD 64 Days Post Sowing-NUE	0.705262	0.022712
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.806516	0.004819
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.798386	0.005623
LYD211	Vectors Sorghum Field Normal	flower	Total Seed Weight /Head gr based on 5 heads-normal	0.782852	0.012611
LYD211	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on 5 plants-normal	0.777638	0.013628
LYD211	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on plot-normal	0.770563	0.015094
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.753009	0.011935
LYD211	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on 5 plants-normal	0.742574	0.02192
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Length cm-NUE	0.739574	0.014492
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.739155	0.014577
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Length cm-NUE	0.737733	0.01487
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.806516	0.004819

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.798386	0.005623
LYD211	Vectors Sorghum Field Normal	flower	Total Seed Weight /Head gr based on 5 heads-normal	0.782852	0.012611
LYD211	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on 5 plants-normal	0.777638	0.013628
LYD211	Vectors Sorghum Field Normal	flag leaf	FW Head/Plant gr based on plot-normal	0.770563	0.015094
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.753009	0.011935
LYD211	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on 5 plants-normal	0.742574	0.02192
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Length cm-NUE	0.739574	0.014492
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.739155	0.014577
LYD211	Vectors Sorghum Field NUE	flower meristem	Average Seed Length cm-NUE	0.737733	0.01487
LYD227	Vectors Sorghum Field NUE	flag leaf	Total Seed Weight /Head gr based on 5 heads-NUE	0.870491	0.00105
LYD227	Vectors Sorghum Field NUE	flower	Final Plant Height cm-NUE	0.792586	0.006251
LYD227	Vectors Sorghum Field NUE	flag leaf	Total Seed Weight /Head gr based on 5 heads-NUE	0.768971	0.00933
LYD227	Vectors Sorghum Field NUE	flag leaf	FW Head/Plant gr based on plot-NUE	0.765842	0.009805
LYD227	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on plot-normal	0.755249	0.018619
LYD227	Vectors Sorghum Field NUE	flower	Leaf SPAD 64 Days Post Sowing-NUE	0.739555	0.014496
LYD227	Vectors Sorghum Field NUE	flag leaf	Total Seed Weight /Head gr based on 5 heads-NUE	0.870491	0.00105
LYD227	Vectors Sorghum Field NUE	flower	Final Plant Height cm-NUE	0.792586	0.006251
LYD227	Vectors Sorghum Field NUE	flag leaf	Total Seed Weight /Head gr based on 5 heads-NUE	0.768971	0.00933
LYD227	Vectors Sorghum Field NUE	flag leaf	FW Head/Plant gr based on plot-NUE	0.765842	0.009805

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD227	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on plot-normal	0.755249	0.018619
LYD227	Vectors Sorghum Field NUE	flower	Leaf SPAD 64 Days Post Sowing-NUE	0.739555	0.014496
LYD228	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on 5 plants-normal	0.873907	0.002068
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Length cm-Drought	0.81557	0.004025
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Length cm-Drought	0.81557	0.004025
LYD228	Vectors Sorghum Field Normal	flower	Total Seed Weight/Head gr based on plot-normal	0.776429	0.013871
LYD228	Vectors Sorghum Field Normal	flower	Total Seed Weight /Head gr based on 5 heads-normal	0.744137	0.021492
LYD228	Vectors Sorghum Field Normal	flower	Head Average Length cm-normal	0.739278	0.022836
LYD228	Vectors Sorghum Field Drought	flower	Head Average Width cm-Drought	0.732502	0.015981
LYD228	Vectors Sorghum Field Drought	flower	Head Average Width cm-Drought	0.732502	0.015981
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Area cm2-Drought	0.730394	0.016445
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Area cm2-Drought	0.730394	0.016445
LYD228	Vectors Sorghum Field Drought	flower	Head Average Area cm2-Drought	0.716072	0.019845
LYD228	Vectors Sorghum Field Drought	flower	Head Average Area cm2-Drought	0.716072	0.019845
LYD228	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.715695	0.01994
LYD228	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.70899	0.021694
LYD228	Vectors Sorghum Field Normal	flower	FW Head/Plant gr based on 5 plants-normal	0.873907	0.002068
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Length cm-Drought	0.81557	0.004025
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Length cm-Drought	0.81557	0.004025
LYD228	Vectors Sorghum Field Normal	flower	Total Seed Weight/Head gr based on plot-normal	0.776429	0.013871

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD228	Vectors Sorghum Field Normal	flower	Total Seed Weight /Head gr based on 5 heads-normal	0.744137	0.021492
LYD228	Vectors Sorghum Field Normal	flower	Head Average Length cm-normal	0.739278	0.022836
LYD228	Vectors Sorghum Field Drought	flower	Head Average Width cm-Drought	0.732502	0.015981
LYD228	Vectors Sorghum Field Drought	flower	Head Average Width cm-Drought	0.732502	0.015981
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Area cm2-Drought	0.730394	0.016445
LYD228	Vectors Sorghum Field Drought	flower meristem	Head Average Area cm2-Drought	0.730394	0.016445
LYD228	Vectors Sorghum Field Drought	flower	Head Average Area cm2-Drought	0.716072	0.019845
LYD228	Vectors Sorghum Field Drought	flower	Head Average Area cm2-Drought	0.716072	0.019845
LYD228	Vectors Sorghum Field NUE	flower meristem	Average Seed Area cm2-NUE	0.715695	0.01994
LYD228	Vectors Sorghum Field NUE	flower meristem	Average Seed Perimeter cm-NUE	0.70899	0.021694
LYD229	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.708295	0.03272
LYD229	Vectors Sorghum Field NUE	flag leaf	Final Plant Height cm-NUE	0.704432	0.022944
LYD229	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.708295	0.03272
LYD229	Vectors Sorghum Field NUE	flag leaf	Final Plant Height cm-NUE	0.704432	0.022944
LYD230	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.759057	0.017696
LYD230	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.732126	0.024914
LYD230	Vectors Sorghum Field Normal	flag leaf	Total Seed Weight/Head gr based on plot-normal	0.720454	0.028562
LYD230	Vectors Sorghum Field Normal	flag leaf	Total Seed Weight/Head gr based on plot-normal	0.71634	0.029928
LYD230	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.759057	0.017696
LYD230	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.732126	0.024914
LYD230	Vectors Sorghum Field Normal	flag leaf	Total Seed Weight/Head gr based on plot-normal	0.720454	0.028562
LYD230	Vectors Sorghum Field Normal	flag leaf	Total Seed Weight/Head gr based on plot-normal	0.71634	0.029928

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.824919	0.006202
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE2 (total biomass/SPAD) (Normal)	0.819131	0.006908
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE2 (total biomass/SPAD) (Normal)	0.797739	0.009991
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.769656	0.015289
LYD231	Vectors Sorghum Field Normal	flag leaf	NUPE [biomass/SPAD](NORMAL)	0.765649	0.016171
LYD231	Vectors Sorghum Field Drought	flower meristem	RGR of Leaf Num-Drought	0.753255	0.03095
LYD231	Vectors Sorghum Field Drought	flower meristem	RGR of Leaf Num-Drought	0.751245	0.03166
LYD231	Vectors Sorghum Field Normal	flower	NUPE [biomass/SPAD](NORMAL)	0.734249	0.024284
LYD231	Vectors Sorghum Field Normal	flag leaf	Total Seed Weight/Head gr based on plot-normal	0.734102	0.024328
LYD231	Vectors Sorghum Field Normal	flag leaf	NUPE [biomass/SPAD](NORMAL)	0.729865	0.025594
LYD231	Vectors Sorghum Field Normal	flower	NUE2 (total biomass/SPAD) (Normal)	0.70267	0.034768
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.824919	0.006202
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE2 (total biomass/SPAD) (Normal)	0.819131	0.006908
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE2 (total biomass/SPAD) (Normal)	0.797739	0.009991
LYD231	Vectors Sorghum Field Normal	flag leaf	NUE [yield /SPAD](NORMAL)	0.769656	0.015289
LYD231	Vectors Sorghum Field Normal	flag leaf	NUPE [biomass/SPAD](NORMAL)	0.765649	0.016171
LYD231	Vectors Sorghum Field Drought	flower meristem	RGR of Leaf Num-Drought	0.753255	0.03095
LYD231	Vectors Sorghum Field Drought	flower meristem	RGR of Leaf Num-Drought	0.751245	0.03166

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expression Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD231	Vectors Sorghum Field Normal	flower	NUPE [biomass/SPAD](NORMAL)	0.734249	0.024284
LYD231	Vectors Sorghum Field Normal	flag leaf	Total Seed Weight/Head gr based on plot-normal	0.734102	0.024328
LYD231	Vectors Sorghum Field Normal	flag leaf	NUPE [biomass/SPAD](NORMAL)	0.729865	0.025594
LYD231	Vectors Sorghum Field Normal	flower	NUE2 (total biomass/SPAD) (Normal)	0.70267	0.034768
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Seed yield per dunam [kg]	0.8712	0.0048
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	0.8712	0.0048
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE yield kg/N applied in soil kg	0.8712	0.0048
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.8457	0.0082
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.8237	0.0120
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE at early grain filling [R1-R2] yield Kg/ N in plant SPAD	0.8124	0.0143
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Yield/stalk width	0.7881	0.0202
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.7863	0.0207
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Yield/LAI	0.7758	0.0236
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 10.8.09	0.7659	0.0267
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE at grain filling [R3-R4] yield Kg/ N in plant SPAD	0.7624	0.0278
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 10.8.09	0.7556	0.0301

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 03.08.09	0.7449	0.0340
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Seed yield per dunam [kg]	0.7423	0.0349
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE yield kg/N applied in soil kg	0.7423	0.0349
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	0.7423	0.0349
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- No of rows per ear	0.7197	0.0441
LYD119_H22	Vectors Maize Normal	Interno de V6-V8	Normal- Plant Height 03.08.09	0.7138	0.0308
LYD119_H22	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.7123	0.0313
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Seed yield per dunam [kg]	0.8712	0.0048
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	0.8712	0.0048
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE yield kg/N applied in soil kg	0.8712	0.0048
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.8457	0.0082
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.8237	0.0120
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE at early grain filling [R1-R2] yield Kg/ N in plant SPAD	0.8124	0.0143
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Yield/stalk width	0.7881	0.0202
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.7863	0.0207
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Yield/LAI	0.7758	0.0236

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 10.8.09	0.7659	0.0267
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE at grain filling [R3-R4] yield Kg/ N in plant SPAD	0.7624	0.0278
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 10.8.09	0.7556	0.0301
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 03.08.09	0.7449	0.0340
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- Seed yield per dunam [kg]	0.7423	0.0349
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- NUE yield kg/N applied in soil kg	0.7423	0.0349
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	0.7423	0.0349
LYD119_H22	Vectors Maize Normal	Grain Distal R4-R5	Normal- No of rows per ear	0.7197	0.0441
LYD119_H22	Vectors Maize Normal	Interno de V6-V8	Normal- Plant Height 03.08.09	0.7138	0.0308
LYD119_H22	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.7123	0.0313
LYD148_H4	Vectors Maize Normal	Grain Distal R4-R5	Normal- Final Leaf Number	0.8457	0.0082
LYD148_H4	Vectors Maize Normal	Grain Distal R4-R5	Normal- Final Leaf Number	0.8451	0.0082
LYD148_H4	Vectors Maize Normal	Interno de R3-R4	Normal- Stalk width 20/08/09 close to TP5	0.7327	0.0387
LYD148_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Final Plant Height	0.7013	0.0353
LYD148_H4	Vectors Maize Normal	Grain Distal R4-R5	Normal- Final Leaf Number	0.8457	0.0082
LYD148_H4	Vectors Maize Normal	Grain Distal R4-R5	Normal- Final Leaf Number	0.8451	0.0082

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD148_H4	Vectors Maize Normal	Interno de R3-R4	Normal- Stalk width 20/08/09 close to TP5	0.7327	0.0387
LYD148_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Final Plant Height	0.7013	0.0353
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 19.7.09	0.8416	0.0088
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 29.07.09	0.7924	0.0190
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 10.08.09	0.7544	0.0305
LYD148_H5	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.7134	0.0309
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Leaf No 3.08.09	0.7109	0.0481
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 19.7.09	0.8416	0.0088
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 29.07.09	0.7924	0.0190
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Plant Height 10.08.09	0.7544	0.0305
LYD148_H5	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.7134	0.0309
LYD148_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Leaf No 3.08.09	0.7109	0.0481
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.8907	0.0013
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear length of filled area cm	0.8319	0.0104
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.8314	0.0055
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 1.9.09 R1-2	0.8154	0.0074

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD196_H2	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 3.8.09	0.7864	0.0206
LYD196_H2	Vectors Maize Normal	Leaf V6-V8	Normal- Stalk width close to TP5 20/08/09	0.7852	0.0071
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear Length cm	0.7700	0.0254
LYD196_H2	Vectors Maize Normal	Leaf V6-V8	Normal- Stalk width close to TP5 20/08/09	0.7690	0.0093
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 1.9.09 R1-2	0.7431	0.0218
LYD196_H2	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7364	0.0372
LYD196_H2	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7354	0.0376
LYD196_H2	Vectors Maize Normal	Leaf V6-V8	Normal- Final Leaf Number	0.7346	0.0155
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear length of filled area cm	0.7234	0.0425
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear Length cm	0.7077	0.0495
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.8907	0.0013
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear length of filled area cm	0.8319	0.0104
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- Final Leaf Number	0.8314	0.0055
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 1.9.09 R1-2	0.8154	0.0074
LYD196_H2	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 3.8.09	0.7864	0.0206
LYD196_H2	Vectors Maize Normal	Leaf V6-V8	Normal- Stalk width close to TP5 20/08/09	0.7852	0.0071
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear Length cm	0.7700	0.0254
LYD196_H2	Vectors Maize Normal	Leaf V6-V8	Normal- Stalk width close to TP5 20/08/09	0.7690	0.0093

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD196_H2	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 1.9.09 R1-2	0.7431	0.0218
LYD196_H2	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7364	0.0372
LYD196_H2	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7354	0.0376
LYD196_H2	Vectors Maize Normal	Leaf V6-V8	Normal- Final Leaf Number	0.7346	0.0155
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear length of filled area cm	0.7234	0.0425
LYD196_H2	Vectors Maize Normal	Interno de R3-R4	Normal- Ear Length cm	0.7077	0.0495
LYD128_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Stalk width 20/08/09 close to TP5	0.9266	0.0009
LYD128_H5	Vectors Maize Normal	Grain Distal R4-R5	Normal- Stalk width 20/08/09 close to TP5	0.9266	0.0009
LYD128_H6	Vectors Maize Normal	Grain Distal R4-R5	Normal- Stalk width 20/08/09 close to TP5	0.9266	0.0009
LYD228_H7	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear Length cm	0.7279	0.0407
LYD228_H7	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 29.7.09	0.7120	0.0475
LYD228_H7	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear Length cm	0.7279	0.0407
LYD228_H7	Vectors Maize Normal	Interno de R3-R4	Normal- SPAD 29.7.09	0.7181	0.0448
LYD228_H7	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 29.7.09	0.7120	0.0475
LYD228_H7	Vectors Maize Normal	Interno de V6-V8	Normal- LAI	0.7084	0.0492
LYD238_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Yield/LAI	0.8504	0.0075

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD238_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Ear Length cm	0.8010	0.0095
LYD238_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Ear length of filled area cm	0.7414	0.0222
LYD238_H4	Vectors Maize Normal	Interno de R3-R4	Normal- Stalk width 20/08/09 close to TP5	0.7132	0.0470
LYD238_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Yield/LAI	0.8504	0.0075
LYD238_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Ear Length cm	0.8010	0.0095
LYD238_H4	Vectors Maize Normal	Interno de V6-V8	Normal- Ear length of filled area cm	0.7414	0.0222
LYD238_H4	Vectors Maize Normal	Interno de R3-R4	Normal- Stalk width 20/08/09 close to TP5	0.7132	0.0470
LYD201_H146	Vectors Maize Normal	Interno de R3-R4	Normal- SPAD 6.9.09 R3-R4	0.7795	0.0226
LYD201_H146	Vectors Maize Normal	Leaf V6-V8	Normal- Final Leaf Number	0.7537	0.0118
LYD201_H146	Vectors Maize Normal	Leaf V6-V8	Normal- Final Leaf Number	0.7412	0.0142
LYD201_H146	Vectors Maize Normal	Grain Distal R4-R5	Normal- Final Plant Height	0.7330	0.0386
LYD201_H146	Vectors Maize Normal	Interno de R3-R4	Normal- SPAD 6.9.09 R3-R4	0.7795	0.0226
LYD201_H146	Vectors Maize Normal	Leaf V6-V8	Normal- Final Leaf Number	0.7537	0.0118
LYD201_H146	Vectors Maize Normal	Leaf V6-V8	Normal- Final Leaf Number	0.7412	0.0142
LYD201_H146	Vectors Maize Normal	Grain Distal R4-R5	Normal- Final Plant Height	0.7330	0.0386
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 29.7.09	0.8859	0.0015
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.8836	0.0016

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear with mm	0.8708	0.0022
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Main Ear Height	0.8612	0.0029
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- NUE at grain filling [R3-R4] yield Kg/ N in plant SPAD	0.8587	0.0030
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- NUE at early grain filling [R1-R2] yield Kg/ N in plant SPAD	0.8554	0.0033
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Seed yield per dunam [kg]	0.8139	0.0076
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- NUE yield kg/N applied in soil kg	0.8139	0.0076
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	0.8139	0.0076
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Yield/stalk width	0.8120	0.0079
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Plant Height	0.7807	0.0130
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear with mm	0.7358	0.0238
LYD201_H147	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7273	0.0409
LYD201_H147	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7218	0.0432
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Main Ear Height	0.7200	0.0287
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear with mm	0.7173	0.0296
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- No of rows per ear	0.7165	0.0299
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Plant Height	0.7109	0.0318

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- No of rows per ear	0.7004	0.0356
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 29.7.09	0.8859	0.0015
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.8836	0.0016
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear with mm	0.8708	0.0022
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Main Ear Height	0.8612	0.0029
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- NUE at grain filling [R3-R4] yield Kg/ N in plant SPAD	0.8587	0.0030
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- NUE at early grain filling [R1-R2] yield Kg/ N in plant SPAD	0.8554	0.0033
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Seed yield per dunam [kg]	0.8139	0.0076
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- NUE yield kg/N applied in soil kg	0.8139	0.0076
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- seed yield per 1 plant rest of the plot [0- RH in Kg]	0.8139	0.0076
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Yield/stalk width	0.8120	0.0079
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Plant Height	0.7807	0.0130
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear with mm	0.7358	0.0238
LYD201_H147	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7273	0.0409
LYD201_H147	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7218	0.0432
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Main Ear Height	0.7200	0.0287

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Ear with mm	0.7173	0.0296
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- No of rows per ear	0.7165	0.0299
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- Final Plant Height	0.7109	0.0318
LYD201_H147	Vectors Maize Normal	Interno de V6-V8	Normal- No of rows per ear	0.7004	0.0356
LYD201_H148	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear length of filled area cm	0.7205	0.0438
LYD201_H148	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 29.7.09	0.7174	0.0296
LYD201_H148	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear length of filled area cm	0.7205	0.0438
LYD201_H148	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 29.7.09	0.7174	0.0296
LYD216_H9	Vectors Maize Normal	Leaf V6-V8	Normal- Ear length of filled area cm	0.7545	0.0117
LYD216_H9	Vectors Maize Normal	Grain Distal R4-R5	Normal- Stalk width 20/08/09 close to TP5	0.7367	0.0371
LYD216_H9	Vectors Maize Normal	Leaf V6-V8	Normal- Ear length of filled area cm	0.7545	0.0117
LYD216_H9	Vectors Maize Normal	Grain Distal R4-R5	Normal- Stalk width 20/08/09 close to TP5	0.7367	0.0371
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 3.8.09	0.8579	0.0064
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.8398	0.0091
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.8112	0.0145
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 29.7.09	0.7661	0.0266
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.7540	0.0307

<i>Gene Name</i>	<i>Vector Set</i>	<i>Expres sion Set</i>	<i>Correlation Vector</i>	<i>R</i>	<i>P</i>
LYD216_H10	Vectors Maize Normal	Interno de R3-R4	Normal- Final Leaf Number	0.7158	0.0458
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 3.8.09	0.8579	0.0064
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.8398	0.0091
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.8112	0.0145
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- SPAD 29.7.09	0.7661	0.0266
LYD216_H10	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear weight per plot (42 plants per plot) [0- RH]	0.7540	0.0307
LYD216_H10	Vectors Maize Normal	Interno de R3-R4	Normal- Final Leaf Number	0.7158	0.0458
LYD227_H4	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 3.8.09	0.8421	0.0044
LYD227_H4	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7830	0.0216
LYD227_H4	Vectors Maize Normal	Interno de V6-V8	Normal- SPAD 3.8.09	0.8421	0.0044
LYD227_H4	Vectors Maize Normal	Grain Distal R4-R5	Normal- Ear with mm	0.7830	0.0216

Table 26: Correlation analyses.

EXAMPLE 10

IDENTIFICATION OF GENES AND HOMOLOGUES THEREOF WHICH

5 INCREASE YIELD, BIOMASS, 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 217 genes which have a major impact on yield, seed yield, oil
10 yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress

tolerance, and/or nitrogen use efficiency when expression thereof is increased in plants. The identified genes (including genes identified by bioinformatics tools and curated sequences thereof), and polypeptide sequences encoded thereby are summarized in Table 27, hereinbelow.

5

Table 27

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

10

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD1	arabidopsis gb165 AT1G03470	arabidopsis	1	488
LYD2	arabidopsis gb165 AT1G22800	arabidopsis	2	489
LYD3	arabidopsis gb165 AT1G32160	arabidopsis	3	490
LYD4	arabidopsis gb165 AT1G34630	arabidopsis	4	491
LYD5	arabidopsis gb165 AT1G67650	arabidopsis	5	492
LYD6	arabidopsis gb165 AT2G15860	arabidopsis	6	493
LYD7	arabidopsis gb165 AT2G25670	arabidopsis	7	494
LYD9	arabidopsis gb165 AT3G01720	arabidopsis	8	495
LYD10	arabidopsis gb165 AT3G15890	arabidopsis	9	496
LYD11	arabidopsis gb165 AT3G53668	arabidopsis	10	497
LYD12	arabidopsis gb165 AT3G60980	arabidopsis	11	498
LYD13	arabidopsis gb165 AT3G61670	arabidopsis	12	499
LYD14	arabidopsis gb165 AT4G04880	arabidopsis	13	500
LYD16	arabidopsis gb165 AT4G20480	arabidopsis	14	501
LYD18	arabidopsis gb165 AT4G24610	arabidopsis	15	502
LYD20	arabidopsis gb165 AT5G10690	arabidopsis	16	503
LYD21	arabidopsis gb165 AT5G36930	arabidopsis	17	504
LYD22	arabidopsis gb165 AT5G51040	arabidopsis	18	505

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD23	arabidopsis gb165 AT5G51080	arabidopsi s	19	506
LYD25	canola gb161 EG019886	canola	20	507
LYD26	medicago 09v1 AL377960	medicago	21	508
LYD27	medicago 09v1 BF632009	medicago	22	509
LYD28	medicago 09v1 BI271781	medicago	23	510
LYD29	medicago 09v1 CRPMT000438	medicago	24	511
LYD33	tomato gb164 AF211815	tomato	25	512
LYD34	tomato gb164 AI483666	tomato	26	513
LYD35	tomato 09v1 AJ306423	tomato	27	514
LYD36	tomato gb164 AI485302	tomato	28	515
LYD37	tomato gb164 AI487977	tomato	29	516
LYD38	tomato gb164 AI773900	tomato	30	517
LYD40	tomato 09v1 AI782539	tomato	31	518
LYD41	tomato 09v1 BF052865	tomato	32	519
LYD42	tomato 09v1 AW036074	tomato	33	520
LYD43	tomato gb164 AW037558	tomato	34	521
LYD44	tomato gb164 AW217297	tomato	35	522
LYD45	tomato gb164 AW618293	tomato	36	523
LYD47	tomato gb164 BG123883	tomato	37	524
LYD48	tomato 09v1 BG123886	tomato	38	525
LYD49	tomato 09v1 BG123989	tomato	39	526
LYD50	tomato 09v1 BG127394	tomato	40	527
LYD51	tomato gb164 BG127506	tomato	41	528
LYD52	tomato 09v1 BG128140	tomato	42	529
LYD53	tomato gb164 BG128949	tomato	43	530
LYD55	tomato gb164 BG131146	tomato	44	531
LYD57	tomato gb164 BG134380	tomato	45	532
LYD58	tomato 09v1 BG134619	tomato	46	533
LYD59	tomato 09v1 BG135632	tomato	47	534
LYD61	tomato 09v1 BG138131	tomato	48	535
LYD62	tomato 09v1 BG734743	tomato	49	536
LYD63	tomato 09v1 BI206677	tomato	50	537
LYD65	tomato 09v1 CK273548	tomato	51	538
LYD66	tomato gb164 CD002407	tomato	52	539
LYD67	tomato 09v1 BF113276	tomato	53	540
LYD69	arabidopsis gb165 AT5G25120	arabidopsi s	54	541
LYD70	canola gb161 CB686084	canola	55	542
LYD71	canola gb161 CD817042	canola	56	543
LYD72	medicago 09v1 AW696637	medicago	57	544
LYD73	tomato gb164 AA824853	tomato	58	545
LYD74	tomato 09v1 BG124100	tomato	59	546
LYD75	tomato gb164 BG134552	tomato	60	547
LYD76	tomato gb164 BP890691	tomato	61	548
LYD78	soybean gb168 AL388558	soybean	62	549
LYD79	soybean gb168 BE820644	soybean	63	550

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD80	arabidopsis gb165 AT1G21920	arabidopsis	64	551
LYD81	medicago 09v1 BF632274	medicago	65	552
LYD82	tomato gb164 BG630963	tomato	66	553
LYD84	arabidopsis gb165 AT5G15254	arabidopsis	67	554
LYD85	arabidopsis gb165 AT4G29905	arabidopsis	68	555
LYD86	arabidopsis gb165 AT5G41010	arabidopsis	69	556
LYD87	tomato gb164 AW930554	tomato	70	557
LYD88	arabidopsis gb165 AT1G68710	arabidopsis	71	558
LYD89	arabidopsis gb165 AT5G42730	arabidopsis	72	559
LYD90	arabidopsis gb165 AT1G18910	arabidopsis	73	560
LYD91	tomato 09v1 BG643473	tomato	74	561
LYD92	arabidopsis gb165 AT1G19240	arabidopsis	75	562
LYD94	arabidopsis gb165 AT1G49660	arabidopsis	76	563
LYD95	arabidopsis gb165 AT1G65295	arabidopsis	77	564
LYD96	arabidopsis gb165 AT1G76970	arabidopsis	78	565
LYD97	arabidopsis gb165 AT2G01090	arabidopsis	79	566
LYD99	arabidopsis gb165 AT3G26380	arabidopsis	80	567
LYD101	arabidopsis gb165 AT4G14930	arabidopsis	81	568
LYD102	arabidopsis gb165 AT4G24800	arabidopsis	82	569
LYD103	arabidopsis gb165 AT5G05060	arabidopsis	83	570
LYD104	arabidopsis gb165 AT5G23070	arabidopsis	84	571
LYD105	arabidopsis gb165 AT5G40540	arabidopsis	85	572
LYD106	arabidopsis gb165 AT5G44930	arabidopsis	86	573
LYD107	arabidopsis gb165 AT5G62630	arabidopsis	87	574
LYD108	canola gb161 EV139574	canola	88	575
LYD109	b_juncealyd3 EVGN00087322220915	b_junce	89	576
LYD110	b_juncealyd3 E6ANDIZ01CHGS1	b_junce	90	577

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD113	b_juncealyd3 H07501	b_juncea	91	578
LYD114	b_juncealgb164 EVGN00337011101441	b_juncea	92	579
LYD117	b_juncealyd3 E6ANDIZ01AGE3G	b_juncea	93	580
LYD118	b_juncealyd3 E6ANDIZ01A3PN5	b_juncea	94	581
LYD119	b_juncealgb164 EVGN01067614512362	b_juncea	95	582
LYD120	b_juncealyd3 X1E6ANDIZ01EAN1T	b_juncea	96	583
LYD122	b_juncealyd3 E6ANDIZ01DUORN	b_juncea	97	584
LYD123	b_juncealgb164 EVGN08545904982944	b_juncea	98	585
LYD124	b_juncealgb164 EVGN10695305591742	b_juncea	99	586
LYD125	medicagolgb157.2 AW171770	medicago	100	587
LYD126	medicagolgb157.2 BE240432	medicago	101	588
LYD127	soybeanlgb166 AW119405	soybean	102	589
LYD128	soybeanlgb166 BE210997	soybean	103	590
LYD129	soybeanlgb166 BE660895	soybean	104	591
LYD132	soybeanlgb168 BF634740	soybean	105	592
LYD133	soybeanlgb168 BI418412	soybean	106	593
LYD134	soybeanlgb168 BU546353	soybean	107	594
LYD136	soybeanlgb168 AW685064	soybean	108	595
LYD139	soybeanlgb168 BI969776	soybean	109	596
LYD140	soybeanlgb168 CF069839	soybean	110	597
LYD142	tomatol09v1 AI779400	tomato	111	598
LYD144	tomatol09v1 BG135622	tomato	112	599
LYD146	tomatolgb164 DV103976	tomato	113	600
LYD148	sorghumlgb161 crplAF047899	sorghum	114	601
LYD149	arabidopsislgb165 AT1G05350	arabidopsis	115	602
LYD150	arabidopsislgb165 AT1G61180	arabidopsis	116	603
LYD152	arabidopsislgb165 AT5G02370	arabidopsis	117	604
LYD153	arabidopsislgb165 AT5G42920	arabidopsis	118	605
LYD156	tomatolgb164 BG125257	tomato	119	606
LYD157	tomatol09v1 BG735318	tomato	120	607
LYD158	tomatolgb164 DB709286	tomato	121	608
LYD159	b_juncealgb164 DT317712	b_juncea	122	609
LYD166	b_juncealgb164 EVGN00118027751203	b_juncea	123	610
LYD167	b_juncealgb164 EVGN00123927221199	b_juncea	124	611
LYD172	b_juncealyd3 E6ANDIZ01ATVGF	b_juncea	125	612
LYD173	b_juncealgb164 EVGN00297423550919	b_juncea	126	613

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Poly pep. SEQ ID NO:</i>
LYD174	b_juncealyd3 E6ANDIZ01AF3YB	b_juncea	127	614
LYD176	b_juncealgb164 EVGN00462208651225	b_juncea	128	615
LYD177	b_juncealgb164 EVGN00465119080454	b_juncea	129	616
LYD178	b_juncealgb164 EVGN00502808481823	b_juncea	130	617
LYD180	b_juncealyd3 E6ANDIZ01A6SGI1	b_juncea	131	618
LYD184	b_juncealyd3 E6ANDIZ01A3ARL	b_juncea	132	619
LYD185	b_juncealgb164 EVGN01300508721002	b_juncea	133	620
LYD186	b_juncealyd3 GENL37642	b_juncea	134	621
LYD187	b_juncealgb164 EVGN01497309140908	b_juncea	135	622
LYD188	b_juncealyd3 CD813443	b_juncea	136	623
LYD190	b_juncealyd3 GENBG543253	b_juncea	137	624
LYD192	b_juncealyd3 A4M2E6ANDIZ01B0ZJK	b_juncea	138	625
LYD193	b_juncealyd3 E6ANDIZ01A79AV1	b_juncea	139	626
LYD194	b_juncealyd3 E6ANDIZ01AFJMD	b_juncea	140	627
LYD195	tomatolgb164 AI483451	tomato	141	628
LYD196	maizelgb170 AI586800	maize	142	629
LYD197	arabidopsis gb165 AT5G63800	arabidopsis	143	630
LYD200	b_juncealyd3 E7FJ1I304DXRGY	b_juncea	144	631
LYD201	b_juncealgb164 EVGN00128110990752	b_juncea	145	632
LYD202	b_juncealgb164 EVGN00179312122996	b_juncea	146	633
LYD204	b_juncealyd3 E6ANDIZ01A9A19	b_juncea	147	634
LYD206	b_juncealgb164 EVGN00955015301700	b_juncea	148	635
LYD208	b_juncealyd3 E6ANDIZ01BZ44C	b_juncea	149	636
LYD209	b_juncealyd3 E6ANDIZ02G6J79	b_juncea	150	637
LYD211	sorghum gb161.crp W59814	sorghum	151	638
LYD212	arabidopsis gb165 AT1G21560	arabidopsis	152	639
LYD213	arabidopsis gb165 AT1G63460	arabidopsis	153	640
LYD214	arabidopsis gb165 AT2G24440	arabidopsis	154	641
LYD215	arabidopsis gb165 AT2G43350	arabidopsis	155	642
LYD216	arabidopsis gb165 AT3G03960	arabidopsis	156	643
LYD217	arabidopsis gb165 AT3G06035	arabidopsis	157	644

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Poly pep. SEQ ID NO:</i>
LYD219	arabidopsis gb165 AT3G51250	arabidopsis	158	645
LYD220	arabidopsis gb165 AT4G16160	arabidopsis	159	646
LYD221	arabidopsis gb165 AT4G35850	arabidopsis	160	647
LYD222	arabidopsis gb165 AT4G35985	arabidopsis	161	648
LYD223	arabidopsis gb165 AT5G13200	arabidopsis	162	649
LYD224	arabidopsis gb165 AT5G58070	arabidopsis	163	650
LYD225	barley gb157 SOLEXA AJ476940	barley	164	651
LYD227	sorghum gb161.crpl BE600694	sorghum	165	652
LYD228	sorghum gb161.crpl AI724169	sorghum	166	653
LYD229	sorghum gb161.crpl AW680415	sorghum	167	654
LYD230	sorghum gb161.crpl AW747687	sorghum	168	655
LYD231	sorghum gb161.crpl CA827765	sorghum	169	656
LYD232	tomato 09v1 AI774782	tomato	170	657
LYD233	tomato gb164 AW032486	tomato	171	658
LYD234	tomato gb164 BG123219	tomato	172	659
LYD235	tomato 09v1 BG132066	tomato	173	660
LYD236	tomato gb164 BG629499	tomato	174	661
LYD238	barley gb157 SOLEXA AL504570	barley	175	662
LYD240	barley gb157 SOLEXA BQ766120	barley	176	663
LYD244	arabidopsis gb165 AT1G70810	arabidopsis	177	664
LYD245	arabidopsis gb165 AT2G36410	arabidopsis	178	665
LYD246	arabidopsis gb165 AT5G17900	arabidopsis	179	666
LYD248	b_juncea gb164 EVGN00459611963354	b_juncea	180	667
LYD250	b_juncea yd3 C1E7FJ1I304DWSVV	b_juncea	181	668
LYD252	b_juncea yd3 E6ANDIZ01CP0S8	b_juncea	182	669
LYD253	b_juncea yd3 G2BG543337	b_juncea	183	670
LYD256	b_juncea yd3 G2ES909931	b_juncea	184	671
LYD257	b_juncea yd3 STE6ANDIZ01D9959	b_juncea	185	672
LYD260	b_juncea yd3 E6ANDIZ01BMZAP	b_juncea	186	673
LYD261	b_juncea yd3 E6ANDIZ01A3LGY	b_juncea	187	674
LYD264	b_juncea yd3 C1E6ANDIZ01B2URL	b_juncea	188	675
LYD266	b_juncea yd3 GENCX189412	b_juncea	189	676
LYD267	b_juncea yd3 E6ANDIZ01BB7PO	b_juncea	190	677
LYD268	b_juncea gb164 EVGN26566813750231	b_juncea	191	678
LYD271	b_juncea gb164 EVGN08627136613786	b_juncea	192	679

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD273	b_juncealyd3 E6ANDIZ01D5PI2	b_juncea	193	680
LYD275	b_juncealyd3 G2CD811838	b_juncea	194	681
LYD276	b_juncealyd3 E7FJ1I302CBAW9	b_juncea	195	682
LYD278	b_juncealyd3 A4M2E6ANDIZ01AZ32J	b_juncea	196	683
LYD279	b_juncealyd3 GENCD837122	b_juncea	197	684
LYD282	b_juncealyd3 G2CD837360	b_juncea	198	685
LYD283	b_juncealyd3 G2H74785	b_juncea	199	686
LYD285	b_juncealyd3 C1E6ANDIZ01A8PO2	b_juncea	200	687
LYD286	b_juncealyd3 TT1E6ANDIZ02HFR5M	b_juncea	201	688
LYD287	arabidopsis gb165 AT5G10860	arabidopsis	202	689
LYD288	b_juncealyd3 E6ANDIZ01AZRCR	b_juncea	203	690
LYD124_H7	canola gb161 ES968317	canola	204	691
LYD128_H1	arabidopsis gb165 AT5G51660	arabidopsis	205	692
LYD267_H0	arabidopsis gb165 AT1G64790	arabidopsis	206	693
LYD271_H0	arabidopsis gb165 AT2G47240	arabidopsis	207	694
LYD89_H0	arabidopsis gb165 AT1G68050	arabidopsis	208	695
LYM104	rice gb157.2 AK072782	rice	209	696
LYM275	barley gb157.3 BE421069	barley	210	697
LYD112	b_juncealgb164 EVGN00224711371076	b_juncea	211	-
LYD115	b_juncealyd3 E6ANDIZ01AL3LA	b_juncea	212	-
LYD259	b_juncealyd3 CN827195	b_juncea	213	-
LYD262	b_juncealyd3 A4M2E6ANDIZ01C3K15	b_juncea	214	-
LYD265	b_juncealgb164 EVGN07822109542425	b_juncea	215	-
LYD269	b_juncealyd3 A4M2E6ANDIZ02J3I20	b_juncea	216	-
LYD270	b_juncealyd3 C1E6ANDIZ01AQ8V8	b_juncea	217	-
LYD124	b_juncealgb164 EVGN10695305591742	b_juncea	99	724
LYD152	arabidopsis gb165 AT5G02370	arabidopsis	117	729
LYD128_H1	arabidopsis gb165 AT5G51660	arabidopsis	205	749
LYD267_H0	arabidopsis gb165 AT1G64790	arabidopsis	206	750

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD12	arabidopsis gb165 AT3G60980	arabidopsi s	218	698
LYD18	arabidopsis gb165 AT4G24610	arabidopsi s	219	502
LYD28	medicago 09v1 BI271781	medicago	220	510
LYD29	medicago 09v1 CRPMT000438	medicago	221	699
LYD35	tomato gb164 AI483874	tomato	222	700
LYD40	tomato gb164 AI782539	tomato	223	701
LYD41	tomato gb164 AJ784615	tomato	224	702
LYD42	tomato gb164 AW036074	tomato	225	520
LYD45	tomato gb164 AW618293	tomato	226	703
LYD48	tomato gb164 BG123886	tomato	227	704
LYD49	tomato gb164 BG123989	tomato	228	705
LYD50	tomato gb164 BG127394	tomato	229	706
LYD52	tomato gb164 BG128140	tomato	230	707
LYD58	tomato gb164 BG134619	tomato	231	708
LYD59	tomato gb164 BG135632	tomato	232	709
LYD61	tomato gb164 BG138131	tomato	233	710
LYD62	tomato gb164 BG734743	tomato	234	711
LYD63	tomato gb164 BI206677	tomato	235	537
LYD65	tomato gb164 BP895649	tomato	236	712
LYD67	tomato gb164 DB701451	tomato	237	713
LYD74	tomato gb164 AI490774	tomato	238	714
LYD82	tomato gb164 BG630963	tomato	239	715
LYD84	arabidopsis gb165 AT5G15254	arabidopsi s	240	716
LYD91	tomato gb164 BG643473	tomato	241	717
LYD106	arabidopsis gb165 AT5G44930	arabidopsi s	242	718
LYD108	canola gb161 EV139574	canola	243	719
LYD118	b_juncealyd3 E6ANDIZ01A3PN5	b_junce	244	720
LYD119	b_juncealgb164 EVGN01067614512 362	b_junce	245	721
LYD120	b_juncealyd3 X1E6ANDIZ01EAN1 T	b_junce	246	722
LYD123	b_juncealgb164 EVGN08545904982 944	b_junce	247	723
LYD127	soybean gb166 AW119405	soybean	248	725
LYD133	soybean gb168 BI418412	soybean	249	593
LYD142	tomato gb164 AI779400	tomato	250	726
LYD144	tomato gb164 AW429188	tomato	251	727
LYD150	arabidopsis gb165 AT1G61180	arabidopsi s	252	728
LYD153	arabidopsis gb165 AT5G42920	arabidopsi s	253	605
LYD157	tomato gb164 BG735318	tomato	254	607
LYD174	b_juncealyd3 E6ANDIZ01AF3YB	b_junce	255	614

<i>Gene Name</i>	<i>Cluster Name</i>	<i>Organism</i>	<i>Polynuc. SEQ ID NO:</i>	<i>Polypep. SEQ ID NO:</i>
LYD185	b_juncealgb164 EVGN01300508721002	b_juncea	256	730
LYD192	b_juncealyd3 A4M2E6ANDIZ01B0ZJK	b_juncea	257	731
LYD208	b_juncealyd3 E6ANDIZ01BZ44C	b_juncea	258	732
LYD212	arabidopsis gb165 AT1G21560	arabidopsis	259	733
LYD222	arabidopsis gb165 AT4G35985	arabidopsis	260	648
LYD231	sorghum gb161.crp CA827765	sorghum	261	734
LYD232	tomato gb164 AI774782	tomato	262	735
LYD235	tomato gb164 BG132066	tomato	263	736
LYD248	b_juncealgb164 EVGN00459611963354	b_juncea	264	737
LYD250	b_juncealyd3 C1E7FJ1I304DWSVV	b_juncea	265	738
LYD252	b_juncealyd3 E6ANDIZ01CP0S8	b_juncea	266	669
LYD260	b_juncealyd3 E6ANDIZ01BMZAP	b_juncea	267	739
LYD261	b_juncealyd3 E6ANDIZ01A3LGY	b_juncea	268	740
LYD264	b_juncealyd3 C1E6ANDIZ01B2URL	b_juncea	269	741
LYD268	b_juncealyd3 C1E6ANDIZ01DMZ45	b_juncea	270	742
LYD271	b_juncealgb164 EVGN08627136613786	b_juncea	271	743
LYD273	b_juncealyd3 E6ANDIZ01D5PI2	b_juncea	272	744
LYD276	b_juncealyd3 E7FJ1I302CBAW9	b_juncea	273	745
LYD278	b_juncealyd3 A4M2E6ANDIZ01AZ32J	b_juncea	274	746
LYD283	b_juncealyd3 G2H74785	b_juncea	275	747
LYD286	b_juncealyd3 TT1E6ANDIZ02HFR5M	b_juncea	276	748
LYD124_H7	canola gb161 ES968317	canola	277	691
LYD112	b_juncealgb164 EVGN00224711371076	b_juncea	278	-
LYD115	b_juncealyd3 E6ANDIZ01AL3LA	b_juncea	279	-
LYD259	b_juncealyd3 CN827195	b_juncea	280	-
LYD262	b_juncealyd3 A4M2E6ANDIZ01C3K15	b_juncea	281	-
LYD265	b_juncealgb164 EVGN07822109542425	b_juncea	282	-
LYD269	b_juncealyd3 A4M2E6ANDIZ02J3I20	b_juncea	283	-
LYD270	b_juncealyd3 C1E6ANDIZ01AQ8V8	b_juncea	284	-

Table 27: Provided are the identified genes, their annotation, organism and polynucleotide and polypeptide sequence identifiers. "polynucl." = polynucleotide; "polypep." = polypeptide.

EXAMPLE 11***IDENTIFICATION OF HOMOLOGOUS SEQUENCES THAT INCREASE SEED YIELD, OIL YIELD, GROWTH RATE, OIL CONTENT, FIBER YIELD, FIBER QUALITY, BIOMASS, VIGOR, ABST AND/OR NUE OF A PLANT***

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

 To identify putative orthologs of the genes affecting plant yield, oil yield, oil content, seed yield, growth rate, vigor, biomass, abiotic stress tolerance and/or nitrogen use efficiency, all sequences were aligned using the BLAST (*Basic Local Alignment*
15 *Search Tool*). Sequences sufficiently similar were tentatively grouped. These putative orthologs were further organized under a Phylogram - a branching diagram (tree) assumed to be a representation of the evolutionary relationships among the biological taxa. Putative ortholog groups were analyzed as to their agreement with the phylogram and in cases of disagreements these ortholog groups were broken accordingly.

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

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

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

The homologous genes may belong to the same gene family. The analysis of a gene family may be carried out using sequence similarity analysis. To perform this analysis one may use standard programs for multiple alignments e.g. Clustal W. A neighbour-joining tree of the proteins homologous to the genes in this invention may be used to provide an overview of structural and ancestral relationships. Sequence identity may be calculated using an alignment program as described above. It is expected that other plants will carry a similar functional gene (ortholog) or a family of similar genes and those genes will provide the same preferred phenotype as the genes presented here. Advantageously, these family members may be useful in the methods of the invention. Example of other plants are included here but not limited to, barley (*Hordeum vulgare*), Arabidopsis (*Arabidopsis thaliana*), maize (*Zea mays*), cotton (*Gossypium*), Oilseed rape (*Brassica napus*), Rice (*Oryza sativa*), Sugar cane (*Saccharum officinarum*),

Sorghum (*Sorghum bicolor*), Soybean (*Glycine max*), Sunflower (*Helianthus annuus*), Tomato (*Lycopersicon esculentum*), Wheat (*Triticum aestivum*).

The above-mentioned analyses for sequence homology can be carried out on a full-length sequence, but may also be based on a comparison of certain regions such as conserved domains. The identification of such domains, would also be well within the realm of the person skilled in the art and would involve, for example, a computer readable format of the nucleic acids of the present invention, the use of alignment software programs and the use of publicly available information on protein domains, conserved motifs and boxes. This information is available in the PRODOM (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 α -helical structures or β -sheet structures). Conservative substitution tables are well known in the art (see for example Creighton (1984) *Proteins*. W.H. Freeman and Company). Homologues of a nucleic acid encompass nucleic acids having nucleotide substitutions, deletions and/or insertions relative to the unmodified nucleic acid in question and having similar biological and functional activity as the unmodified nucleic acid from which they are derived.

Table 28, hereinbelow, lists a summary of orthologous and homologous sequences of the polynucleotide sequences and polypeptide sequences presented in

Table 27 above, which were identified from the databases using the NCBI BLAST software (e.g., using the Blastp and tBlastn algorithms) and needle (EMBOSS package) as being at least 80% homologous to the selected polynucleotides and polypeptides, and which are expected to increase plant yield, seed yield, oil yield, oil content, growth rate, fiber yield, fiber quality, biomass, vigor, ABST and/or NUE of a plant.

Table 28

Homologous polynucleotides and polypeptides which can increase plant yield, seed yield, oil yield, oil content, growth rate, fiber yield, fiber quality, biomass, vigor, ABST and/or NUE of a plant

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
814	LYD1	arabidopsis_lyratal09v1IJGI AL000277_P1	4852	488	88.1	globlastp
815	LYD2	arabidopsis_lyratal09v1IJGI AL002442_T1	4853	489	95.28	glotblastn
816	LYD2	radishlgb164IEV527506_P1	4854	489	85.1	globlastp
817	LYD2	radishlgb164IEV543672_T1	4855	489	84.15	glotblastn
818	LYD3	arabidopsis_lyratal09v1IJGI AL003335_P1	4856	490	97	globlastp
819	LYD3	canola10v1ICD816459_P1	4857	490	87.3	globlastp
820	LYD3	canolalgb161ICD816459_P1	4858	490	87	globlastp
821	LYD3	radishlgb164IEV536106_P1	4859	490	83.8	globlastp
822	LYD4	arabidopsis_lyratal09v1IJGI AL003600_P1	4860	491	96.3	globlastp
823	LYD4	canolalgb161IDY022340_P1	4861	491	81.1	globlastp
824	LYD4	canola10v1IDY022340_P1	4862	491	80.9	globlastp
825	LYD5	arabidopsis_lyratal09v1IJGI AL006945_P1	4863	492	88.9	globlastp
826	LYD6	arabidopsis_lyratal09v1IJGI AL011942_P1	4864	493	94.6	globlastp
827	LYD6	canola10v1IEE470649_P1	4865	493	83.6	globlastp
828	LYD6	canolalgb161ICD835605_T1	4866	493	83.46	glotblastn
829	LYD6	canola10v1IDY005922_P1	4867	493	82.6	globlastp
830	LYD7	arabidopsis_lyratal09v1IJGI AL013304_P1	4868	494	95.3	globlastp
831	LYD7	radishlgb164IEV526280_P1	4869	494	84.2	globlastp
832	LYD7	canola10v1IEE464842_P1	4870	494	81.4	globlastp
833	LYD7	b_rapalgb162IDN960346_P1	4871	494	81.4	globlastp
834	LYD9	arabidopsis_lyratal09v1IJGI AL008425_P1	4872	495	96.8	globlastp
835	LYD9	canola10v1ICX188920_P1	4873	495	87.5	globlastp
836	LYD9	canolalgb161ICX188920_P1	4874	495	87.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
837	LYD1 0	arabidopsis_lyratal09v1IJGI AL010075_P1	4875	496	94.2	globlastp
838	LYD1 1	arabidopsis_lyratal09v1IJGI AL018613_P1	4876	497	91.7	globlastp
839	LYD1 2	arabidopsis_lyratal09v1IJGI AL019555_P1	4877	498	80.3	globlastp
840	LYD1 3	arabidopsis_lyratal09v1IJGI AL019486_T1	4878	499	94.88	glotblastn
841	LYD1 4	arabidopsis_lyratal09v1IJGI AL023385_P1	4879	500	94.1	globlastp
842	LYD1 4	canolal10v1ICD829595_P1	4880	500	87.9	globlastp
843	LYD1 4	canolalgb161ICD829595_P1	4880	500	87.9	globlastp
844	LYD1 4	radishlgb164IEY944220_P1	4881	500	83.9	globlastp
845	LYD1 8	arabidopsis_lyratal09v1IJGI AL025644_P1	4882	502	98	globlastp
846	LYD2 0	arabidopsis_lyratal09v1IJGI AL020751_T1	4883	503	93.97	glotblastn
847	LYD2 2	arabidopsis_lyratal09v1IJGI AL029529_P1	4884	505	93.6	globlastp
848	LYD2 2	canolal10v1IH07584_P1	4885	505	86.2	globlastp
849	LYD2 2	canolalgb161IH07584_P1	4885	505	86.2	globlastp
850	LYD2 2	canolal10v1ICD822100_P1	4886	505	85.1	globlastp
851	LYD2 2	canolalgb161ICD822100_P1	4886	505	85.1	globlastp
852	LYD2 2	radishlgb164IEV538885_P1	4887	505	85.1	globlastp
853	LYD2 2	thellungiellalgb167IDN7729 03_P1	4888	505	85.1	globlastp
854	LYD2 2	b_junceal10v2IE6ANDIZ01 CL8L1_P1	4889	505	84.6	globlastp
855	LYD2 2	canolal10v1IEG020309_P1	4890	505	84.6	globlastp
856	LYD2 2	canolalgb161IEG020309_P1	4890	505	84.6	globlastp
857	LYD2 2	radishlgb164IEV537868_P1	4891	505	84.6	globlastp
858	LYD2 2	b_rapalgb162IEX016229_P1	4892	505	84	globlastp
859	LYD2 2	radishlgb164IEV525209_P1	4893	505	84	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
860	LYD2 2	radishlgb164 EV537841_P1	4894	505	84	globlastp
861	LYD2 2	radishlgb164 EW732032_P1	4895	505	83.5	globlastp
862	LYD2 3	arabidopsis_lyrata 09v1 JGI AL029534_P1	4896	506	85.5	globlastp
863	LYD2 5	radishlgb164 EV527157_T1	4897	507	92.39	glotblastn
864	LYD2 5	b_rapalgb162 EX019886_P1	4898	507	86.4	globlastp
865	LYD2 5	radishlgb164 EV528812_P1	4899	507	86.4	globlastp
866	LYD2 5	b_oleracealgb161 EH428988 _P1	4900	507	86.1	globlastp
867	LYD2 5	arabidopsis_lyrata 09v1 JGI AL027442_P1	4901	507	83.5	globlastp
868	LYD2 5	arabidopsis 10v1 AT5G4203 0_P1	4902	507	83.3	globlastp
869	LYD2 6	soybeanlgb168 BU547748_P 1	4903	508	83.8	globlastp
870	LYD2 6	pigeonpeal 10v1 SRR054580 S0003992_P1	4904	508	83.5	globlastp
871	LYD2 6	soybeanlgb168 AL377960_P 1	4905	508	83.5	globlastp
872	LYD2 6	peanut 10v1 ES759373_P1	4906	508	80.7	globlastp
873	LYD2 6	beanlgb167 FD790445_P1	4907	508	80.4	globlastp
874	LYD2 9	lotus 09v1 BP083688_P1	4908	511	81.6	globlastp
875	LYD2 9	soybeanlgb168 CB891857_P 1	4909	511	80.3	globlastp
876	LYD3 3	potatolgb157.2 BG351683_P 1	4910	512	96.5	globlastp
877	LYD3 3	solanum_phurejal 09v1 SPH AF211815_P1	4910	512	96.5	globlastp
878	LYD3 3	potatol 10v1 BG351683_P1	4910	512	96.5	globlastp
879	LYD3 3	potatolgb157.2 CK718359_T 1	4911	512	91.67	glotblastn
880	LYD3 3	eggplant 10v1 FS026710_P1	4912	512	89.9	globlastp
881	LYD3 3	pepperlgb171 CO776598_P1	4913	512	87.6	globlastp
882	LYD3 3	tobacco gb162 DV161243_P 1	4914	512	83.8	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
883	LYD3 3	solanum_phurejal09v1 SPH AW622515_T1	4915	512	80.21	glotblastn
884	LYD3 4	solanum_phurejal09v1 SPH AI483666_P1	4916	513	98.1	globlastp
885	LYD3 4	pepperlgb171 BM062207_P 1	4917	513	92.7	globlastp
886	LYD3 5	solanum_phurejal09v1 SPH AJ306423_P1	4918	514	91.6	globlastp
887	LYD3 5	potatolgb157.2 AJ306423_P 1	4919	514	91.1	globlastp
888	LYD3 5	potatol10v1 AJ306423_P1	4920	514	90.9	globlastp
889	LYD3 5	pepperlgb171 CA515906_P1	4921	514	82.5	globlastp
890	LYD3 5	nicotiana_benthamianalgb16 2 CK280498_P1	4922	514	80.7	globlastp
891	LYD3 6	solanum_phurejal09v1 SPH AI485302_P1	4923	515	95.8	globlastp
892	LYD3 6	pepperlgb171 BM064313_P 1	4924	515	89.4	globlastp
893	LYD3 7	potatol10v1 BE921890_P1	4925	516	89.1	globlastp
894	LYD3 7	potatolgb157.2 BE921890_P 1	4925	516	89.1	globlastp
895	LYD3 7	solanum_phurejal09v1 SPH AI487977_T1	4926	516	88.24	glotblastn
896	LYD3 7	eggplantl10v1 FS013887_P1	4927	516	85.3	globlastp
897	LYD3 7	solanum_phurejal09v1 SPH BW686911_T1	4928	516	83.68	glotblastn
898	LYD3 7	solanum_phurejal09v1 SPH CRPSP002839_T1	4929	516	83.26	glotblastn
899	LYD3 7	pepperlgb171 CA522394_P1	4930	516	80.7	globlastp
900	LYD3 7	solanum_phurejal09v1 SPH CRPSP002387_P1	4931	516	80.1	globlastp
901	LYD4 0	solanum_phurejal09v1 SPH AI782539_P1	4932	518	89.5	globlastp
902	LYD4 1	potatol10v1 BF052865_P1	4933	519	84	globlastp
903	LYD4 1	nicotiana_benthamianalgb16 2 CK280334_T1	4934	519	80	glotblastn
904	LYD4 2	potatol10v1 BE919699_P1	4935	520	87.4	globlastp
905	LYD4 2	solanum_phurejal09v1 SPH AW036074_P1	4936	520	87.4	globlastp

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906	LYD4 2	potatolgb157.2 BE919699_T 1	4937	520	86.94	glotblastn
907	LYD4 3	solanum_phurejal09v1 SPH AW037558_P1	4938	521	95.9	globlastp
908	LYD4 3	eggplantl10v1 FS004461_P1	4939	521	90.3	globlastp
909	LYD4 3	pepperlgb171 EB084651_P1	4940	521	88.4	globlastp
910	LYD4 3	tobacco gb162 EB429609_P 1	4941	521	88.3	globlastp
911	LYD4 3	petunialgb171 FN008650_P1	4942	521	86.9	globlastp
912	LYD4 4	solanum_phurejal09v1 SPH AW217297_P1	4943	522	91.1	globlastp
913	LYD4 4	eggplantl10v1 FS043660_P1	4944	522	90.3	globlastp
914	LYD4 4	potatolgb157.2 BQ514775_P 1	4945	522	90.3	globlastp
915	LYD4 4	pepperlgb171 GD056569_P1	4946	522	86.6	globlastp
916	LYD4 4	tobacco gb162 AF211657_T 1	4947	522	83.12	glotblastn
917	LYD4 7	potatolgb157.2 BG095639_P 1	4948	524	97.1	globlastp
918	LYD4 7	potato 10v1 BG095639_P1	4949	524	96.4	globlastp
919	LYD4 7	solanum_phurejal09v1 SPH BG123883_P1	4950	524	95.7	globlastp
920	LYD4 7	potatolgb157.2 BG097730_P 1	4951	524	95.3	globlastp
921	LYD4 7	eggplantl10v1 FS002881_P1	4952	524	89.5	globlastp
922	LYD4 7	pepperlgb171 BM063195_P 1	4953	524	89.5	globlastp
923	LYD4 7	tobacco gb162 EB426460_P 1	4954	524	83	globlastp
924	LYD4 8	solanum_phurejal09v1 SPH BG123886_T1	4955	525	92.64	glotblastn
925	LYD4 8	eggplantl10v1 FS025632_P1	4956	525	88.7	globlastp
926	LYD4 8	potato 10v1 CV503109_T1	4957	525	87.94	glotblastn
927	LYD5 0	solanum_phurejal09v1 SPH BG127394_P1	4958	527	94.1	globlastp
928	LYD5 0	pepperlgb171 BM064159_P 1	4959	527	87.7	globlastp

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929	LYD5 0	pepper gb171 CA517048_P1	4960	527	80.7	globlastp
930	LYD5 0	tomato 09v1 BG131854_P1	4961	527	80.7	globlastp
931	LYD5 0	tomato gb164 BG131854_P1	4961	527	80.7	globlastp
932	LYD5 0	potato 10v1 BI406827_T1	4962	527	80.67	glotblastn
933	LYD5 0	potato gb157.2 BI406827_T 1	4962	527	80.67	glotblastn
934	LYD5 0	solanum_phureja 09v1 SPH BG131854_P1	4963	527	80.3	globlastp
935	LYD5 0	tobacco gb162 CN498866_P 1	4964	527	80.1	globlastp
936	LYD5 1	potato gb157.2 CK851783_P 1	4965	528	98.9	globlastp
937	LYD5 1	potato 10v1 BG887178_P1	4965	528	98.9	globlastp
938	LYD5 1	potato gb157.2 CV286494_P 1	4966	528	98.4	globlastp
939	LYD5 1	potato gb157.2 BG887178_P 1	4967	528	95.7	globlastp
940	LYD5 1	solanum_phureja 09v1 SPH BG127506_P1	4968	528	95.7	globlastp
941	LYD5 1	pepper gb171 CO776357_P1	4969	528	91.4	globlastp
941	LYD2 24	pepper gb171 CO776357_P1	4969	650	80.1	globlastp
942	LYD5 1	eggplant 10v1 FS010852_P1	4970	528	88.6	globlastp
943	LYD5 1	tobacco gb162 DV157738_P 1	4971	528	88.1	globlastp
944	LYD5 1	tobacco gb162 EB446434_P 1	4972	528	86.5	globlastp
944	LYD2 24	tobacco gb162 EB446434_P 1	4972	650	81.2	globlastp
945	LYD5 1	tomato 09v1 BG135563_P1	4973	528	84.3	globlastp
946	LYD5 1	tomato gb164 BG135563_P1	4973	528	84.3	globlastp
947	LYD5 1	papaya gb165 AM903594_P 1	4974	528	83.2	globlastp
948	LYD5 1	tripphysaria gb164 DR172528 _P1	4975	528	83.2	globlastp
948	LYD2 24	tripphysaria gb164 DR172528 _P1	4975	650	82.8	globlastp

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949	LYD5 1	antirrhinum gb166 AJ79273 1_P1	4976	528	82.8	globlastp
949	LYD2 24	antirrhinum gb166 AJ79273 1_P1	4976	650	80.7	globlastp
950	LYD5 1	cacaolgb167 CU507814_P1	4977	528	82.7	globlastp
951	LYD5 1	potatol10v1 BG890660_P1	4978	528	82.7	globlastp
952	LYD5 1	potatolgb157.2 BG890660_P 1	4978	528	82.7	globlastp
953	LYD5 1	triphysarial10v1 DR172528_ P1	4979	528	82.7	globlastp
953	LYD2 24	triphysarial10v1 DR172528_ P1	4979	650	82.3	globlastp
954	LYD5 1	castorbean 09v1 XM002523 459_P1	4980	528	82.4	globlastp
955	LYD5 1	ipomoea_nill10v1 BJ557864 _P1	4981	528	82.3	globlastp
956	LYD5 1	ipomoealgb157.2 BJ557864_ P1	4982	528	82.3	globlastp
957	LYD5 1	petunialgb171 FN009866_T 1	4983	528	82.26	glotblastn
958	LYD5 1	cotton 10v1 BG440664_P1	4984	528	82.2	globlastp
959	LYD5 1	pepper gb171 CO910024_P1	4985	528	82.2	globlastp
960	LYD5 1	blueberry 10v1 CV090845_P 1	4986	528	81.6	globlastp
961	LYD5 1	cotton gb164 BG440664_P1	4987	528	81.6	globlastp
962	LYD5 1	peanut 10v1 ES719286_P1	4988	528	81.6	globlastp
963	LYD5 1	peanut gb171 EH042075_P1	4988	528	81.6	globlastp
964	LYD5 1	solanum_phurejal09v1 SPH BI203337_P1	4989	528	81.6	globlastp
965	LYD5 1	walnutslgb166 CV195852_P 1	4990	528	81.6	globlastp
966	LYD5 1	poplar gb170 BI068309_P1	4991	528	81.2	globlastp
967	LYD5 1	chestnut gb170 SRR006295S 0012962_P1	4992	528	81.1	globlastp
968	LYD5 1	lettuce 10v1 DW075260_P1	4993	528	81.1	globlastp
969	LYD5 1	lettuce gb157.2 DW075260_ P1	4993	528	81.1	globlastp

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970	LYD5 1	lettucelgb157.2 DW138454_ P1	4994	528	81.1	globlastp
971	LYD5 1	oil_palm gb166 ES370588_ T1	4995	528	81.08	glotblastn
972	LYD5 1	poplar 10v1 BI068309_P1	4996	528	80.6	globlastp
973	LYD5 1	dandelion 10v1 DR399893_ P1	4997	528	80.5	globlastp
974	LYD5 1	oak 10v1 SRR006307S0007 944_P1	4998	528	80.5	globlastp
975	LYD5 1	cichorium gb171 EH690884_ P1	4999	528	80.5	globlastp
976	LYD5 1	lettucelgb157.2 DW145838_ P1	5000	528	80.5	globlastp
977	LYD5 1	monkeyflower 09v1 CV5204 88_P1	5001	528	80.5	globlastp
978	LYD5 1	monkeyflower 10v1 CV5204 88_P1	5001	528	80.5	globlastp
979	LYD5 1	lettucel10v1 DW043917_P1	5000	528	80.5	globlastp
980	LYD5 1	eschscholzia 10v1 CD47675 4_P1	5002	528	80.2	globlastp
981	LYD5 1	curcuma 10v1 DY383234_P 1	5003	528	80.1	globlastp
982	LYD5 1	nasturtium 10v1 GH162572_ P1	5004	528	80.1	globlastp
983	LYD5 1	tamarix gb166 CF199524_P 1	5005	528	80.1	globlastp
984	LYD5 1	cassava 09v1 CK652227_T1	5006	528	80	glotblastn
985	LYD5 1	heritiera 10v1 SRR005794S0 007518_P1	5007	528	80	globlastp
986	LYD5 1	oak 10v1 CR627779_P1	5008	528	80	globlastp
987	LYD5 1	oak 10v1 FN742298_P1	5008	528	80	globlastp
988	LYD5 1	kiwi gb166 FG411068_P1	5009	528	80	globlastp
989	LYD5 1	lettucelgb157.2 DW043917_ P1	5010	528	80	globlastp
990	LYD5 1	monkeyflower 09v1 GO9641 50_P1	5011	528	80	globlastp
991	LYD5 1	oak gb170 DB996542_T1	5012	528	80	glotblastn
992	LYD5 1	oak gb170 SRR006309S002 0036_P1	5013	528	80	globlastp

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993	LYD5 2	solanum_phurejal09v1 SPH BG128140_P1	5014	529	92	globlastp
994	LYD5 2	tomatol09v1 BF052558_P1	5015	529	80.4	globlastp
995	LYD5 3	solanum_phurejal09v1 SPH BG128949_P1	5016	530	89.7	globlastp
996	LYD5 3	potatol10v1 CK718279_T1	5017	530	88.79	glotblastn
997	LYD5 3	potatolgb157.2 CK718279_T 1	5018	530	87	glotblastn
998	LYD5 3	solanum_phurejal09v1 SPH AJ785469_P1	5019	530	82.5	globlastp
999	LYD5 5	potatolgb157.2 BG591939_P 1	5020	531	90.1	globlastp
1000	LYD5 5	solanum_phurejal09v1 SPH BG131146_P1	5021	531	89.4	globlastp
1001	LYD5 5	eggplantl10v1 FS010619_P1	5022	531	86.5	globlastp
1002	LYD5 5	potatol10v1 BG591939_P1	5023	531	84.6	globlastp
1003	LYD5 5	pepperlgb171 BM062230_P 1	5024	531	80	globlastp
1004	LYD5 7	solanum_phurejal09v1 SPH BG134380_P1	5025	532	91.3	globlastp
1005	LYD5 7	pepperlgb171 BM063304_T 1	5026	532	88.37	glotblastn
1006	LYD5 8	solanum_phurejal09v1 SPH BG134619_T1	5027	533	83.21	glotblastn
1007	LYD5 8	solanum_phurejal09v1 SPH BG627533_P1	5028	533	81.3	globlastp
1008	LYD5 9	solanum_phurejal09v1 SPH BG135632_P1	5029	534	97.7	globlastp
1009	LYD5 9	potatol10v1 BE920142_P1	5030	534	97.5	globlastp
1010	LYD5 9	potatolgb157.2 BE920142_P 1	5030	534	97.5	globlastp
1011	LYD5 9	eggplantl10v1 FS003439_P1	5031	534	93.8	globlastp
1012	LYD5 9	tomatol09v1 TOMTRALTB E_P1	5032	534	83.4	globlastp
1013	LYD5 9	tomatolgb164 TOMTRALT BE_P1	5032	534	83.4	globlastp
1014	LYD5 9	grapelgb160 BQ796337_P1	5033	534	81.6	globlastp
1015	LYD5 9	monkeyflowerl10v1 GO9707 70_P1	5034	534	80.7	globlastp

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1016	LYD5 9	prunus 10v1 BU039926_P1	5035	534	80.2	globlastp
1017	LYD5 9	chestnut gb170 AF417293_T 1	5036	534	80.18	glotblastn
1018	LYD5 9	poplar 10v1 BU823552_P1	5037	534	80	globlastp
1019	LYD6 1	solanum_phurejal09v1 SPH BG138131_P1	5038	535	98.5	globlastp
1020	LYD6 1	potato 10v1 BG889997_P1	5039	535	98.2	globlastp
1021	LYD6 1	potato gb157.2 BG889997_P 1	5040	535	97.9	globlastp
1022	LYD6 1	eggplant 10v1 FS032594_P1	5041	535	93.9	globlastp
1023	LYD6 2	solanum_phurejal09v1 SPH CV504049_P1	5042	536	90.5	globlastp
1024	LYD6 2	potato gb157.2 CV504049_P 1	5043	536	88.5	globlastp
1025	LYD6 5	potato 10v1 CK273548_P1	5044	538	83.6	globlastp
1026	LYD6 5	potato gb157.2 CK273548_P 1	5044	538	83.6	globlastp
1027	LYD6 5	solanum_phurejal09v1 SPH CK273548_P1	5045	538	83.3	globlastp
1028	LYD6 6	solanum_phurejal09v1 SPH CD002407_P1	5046	539	96.4	globlastp
1029	LYD6 6	tomato 09v1 FG549581_P1	5047	539	95.2	globlastp
1030	LYD6 6	solanum_phurejal09v1 SPH GO374369_P1	5048	539	95.2	globlastp
1031	LYD6 6	potato 10v1 EG013178_P1	5049	539	92.8	globlastp
1032	LYD6 6	solanum_phurejal09v1 SPH AI486008_P1	5050	539	92.8	globlastp
1033	LYD6 6	solanum_phurejal09v1 SPH CK468681_P1	5051	539	91.6	globlastp
1034	LYD6 6	solanum_phurejal09v1 SPHS RR015435S0258823_P1	5052	539	90.4	globlastp
1035	LYD6 6	pepper gb171 GD112009_P1	5053	539	88	globlastp
1036	LYD6 6	tomato 09v1 AI486008_P1	5054	539	86.7	globlastp
1037	LYD6 6	pepper gb171 CA524720_P1	5055	539	86.7	globlastp
1038	LYD6 6	tomato gb164 AI486008_P1	5054	539	86.7	globlastp

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1039	LYD6 6	eggplant 10v1 FS049175_P1	5056	539	85.7	globlastp
1040	LYD6 6	petunia gb171 FN013481_P1	5057	539	82.6	globlastp
1041	LYD6 6	petunia gb171 CV294587_P 1	5058	539	81.4	globlastp
1042	LYD6 6	tobacco gb162 EB451442_P 1	5059	539	80.5	globlastp
1043	LYD6 7	solanum_phureja 09v1 SPH BF113276_P1	5060	540	96.7	globlastp
1044	LYD6 7	potato 10v1 BQ514597_P1	5061	540	87.7	globlastp
1045	LYD6 7	potato gb157.2 BQ514597_P 1	5061	540	87.7	globlastp
1046	LYD6 9	arabidopsis_lyrata 09v1 JGI AL022233_P1	5062	541	91.5	globlastp
1047	LYD6 9	arabidopsis 10v1 AT5G2513 0_P1	5063	541	90.9	globlastp
1048	LYD6 9	arabidopsis gb165 AT5G251 30_P1	5063	541	90.9	globlastp
1049	LYD6 9	arabidopsis 10v1 AT5G2514 0_P1	5064	541	81.9	globlastp
1050	LYD6 9	arabidopsis 10v1 AT5G2518 0_P1	5065	541	81	globlastp
1051	LYD7 0	b_rapa gb162 CO749669_P1	5066	542	99	globlastp
1052	LYD7 0	canola 10v1 CB686270_P1	5067	542	87.8	globlastp
1053	LYD7 0	canola gb161 CB686270_P1	5067	542	87.8	globlastp
1054	LYD7 0	b_oleracea gb161 DY026133 _T1	5068	542	87.18	glotblastn
1055	LYD7 0	radish gb164 AF052690_P1	5069	542	86.1	globlastp
1056	LYD7 0	thellungiella gb167 BM9855 18_T1	5070	542	80.26	glotblastn
1057	LYD7 1	b_oleracea gb161 DY027446 _P1	543	543	100	globlastp
1058	LYD7 1	canola gb161 CD817725_P1	5071	543	97.1	globlastp
1059	LYD7 1	b_rapa gb162 CV544359_P1	5072	543	96.3	globlastp
1060	LYD7 1	b_junceal 10v2 E6ANDIZ01 BK9AI_P1	5073	543	94.2	globlastp
1061	LYD7 2	canola 10v1 CD818215_P1	5074	544	81.7	globlastp

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1062	LYD7 2	canola gb161 CD825357_P1	5075	544	81.7	globlastp
1063	LYD7 2	canola 10v1 CD836921_P1	5076	544	81.5	globlastp
1064	LYD7 2	cucumber 09v1 CK755361_P1	5077	544	81.4	globlastp
1065	LYD7 2	sunflower 10v1 CD848269_P1	5078	544	81.2	globlastp
1066	LYD7 2	melon 10v1 DV634181_P1	5079	544	81	globlastp
1067	LYD7 2	artemisia gb164 EY053079_T1	5080	544	80.94	glotblastn
1068	LYD7 2	tomato 09v1 AI779245_P1	5081	544	80.9	globlastp
1069	LYD7 2	monkeyflower 09v1 GO998343_P1	5082	544	80.7	globlastp
1070	LYD7 2	monkeyflower 10v1 GO998343_P1	5082	544	80.7	globlastp
1071	LYD7 2	radish gb164 EW716526_P1	5083	544	80.7	globlastp
1072	LYD7 2	dandelion 10v1 DY820612_T1	5084	544	80.68	glotblastn
1073	LYD7 2	arabidopsis 10v1 AT4G27070_T1	5085	544	80.68	glotblastn
1074	LYD7 2	arabidopsis_lyrata 09v1 JGI AL030016_P1	5086	544	80.3	globlastp
1075	LYD7 2	nasturtium 10v1 SRR032558 S0038114_P1	5087	544	80.1	globlastp
1076	LYD7 3	solanum_phureja 09v1 SPH AA824853_T1	5088	545	97.84	glotblastn
1077	LYD7 3	monkeyflower 10v1 GR111848_P1	5089	545	83.2	globlastp
1078	LYD7 3	tripphysaria 10v1 EY174824_P1	5090	545	82.7	globlastp
1079	LYD7 3	monkeyflower 09v1 GR111848_T1	5091	545	82.66	glotblastn
1080	LYD7 3	tripphysaria gb164 EY174824_T1	5092	545	82.11	glotblastn
1081	LYD7 3	pigeonpea 10v1 SRR054580 S0040813_P1	5093	545	81	globlastp
1082	LYD7 3	apple gb171 CN444478_P1	5094	545	80.8	globlastp
1083	LYD7 3	prunus gb167 AJ872422_P1	5095	545	80.5	globlastp
1084	LYD7 3	soybean gb168 AL380796_P1	5096	545	80.4	globlastp

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1085	LYD7 3	prunus 10v1 CN445461_T1	5097	545	80.27	glotblastn
1086	LYD7 3	cowpea gb166 FF394654_T1	5098	545	80.22	glotblastn
1087	LYD7 4	potato gb157.2 BE919413_P 1	5099	546	96.3	globlastp
1088	LYD7 4	solanum_phureja 09v1 SPH AA824836_P1	5099	546	96.3	globlastp
1089	LYD7 4	potato 10v1 BE919413_P1	5099	546	96.3	globlastp
1090	LYD7 4	potato gb157.2 CK262220_P 1	5100	546	94.3	globlastp
1091	LYD7 4	potato gb157.2 BG890062_P 1	5101	546	93.5	globlastp
1092	LYD7 4	tomato 09v1 TOMPSI_P1	5102	546	93.5	globlastp
1093	LYD7 4	tomato gb164 TOMPSI_P1	5102	546	93.5	globlastp
1094	LYD7 4	potato gb157.2 BE921836_P 1	5103	546	93.1	globlastp
1095	LYD7 4	solanum_phureja 09v1 SPH TOMPSI_P1	5103	546	93.1	globlastp
1096	LYD7 4	potato 10v1 BE921836_P1	5103	546	93.1	globlastp
1097	LYD7 4	pepper gb171 AA840636_P1	5104	546	91.9	globlastp
1098	LYD7 4	eggplant 10v1 FS024905_P1	5105	546	91.1	globlastp
1099	LYD7 4	tobacco gb162 CV017194_P 1	5106	546	91.1	globlastp
1100	LYD7 4	nicotiana_benthamiana gb16 2 CN655516_P1	5107	546	90.7	globlastp
1101	LYD7 4	tobacco gb162 CO046507_P 1	5108	546	90.7	globlastp
1102	LYD7 4	tobacco gb162 CV016100_P 1	5109	546	90.7	globlastp
1103	LYD7 4	nicotiana_benthamiana gb16 2 CN655239_P1	5110	546	90.2	globlastp
1104	LYD7 4	tobacco gb162 BU673932_P 1	5110	546	90.2	globlastp
1105	LYD7 4	nicotiana_benthamiana gb16 2 CN741940_P1	5111	546	89.8	globlastp
1106	LYD7 4	petunia gb171 CV295755_P 1	5112	546	89.4	globlastp
1107	LYD7 4	nicotiana_benthamiana gb16 2 CN742501_P1	5113	546	89	globlastp

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1108	LYD7 4	lettucelgb157.2 DW043670_ P1	5114	546	87.9	globlastp
1109	LYD7 4	lettucelgb157.2 DW145751_ P1	5114	546	87.9	globlastp
1110	LYD7 4	lettucel10v1 CV700018_P1	5114	546	87.9	globlastp
1111	LYD7 4	antirrhinum gb166 AJ79088 0_P1	5115	546	87.8	globlastp
1112	LYD7 4	lettucelgb157.2 CV700018_ P1	5116	546	87.4	globlastp
1113	LYD7 4	lettucel10v1 DW074491_P1	5117	546	87.4	globlastp
1114	LYD7 4	lettucelgb157.2 DW074491_ P1	5117	546	87.4	globlastp
1115	LYD7 4	prunus gb167 AJ872311_P1	5118	546	86.8	globlastp
1116	LYD7 4	kiwi gb166 FG400771_P1	5119	546	86.7	globlastp
1117	LYD7 4	centaurealgb166 EL930984_ P1	5120	546	86.6	globlastp
1118	LYD7 4	dandelion 10v1 DQ160108_ P1	5121	546	86.6	globlastp
1119	LYD7 4	dandelion gb161 DQ160108 _P1	5121	546	86.6	globlastp
1120	LYD7 4	lettucelgb157.2 DW047470_ P1	5122	546	86.6	globlastp
1121	LYD7 4	cucumber 09v1 CK085482_ P1	5123	546	86.2	globlastp
1122	LYD7 4	apple gb171 AY347803_P1	5124	546	86	globlastp
1123	LYD7 4	apple gb171 CN878571_P1	5125	546	86	globlastp
1124	LYD7 4	melon 10v1 DV631727_P1	5126	546	85.8	globlastp
1125	LYD7 4	artemisia 10v1 EY032037_P 1	5127	546	85.8	globlastp
1126	LYD7 4	artemisia gb164 EY032037_ P1	5128	546	85.8	globlastp
1127	LYD7 4	artemisia gb164 EY033150_ P1	5127	546	85.8	globlastp
1128	LYD7 4	seneciolgb170 DY658127_P 1	5129	546	85.8	globlastp
1129	LYD7 4	strawberry gb164 CO816702 _P1	5130	546	85.8	globlastp
1130	LYD7 4	sunflower gb162 BU672054 _P1	5131	546	85.8	globlastp

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1131	LYD7 4	sunflower 10v1 BU672054_ P1	5132	546	85.4	globlastp
1132	LYD7 4	catharanthus gb166 EG5545 91_P1	5133	546	85.4	globlastp
1133	LYD7 4	sunflower 10v1 CD845700_ P1	5134	546	85.4	globlastp
1134	LYD7 4	cotton 10v1 CA993646_P1	5135	546	85.1	globlastp
1135	LYD7 4	cotton 10v1 CD485707_P1	5136	546	85	globlastp
1136	LYD7 4	beet gb162 BQ487964_P1	5137	546	85	globlastp
1137	LYD7 4	castorbean 09v1 EG656437_ P1	5138	546	85	globlastp
1138	LYD7 4	chestnut gb170 SRR006295S 0033318_P1	5139	546	85	globlastp
1139	LYD7 4	cynara gb167 GE589113_P1	5140	546	85	globlastp
1140	LYD7 4	poplar 10v1 BI068408_P1	5141	546	85	globlastp
1141	LYD7 4	spurge gb161 DV128345_P1	5142	546	85	globlastp
1142	LYD7 4	sunflower gb162 CD845700_ P1	5143	546	85	globlastp
1143	LYD7 4	triphysaria gb164 EY127386_ P1	5144	546	85	globlastp
1144	LYD7 4	ipomoea_nill 10v1 BJ554139_ P1	5145	546	84.8	globlastp
1145	LYD7 4	ipomoea_batatas 10v1 BM87 8729_P1	5146	546	84.7	globlastp
1146	LYD7 4	cotton gb164 CA993646_P1	5147	546	84.7	globlastp
1147	LYD7 4	triphysaria 10v1 EY127386_ P1	5148	546	84.6	globlastp
1148	LYD7 4	triphysaria 10v1 SRR023500 S0001172_P1	5149	546	84.6	globlastp
1149	LYD7 4	cassava 09v1 DV443354_P1	5150	546	84.6	globlastp
1150	LYD7 4	cassava gb164 DV443354_P 1	5150	546	84.6	globlastp
1151	LYD7 4	citrus gb166 BQ623380_P1	5151	546	84.6	globlastp
1152	LYD7 4	poplar gb170 BI068408_P1	5152	546	84.6	globlastp
1153	LYD7 4	cleome_gynandra 10v1 SRR 015532S0002528_P1	5153	546	84.3	globlastp

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1154	LYD7 4	cleome_spinosal10v1 SRR01 5531S0000163_P1	5154	546	84.3	globlastp
1155	LYD7 4	soybean gb168 BE316989_P 1	5155	546	84.3	globlastp
1156	LYD7 4	soybean gb168 BE324912_P 1	5156	546	84.3	globlastp
1157	LYD7 4	b_junceal10v2 E6ANDIZ01 A1BN1_P1	5157	546	84.1	globlastp
1158	LYD7 4	cassaval09v1 CK644716_P1	5158	546	84.1	globlastp
1159	LYD7 4	b_junceal10v2 E6ANDIZ01 AVS2X_P1	5159	546	84.1	globlastp
1160	LYD7 4	b_junceal10v2 E6ANDIZ01 AH1XS_P1	5160	546	84.1	globlastp
1161	LYD7 4	b_junceal10v2 E6ANDIZ01 A1C0H_P1	5161	546	84.1	globlastp
1162	LYD7 4	b_juncealgb164 EVGN0014 7211371919_P1	5161	546	84.1	globlastp
1163	LYD7 4	b_rapalgb162 CO750665_P1	5162	546	84.1	globlastp
1164	LYD7 4	lotus 09v1 LLCN824968_P1	5163	546	84.1	globlastp
1165	LYD7 4	maize gb170 LLDQ245113_ P1	5161	546	84.1	globlastp
1166	LYD7 4	radish gb164 EW722654_P1	5164	546	84.1	globlastp
1167	LYD7 4	radish gb164 EV524798_P1	5165	546	83.9	globlastp
1168	LYD7 4	tragopogon 10v1 SRR02020 5S0005883_T1	5166	546	83.81	glotblastn
1169	LYD7 4	ginsengl10v1 DV553807_P1	5167	546	83.8	globlastp
1170	LYD7 4	cacaolgb167 CA798006_P1	5168	546	83.8	globlastp
1171	LYD7 4	b_junceal10v2 E6ANDIZ01 A31EZ_P1	5169	546	83.7	globlastp
1172	LYD7 4	b_junceal10v2 E6ANDIZ01 AJQWT_P1	5170	546	83.7	globlastp
1173	LYD7 4	canolal10v1 BQ704518_P1	5171	546	83.7	globlastp
1174	LYD7 4	heritieral10v1 SRR005794S0 008009_P1	5172	546	83.7	globlastp
1175	LYD7 4	b_juncealgb164 EVGN0012 0108451580_P1	5173	546	83.7	globlastp
1176	LYD7 4	b_junceal10v2 E6ANDIZ01 A2E3P_P1	5174	546	83.7	globlastp

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1177	LYD7 4	b_juncealgb164 EVGN0014 5618710181_P1	5174	546	83.7	globlastp
1178	LYD7 4	banana 10v1 DN238032_P1	5175	546	83.7	globlastp
1179	LYD7 4	canolalgb161 BQ704518_P1	5171	546	83.7	globlastp
1180	LYD7 4	canolal 10v1 CX281752_P1	5170	546	83.7	globlastp
1181	LYD7 4	coffeal 10v1 DV667224_P1	5176	546	83.7	globlastp
1182	LYD7 4	coffealgb157.2 DV667224_P 1	5176	546	83.7	globlastp
1183	LYD7 4	grapelgb160 BM436396_P1	5177	546	83.7	globlastp
1184	LYD7 4	pigeonpealgb171 GR472607 _P1	5178	546	83.7	globlastp
1185	LYD7 4	radish gb164 EX754159_P1	5179	546	83.5	globlastp
1186	LYD7 4	arabidopsis_lyratal09v1 JGI AL018741_P1	5180	546	83.4	globlastp
1187	LYD7 4	b_junceal 10v2 E6ANDIZ01 A04A0_P1	5181	546	83.4	globlastp
1188	LYD7 4	canolal 10v1 H07415_P1	5182	546	83.4	globlastp
1189	LYD7 4	artemisial 10v1 EY036894_P 1	5183	546	83.4	globlastp
1190	LYD7 4	artemisialgb164 EY036894_ P1	5184	546	83.4	globlastp
1191	LYD7 4	b_juncealgb164 EVGN0004 9825240489_P1	5182	546	83.4	globlastp
1192	LYD7 4	b_oleracealgb161 AM38505 5_P1	5185	546	83.4	globlastp
1193	LYD7 4	b_rapalgb162 L37611_P1	5181	546	83.4	globlastp
1194	LYD7 4	canolalgb161 CB686447_P1	5182	546	83.4	globlastp
1195	LYD7 4	canolal 10v1 CX281522_P1	5181	546	83.4	globlastp
1196	LYD7 4	thellungiellalgb167 DN7727 61_P1	5186	546	83.4	globlastp
1197	LYD7 4	pigeonpeal 10v1 GW358832_ T1	5187	546	83.33	glotblastn
1198	LYD7 4	aquilegial 10v1 DR939805_P 1	5188	546	83.3	globlastp
1199	LYD7 4	b_junceal 10v2 E6ANDIZ01 A1B2W_P1	5189	546	83.3	globlastp

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1200	LYD7 4	b_juncealgb164 EVGN0001 6619570173_P1	5189	546	83.3	globlastp
1201	LYD7 4	b_oleracealgb161 CO729370 _P1	5189	546	83.3	globlastp
1202	LYD7 4	canola 10v1 CN728998_P1	5189	546	83.3	globlastp
1203	LYD7 4	canola gb161 CN728998_P1	5189	546	83.3	globlastp
1204	LYD7 4	cassava gb164 CK644716_P 1	5190	546	83.3	globlastp
1205	LYD7 4	cowpea gb166 FC458212_P 1	5191	546	83.3	globlastp
1206	LYD7 4	iceplant gb164 BE034750_P 1	5192	546	83.3	globlastp
1207	LYD7 4	eucalyptus gb166 ES588553 _P1	5193	546	83.1	globlastp
1208	LYD7 4	oak 10v1 CU657211_P1	5194	546	83	globlastp
1209	LYD7 4	oak 10v1 FP027604_P1	5194	546	83	globlastp
1210	LYD7 4	oak 10v1 FP030258_P1	5194	546	83	globlastp
1211	LYD7 4	arabidopsis 10v1 AT3G5489 0_P1	5195	546	83	globlastp
1212	LYD7 4	poplar 10v1 BI068471_P1	5196	546	83	globlastp
1213	LYD7 4	poplar gb170 BI068471_P1	5196	546	83	globlastp
1214	LYD7 4	curcuma 10v1 DY387256_P 1	5197	546	82.7	globlastp
1215	LYD7 4	nasturtium 10v1 SRR032558 S0028852_P1	5198	546	82.6	globlastp
1216	LYD7 4	oak gb170 CU657211_P1	5199	546	82.6	globlastp
1217	LYD7 4	bean gb167 CB280571_P1	5200	546	82.5	globlastp
1218	LYD7 4	liriodendron gb166 FD48979 7_P1	5201	546	82.5	globlastp
1219	LYD7 4	peanut 10v1 EC391290_P1	5202	546	82.5	globlastp
1220	LYD7 4	peanut gb171 EC391290_P1	5202	546	82.5	globlastp
1221	LYD7 4	monkeyflower 09v1 DV2077 96_P1	5203	546	82.3	globlastp
1222	LYD7 4	monkeyflower 10v1 DV2077 96_P1	5203	546	82.3	globlastp

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1223	LYD7 4	canola gb161 CX281522_P1	5204	546	82.2	globlastp
1224	LYD7 4	peanut 10v1 DT044319_P1	5205	546	82.1	globlastp
1225	LYD7 4	banana gb167 DN238553_P 1	5206	546	82.1	globlastp
1226	LYD7 4	walnut gb166 EL891496_P 1	5207	546	82.1	globlastp
1227	LYD7 4	walnut gb166 EL891497_P 1	5208	546	81.9	globlastp
1228	LYD7 4	papaya gb165 EX243398_P1	5209	546	81.5	globlastp
1229	LYD7 4	eschscholzia 10v1 CD48124 3_P1	5210	546	81.3	globlastp
1230	LYD7 4	monkeyflower 09v1 GO9754 34_P1	5211	546	81	globlastp
1231	LYD7 4	rose gb157.2 EC586509_P1	5212	546	81	globlastp
1232	LYD7 4	medicago 09v1 LLBE31698 9_P1	5213	546	80.6	globlastp
1233	LYD7 4	canola gb161 CX281752_P1	5214	546	80.5	globlastp
1234	LYD7 4	acacia 10v1 FS585491_P1	5215	546	80.2	globlastp
1235	LYD7 4	amborella gb166 CD482049 _T1	5216	546	80.08	glotblastn
1236	LYD7 5	solanum_phureja 09v1 SPH BG134552_P1	5217	547	98.5	globlastp
1237	LYD7 5	tomato 09v1 BG133027_P1	5218	547	91.1	globlastp
1238	LYD7 5	pepper gb171 BM063537_P 1	5219	547	90.5	globlastp
1239	LYD7 5	solanum_phureja 09v1 SPH BG133027_P1	5220	547	90.3	globlastp
1240	LYD7 5	potato 10v1 BF052754_P1	5221	547	89.8	globlastp
1241	LYD7 5	potato gb157.2 BF052754_P 1	5221	547	89.8	globlastp
1242	LYD7 5	tomato gb164 AI485840_P1	5222	547	89.8	globlastp
1243	LYD7 5	solanum_phureja 09v1 SPH AI485840_P1	5223	547	89.4	globlastp
1244	LYD7 5	triphysaria 10v1 DR173408_ P1	5224	547	86.2	globlastp
1245	LYD7 5	cotton gb164 AI727065_P1	5225	547	86.1	globlastp

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1246	LYD7 5	cotton 10v1 AI727065_P1	5225	547	86.1	globlastp
1247	LYD7 5	triphysarial 10v1 EY145965_ P1	5226	547	86	globlastp
1248	LYD7 5	cacaolgb167 CU473969_P1	5227	547	85.7	globlastp
1249	LYD7 5	monkeyflower 09v1 GO9604 96_P1	5228	547	85.6	globlastp
1250	LYD7 5	monkeyflower 10v1 GO9451 38_P1	5228	547	85.6	globlastp
1251	LYD7 5	cassaval09v1 DV450411_P1	5229	547	85.5	globlastp
1252	LYD7 5	catharanthus gb166 EG5541 52_T1	5230	547	85.31	glotblastn
1253	LYD7 5	monkeyflower 09v1 GO9451 38_P1	5231	547	85.3	globlastp
1254	LYD7 5	salvial 10v1 CV163176_P1	5232	547	85.1	globlastp
1255	LYD7 5	tomato 09v1 AI485840_P1	5233	547	85.1	globlastp
1256	LYD7 5	castorbean 09v1 EG665428_ P1	5234	547	85	globlastp
1257	LYD7 5	poplar gb170 BI124433_P1	5235	547	85	globlastp
1258	LYD7 5	poplar 10v1 BI124433_P1	5236	547	84.8	globlastp
1259	LYD7 5	cotton gb164 CO071822_T1	5237	547	84.42	glotblastn
1260	LYD7 5	poplar 10v1 BI070420_P1	5238	547	84.4	globlastp
1261	LYD7 5	poplar gb170 BI070420_P1	5238	547	84.4	globlastp
1262	LYD7 5	kiwilgb166 FG459967_P1	5239	547	84.3	globlastp
1263	LYD7 5	cotton 10v1 AI054730_T1	5240	547	83.97	glotblastn
1264	LYD7 5	kiwilgb166 FG397568_P1	5241	547	83.9	globlastp
1265	LYD7 5	citrus gb166 CD575199_P1	5242	547	83.8	globlastp
1266	LYD7 5	strawberry gb164 CO381295 _P1	5243	547	83.8	globlastp
1267	LYD7 5	cotton 10v1 AI726226_P1	5244	547	83.5	globlastp
1268	LYD7 5	melon 10v1 AM719548_P1	5245	547	83.5	globlastp

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1269	LYD7 5	cotton gb164 AI054730_P1	5246	547	83.5	globlastp
1270	LYD7 5	cucumber 09v1 AM718341_P1	5247	547	83.4	globlastp
1271	LYD7 5	chestnut gb170 SRR006295S0000051_P1	5248	547	83.2	globlastp
1272	LYD7 5	pigeonpea 10v1 GR464336_P1	5249	547	83	globlastp
1273	LYD7 5	oak 10v1 DN949810_P1	5250	547	82.8	globlastp
1274	LYD7 5	grape gb160 BQ792527_P1	5251	547	82.7	globlastp
1275	LYD7 5	soybean gb168 AA660206_P1	5252	547	82.7	globlastp
1276	LYD7 5	prunus 10v1 CB819938_P1	5253	547	82.4	globlastp
1277	LYD7 5	apple gb171 CN444703_P1	5254	547	82.1	globlastp
1278	LYD7 5	bean gb167 FE691109_P1	5255	547	81.6	globlastp
1279	LYD7 5	prunus gb167 CB819938_P1	5256	547	81.4	globlastp
1280	LYD7 5	peanut 10v1 ES717548_P1	5257	547	81.3	globlastp
1281	LYD7 5	peanut gb171 ES708081_P1	5258	547	81.3	globlastp
1282	LYD7 5	artemisia 10v1 EY091466_P1	5259	547	80.7	globlastp
1283	LYD7 5	medicago 09v1 AA660206_P1	5260	547	80.7	globlastp
1284	LYD7 5	b_rapa gb162 CX265583_T1	5261	547	80.6	glotblastn
1285	LYD7 5	canola gb161 CN727227_T1	5262	547	80.6	glotblastn
1286	LYD7 5	soybean gb168 AW685689_T1	5263	547	80.54	glotblastn
1287	LYD7 5	artemisia 10v1 EY108330_P1	5264	547	80.5	globlastp
1288	LYD7 5	canola 10v1 CN727227_P1	5265	547	80.4	globlastp
1289	LYD7 5	switchgrass gb167 DN146648_P1	5266	547	80.4	globlastp
1290	LYD7 5	nasturtium 10v1 SRR032558S0114794_P1	5267	547	80.3	globlastp
1291	LYD7 5	artemisia gb164 EY091466_P1	5268	547	80.3	globlastp

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1292	LYD7 5	arabidopsis_lyrata 09v1 JGI AL023205_P1	5269	547	80.2	globlastp
1293	LYD7 5	lettuce 10v1 DW114885_P1	5270	547	80.1	globlastp
1294	LYD7 5	lettuce gb157.2 DW114885_ P1	5270	547	80.1	globlastp
1295	LYD7 5	arabidopsis 10v1 AT4G1182 0_P1	5271	547	80	globlastp
1296	LYD7 5	arabidopsis gb165 AT4G118 20_P1	5271	547	80	globlastp
1297	LYD7 5	b_juncea gb164 AF148847_ P1	5272	547	80	globlastp
1298	LYD7 5	soybean gb168 AW428876_ P1	5273	547	80	globlastp
1299	LYD7 6	potato 10v1 BG887381_P1	5274	548	94.3	globlastp
1300	LYD7 6	potato gb157.2 BG887381_T 1	5275	548	93.63	glotblastn
1301	LYD7 6	solanum_phureja 09v1 SPH AI894730_P1	5276	548	93.6	globlastp
1302	LYD7 6	potato gb157.2 CN464137_P 1	5277	548	92.5	globlastp
1303	LYD7 6	tomato gb164 AW035287_P 1	5278	548	92.5	globlastp
1304	LYD7 6	solanum_phureja 09v1 SPH BG886634_P1	5279	548	91.7	globlastp
1305	LYD7 6	tomato gb164 AI894730_P1	5280	548	91.2	globlastp
1306	LYD7 6	tomato gb164 BE435253_P1	5281	548	90.6	globlastp
1307	LYD7 6	potato 10v1 BG597973_P1	5282	548	90	globlastp
1308	LYD7 6	pepper gb171 CA523398_P1	5283	548	90	globlastp
1309	LYD7 6	pepper gb171 AY284925_P1	5284	548	89.4	globlastp
1310	LYD7 6	potato gb157.2 BG597973_P 1	5285	548	89.4	globlastp
1311	LYD7 6	solanum_phureja 09v1 SPH BG886552_P1	5286	548	87.8	globlastp
1312	LYD7 6	potato 10v1 BG886634_P1	5287	548	87.3	globlastp
1313	LYD7 6	potato gb157.2 BG886634_P 1	5287	548	87.3	globlastp
1314	LYD7 6	potato gb157.2 BQ513303_P 1	5288	548	87.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
1315	LYD7 6	tomatolgb164 CD002116_P1	5289	548	87.2	globlastp
1316	LYD7 6	potatol10v1 BG886552_P1	5290	548	87.2	globlastp
1317	LYD7 6	potatolgb157.2 BG886552_T 1	5291	548	86.54	glotblastn
1318	LYD7 6	eggplantl10v1 FS003064_P1	5292	548	86.5	globlastp
1319	LYD7 6	solanum_phurejal09v1 SPH BP891733_P1	5293	548	85.9	globlastp
1320	LYD7 6	solanum_phurejal09v1 SPH CV499099_P1	5294	548	85	globlastp
1321	LYD7 6	potatolgb157.2 CV499099_P 1	5295	548	84.9	globlastp
1322	LYD7 6	tobaccolgb162 AY329046_P 1	5296	548	84.4	globlastp
1323	LYD7 6	potatolgb157.2 BF053339_T 1	5297	548	84.38	glotblastn
1324	LYD7 6	tobaccolgb162 AY329052_P 1	5298	548	83.8	globlastp
1325	LYD7 6	tobaccolgb162 EB429178_P 1	5299	548	83.1	globlastp
1326	LYD7 6	potatolgb157.2 BG098017_P 1	5300	548	82.7	globlastp
1327	LYD7 6	potatol10v1 BI406549_P1	5300	548	82.7	globlastp
1328	LYD7 6	potatolgb157.2 EG013355_P 1	5301	548	82.1	globlastp
1329	LYD7 6	solanum_phurejal09v1 SPH BI406549_P1	5302	548	82.1	globlastp
1330	LYD7 6	potatolgb157.2 BI406549_P1	5303	548	81.4	globlastp
1331	LYD7 6	triphysarial10v1 EY002368_ P1	5304	548	80.9	globlastp
1332	LYD7 6	tobaccolgb162 AY329063_P 1	5305	548	80.8	globlastp
1333	LYD7 6	monkeyflowerl09v1 GR0069 39_P1	5306	548	80.7	globlastp
1334	LYD7 6	monkeyflowerl10v1 GR0069 39_P1	5306	548	80.7	globlastp
1335	LYD7 6	monkeyflowerl10v1 CRPM G033362_P1	5307	548	80.3	globlastp
1336	LYD7 6	monkeyflowerl10v1 GR1094 76_P1	5308	548	80.1	globlastp
1337	LYD7 6	triphysarial10v1 EY020547_ P1	5309	548	80.1	globlastp

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1338	LYD7 6	cacaolgb167 CU595931_P1	5310	548	80	globlastp
1339	LYD7 6	melon 10v1 DV632570_P1	5311	548	80	globlastp
1340	LYD7 6	tobacco gb162 AF166277_P 1	5312	548	80	globlastp
1341	LYD7 8	pigeonpeal10v1 SRR054580 S0035478_P1	5313	549	92.5	globlastp
1342	LYD7 8	bean gb167 CB543362_P1	5314	549	90.2	globlastp
1343	LYD7 8	medicagol09v1 AL388558_P 1	5315	549	84	globlastp
1344	LYD7 8	lotus 09v1 BP051777_P1	5316	549	83.8	globlastp
1345	LYD7 8	cowpea gb166 FF399864_T1	5317	549	83.01	glotblastn
1346	LYD7 9	soybean gb168 AA660469_P 1	5318	550	98.4	globlastp
1347	LYD7 9	pigeonpeal10v1 SRR054580 S0042661_P1	5319	550	96.8	globlastp
1348	LYD7 9	bean gb167 CA911516_P1	5319	550	96.8	globlastp
1349	LYD7 9	cowpea gb166 FF539866_P1	5320	550	96.8	globlastp
1350	LYD7 9	liquorice gb171 FS243942_P 1	5321	550	93.7	globlastp
1351	LYD7 9	medicagol09v1 AA660469_ P1	5322	550	92.1	globlastp
1352	LYD7 9	acacia 10v1 GR481860_P1	5323	550	90.5	globlastp
1353	LYD7 9	peanut 10v1 ES705666_P1	5324	550	90.5	globlastp
1354	LYD7 9	peanut 10v1 SRR042413S00 25060_P1	5324	550	90.5	globlastp
1355	LYD7 9	peanut gb171 ES705666_P1	5324	550	90.5	globlastp
1356	LYD7 9	cassava 09v1 DV454356_P1	5325	550	85.7	globlastp
1357	LYD7 9	cassava gb164 DV454356_P 1	5325	550	85.7	globlastp
1358	LYD7 9	citrus gb166 CB610995_P1	5326	550	85.7	globlastp
1359	LYD7 9	poplar 10v1 BU897706_P1	5327	550	82.5	globlastp
1360	LYD7 9	poplar gb170 BU897706_P1	5327	550	82.5	globlastp

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1361	LYD7 9	lotus 09v1 BW596764_P1	5328	550	81.5	globlastp
1362	LYD7 9	coffealgb157.2 DV693211_T 1	5329	550	81.25	glotblastn
1363	LYD7 9	coffeal10v1 DV693211_P1	5330	550	81.2	globlastp
1364	LYD7 9	orobanche 10v1 SRR023189 S0007343_P1	5331	550	81	globlastp
1365	LYD7 9	grape gb160 BQ792370_P1	5332	550	81	globlastp
1366	LYD7 9	prunus gb167 AJ823531_P1	5333	550	81	globlastp
1367	LYD7 9	prunus gb167 FC864840_P1	5333	550	81	globlastp
1368	LYD7 9	oak 10v1 FP038176_T1	5334	550	80.95	glotblastn
1369	LYD7 9	chestnut gb170 SRR006295S 0047496_T1	5334	550	80.95	glotblastn
1370	LYD8 0	arabidopsis_lyrata 09v1 JGI AL002319_T1	5335	551	95.44	glotblastn
1371	LYD8 0	canola 10v1 EE449185_P1	5336	551	85.7	globlastp
1372	LYD8 0	canola gb161 EL590482_P1	5337	551	82.4	globlastp
1373	LYD8 1	peanut 10v1 ES721579_T1	5338	552	80.87	glotblastn
1374	LYD8 4	arabidopsis_lyrata 09v1 JGI AL021222_P1	5339	554	95.3	globlastp
1375	LYD8 5	arabidopsis_lyrata 09v1 JGI AL025065_P1	5340	555	97	globlastp
1376	LYD8 5	canola 10v1 CD818889_P1	5341	555	94	globlastp
1377	LYD8 5	canola 10v1 CD821386_P1	5342	555	94	globlastp
1378	LYD8 5	canola gb161 CD821386_P1	5342	555	94	globlastp
1379	LYD8 5	b_oleracealgb161 DY019746 _P1	5343	555	92.5	globlastp
1380	LYD8 5	canola 10v1 EE451644_P1	5344	555	92.5	globlastp
1381	LYD8 5	canola gb161 CD818889_P1	5344	555	92.5	globlastp
1382	LYD8 5	canola 10v1 EV007961_P1	5345	555	92.5	globlastp
1383	LYD8 5	canola gb161 EV007961_P1	5345	555	92.5	globlastp

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1384	LYD8 5	radish gb164 FD935048_T1	5346	555	91.04	glotblastn
1385	LYD8 5	b_rapa gb162 EX069163_P1	5347	555	91	globlastp
1386	LYD8 5	radish gb164 EV538503_P1	5347	555	91	globlastp
1387	LYD8 5	cleome_gynandra 10v1 SRR 015532S0082161_P1	5348	555	80.6	globlastp
1388	LYD8 6	thellungiella gb167 BY8305 02_P1	5349	556	98	globlastp
1389	LYD8 6	thellungiella gb167 DN7740 53_P1	5350	556	98	globlastp
1390	LYD8 6	b_junceal 10v2 E6ANDIZ01 AGKLO_P1	5351	556	96.1	globlastp
1391	LYD8 6	b_junceal 10v2 E6ANDIZ01 C9M4I_P1	5351	556	96.1	globlastp
1392	LYD8 6	b_junceal 10v2 E6ANDIZ01 EOWBA_P1	5351	556	96.1	globlastp
1393	LYD8 6	b_junceal 10v2 E6ANDIZ02 FW8ZO_P1	5351	556	96.1	globlastp
1394	LYD8 6	canola 10v1 CD818375_P1	5351	556	96.1	globlastp
1395	LYD8 6	canola 10v1 CN725716_P1	5351	556	96.1	globlastp
1396	LYD8 6	b_junceal gb164 EVGN0045 9709681320_P1	5351	556	96.1	globlastp
1397	LYD8 6	b_oleraceal gb161 AM05760 9_P1	5351	556	96.1	globlastp
1398	LYD8 6	b_rapa gb162 DY010357_P1	5351	556	96.1	globlastp
1399	LYD8 6	canola 10v1 CD817105_P1	5351	556	96.1	globlastp
1400	LYD8 6	canola gb161 CD817105_P1	5351	556	96.1	globlastp
1401	LYD8 6	canola gb161 CD818375_P1	5351	556	96.1	globlastp
1402	LYD8 6	canola 10v1 CN730342_P1	5351	556	96.1	globlastp
1403	LYD8 6	canola gb161 CN730342_P1	5351	556	96.1	globlastp
1404	LYD8 6	radish gb164 EV568513_P1	5351	556	96.1	globlastp
1405	LYD8 6	radish gb164 EV570136_P1	5351	556	96.1	globlastp
1406	LYD8 6	b_oleraceal gb161 EE534616 _T1	5352	556	96.08	glotblastn

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1407	LYD8 6	canola gb161 CN725716_T1	5353	556	96.08	glotblastn
1408	LYD8 6	arabidopsis_lyrata 09v1 BQ8 34513_P1	5354	556	94.2	globlastp
1409	LYD8 6	sunflower 10v1 AJ318305_P 1	5355	556	94.1	globlastp
1410	LYD8 6	sunflower 10v1 SFSLX0015 3819D2_P1	5355	556	94.1	globlastp
1411	LYD8 6	radish gb164 FD542635_P1	5356	556	94.1	globlastp
1412	LYD8 6	artemisia 10v1 SRR019547S 0037450_P1	5357	556	92.2	globlastp
1413	LYD8 6	cleome_gynandra 10v1 SRR 015532S0003909_P1	5358	556	92.2	globlastp
1414	LYD8 6	cleome_spinosa 10v1 SRR01 5531S0004445_P1	5359	556	92.2	globlastp
1415	LYD8 6	heritiera 10v1 SRR005795S0 007963_P1	5360	556	92.2	globlastp
1416	LYD8 6	nasturtium 10v1 SRR032558 S0118083_P1	5361	556	92.2	globlastp
1417	LYD8 6	artemisia 10v1 EX980187_P 1	5357	556	92.2	globlastp
1418	LYD8 6	artemisia gb164 EX980187_ P1	5357	556	92.2	globlastp
1419	LYD8 6	caca gb167 CU501402_P1	5360	556	92.2	globlastp
1420	LYD8 6	cotton gb164 BE053773_P1	5360	556	92.2	globlastp
1421	LYD8 6	cotton gb164 CO120014_P1	5360	556	92.2	globlastp
1422	LYD8 6	gerbera 09v1 AJ762308_P1	5357	556	92.2	globlastp
1423	LYD8 6	gerbera 09v1 AJ762481_P1	5357	556	92.2	globlastp
1424	LYD8 6	lettuce 10v1 DW045900_P1	5357	556	92.2	globlastp
1425	LYD8 6	lettuce gb157.2 DW045900_ P1	5357	556	92.2	globlastp
1426	LYD8 6	lettuce 10v1 DW077419_P1	5362	556	92.2	globlastp
1427	LYD8 6	lettuce gb157.2 DW077419_ P1	5362	556	92.2	globlastp
1428	LYD8 6	lettuce 10v1 DW084501_P1	5357	556	92.2	globlastp
1429	LYD8 6	lettuce gb157.2 DW084501_ P1	5357	556	92.2	globlastp

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1430	LYD8 6	lettuce 10v1 DW146736_P1	5357	556	92.2	globlastp
1431	LYD8 6	safflower gb162 EL511108_ P1	5357	556	92.2	globlastp
1432	LYD8 6	cotton 10v1 BE053773_P1	5360	556	92.2	globlastp
1433	LYD8 6	cleome_gynandra 10v1 SRR 015532S0086075_T1	5363	556	90.2	glotblastn
1434	LYD8 6	cleome_spinosa 10v1 SRR01 5531S0019603_P1	5364	556	90.2	globlastp
1435	LYD8 6	cyamopsis 10v1 EG983537_ P1	5365	556	90.2	globlastp
1436	LYD8 6	dandelion 10v1 GO663055_ P1	5366	556	90.2	globlastp
1437	LYD8 6	ginseng 10v1 GR874677_P1	5365	556	90.2	globlastp
1438	LYD8 6	orobanche 10v1 SRR023189 S0000905_P1	5365	556	90.2	globlastp
1439	LYD8 6	orobanche 10v1 SRR023189 S0034846_P1	5365	556	90.2	globlastp
1440	LYD8 6	beet gb162 EG550343_P1	5365	556	90.2	globlastp
1441	LYD8 6	canola gb161 EV056789_P1	5367	556	90.2	globlastp
1442	LYD8 6	catharanthus gb166 FD4152 78_T1	5368	556	90.2	glotblastn
1443	LYD8 6	centaurea gb166 EH747270_ P1	5369	556	90.2	globlastp
1444	LYD8 6	coffea 10v1 DV689480_P1	5365	556	90.2	globlastp
1445	LYD8 6	coffea gb157.2 DV689480_P 1	5365	556	90.2	globlastp
1446	LYD8 6	cotton gb164 BF275857_P1	5370	556	90.2	globlastp
1447	LYD8 6	cynara gb167 GE588082_P1	5371	556	90.2	globlastp
1448	LYD8 6	grape gb160 BM436961_P1	5365	556	90.2	globlastp
1449	LYD8 6	grape gb160 CB005160_P1	5365	556	90.2	globlastp
1450	LYD8 6	iceplant gb164 BE130459_T 1	5372	556	90.2	glotblastn
1451	LYD8 6	kiwi gb166 FG438126_P1	5365	556	90.2	globlastp
1452	LYD8 6	monkeyflower 09v1 DV2063 92_P1	5373	556	90.2	globlastp

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1453	LYD8 6	petunialgb171 CV294446_T 1	5374	556	90.2	glotblastn
1454	LYD8 6	brachypodiuml09v1 DV4776 56_P1	5375	556	88.5	globlastp
1455	LYD8 6	oatl10v2 CN816027_P1	5376	556	88.5	globlastp
1456	LYD8 6	banana10v1 DN238995_P1	5377	556	88.5	globlastp
1457	LYD8 6	bananalgb167 DN238995_P 1	5377	556	88.5	globlastp
1458	LYD8 6	brachypodiumlgb169 DV477 656_P1	5375	556	88.5	globlastp
1459	LYD8 6	cowpealgb166 FC458602_T 1	5378	556	88.24	glotblastn
1460	LYD8 6	ipomoealgb157.2 EE876485 _T1	5379	556	88.24	glotblastn
1461	LYD8 6	melonlgb165 AM713586_T1	5380	556	88.24	glotblastn
1462	LYD8 6	oil_palm gb166 EL693216_ T1	5381	556	88.24	glotblastn
1463	LYD8 6	petunialgb171 DC240311_T 1	-	556	88.24	glotblastn
1464	LYD8 6	cassaval09v1 DB935598_P1	5382	556	88.2	globlastp
1465	LYD8 6	cucumberl09v1 AM713586_ P1	5383	556	88.2	globlastp
1466	LYD8 6	eschscholzial10v1 SRR0141 16S0008646_P1	5383	556	88.2	globlastp
1467	LYD8 6	flaxl09v1 EH791278_P1	5384	556	88.2	globlastp
1468	LYD8 6	ipomoea_batatasl10v1 EE87 6485_P1	5385	556	88.2	globlastp
1469	LYD8 6	melonl10v1 AM713586_P1	5383	556	88.2	globlastp
1470	LYD8 6	nasturtiuml10v1 GH170854_ P1	5386	556	88.2	globlastp
1471	LYD8 6	pigeonpeal10v1 GW352442_ P1	5382	556	88.2	globlastp
1472	LYD8 6	salvial10v1 SRR014553S000 3727_P1	5387	556	88.2	globlastp
1473	LYD8 6	basilicuml10v1 DY322542_ P1	5388	556	88.2	globlastp
1474	LYD8 6	beanlgb167 CA902205_P1	5382	556	88.2	globlastp
1475	LYD8 6	beechlgb170 SRR006293S00 04143_P1	5389	556	88.2	globlastp

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1476	LYD8 6	bruguieralgb166 BP938976_ P1	5382	556	88.2	globlastp
1477	LYD8 6	castorbean 09v1 XM002527 470_P1	5383	556	88.2	globlastp
1478	LYD8 6	cichoriumlgb171 EH707102 _P1	5390	556	88.2	globlastp
1479	LYD8 6	citruslgb166 BE205724_P1	5382	556	88.2	globlastp
1480	LYD8 6	liquoricelgb171 FS240673_P 1	5382	556	88.2	globlastp
1481	LYD8 6	liquoricelgb171 FS244039_P 1	5382	556	88.2	globlastp
1482	LYD8 6	liriodendronlgb166 FD49028 2_P1	5391	556	88.2	globlastp
1483	LYD8 6	lotus 09v1 LLBU494472_P1	5382	556	88.2	globlastp
1484	LYD8 6	medicagol09v1 LLCX53191 4_P1	5392	556	88.2	globlastp
1485	LYD8 6	poplar 10v1 BU809765_P1	5382	556	88.2	globlastp
1486	LYD8 6	poplarlgb170 BU809765_P1	5382	556	88.2	globlastp
1487	LYD8 6	soybeanlgb168 BU494472_P 1	5382	556	88.2	globlastp
1488	LYD8 6	soybeanlgb168 CA851270_P 1	5382	556	88.2	globlastp
1489	LYD8 6	walnutslgb166 CB303734_P 1	5382	556	88.2	globlastp
1490	LYD8 6	medicagol09v1 BE316988_P 1	5392	556	88.2	globlastp
1491	LYD8 6	cryptomeria lgb166 BW9947 02_P1	5393	556	86.8	globlastp
1492	LYD8 6	wheatlgb164 BE414948_T1	5394	556	86.54	glotblastn
1493	LYD8 6	wheatlgb164 CA625348_T1	5395	556	86.54	glotblastn
1494	LYD8 6	wheatlgb164 CD894479_T1	5396	556	86.54	glotblastn
1495	LYD8 6	barley 10v1 BG299304_P1	5397	556	86.5	globlastp
1496	LYD8 6	barley 10v1 BG414327_P1	5397	556	86.5	globlastp
1497	LYD8 6	eggplant 10v1 FS019985_P1	5398	556	86.5	globlastp
1498	LYD8 6	millet 10v1 EVO454PM061 746_P1	5399	556	86.5	globlastp

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1499	LYD8 6	maize 10v1 AI372144_P1	5399	556	86.5	globlastp
1500	LYD8 6	maize gb170 AI372144_P1	5399	556	86.5	globlastp
1501	LYD8 6	nuphar gb166 CO997227_P1	5400	556	86.5	globlastp
1502	LYD8 6	pepper gb171 GD067147_P1	5398	556	86.5	globlastp
1503	LYD8 6	potato gb157.2 BG590800_P 1	5398	556	86.5	globlastp
1504	LYD8 6	potato gb157.2 CN515437_P 1	5398	556	86.5	globlastp
1505	LYD8 6	rice gb170 OS01G34614_P1	5399	556	86.5	globlastp
1506	LYD8 6	solanum_phureja 09v1 SPH BG627534_P1	5398	556	86.5	globlastp
1507	LYD8 6	sorghum 09v1 SB02G01066 0_P1	5399	556	86.5	globlastp
1508	LYD8 6	sorghum 09v1 SB07G00543 5_P1	5399	556	86.5	globlastp
1509	LYD8 6	sugarcane 10v1 CA072079_ P1	5399	556	86.5	globlastp
1510	LYD8 6	sugarcane gb157.3 CA07207 9_P1	5399	556	86.5	globlastp
1511	LYD8 6	sugarcane 10v1 CA090932_ P1	5399	556	86.5	globlastp
1512	LYD8 6	sugarcane gb157.3 CA09093 2_P1	5399	556	86.5	globlastp
1513	LYD8 6	switchgrass gb167 DN14723 5_P1	5399	556	86.5	globlastp
1514	LYD8 6	switchgrass gb167 FL72581 8_P1	5399	556	86.5	globlastp
1515	LYD8 6	switchgrass gb167 FL73449 2_P1	5399	556	86.5	globlastp
1516	LYD8 6	tobacco gb162 CV019381_P 1	5398	556	86.5	globlastp
1517	LYD8 6	tomato 09v1 BG627534_P1	5398	556	86.5	globlastp
1518	LYD8 6	tomato gb164 BG627534_P1	5398	556	86.5	globlastp
1519	LYD8 6	wheat gb164 BE401020_P1	5397	556	86.5	globlastp
1520	LYD8 6	wheat gb164 BE402150_P1	5397	556	86.5	globlastp
1521	LYD8 6	wheat gb164 CA634446_P1	5397	556	86.5	globlastp

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1522	LYD8 6	potatol10v1 BG590800_P1	5398	556	86.5	globlastp
1523	LYD8 6	ipomoea_nill10v1 CJ745906_P1	5401	556	86.3	globlastp
1523	LYD8 6	ipomoealgb157.2 CJ745906_T1	5408	556	86.27	glotblastn
1524	LYD8 6	oakl10v1 FP042379_P1	5402	556	86.3	globlastp
1525	LYD8 6	oakl10v1 FP042823_P1	5402	556	86.3	globlastp
1526	LYD8 6	oakl10v1 FP044622_P1	5402	556	86.3	globlastp
1527	LYD8 6	triphysarial10v1 SRR023500 S0014025_P1	5403	556	86.3	globlastp
1528	LYD8 6	triphysarial10v1 SRR023500 S0018952_P1	5403	556	86.3	globlastp
1529	LYD8 6	basilicum gb157.3 DY32254 2_P1	5404	556	86.3	globlastp
1530	LYD8 6	bruguieralgb166 BP949765_P1	5405	556	86.3	globlastp
1531	LYD8 6	chestnut gb170 SRR006295S 0023708_P1	5402	556	86.3	globlastp
1532	LYD8 6	chestnut gb170 SRR006295S 0041620_P1	5402	556	86.3	globlastp
1533	LYD8 6	oak gb170 DN949877_P1	5402	556	86.3	globlastp
1534	LYD8 6	peanut gb171 EE123506_P1	5406	556	86.3	globlastp
1535	LYD8 6	peal09v1 CD860415_P1	5407	556	86.3	globlastp
1536	LYD8 6	spurgelgb161 DV154503_T1	5409	556	86.27	glotblastn
1537	LYD8 6	cryptomeria gb166 BW9962 32_T1	5410	556	84.91	glotblastn
1538	LYD8 6	spruce gb162 CO218164_T1	5411	556	84.91	glotblastn
1539	LYD8 6	zamialgb166 DY033916_T1	5412	556	84.91	glotblastn
1540	LYD8 6	pinel10v1 AW056457_P1	5413	556	84.9	globlastp
1541	LYD8 6	pinelgb157.2 AW056457_P1	5413	556	84.9	globlastp
1542	LYD8 6	cynodon 10v1 ES300626_P1	5414	556	84.6	globlastp
1543	LYD8 6	amborella gb166 FD435944_P1	5415	556	84.6	globlastp

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1544	LYD8 6	peanut 10v1 ES710826_T1	5416	556	84.31	glotblastn
1545	LYD8 6	peanut 10v1 GO341045_T1	5417	556	84.31	glotblastn
1546	LYD8 6	eucalyptus gb166 CB967699 _T1	5418	556	84.31	glotblastn
1547	LYD8 6	peanut 10v1 EE123506_T1	5419	556	84.31	glotblastn
1548	LYD8 6	pine 10v1 AA740051_P1	5420	556	83	globlastp
1549	LYD8 6	pine gb157.2 AA740051_P1	5420	556	83	globlastp
1550	LYD8 6	spruce gb162 CO216054_P1	5420	556	83	globlastp
1551	LYD8 6	sunflower gb162 AJ318305_ P1	5421	556	82.8	globlastp
1552	LYD8 6	millet 10v1 EVO454PM026 113_P1	5422	556	82.7	globlastp
1553	LYD8 6	poppy gb166 FE968146_P1	5423	556	82.7	globlastp
1554	LYD8 6	prunus 10v1 CV044517_P1	5424	556	82.4	globlastp
1555	LYD8 6	poppy gb166 FE966049_P1	5425	556	82.4	globlastp
1556	LYD8 6	prunus 10v1 CB818579_P1	5424	556	82.4	globlastp
1557	LYD8 6	prunus gb167 CB818579_P1	5424	556	82.4	globlastp
1558	LYD8 6	prunus gb167 CB820508_P1	5424	556	82.4	globlastp
1559	LYD8 6	prunus gb167 CV044517_P1	5424	556	82.4	globlastp
1560	LYD8 6	radish gb164 EY904176_P1	5426	556	82.4	globlastp
1561	LYD8 6	lovegrass gb167 EH194086_ T1	5427	556	82.35	glotblastn
1562	LYD8 6	monkeyflower 10v1 DV2063 92_T1	5428	556	82.35	glotblastn
1563	LYD8 6	solanum_phureja 09v1 SPH DN980135_T1	5429	556	82.35	glotblastn
1564	LYD8 6	peanut 10v1 SRR042421S00 83859_T1	-	556	82.35	glotblastn
1565	LYD8 6	marchantia gb166 BJ851604 _P1	5430	556	81.8	globlastp
1566	LYD8 6	physcomitrella 10v1 BJ1856 20_P1	5431	556	80.8	globlastp

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1567	LYD8 6	applelgb171 CN490502_P1	5432	556	80.8	globlastp
1568	LYD8 6	gingerlgb164 DY360661_P1	5433	556	80.8	globlastp
1569	LYD8 6	switchgrasslgb167 DN15117 0_T1	-	556	80.77	glotblastn
1570	LYD8 6	fernlgb171 BP917328_T1	5434	556	80.39	glotblastn
1571	LYD8 6	fernlgb171 DK945205_T1	5434	556	80.39	glotblastn
1572	LYD8 6	lettucel10v1 DW146230_T1	5435	556	80.39	glotblastn
1573	LYD8 6	lettucelgb157.2 DW146230_ T1	5435	556	80.39	glotblastn
1574	LYD8 6	orobanche10v1 SRR023497 S0014234_T1	-	556	80.39	glotblastn
1575	LYD8 7	potatolgb157.2 BQ504596_T 1	5436	557	94.44	glotblastn
1576	LYD8 7	potatol10v1 CV505175_T1	-	557	93.06	glotblastn
1577	LYD8 7	eggplantl10v1 FS004333_P1	5437	557	88.7	globlastp
1578	LYD8 7	potatol10v1 BQ504596_T1	-	557	87.5	glotblastn
1579	LYD8 7	solanum_phurejal09v1 SPH AW930554_P1	5438	557	83.1	globlastp
1580	LYD8 7	solanum_phurejal09v1 SPH AW930554_T1	-	557	80.56	glotblastn
1581	LYD8 8	arabidopsis_lyratal09v1 JGI AL007072_P1	5439	558	97.9	globlastp
1582	LYD8 8	arabidopsis_lyratal09v1 JGI AL002750_P1	5440	558	80.7	globlastp
1583	LYD8 8	arabidopsislgb165 AT1G261 30_P1	5441	558	80.7	globlastp
1584	LYD8 9	arabidopsisl10v1 AT1G6805 0_T1	695	559	81.16	glotblastn
1585	LYD9 0	arabidopsis_lyratal09v1 JGI AL001987_P1	5442	560	92.5	globlastp
1586	LYD9 1	potatol10v1 CN215887_P1	5443	561	94.1	globlastp
1587	LYD9 1	potatolgb157.2 CN215887_P 1	5443	561	94.1	globlastp
1588	LYD9 1	solanum_phurejal09v1 SPH BG643473_P1	5443	561	94.1	globlastp
1589	LYD9 1	eggplantl10v1 FS027048_P1	5444	561	85.8	globlastp

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1590	LYD9 2	arabidopsis_lyratal09v1 JGI AL002019_P1	5445	562	91.3	globlastp
1591	LYD9 2	radish gb164 EX746761_P1	5446	562	81.7	globlastp
1592	LYD9 4	arabidopsis_lyratal09v1 JGI AL004398_P1	5447	563	90.9	globlastp
1593	LYD9 5	arabidopsis_lyratal09v1 JGI AL006360_P1	5448	564	94.8	globlastp
1594	LYD9 5	thellungiella gb167 BY8060 85_P1	5449	564	85.3	globlastp
1595	LYD9 5	canola 10v1 EE555701_P1	5450	564	80.2	globlastp
1596	LYD9 5	b_rapa gb162 DY010324_P1	5451	564	80.2	globlastp
1597	LYD9 5	radish gb164 EV547048_P1	5452	564	80.2	globlastp
1598	LYD9 6	arabidopsis_lyratal09v1 JGI AL007972_P1	5453	565	91.1	globlastp
1599	LYD9 7	b_junceal10v2 E6ANDIZ01 AHC UW_T1	5454	566	83.87	glotblastn
1600	LYD9 7	b_junceal10v2 E6ANDIZ01 DGCSI_T1	5454	566	83.87	glotblastn
1601	LYD9 7	cleome_gynandra 10v1 SRR 015532S0011847_T1	5455	566	83.87	glotblastn
1602	LYD9 7	cleome_spinosa 10v1 SRR01 5531S0012286_T1	5456	566	83.87	glotblastn
1603	LYD9 7	prunus 10v1 CN444116_T1	5457	566	83.87	glotblastn
1604	LYD9 7	b_rapa gb162 EE527302_T1	5458	566	83.87	glotblastn
1605	LYD9 7	chestnut gb170 SRR006295S 0004400_T1	5459	566	83.87	glotblastn
1606	LYD9 7	citrus gb166 CF509977_T1	5460	566	83.87	glotblastn
1607	LYD9 7	arabidopsis_lyratal09v1 JGI AL016247_P1	5461	566	83.6	globlastp
1608	LYD9 7	artemisia 10v1 SRR019552S 0293476_T1	5462	566	82.26	glotblastn
1609	LYD9 7	b_junceal10v2 BJ1SLX0005 2468D2_T1	5463	566	82.26	glotblastn
1610	LYD9 7	canola 10v1 CD812513_T1	5463	566	82.26	glotblastn
1611	LYD9 7	canola 10v1 CD813050_T1	5464	566	82.26	glotblastn
1612	LYD9 7	oak 10v1 DN950354_T1	5465	566	82.26	glotblastn

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1613	LYD9 7	oak 10v1 FP044338_T1	5465	566	82.26	glotblastn
1614	LYD9 7	b_juncealgb164 EVGN0059 9610960902_T1	5466	566	82.26	glotblastn
1615	LYD9 7	b_juncealgb164 EVGN0082 0308641772_T1	5467	566	82.26	glotblastn
1616	LYD9 7	b_junceal10v2 E6ANDIZ01 A4PGS_T1	5463	566	82.26	glotblastn
1617	LYD9 7	b_juncealgb164 EVGN0087 1713963261_T1	5463	566	82.26	glotblastn
1618	LYD9 7	b_oleracealgb161 ES949849 _T1	5464	566	82.26	glotblastn
1619	LYD9 7	b_rapalgb162 EE517284_T1	5463	566	82.26	glotblastn
1620	LYD9 7	canolalgb161 CD812513_T1	5463	566	82.26	glotblastn
1621	LYD9 7	canolalgb161 CD813050_T1	5464	566	82.26	glotblastn
1622	LYD9 7	canolalgb161 CN736915_T1	5463	566	82.26	glotblastn
1623	LYD9 7	oak gb170 DN950354_T1	5465	566	82.26	glotblastn
1624	LYD9 7	radish gb164 EW714476_T1	5468	566	82.26	glotblastn
1625	LYD9 7	spurge gb161 DV139037_T1	5469	566	82.26	glotblastn
1626	LYD9 7	canola 10v1 CN736915_T1	5463	566	82.26	glotblastn
1627	LYD9 7	b_oleracealgb161 AM05718 4_T1	5470	566	82.26	glotblastn
1628	LYD9 7	canola 10v1 CD811653_T1	5470	566	82.26	glotblastn
1629	LYD9 7	canolalgb161 CD811653_T1	5470	566	82.26	glotblastn
1630	LYD9 7	canola 10v1 CD838423_T1	5470	566	82.26	glotblastn
1631	LYD9 7	canolalgb161 CD838423_T1	5470	566	82.26	glotblastn
1632	LYD9 7	acacial10v1 FS588284_T1	5471	566	80.65	glotblastn
1633	LYD9 7	arabidopsis_lyratal09v1 BQ8 34172_T1	5472	566	80.65	glotblastn
1634	LYD9 7	b_junceal10v2 E6ANDIZ01 A3GHB_T1	5473	566	80.65	glotblastn
1635	LYD9 7	b_junceal10v2 E6ANDIZ01 AT806_T1	5474	566	80.65	glotblastn

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1636	LYD9 7	b_junceal10v2IE6ANDIZ01 CWXC3_T1	5475	566	80.65	glotblastn
1637	LYD9 7	melonl10v1IAM723468_T1	5476	566	80.65	glotblastn
1638	LYD9 7	nasturtiuml10v1ISRR032558 S0093244_T1	5477	566	80.65	glotblastn
1639	LYD9 7	avocadol10v1IFD505830_T1	5478	566	80.65	glotblastn
1640	LYD9 7	avocadolgb164IFD505830_T 1	5478	566	80.65	glotblastn
1641	LYD9 7	cacaolgb167ICU469972_T1	5479	566	80.65	glotblastn
1642	LYD9 7	nupharlgb166ICD474040_T1	5480	566	80.65	glotblastn
1643	LYD9 7	poplarlgb170IBI123662_T1	5481	566	80.65	glotblastn
1644	LYD9 7	radishlgb164IEV535996_T1	5482	566	80.65	glotblastn
1645	LYD9 7	radishlgb164IEX762610_T1	5483	566	80.65	glotblastn
1646	LYD9 7	radishlgb164IEX889839_T1	5472	566	80.65	glotblastn
1647	LYD9 7	teal10v1IGE651392_T1	5484	566	80.65	glotblastn
1648	LYD9 7	tealgb171IGE651392_T1	5484	566	80.65	glotblastn
1649	LYD9 7	b_junceal10v2IBJ1SLX0044 6286D1_P1	5485	566	80.6	globlastp
1650	LYD9 9	arabidopsis_lyratal09v1JGI AL016742_P1	5486	567	93.7	globlastp
1651	LYD9 9	canolal10v1ICD824755_P1	5487	567	84.3	globlastp
1652	LYD9 9	canolalgb161ICD824755_T1	5488	567	83.98	glotblastn
1653	LYD1 01	arabidopsis_lyratal09v1JGI AL026794_T1	5489	568	94.94	glotblastn
1654	LYD1 01	thellungiellalgb167IBY8185 27_P1	5490	568	84.8	globlastp
1655	LYD1 01	canolalgb161ICD814430_T1	5491	568	84.13	glotblastn
1656	LYD1 01	radishlgb164IEX754941_T1	5492	568	82.97	glotblastn
1657	LYD1 01	canolalgb161ICN733694_P1	5493	568	82.9	globlastp
1658	LYD1 01	canolal10v1IDY006642_P1	5494	568	82.9	globlastp

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1659	LYD1 01	b_rapalgb162 EE520760_P1	5495	568	81.7	globlastp
1660	LYD1 02	arabidopsis_lyratal09v1 JGI AL025624_T1	5496	569	95.3	glotblastn
1661	LYD1 03	arabidopsis 10v1 AT5G0504 0_P1	5497	570	94.8	globlastp
1662	LYD1 04	arabidopsis_lyratal09v1 JGI AL021995_P1	5498	571	85.8	globlastp
1663	LYD1 05	canola 10v1 ES900634_P1	5499	572	89	globlastp
1664	LYD1 05	canola gb161 ES900634_P1	5499	572	89	globlastp
1665	LYD1 05	radish gb164 EX770229_T1	5500	572	88.67	glotblastn
1666	LYD1 05	prunus 10v1 DY255399_P1	5501	572	80.6	globlastp
1667	LYD1 05	poplar 10v1 BU896271_T1	5502	572	80.51	glotblastn
1668	LYD1 05	poplar gb170 BU896271_T1	5502	572	80.51	glotblastn
1669	LYD1 05	castorbean 09v1 XM002521 435_P1	5503	572	80.2	globlastp
1670	LYD1 05	poplar 10v1 CB240481_T1	5504	572	80.17	glotblastn
1671	LYD1 05	poplar gb170 CB240481_T1	5504	572	80.17	glotblastn
1672	LYD1 07	arabidopsis_lyratal09v1 JGI AL030915_P1	5505	574	95.3	globlastp
1673	LYD1 08	arabidopsis 10v1 AT1G6926 0_P1	5506	575	80.4	globlastp
1674	LYD1 08	arabidopsis_lyratal09v1 JGI AL007132_T1	5507	575	80.39	glotblastn
1675	LYD1 09	canola 10v1 CX191086_P1	5508	576	98.1	globlastp
1676	LYD1 09	b_rapalgb162 CV545543_P1	5509	576	98.1	globlastp
1677	LYD1 09	canola gb161 CD827969_P1	5510	576	94.2	globlastp
1678	LYD1 09	cotton 10v1 CO090506_P1	5511	576	81.7	globlastp
1679	LYD1 09	sunflower gb162 DY905124 _P1	5512	576	81.2	globlastp
1680	LYD1 09	centaurea gb166 EH713977_ T1	5513	576	81.16	glotblastn
1681	LYD1 09	artemisia gb164 EY095004_ P1	5514	576	81	globlastp

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1682	LYD1 09	cassava 09v1 DV454624_P1	5515	576	80.8	globlastp
1683	LYD1 09	cotton gb164 CO090506_P1	5516	576	80.7	globlastp
1684	LYD1 09	cynara gb167 GE577297_T1	5517	576	80.51	glotblastn
1685	LYD1 09	artemisia 10v1 EY095004_P 1	5518	576	80.4	globlastp
1686	LYD1 09	sunflower 10v1 DY905124_ T1	5519	576	80.17	glotblastn
1687	LYD1 09	cichorium gb171 EH674636 _P1	5520	576	80	globlastp
1688	LYD1 10	arabidopsis_lyrata 09v1 JGI AL020149_P1	5521	577	93.1	globlastp
1689	LYD1 10	arabidopsis gb165 AT5G049 50_P1	5522	577	93.1	globlastp
1690	LYD1 10	arabidopsis 10v1 AT5G0495 0_P1	5522	577	93.1	globlastp
1691	LYD1 13	arabidopsis_lyrata 09v1 JGI AL025749_P1	5523	578	80.7	globlastp
1692	LYD1 13	arabidopsis 10v1 AT4G2360 0_P1	5524	578	80.4	globlastp
1693	LYD1 13	arabidopsis gb165 AT4G236 00_P1	5524	578	80.4	globlastp
1694	LYD1 17	canola gb161 ES899985_T1	5525	580	98.33	glotblastn
1695	LYD1 17	canola 10v1 ES899985_P1	5526	580	98.3	globlastp
1696	LYD1 17	b_juncea gb164 EVGN0085 3408702074_P1	5527	580	96.7	globlastp
1697	LYD1 17	arabidopsis_lyrata 09v1 JGI AL010445_P1	5528	580	85	globlastp
1698	LYD1 17	arabidopsis 10v1 AT3G1903 0_P1	5529	580	85	globlastp
1699	LYD1 17	arabidopsis gb165 AT3G190 30_P1	5529	580	85	globlastp
1700	LYD1 17	canola 10v1 DV643336_P1	5530	580	85	globlastp
1701	LYD1 17	canola gb161 DV643336_T1	5531	580	85	glotblastn
1702	LYD1 17	thellungiella gb167 BY8306 57_P1	5532	580	85	globlastp
1703	LYD1 17	b_juncea gb164 DT317662_ T1	5533	580	83.33	glotblastn
1704	LYD1 17	b_juncea 10v2 DT317662_P 1	5534	580	83.3	globlastp

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1705	LYD1 17	b_rapalgb162 DN960553_T1	5535	580	81.67	glotblastn
1706	LYD1 17	b_rapalgb162 EX140655_P1	5536	580	80	globlastp
1707	LYD1 17	radishlgb164 EV529011_P1	5537	580	80	globlastp
1708	LYD1 18	canolalgb161 CD817267_P1	5538	581	95.2	globlastp
1709	LYD1 18	canolal10v1 CD817267_T1	5539	581	93.98	glotblastn
1710	LYD1 20	canolal10v1 AI352738_P1	5540	583	96.7	globlastp
1711	LYD1 20	b_rapalgb162 CV523156_P1	5541	583	94.6	globlastp
1712	LYD1 20	canolalgb161 AI352738_P1	5542	583	91.6	globlastp
1713	LYD1 20	radishlgb164 EW722416_P1	5543	583	85.2	globlastp
1714	LYD1 22	canolal10v1 CD823303_P1	5544	584	97.8	globlastp
1715	LYD1 22	b_rapalgb162 CX268424_P1	5545	584	97.8	globlastp
1716	LYD1 22	canolalgb161 CD833389_P1	5544	584	97.8	globlastp
1717	LYD1 22	canolal10v1 CD833389_T1	5546	584	95.52	glotblastn
1718	LYD1 22	canolal10v1 H07385_P1	5547	584	94.6	globlastp
1719	LYD1 22	radishlgb164 EV527743_P1	5548	584	85.9	globlastp
1720	LYD1 22	b_oleracealgb161 CO729358_T1	5549	584	84.06	glotblastn
1721	LYD1 22	radishlgb164 EV535258_P1	5550	584	83.3	globlastp
1722	LYD1 22	radishlgb164 EW724035_P1	5550	584	83.3	globlastp
1723	LYD1 22	b_rapalgb162 CX272620_P1	5551	584	82	globlastp
1724	LYD1 22	canolal10v1 CD828378_P1	5552	584	82	globlastp
1725	LYD1 22	canolalgb161 CD828378_P1	5552	584	82	globlastp
1726	LYD1 22	radishlgb164 EX890296_P1	5553	584	81.9	globlastp
1727	LYD1 22	b_junceal10v2 E6ANDIZ01 B5P5S_P1	5554	584	81.7	globlastp

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1728	LYD1 22	b_juncealgb164 EVGN0102 3309282188_P1	5555	584	81.7	globlastp
1729	LYD1 22	radishlgb164 EX760929_P1	5556	584	81.4	globlastp
1730	LYD1 22	arabidopsis_lyratal09v1 JGI AL009885_P1	5557	584	80.2	globlastp
1731	LYD1 22	radishlgb164 EV567933_P1	5558	584	80.1	globlastp
1732	LYD1 22	radishlgb164 FD557550_T1	5559	584	80.09	glotblastn
1733	LYD1 23	canolal10v1 H07806_P1	5560	585	96.3	globlastp
1734	LYD1 23	canolalgb161 H07806_P1	5560	585	96.3	globlastp
1735	LYD1 23	b_rapalgb162 CO750130_P1	5561	585	95.9	globlastp
1736	LYD1 23	b_rapalgb162 CX265903_P1	5562	585	82.9	globlastp
1737	LYD1 28	soybeanlgb168 AL369494_T 1	5563	590	98.77	glotblastn
1738	LYD1 28	oakl10v1 FN715603_T1	5564	590	92.92	glotblastn
1739	LYD1 28	cottonl10v1 CO092231_T1	5565	590	90.74	glotblastn
1740	LYD1 28	citruslgb166 CF829285_T1	5566	590	90.15	glotblastn
1741	LYD1 28	cassaval09v1 DB929656_T1	5567	590	90.12	glotblastn
1742	LYD1 28	prunusl10v1 CN900288_T1	5568	590	88.92	glotblastn
1743	LYD1 28	castorbeanl09v1 EG658310_ T1	5569	590	88.62	glotblastn
1744	LYD1 28	cucumberl09v1 CSCRPO025 09_P1	5570	590	87	globlastp
1745	LYD1 28	poplarl10v1 BU825993_T1	5571	590	86.46	glotblastn
1746	LYD1 28	poplarlgb170 BU825993_T1	5572	590	86.46	glotblastn
1747	LYD1 28	nasturtiuml10v1 SRR032559 S0102172_P1	5573	590	85.1	globlastp
1748	LYD1 28	aquilegal10v1 DT733538_T 1	5574	590	83.69	glotblastn
1749	LYD1 28	aquilegalgb157.3 DT733538 _T1	5574	590	83.69	glotblastn
1750	LYD1 28	spurgelgb161 DV123236_P1	5575	590	83.6	globlastp

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1751	LYD1 28	artemisia 10v1 EY105477_T 1	5576	590	82.72	glotblastn
1752	LYD1 28	pigeonpea 10v1 SRR054580 S0061350_P1	5577	590	82.7	globlastp
1753	LYD1 28	monkeyflower 10v1 DV2102 21_T1	5578	590	82.46	glotblastn
1754	LYD1 28	arabidopsis 10v1 AT5G5166 0_T1	692	590	82.41	glotblastn
1755	LYD1 28	artemisia gb164 EY105477_ P1	5579	590	82.3	globlastp
1756	LYD1 28	lettuce 10v1 DW076329_P1	5580	590	82.2	globlastp
1757	LYD1 28	arabidopsis_lyrata 09v1 JGI AL029590_T1	5581	590	82.1	glotblastn
1757	LYD1 28_H 1	arabidopsis_lyrata 09v1 JGI AL029590_P1	5581	692	96.1	globlastp
1758	LYD1 28	solanum_phureja 09v1 SPH AW033433_T1	5582	590	81.54	glotblastn
1759	LYD1 28	tomato 09v1 AW033433_T1	5583	590	81.54	glotblastn
1760	LYD1 28	tomato gb164 AW033433_T 1	5584	590	80.92	glotblastn
1761	LYD1 28	maize gb170 AW267531_T1	5585	590	80.86	glotblastn
1762	LYD1 28	maize gb170 LLAW267531_ T1	5586	590	80.86	glotblastn
1763	LYD1 28	sorghum 09v1 SB06G00357 0_T1	5587	590	80.56	glotblastn
1764	LYD1 28	switchgrass gb167 FE61695 6_T1	5588	590	80.25	glotblastn
1765	LYD1 29	soybean gb168 BI967184_P 1	5589	591	95.9	globlastp
1766	LYD1 29	lotus 09v1 AV425312_P1	5590	591	83	globlastp
1767	LYD1 29	medicago 09v1 AL369300_P 1	5591	591	81.4	globlastp
1768	LYD1 32	soybean gb168 AW693844_ P1	5592	592	99.3	globlastp
1769	LYD1 32	soybean gb168 BF004853_P 1	5593	592	91.5	globlastp
1770	LYD1 32	pigeonpea 10v1 SRR054580 S0087423_P1	5594	592	83.9	globlastp
1771	LYD1 32	cowpea gb166 FF384575_P1	5595	592	80.7	globlastp
1772	LYD1 32	medicago 09v1 AW191239_ P1	5596	592	80.7	globlastp

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1773	LYD1 33	soybean gb168 CD393324_P 1	5597	593	91.8	globlastp
1774	LYD1 33	cowpea gb166 FF385910_P1	5598	593	88.1	globlastp
1775	LYD1 33	medicago 09v1 LLAI737587 _T1	5599	593	82.58	glotblastn
1776	LYD1 33	pea 09v1 AJ784963_P1	5600	593	80.7	globlastp
1777	LYD1 34	soybean gb168 BI969393_P 1	5601	594	90.8	globlastp
1778	LYD1 34	pigeonpea 10v1 SRR054580 S0012839_P1	5602	594	82.6	globlastp
1779	LYD1 34	cowpea gb166 FG838398_P 1	5603	594	81.6	globlastp
1780	LYD1 36	soybean gb168 BE239778_P 1	5604	595	96.5	globlastp
1781	LYD1 36	cowpea gb166 EG594237_P 1	5605	595	92.3	globlastp
1782	LYD1 36	peanut 10v1 ES704221_P1	5606	595	85.3	globlastp
1783	LYD1 36	medicago 09v1 AW685064_ P1	5607	595	85.3	globlastp
1784	LYD1 36	cotton gb164 AI726457_P1	5608	595	84	globlastp
1785	LYD1 36	poplar gb170 BI130072_P1	5609	595	82.9	globlastp
1786	LYD1 36	poplar 10v1 BI130072_P1	5610	595	82.8	globlastp
1787	LYD1 36	chestnut gb170 SRR006295S 0010383_T1	5611	595	82.78	glotblastn
1788	LYD1 36	citrus gb166 BQ623379_P1	5612	595	82.3	globlastp
1789	LYD1 36	poplar 10v1 AI163151_P1	5613	595	82.3	globlastp
1790	LYD1 36	poplar gb170 AI163151_P1	5613	595	82.3	globlastp
1791	LYD1 36	castorbean 09v1 EG665587_ P1	5614	595	82.1	globlastp
1792	LYD1 36	cucumber 09v1 DN909551_ P1	5615	595	81.6	globlastp
1793	LYD1 36	cotton 10v1 CO092102_P1	5616	595	81.6	globlastp
1794	LYD1 36	cotton gb164 CO092102_P1	5617	595	81.6	globlastp
1795	LYD1 36	cassava 09v1 FF380826_P1	5618	595	80.1	globlastp

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1796	LYD1 39	soybeanlgb168 BE998145_P 1	5619	596	94.1	globlastp
1797	LYD1 39	pigeonpeal10v1 SRR054580 S0001303_P1	5620	596	88.8	globlastp
1798	LYD1 39	beanlgb167 CA911135_P1	5621	596	85.8	globlastp
1799	LYD1 39	cowpealgb166 FF543055_P1	5622	596	81.3	globlastp
1800	LYD1 39	lotusl09v1 BP035957_P1	5623	596	80.8	globlastp
1801	LYD1 39	peanutl10v1 SRR042413S00 28830_P1	5624	596	80.5	globlastp
1802	LYD1 40	soybeanlgb168 CA912345_T 1	5625	597	95.28	glotblastn
1803	LYD1 40	soybeanlgb168 BF645424_P 1	5626	597	89.7	globlastp
1804	LYD1 40	beanlgb167 CA912345_T1	5627	597	87.61	glotblastn
1805	LYD1 40	cowpealgb166 FF382497_P1	5628	597	87.1	globlastp
1806	LYD1 40	cowpealgb166 FF393151_P1	5629	597	84.1	globlastp
1807	LYD1 40	medicagol09v1 BF645424_P 1	5630	597	83.7	globlastp
1808	LYD1 40	peanutl10v1 GO325551_P1	5631	597	82	globlastp
1809	LYD1 42	potatol10v1 BQ518275_P1	5632	598	92.2	globlastp
1810	LYD1 42	potatolgb157.2 BQ518275_P 1	5632	598	92.2	globlastp
1811	LYD1 42	solanum_phurejal09v1 SPH AI779400_P1	5633	598	91.1	globlastp
1812	LYD1 46	potatol10v1 DN589883_P1	5634	600	97	globlastp
1813	LYD1 46	potatolgb157.2 DN589883_P 1	5634	600	97	globlastp
1814	LYD1 46	solanum_phurejal09v1 SPH DN589883_P1	5634	600	97	globlastp
1815	LYD1 46	peanutl10v1 SRR042421S00 18443_P1	5635	600	83.3	globlastp
1816	LYD1 46	liquoricelgb171 FS241344_P 1	5636	600	83.3	globlastp
1817	LYD1 46	pepperlgb171 GD081638_P1	5637	600	82.6	globlastp
1818	LYD1 46	soybeanlgb168 BM528198_ P1	5638	600	80.6	globlastp

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1819	LYD1 46	coffeal10v1 EG328835_P1	5639	600	80.3	globlastp
1820	LYD1 46	heritiera10v1 SRR005795S0 062589_P1	5640	600	80.3	globlastp
1821	LYD1 46	ipomoea_batatas10v1 EE88 0432XX1_P1	5641	600	80.3	globlastp
1822	LYD1 46	chickpeal09v2 GR390849_P 1	5642	600	80.3	globlastp
1823	LYD1 46	cotton10v1 DW509770_P1	5643	600	80.3	globlastp
1824	LYD1 46	cotton1gb164 DW509770_P1	5644	600	80.3	globlastp
1825	LYD1 46	ipomoea1gb157.2 EE880432 _P1	5641	600	80.3	globlastp
1826	LYD1 48	sugarcane1gb157.3 CA08696 6_P1	5645	601	97.5	globlastp
1827	LYD1 48	sugarcane10v1 CA086966_ P1	5645	601	97.5	globlastp
1828	LYD1 48	sugarcane1gb157.3 CA08696 4_P1	5646	601	92.9	globlastp
1829	LYD1 48	sugarcane1gb157.3 CA13320 1_P1	5647	601	92.9	globlastp
1830	LYD1 48	maize10v1 AI855415_P1	5648	601	92.1	globlastp
1831	LYD1 48	maize1gb170 AI855415_P1	5648	601	92.1	globlastp
1832	LYD1 48	switchgrass1gb167 DN14335 2_P1	5649	601	91.2	globlastp
1833	LYD1 48	sugarcane1gb157.3 BQ53504 7_P1	5650	601	90.8	globlastp
1834	LYD1 48	sugarcane1gb157.3 CA06695 0_P1	5651	601	90.8	globlastp
1835	LYD1 48	sugarcane10v1 BQ535149_ P1	5650	601	90.8	globlastp
1836	LYD1 48	switchgrass1gb167 FE63981 8_P1	5652	601	90.8	globlastp
1837	LYD1 48	millet10v1 EVO454PM002 672_P1	5653	601	90.4	globlastp
1838	LYD1 48	millet10v1 PMSLX0001952 D2_P1	5653	601	90.4	globlastp
1839	LYD1 48	sorghum109v1 SB08G00285 0_P1	5654	601	90.4	globlastp
1840	LYD1 48	sugarcane1gb157.3 BQ47902 0_P1	5655	601	90.4	globlastp
1841	LYD1 48	wheat1gb164 CA484173_P1	5656	601	90.4	globlastp

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1842	LYD1 48	maize 10v1 T27554_P1	5657	601	89.2	globlastp
1843	LYD1 48	maize gb170 T27554_P1	5657	601	89.2	globlastp
1844	LYD1 48	millet 10v1 EVO454PM000 212_P1	5658	601	89.1	globlastp
1845	LYD1 48	leymus gb166 CN465810_P 1	5659	601	89.1	globlastp
1846	LYD1 48	pseudoroegneria gb167 FF34 0328_P1	5660	601	89.1	globlastp
1847	LYD1 48	switchgrass gb167 FE59934 6_P1	5661	601	88.9	globlastp
1848	LYD1 48	wheat gb164 BE403756_P1	5662	601	88.7	globlastp
1849	LYD1 48	wheat gb164 BE399235_P1	5663	601	88.3	globlastp
1850	LYD1 48	wheat gb164 WHTWALI_P 1	5664	601	88.3	globlastp
1851	LYD1 48	cynodon 10v1 ES293788_P1	5665	601	87.9	globlastp
1852	LYD1 48	barley 10v1 BE421842_P1	5666	601	87.9	globlastp
1853	LYD1 48	barley gb157 SOLEXA BE42 1842_P1	5666	601	87.9	globlastp
1854	LYD1 48	switchgrass gb167 FE60736 1_P1	5667	601	87.7	globlastp
1855	LYD1 48	fescue gb161 DT682653_P1	5668	601	87.4	globlastp
1856	LYD1 48	oat 10v2 GO585949_P1	5669	601	87	globlastp
1857	LYD1 48	brachypodium 09v1 DV4695 30_P1	5670	601	86.8	globlastp
1858	LYD1 48	brachypodium gb169 WHT WALI_P1	5670	601	86.8	globlastp
1859	LYD1 48	rice gb170 OS11G05050_P1	5671	601	86.6	globlastp
1860	LYD1 48	rice gb170 OS12G05050_P1	5672	601	86.2	globlastp
1861	LYD1 48	sugarcane 10v1 BQ535105_ P1	5673	601	82.1	globlastp
1862	LYD1 48	sugarcane gb157.3 CA06955 3_T1	5674	601	80.33	glotblastn
1863	LYD1 49	arabidopsis_lyrata 09v1 JGI AL000485_T1	5675	602	97.98	glotblastn
1864	LYD1 50	arabidopsis 10v1 AT1G6131 0_P1	5676	603	85.4	globlastp

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1865	LYD1 52	arabidopsis_lyratal09v1 JGI AL019864_P1	5677	604	87.1	globlastp
1866	LYD1 53	arabidopsis_lyratal09v1 JGI AL028781_P1	5678	605	94.7	globlastp
1867	LYD1 53	canola 10v1 CD834597_T1	5679	605	86.09	glotblastn
1868	LYD1 56	solanum_phurejal09v1 SPH BG125257_P1	5680	606	93.4	globlastp
1869	LYD1 56	tobacco gb162 DW003871_ P1	5681	606	86.2	globlastp
1870	LYD1 57	solanum_phurejal09v1 SPH BG735318_P1	5682	607	97.8	globlastp
1871	LYD1 57	tobacco gb162 EB443875_T 1	5683	607	92.45	glotblastn
1872	LYD1 57	triphysarial10v1 DR173387_ P1	5684	607	81	globlastp
1873	LYD1 57	monkeyflower 09v1 DV2062 93_T1	5685	607	80.41	glotblastn
1874	LYD1 57	monkeyflower 10v1 DV2062 93_P1	5686	607	80.3	globlastp
1875	LYD1 58	solanum_phurejal09v1 SPH CV302355_P1	5687	608	92.1	globlastp
1876	LYD1 59	canola 10v1 CD840853_P1	5688	609	99.4	globlastp
1877	LYD1 59	b_rapa gb162 CV433375_P1	5689	609	97.5	globlastp
1878	LYD1 59	canola 10v1 CX188057_P1	5690	609	97.5	globlastp
1879	LYD1 59	canola gb161 CX188057_P1	5690	609	97.5	globlastp
1880	LYD1 59	radish gb164 EV526121_P1	5691	609	96.3	globlastp
1881	LYD1 59	arabidopsis_lyratal09v1 BQ8 34364_P1	5692	609	95.1	globlastp
1882	LYD1 59	arabidopsis 10v1 AT1G8092 0_P1	5692	609	95.1	globlastp
1883	LYD1 59	arabidopsis gb165 AT1G809 20_P1	5692	609	95.1	globlastp
1884	LYD1 59	arabidopsis_lyratal09v1 TM PLEW733261T1_T1	5693	609	95.09	glotblastn
1885	LYD1 59	radish gb164 EW713954_P1	5694	609	86.4	globlastp
1886	LYD1 59	radish gb164 EV524864_P1	5695	609	83.3	globlastp
1887	LYD1 66	canola 10v1 BQ704758_P1	5696	610	99.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
1888	LYD1 66	canola gb161 BQ704758_P1	5696	610	99.2	globlastp
1889	LYD1 66	radish gb164 EV534875_P1	5697	610	99.2	globlastp
1890	LYD1 66	radish gb164 EV540019_P1	5698	610	99.2	globlastp
1891	LYD1 66	b_junceal10v2 E6ANDIZ01 A0QZN_P1	5699	610	98.7	globlastp
1892	LYD1 66	b_oleracealgb161 DY015712 _P1	5700	610	98.4	globlastp
1893	LYD1 66	arabidopsis 10v1 AT1G0934 0_P1	5701	610	96.8	globlastp
1894	LYD1 66	arabidopsis gb165 AT1G093 40_P1	5701	610	96.8	globlastp
1895	LYD1 66	arabidopsis_lyratal09v1 JGI AL000901_P1	5702	610	96	globlastp
1896	LYD1 66	cleome_gynandra 10v1 SRR 015532S0001942_P1	5703	610	90.8	globlastp
1897	LYD1 66	cleome_spinosal10v1 GR935 323_P1	5704	610	90	globlastp
1898	LYD1 66	cleome_spinosal10v1 GR933 224_P1	5705	610	89.4	globlastp
1899	LYD1 66	oak 10v1 CU640621_P1	5706	610	86.8	globlastp
1900	LYD1 66	aquilegal10v1 DR912555_P 1	5707	610	86.8	globlastp
1901	LYD1 66	chestnut gb170 SRR006296S 0063232_P1	5706	610	86.8	globlastp
1902	LYD1 66	b_juncealgb164 EVGN0010 1514270624_P1	5708	610	86.5	globlastp
1903	LYD1 66	cassava gb164 CK651731_P 1	5709	610	86.3	globlastp
1904	LYD1 66	citrus gb166 CF417618_P1	5710	610	86.1	globlastp
1905	LYD1 66	cassava 09v1 MESCRP0310 23_P1	5711	610	85.8	globlastp
1906	LYD1 66	castorbean 09v1 XM002512 495_P1	5712	610	85.8	globlastp
1907	LYD1 66	radish gb164 EV535299_P1	5713	610	85.7	globlastp
1908	LYD1 66	melon 10v1 AM724794_P1	5714	610	85.5	globlastp
1909	LYD1 66	antirrhinum gb166 AJ79086 3_T1	5715	610	85.45	glotblastn
1910	LYD1 66	ipomoea gb157.2 BJ556545_ P1	5716	610	85.3	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
1911	LYD1 66	melon gb165 AM724794_P1	5717	610	85.3	globlastp
1912	LYD1 66	walnuts gb166 EL890919_T 1	5718	610	85.19	glotblastn
1913	LYD1 66	prunus 10v1 BU044092_P1	5719	610	85.1	globlastp
1914	LYD1 66	cotton 10v1 CO070417_P1	5720	610	85	globlastp
1915	LYD1 66	monkeyflower 09v1 DV2067 23_P1	5721	610	85	globlastp
1916	LYD1 66	monkeyflower 10v1 DV2067 23_P1	5721	610	85	globlastp
1917	LYD1 66	papaya gb165 EX256506_P1	5722	610	85	globlastp
1918	LYD1 66	prunus gb167 BU044092_P1	5723	610	84.9	globlastp
1919	LYD1 66	tobacco gb162 DV159774_P 1	5724	610	84.9	globlastp
1920	LYD1 66	cotton gb164 CO070417_P1	5725	610	84.7	globlastp
1921	LYD1 66	cucumber 09v1 AM724794_ P1	5726	610	84.5	globlastp
1922	LYD1 66	triphysarial 10v1 EY144050_ P1	5727	610	84.5	globlastp
1923	LYD1 66	cowpea gb166 FC457398_P 1	5728	610	84.4	globlastp
1924	LYD1 66	oak gb170 CU640621_P1	5729	610	84.4	globlastp
1925	LYD1 66	salvia 10v1 FE536314_P1	5730	610	84.2	globlastp
1926	LYD1 66	poplar gb170 BI068409_P1	5731	610	84.2	globlastp
1927	LYD1 66	poplar gb170 BU880077_P1	5732	610	84.2	globlastp
1928	LYD1 66	clover gb162 BB903013_P1	5733	610	84.1	globlastp
1929	LYD1 66	poplar 10v1 BU880077_P1	5734	610	83.9	globlastp
1930	LYD1 66	poplar 10v1 BI068409_P1	5735	610	83.7	globlastp
1931	LYD1 66	strawberry gb164 DY667768 _T1	5736	610	83.42	glotblastn
1932	LYD1 66	tomato 09v1 BG123220_P1	5737	610	83.4	globlastp
1933	LYD1 66	tomato gb164 BG123220_P1	5737	610	83.4	globlastp

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1934	LYD1 66	apple gb171 CN444185_P1	5738	610	83.3	globlastp
1935	LYD1 66	apple gb171 CN489833_P1	5739	610	83.3	globlastp
1936	LYD1 66	bean gb167 CB280711_P1	5740	610	83.1	globlastp
1937	LYD1 66	grape gb160 CA810251_P1	5741	610	83.1	globlastp
1938	LYD1 66	potato 10v1 BE919563_P1	5742	610	83.1	globlastp
1939	LYD1 66	potato gb157.2 BE919563_P 1	5742	610	83.1	globlastp
1940	LYD1 66	solanum_phureja 09v1 SPH BG123220_P1	5742	610	83.1	globlastp
1941	LYD1 66	soybean gb168 AW697089_ P1	5743	610	83.1	globlastp
1942	LYD1 66	soybean gb168 BF519945_P 1	5744	610	83.1	globlastp
1943	LYD1 66	lotus 09v1 AV411209_P1	5745	610	82.8	globlastp
1944	LYD1 66	eggplant 10v1 FS064026_P1	5746	610	82.3	globlastp
1945	LYD1 66	rhizophora 10v1 SRR005792 S0001147_P1	5747	610	82.2	globlastp
1946	LYD1 66	artemisia 10v1 EY037995_P 1	5748	610	81.5	globlastp
1947	LYD1 66	artemisia gb164 EY037995_ P1	5748	610	81.5	globlastp
1948	LYD1 66	nicotiana_benthamiana gb16 2 CN746126_P1	5749	610	81.2	globlastp
1949	LYD1 66	centaurea gb166 EH725433_ T1	5750	610	80.95	glotblastn
1950	LYD1 66	cichorium gb171 EH694497_ T1	5751	610	80.42	glotblastn
1951	LYD1 66	cynara gb167 GE585828_P1	5752	610	80.2	globlastp
1952	LYD1 66	peanut 10v1 CD037653_P1	5753	610	80.2	globlastp
1953	LYD1 66	peanut gb171 CD037653_P1	5754	610	80.2	globlastp
1954	LYD1 66	lettuce 10v1 CV699894_T1	5755	610	80.16	glotblastn
1955	LYD1 66	sunflower 10v1 BU671862_ P1	5756	610	80.1	globlastp
1956	LYD1 67	radish gb164 EV525510_P1	5757	611	99	globlastp

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1957	LYD1 67	radish gb164 EV536182_P1	5758	611	99	globlastp
1958	LYD1 67	b_oleracealgb161 EH425281_P1	5759	611	97.4	globlastp
1959	LYD1 67	canola 10v1 CB686097_P1	5759	611	97.4	globlastp
1960	LYD1 67	canola gb161 CB686097_P1	5759	611	97.4	globlastp
1961	LYD1 67	b_juncealgb164 DT317679_P1	5760	611	96.9	globlastp
1962	LYD1 67	b_rapalgb162 L37994_P1	5760	611	96.9	globlastp
1963	LYD1 67	canola 10v1 CD812237_P1	5760	611	96.9	globlastp
1964	LYD1 67	canola gb161 CB686288_P1	5760	611	96.9	globlastp
1965	LYD1 67	canola gb161 CX281643_P1	5761	611	93.9	globlastp
1966	LYD1 67	canola gb161 EE430594_P1	5762	611	93.9	globlastp
1967	LYD1 67	canola 10v1 EE430594_P1	5763	611	93.4	globlastp
1968	LYD1 67	b_rapalgb162 AT002236_P1	5764	611	93.4	globlastp
1969	LYD1 67	canola 10v1 CX281643_P1	5765	611	93.4	globlastp
1970	LYD1 67	b_junceal10v2 BJ1SLX00005575D1_P1	5766	611	92.9	globlastp
1971	LYD1 67	b_junceal10v2 E6ANDIZ01A3IXY_P1	5767	611	92.9	globlastp
1972	LYD1 67	b_juncealgb164 EVGN00251514510715_P1	5768	611	92.9	globlastp
1973	LYD1 67	b_rapalgb162 CV432763_P1	5769	611	92.3	globlastp
1974	LYD1 67	b_junceal10v2 OXBJ1SLX00018566D1T1_P1	5770	611	91.8	globlastp
1975	LYD1 67	radish gb164 EX749211_P1	5771	611	91.8	globlastp
1976	LYD1 67	b_junceal10v2 E6ANDIZ01A8TWA_P1	5772	611	91.3	globlastp
1977	LYD1 67	b_junceal10v2 OXBJ1SLX00001660D1T1_P1	5773	611	90.3	globlastp
1978	LYD1 67	arabidopsis 10v1 AT3G22840_P1	5774	611	89.4	globlastp
1979	LYD1 67	thellungiellalgb167 DN772992_P1	5775	611	87.3	globlastp

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1980	LYD1 67	arabidopsis_lyrata 09v1 JGI AL010903_P1	5776	611	87.2	globlastp
1981	LYD1 73	b_rapalgb162 L46564_P1	5777	613	99.5	globlastp
1982	LYD1 73	canola 10v1 H07553_P1	5777	613	99.5	globlastp
1983	LYD1 73	canola gb161 H07553_P1	5777	613	99.5	globlastp
1984	LYD1 73	b_oleracealgb161 AM38615 9_P1	5778	613	99.1	globlastp
1985	LYD1 73	canola 10v1 CD818135_P1	5778	613	99.1	globlastp
1986	LYD1 73	canola gb161 CD818135_P1	5778	613	99.1	globlastp
1987	LYD1 73	b_juncealgb164 EVGN0019 3213831087_P1	5779	613	98.1	globlastp
1988	LYD1 73	b_junceal10v2 E6ANDIZ01 A2QZJ_P1	5780	613	96.7	globlastp
1989	LYD1 73	radish gb164 EV526485_P1	5781	613	96.7	globlastp
1990	LYD1 73	radish gb164 EX757513_P1	5782	613	96.7	globlastp
1991	LYD1 73	radish gb164 EV537108_P1	5783	613	94.8	globlastp
1992	LYD1 73	radish gb164 EX905183_P1	5784	613	94.8	globlastp
1993	LYD1 73	radish gb164 EV546803_P1	5785	613	94.4	globlastp
1994	LYD1 73	radish gb164 EY902155_T1	5786	613	94.37	glotblastn
1995	LYD1 73	b_junceal10v2 E6ANDIZ01 A0NM0_T1	5787	613	87.85	glotblastn
1996	LYD1 73	thellungiella gb167 DN7733 41_P1	5788	613	85	globlastp
1997	LYD1 73	arabidopsis 10v1 AT1G1957 0_P1	5789	613	84	globlastp
1998	LYD1 73	arabidopsis gb165 AT1G195 70_P1	5789	613	84	globlastp
1999	LYD1 73	b_junceal10v2 E6ANDIZ01 A566R_P1	5790	613	83.6	globlastp
2000	LYD1 73	radish gb164 EX747007_P1	5791	613	82.2	globlastp
2001	LYD1 73	radish gb164 EW725652_P1	5792	613	81.7	globlastp
2002	LYD1 73	radish gb164 EV534906_P1	5793	613	81.2	globlastp

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2003	LYD1 73	arabidopsis_lyratal09v1 JGI AL002059_T1	5794	613	80.75	glotblastn
2004	LYD1 73	arabidopsis_lyratal09v1 JGI AL007795_P1	5795	613	80.3	globlastp
2005	LYD1 73	cleome_gynandra10v1 SRR 015532S0012442_P1	5796	613	80.3	globlastp
2006	LYD1 74	canola10v1 CD813876_P1	5797	614	99.8	globlastp
2007	LYD1 74	canola1gb161 CD813876_P1	5797	614	99.8	globlastp
2008	LYD1 74	b_oleracealgb161 AY065840 _P1	5798	614	99.2	globlastp
2009	LYD1 74	radish1gb164 EW714178_P1	5799	614	97.6	globlastp
2010	LYD1 74	canola10v1 CD815711_P1	5800	614	97	globlastp
2011	LYD1 74	arabidopsis1gb165 AT1G227 10_P1	5801	614	94.5	globlastp
2011	LYD1 74	arabidopsis10v1 AT1G2271 0_P1	5803	614	93.6	globlastp
2012	LYD1 74	canola1gb161 CD825116_P1	5802	614	94	globlastp
2013	LYD1 74	arabidopsis_lyratal09v1 JGI AL002431_P1	5804	614	93.2	globlastp
2014	LYD1 74	canola10v1 DW998857_P1	5805	614	81.1	globlastp
2015	LYD1 76	canola10v1 BQ704660_P1	5806	615	92.9	globlastp
2016	LYD1 76	canola1gb161 CX187649_P1	5806	615	92.9	globlastp
2017	LYD1 76	b_rapalgb162 BG543075_P1	5807	615	91.8	globlastp
2018	LYD1 76	canola10v1 CN727120_P1	5808	615	91.3	globlastp
2019	LYD1 76	canola1gb161 CN727120_P1	5808	615	91.3	globlastp
2020	LYD1 76	maize1gb170 LLDQ245199_ P1	5808	615	91.3	globlastp
2021	LYD1 76	b_oleracealgb161 X94979_P 1	5809	615	91	globlastp
2022	LYD1 76	b_nigral09v1 GT069756_P1	5810	615	87.9	globlastp
2023	LYD1 76	b_juncealgb164 EVGN0114 4714190893_P1	5811	615	87.1	globlastp
2024	LYD1 76	b_oleracealgb161 AM38645 1_P1	5812	615	87	globlastp

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2025	LYD1 76	b_rapalgb162 CV544363_P1	5813	615	87	globlastp
2026	LYD1 76	canolal10v1 EG021017_P1	5813	615	87	globlastp
2027	LYD1 76	canolalgb161 EG021017_P1	5813	615	87	globlastp
2028	LYD1 76	b_junceal10v2 E6ANDIZ01 AKW0S_P1	5814	615	86.5	globlastp
2029	LYD1 76	canolal10v1 CN729310_P1	5815	615	86	globlastp
2030	LYD1 76	canolalgb161 CN729310_P1	5815	615	86	globlastp
2031	LYD1 76	radishlgb164 EV524460_P1	5816	615	85.9	globlastp
2032	LYD1 76	thellungiellalgb167 DN7730 90_P1	5817	615	84.8	globlastp
2033	LYD1 76	b_rapalgb162 L47867_P1	5818	615	84.4	globlastp
2034	LYD1 76	canolal10v1 DY018032_P1	5818	615	84.4	globlastp
2035	LYD1 76	canolalgb161 DY018032_P1	5818	615	84.4	globlastp
2036	LYD1 76	b_junceal10v2 E6ANDIZ01 A94EP_P1	5819	615	84.2	globlastp
2037	LYD1 76	b_juncealgb164 EVGN0034 4614610857_P1	5819	615	84.2	globlastp
2038	LYD1 76	b_junceal10v2 E6ANDIZ01 A1KFY1_P1	5820	615	83.6	globlastp
2039	LYD1 76	radishlgb164 EW726459_T1	5821	615	83.41	glotblastn
2040	LYD1 76	radishlgb164 EX771849_P1	5822	615	83.4	globlastp
2041	LYD1 76	radishlgb164 EV535313_P1	5823	615	82.5	globlastp
2042	LYD1 76	canolal10v1 H74597_T1	5824	615	82.41	glotblastn
2043	LYD1 76	canolalgb161 H74597_T1	5824	615	82.41	glotblastn
2044	LYD1 76	canolalgb161 EV176190_T1	5825	615	82.14	glotblastn
2045	LYD1 77	b_rapalgb162 CV546358_P1	5826	616	99	globlastp
2046	LYD1 77	canolalgb161 EE462120_P1	5827	616	99	globlastp
2047	LYD1 77	canolal10v1 CX190522_P1	5828	616	95.9	globlastp

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2048	LYD1 77	canola 10v1 EE462120_P1	5828	616	95.9	globlastp
2049	LYD1 77	canola gb161 CX190522_P1	5828	616	95.9	globlastp
2050	LYD1 77	maize gb170 LLDQ244995_ P1	5828	616	95.9	globlastp
2051	LYD1 77	b_olerace gb161 AM05757 7_P1	5829	616	94.8	globlastp
2052	LYD1 77	b_junceal gb164 EVGN0006 5426350167_P1	5830	616	93.8	globlastp
2053	LYD1 77	radish gb164 EV538277_P1	5831	616	93.8	globlastp
2054	LYD1 77	b_junceal 10v2 E6ANDIZ01 A9K6V_P1	5832	616	92.8	globlastp
2055	LYD1 77	b_junceal gb164 EVGN0036 9325751180_P1	5833	616	90.7	globlastp
2056	LYD1 77	b_junceal 10v2 E6ANDIZ01 A42M6_P1	5834	616	84.5	globlastp
2057	LYD1 78	maize gb170 LLDQ245347_ P1	5835	617	99.3	globlastp
2058	LYD1 78	canola 10v1 CN728812_P1	5836	617	92	globlastp
2059	LYD1 78	b_rapa gb162 EX058232_P1	5837	617	90.9	globlastp
2060	LYD1 78	canola gb161 CN728812_P1	5838	617	89.3	globlastp
2061	LYD1 78	canola gb161 CN729053_P1	5839	617	86.8	globlastp
2062	LYD1 78	b_junceal gb164 EVGN0160 2408322025_T1	5840	617	84.11	glotblastn
2063	LYD1 78	b_rapa gb162 BG543037_T1	5841	617	84.11	glotblastn
2064	LYD1 78	canola gb161 H07680_T1	5842	617	84.11	glotblastn
2065	LYD1 78	b_junceal 10v2 OXB1SLX0 0002305D1T1_P1	5843	617	84.1	globlastp
2066	LYD1 78	b_oleraceal gb161 EH415446 _P1	5844	617	84.1	globlastp
2067	LYD1 78	radish gb164 EV539169_T1	5845	617	84	glotblastn
2068	LYD1 78	radish gb164 EV528495_P1	5846	617	82.8	globlastp
2069	LYD1 78	radish gb164 EV536377_P1	5847	617	82.8	globlastp
2070	LYD1 78	b_oleraceal gb161 EH425722 _T1	5848	617	80.67	glotblastn

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2071	LYD1 78	canola gb161 CD812131_T1	5849	617	80.13	glotblastn
2072	LYD1 78	radish gb164 EX764872_T1	5850	617	80.13	glotblastn
2073	LYD1 78	canola 10v1 H07680_P1	5851	617	80.1	globlastp
2074	LYD1 80	canola 10v1 CB686396_P1	5852	618	99.4	globlastp
2075	LYD1 80	b_rapa gb162 DN961358_P1	5853	618	99.4	globlastp
2076	LYD1 80	canola gb161 CB686396_P1	5852	618	99.4	globlastp
2077	LYD1 80	b_juncea gb164 EVGN0052 9314222143_P1	5854	618	97	globlastp
2078	LYD1 80	b_oleracea gb161 AM38861 7_P1	5854	618	97	globlastp
2079	LYD1 80	canola 10v1 CD815087_P1	5854	618	97	globlastp
2080	LYD1 80	canola gb161 CD815087_P1	5854	618	97	globlastp
2081	LYD1 80	maize gb170 LLDQ246015_ P1	5854	618	97	globlastp
2082	LYD1 80	canola 10v1 DY016051_P1	5855	618	96	globlastp
2083	LYD1 80	b_juncea 10v2 E6ANDIZ01 A2BHS_P1	5856	618	94.7	globlastp
2084	LYD1 80	b_juncea 10v2 E6ANDIZ01 AINAF_P1	5857	618	94.7	globlastp
2085	LYD1 80	b_juncea 10v2 E6ANDIZ01 AY5KE_P1	5858	618	93.5	globlastp
2086	LYD1 80	radish gb164 EV526021_P1	5859	618	93.5	globlastp
2087	LYD1 80	radish gb164 EV565725_P1	5859	618	93.5	globlastp
2088	LYD1 80	radish gb164 EV535131_P1	5860	618	92.9	globlastp
2089	LYD1 80	radish gb164 FD538226_P1	5861	618	92.9	globlastp
2090	LYD1 80	b_nigral 09v1 GT069546_P1	5862	618	90.5	globlastp
2091	LYD1 80	thellungiella gb167 BM9859 57_P1	5863	618	86.9	globlastp
2092	LYD1 80	b_juncea 10v2 E6ANDIZ01 A4TK8_P1	5864	618	86.6	globlastp
2093	LYD1 80	b_rapa gb162 EX017672_P1	5865	618	84.8	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2094	LYD1 80	canola gb161 DY030344_P1	5865	618	84.8	globlastp
2095	LYD1 80	radish gb164 EV572930_P1	5866	618	83.4	globlastp
2096	LYD1 80	arabidopsis 10v1 AT1G0931 O_P1	5867	618	82.8	globlastp
2097	LYD1 80	radish gb164 EW734914_P1	5868	618	82.8	globlastp
2098	LYD1 80	arabidopsis_lyrata 09v1 JGI AL000898_P1	5869	618	82.3	globlastp
2099	LYD1 80	radish gb164 EV535701_T1	5870	618	82.25	glotblastn
2100	LYD1 80	canola 10v1 DY030344_P1	5871	618	82.1	globlastp
2101	LYD1 80	radish gb164 EW735869_P1	5872	618	82.1	globlastp
2102	LYD1 80	radish gb164 EV539268_P1	5873	618	81.5	globlastp
2103	LYD1 80	radish gb164 EV547459_P1	5874	618	81.5	globlastp
2104	LYD1 80	radish gb164 EV569517_P1	5875	618	81.5	globlastp
2105	LYD1 80	radish gb164 EV528599_P1	5876	618	80.4	globlastp
2106	LYD1 84	canola 10v1 EV128279_P1	5877	619	98.9	globlastp
2107	LYD1 84	b_rapa gb162 EX072399_P1	5877	619	98.9	globlastp
2108	LYD1 84	canola gb161 EV128279_P1	5877	619	98.9	globlastp
2109	LYD1 84	canola 10v1 EE427730_P1	5878	619	97.8	globlastp
2110	LYD1 84	canola gb161 EE427730_P1	5878	619	97.8	globlastp
2111	LYD1 84	b_junceal 10v2 E6ANDIZ01 A5CK0_P1	5879	619	93.3	globlastp
2112	LYD1 84	b_junceal gb164 EVGN0091 1914081701_P1	5880	619	93.3	globlastp
2113	LYD1 84	radish gb164 EX890482_P1	5881	619	90.5	globlastp
2114	LYD1 84	b_junceal 10v2 E6ANDIZ01 A2PDG_P1	5882	619	89.4	globlastp
2115	LYD1 84	b_junceal gb164 EVGN0116 9814532136_P1	5883	619	88.3	globlastp
2116	LYD1 84	canola 10v1 DY000970_P1	5884	619	86.7	globlastp

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2117	LYD1 84	b_rapalgb162 L38150_P1	5885	619	86.1	globlastp
2118	LYD1 84	canolalgb161 DY000970_P1	5886	619	86.1	globlastp
2119	LYD1 84	radishlgb164 EV538405_P1	5887	619	86	globlastp
2120	LYD1 84	b_junceal10v2 E6ANDIZ01 A05Y0_P1	5888	619	85.6	globlastp
2121	LYD1 84	radishlgb164 EX749350_T1	5889	619	84.92	glotblastn
2122	LYD1 84	b_junceal10v2 E6ANDIZ01 AMLKU_P1	5890	619	84.9	globlastp
2123	LYD1 85	b_rapalgb162 L33587_P1	5891	620	96.9	globlastp
2124	LYD1 85	canolal10v1 CX192408_P1	5892	620	96.2	globlastp
2125	LYD1 85	canolalgb161 CX192408_P1	5893	620	94.7	globlastp
2126	LYD1 85	canolalgb161 CX191335_P1	5894	620	87.9	globlastp
2127	LYD1 85	canolal10v1 H74507_P1	5895	620	86.2	globlastp
2128	LYD1 85	canolal10v1 CX191541_P1	5896	620	86	globlastp
2129	LYD1 85	thellungiellalgb167 DN7782 69_P1	5897	620	81.7	globlastp
2130	LYD1 85	canolalgb161 CD837602_P1	5898	620	81.6	globlastp
2131	LYD1 85	arabidopsis_lyratal09v1 JGI AL002946_P1	5899	620	80.8	globlastp
2132	LYD1 86	thellungiellalgb167 BY8060 15_P1	5900	621	94.1	globlastp
2133	LYD1 86	arabidopsis 10v1 AT1G5670 0_P1	5901	621	93.2	globlastp
2134	LYD1 86	arabidopsis_lyratal09v1 JGI AL005325_T1	5902	621	90.91	glotblastn
2135	LYD1 86	cleome_gynandra 10v1 SRR 015532S0000444_T1	5903	621	80	glotblastn
2136	LYD1 87	b_oleracealgb161 AM38840 5_P1	5904	622	97.4	globlastp
2137	LYD1 87	canolalgb161 CX190300_P1	5904	622	97.4	globlastp
2138	LYD1 87	radishlgb164 EV536333_P1	5905	622	97.4	globlastp
2139	LYD1 87	radishlgb164 EV550518_P1	5906	622	97.4	globlastp

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2140	LYD1 87	canola 10v1 CB686142_P1	5904	622	97.4	globlastp
2141	LYD1 87	b_oleracealgb161 DY027529_P1	5907	622	97	globlastp
2142	LYD1 87	b_rapalgb162 BG543670_P1	5908	622	97	globlastp
2143	LYD1 87	canola gb161 CB686142_P1	5908	622	97	globlastp
2144	LYD1 87	b_junceal10v2 E6ANDIZ01 BJ4IL_P1	5909	622	96.6	globlastp
2145	LYD1 87	canola 10v1 BQ704355_P1	5910	622	96.6	globlastp
2146	LYD1 87	radish gb164 EV527800_P1	5911	622	96.6	globlastp
2147	LYD1 87	b_juncealgb164 EVGN0022 8415001818_P1	5912	622	96.2	globlastp
2148	LYD1 87	b_rapalgb162 CA991704_P1	5912	622	96.2	globlastp
2149	LYD1 87	canola 10v1 H07333_P1	5912	622	96.2	globlastp
2150	LYD1 87	canola gb161 AI352825_P1	5912	622	96.2	globlastp
2151	LYD1 87	canola gb161 BQ704355_P1	5913	622	96.2	globlastp
2152	LYD1 87	canola gb161 DW998915_P 1	5912	622	96.2	globlastp
2153	LYD1 87	b_oleracealgb161 DY026491_P1	5914	622	95.8	globlastp
2154	LYD1 87	arabidopsis_lyratal09v1 BQ8 34357_P1	5915	622	95.3	globlastp
2155	LYD1 87	b_junceal10v2 E6ANDIZ01 A4TV8_P1	5916	622	95.3	globlastp
2156	LYD1 87	b_junceal10v2 E7FJ1I304D WYFK1_T1	5917	622	94.87	glotblastn
2157	LYD1 87	arabidopsis 10v1 AT5G1914 0_P1	5918	622	94.4	globlastp
2158	LYD1 87	thellungiella gb167 BM9858 60_P1	5919	622	92.3	globlastp
2159	LYD1 87	radish gb164 EX747604_P1	5920	622	91.5	globlastp
2160	LYD1 87	b_junceal10v2 E6ANDIZ01 A2LN8_P1	5921	622	89	globlastp
2161	LYD1 87	canola gb161 BQ705035_P1	5922	622	88.5	globlastp
2162	LYD1 87	cleome_spinosal10v1 GR934 264_P1	5923	622	83.5	globlastp

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2163	LYD1 87	cleome_gynandra 10v1 SRR 015532S0000079_P1	5924	622	83.1	globlastp
2164	LYD1 87	poppy gb166 FG605794_P1	5925	622	81.8	globlastp
2165	LYD1 87	prunus 10v1 BF717221_P1	5926	622	81.4	globlastp
2166	LYD1 87	prunus gb167 BF717221_P1	5926	622	81.4	globlastp
2167	LYD1 87	chestnut gb170 SRR006295S 0001356_P1	5927	622	80.9	globlastp
2168	LYD1 87	liquorice gb171 FS239166_P 1	5928	622	80.9	globlastp
2169	LYD1 87	walnuts gb166 CB303568_P 1	5929	622	80.9	globlastp
2170	LYD1 87	walnuts gb166 CV195685_P 1	5930	622	80.9	globlastp
2171	LYD1 87	nasturtium 10v1 GH162655_ P1	5931	622	80.5	globlastp
2172	LYD1 87	apple gb171 CN489391_P1	5932	622	80.5	globlastp
2173	LYD1 87	citrus gb166 BE208893_P1	5933	622	80.5	globlastp
2174	LYD1 87	cotton gb164 AI054521_P1	5934	622	80.5	globlastp
2175	LYD1 87	oak 10v1 DB997378_T1	5935	622	80.34	glotblastn
2176	LYD1 87	oak 10v1 FN697150_T1	5935	622	80.34	glotblastn
2177	LYD1 87	oak 10v1 FN698586_T1	5935	622	80.34	glotblastn
2178	LYD1 87	oak 10v1 FN699485_T1	5935	622	80.34	glotblastn
2179	LYD1 87	oak 10v1 FN710897_T1	5935	622	80.34	glotblastn
2180	LYD1 87	oak 10v1 FN715237_T1	5935	622	80.34	glotblastn
2181	LYD1 87	oak 10v1 FN755290_T1	5935	622	80.34	glotblastn
2182	LYD1 87	oak 10v1 FP051976_T1	5935	622	80.34	glotblastn
2183	LYD1 87	oak 10v1 FP056365_T1	5935	622	80.34	glotblastn
2184	LYD1 87	oak 10v1 SRR006307S0013 969_T1	5935	622	80.34	glotblastn
2185	LYD1 87	oak 10v1 SRR006307S0041 858_T1	5936	622	80.34	glotblastn

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2186	LYD1 87	oak 10v1 SRR006310S0001 406_T1	5935	622	80.34	glotblastn
2187	LYD1 87	oak 10v1 SRR039734S0072 419_T1	5937	622	80.34	glotblastn
2188	LYD1 87	oak 10v1 SRR039739S0033 686_T1	5935	622	80.34	glotblastn
2189	LYD1 87	oak 10v1 SRR039740S0005 760_T1	5938	622	80.34	glotblastn
2190	LYD1 87	clover gb162 BB904019_T1	5939	622	80.34	glotblastn
2191	LYD1 87	kiwi gb166 FG405871_T1	5940	622	80.34	glotblastn
2192	LYD1 87	radish gb164 EV542281_P1	5941	622	80.3	globlastp
2193	LYD1 87	nasturtium 10v1 GH168619_ P1	5942	622	80.1	globlastp
2194	LYD1 87	oak 10v1 FP041304_P1	5943	622	80.1	globlastp
2195	LYD1 87	apple gb171 CN865201_P1	5944	622	80.1	globlastp
2196	LYD1 87	cotton 10v1 AI054521_P1	5945	622	80.1	globlastp
2197	LYD1 87	oak gb170 DB997378_P1	5946	622	80.1	globlastp
2198	LYD1 87	soybean gb168 AI967327_P 1	5947	622	80.1	globlastp
2199	LYD1 87	soybean gb168 AW329810_ P1	5948	622	80.1	globlastp
2200	LYD1 87	soybean gb168 AW348574_ P1	5949	622	80.1	globlastp
2201	LYD1 88	b_junceal 10v2 E6ANDIZ01 BEAXG_P1	5950	623	87.5	globlastp
2202	LYD1 90	arabidopsis_lyrata 09v1 JGI AL000673_P1	5951	624	87.3	globlastp
2203	LYD1 90	arabidopsis 10v1 AT1G0714 0_P1	5952	624	86.9	globlastp
2204	LYD1 90	arabidopsis gb165 AT1G071 40_P1	5952	624	86.9	globlastp
2205	LYD1 90	canola gb161 CN729032_T1	5953	624	83.56	glotblastn
2206	LYD1 90	canola 10v1 FG564672_P1	5954	624	83.1	globlastp
2207	LYD1 90	cleome_spinosal 10v1 GR931 255_P1	5955	624	81	globlastp
2208	LYD1 93	canola 10v1 CD819193_P1	5956	626	97.9	globlastp

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2209	LYD1 93	canola 10v1 CN828571_P1	5956	626	97.9	globlastp
2210	LYD1 93	canola 10v1 CX189824_P1	5956	626	97.9	globlastp
2211	LYD1 93	canola gb161 CD819193_P1	5956	626	97.9	globlastp
2212	LYD1 93	b_oleracealgb161 AM38535 2_P1	5957	626	97.5	globlastp
2213	LYD1 93	b_junceal10v2 E6ANDIZ01 A1JPM_P1	5958	626	88.3	globlastp
2214	LYD1 93	b_oleracealgb161 AM38877 0_P1	5959	626	86.2	globlastp
2215	LYD1 93	canola 10v1 EE475907_P1	5960	626	86.2	globlastp
2216	LYD1 93	canola gb161 EE475907_P1	5961	626	83.7	globlastp
2217	LYD1 93	arabidopsis 10v1 AT4G2026 0_P1	5962	626	82.7	globlastp
2218	LYD1 93	arabidopsis gb165 AT4G202 60_P1	5962	626	82.7	globlastp
2219	LYD1 93	arabidopsis_lyrata 09v1 JGI AL026112_P1	5963	626	81.4	globlastp
2220	LYD1 94	canola 10v1 CD812567_P1	627	627	100	globlastp
2221	LYD1 94	canola 10v1 CN732445_P1	627	627	100	globlastp
2222	LYD1 94	b_oleracealgb161 AM39435 9_P1	627	627	100	globlastp
2223	LYD1 94	canola gb161 CD812567_P1	627	627	100	globlastp
2224	LYD1 94	canola gb161 CN732445_P1	627	627	100	globlastp
2225	LYD1 94	b_junceal10v2 E6ANDIZ01 A562G_P1	5964	627	98.7	globlastp
2226	LYD1 94	b_junceal10v2 E6ANDIZ01 ETA4O_P1	5964	627	98.7	globlastp
2227	LYD1 94	b_junceal10v2 E6ANDIZ01 AQJZN_P1	5964	627	98.7	globlastp
2228	LYD1 94	b_juncealgb164 EVGN0041 4408181524_P1	5964	627	98.7	globlastp
2229	LYD1 94	b_junceal10v2 BJ1SLX0001 7689D2_P1	5964	627	98.7	globlastp
2230	LYD1 94	b_oleracealgb161 AM05751 5_P1	5964	627	98.7	globlastp
2231	LYD1 94	b_rapalgb162 CO749437_P1	5964	627	98.7	globlastp

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2232	LYD1 94	b_rapalgb162 EE526209_P1	5965	627	98.7	globlastp
2233	LYD1 94	canola 10v1 CD812518_P1	5964	627	98.7	globlastp
2234	LYD1 94	canola gb161 CD812518_P1	5964	627	98.7	globlastp
2235	LYD1 94	canola 10v1 DY001783_P1	5964	627	98.7	globlastp
2236	LYD1 94	canola gb161 DY001783_P1	5964	627	98.7	globlastp
2237	LYD1 94	canola 10v1 H74432_P1	5964	627	98.7	globlastp
2238	LYD1 94	thellungiella gb167 BM9859 87_P1	5964	627	98.7	globlastp
2239	LYD1 94	radish gb164 EV524387_P1	5966	627	97.4	globlastp
2240	LYD1 94	dandelion 10v1 DY803351_ P1	5967	627	94.9	globlastp
2241	LYD1 94	dandelion gb161 DY803351_ P1	5967	627	94.9	globlastp
2242	LYD1 94	dandelion 10v1 DY825659_ P1	5968	627	94.9	globlastp
2243	LYD1 94	gerbera 09v1 AJ751548_P1	5969	627	94.9	globlastp
2244	LYD1 94	safflower gb162 EL511059_ P1	5968	627	94.9	globlastp
2245	LYD1 94	sunflower gb162 CD849312_ P1	5968	627	94.9	globlastp
2246	LYD1 94	sunflower gb162 DY937622_ P1	5967	627	94.9	globlastp
2247	LYD1 94	sunflower 10v1 SFSLX0005 9942D2_P1	5968	627	94.9	globlastp
2248	LYD1 94	sunflower gb162 DY953791_ P1	5968	627	94.9	globlastp
2249	LYD1 94	sunflower 10v1 OXSFSLX0 0055287D2T1_P1	5968	627	94.9	globlastp
2250	LYD1 94	tragopogon 10v1 SRR02020 5S0005820_P1	5970	627	93.6	globlastp
2251	LYD1 94	arabidopsis 10v1 AT2G2309 0_P1	5971	627	93.6	globlastp
2252	LYD1 94	lettuce gb157.2 DW043603_ P1	5972	627	93.6	globlastp
2253	LYD1 94	lettuce 10v1 DW075022_P1	5972	627	93.6	globlastp
2254	LYD1 94	lettuce gb157.2 DW075022_ P1	5972	627	93.6	globlastp

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2255	LYD1 94	lettucelgb157.2 DW103809_ P1	5972	627	93.6	globlastp
2256	LYD1 94	lettucel10v1 DW147737_P1	5972	627	93.6	globlastp
2257	LYD1 94	lettucelgb157.2 DW147737_ P1	5972	627	93.6	globlastp
2258	LYD1 94	lettucel10v1 DW043603_P1	5972	627	93.6	globlastp
2259	LYD1 94	cichoriumlgb171 DT210820 _T1	5973	627	92.31	glotblastn
2260	LYD1 94	arabidopsis_lyratal09v1 BQ8 34396_P1	5974	627	92.3	globlastp
2261	LYD1 94	gerberal09v1 AJ750006_P1	5975	627	92.3	globlastp
2262	LYD1 94	artemisialgb164 EY036549_ P1	5976	627	91	globlastp
2263	LYD1 94	sunflowerlgb162 CD849585 _P1	5977	627	91	globlastp
2264	LYD1 94	sunflowerl10v1 SFSLX0013 2901D2_P1	5977	627	91	globlastp
2265	LYD1 94	sunflowerlgb162 DY948679 _P1	5977	627	91	globlastp
2266	LYD1 94	sunflowerlgb162 DY954159 _P1	5977	627	91	globlastp
2267	LYD1 94	sunflowerl10v1 DY937622_ P1	5978	627	89.7	globlastp
2268	LYD1 94	centaurealgb166 EH747727_ P1	5979	627	89.7	globlastp
2269	LYD1 94	cottonlgb164 DT049285_P1	5980	627	89.7	globlastp
2270	LYD1 94	cottonl10v1 BF277062_P1	5980	627	89.7	globlastp
2271	LYD1 94	ipomoea_nill10v1 BJ553105 _P1	5981	627	88.5	globlastp
2272	LYD1 94	basilicumlgb157.3 DY32376 6_P1	5982	627	88.5	globlastp
2273	LYD1 94	cottonlgb164 BF277062_P1	5983	627	88.5	globlastp
2274	LYD1 94	iceplantlgb164 BE034180_P 1	5984	627	88.5	globlastp
2275	LYD1 94	ipomoealgb157.2 BJ553105_ P1	5981	627	88.5	globlastp
2276	LYD1 94	sunflowerl10v1 AF495716_ T1	5985	627	88.46	glotblastn
2277	LYD1 94	cleome_spinosal10v1 SRR01 5531S0016978_P1	5986	627	87.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2278	LYD1 94	ipomoea_batatas 10v1 BU69 0434_P1	5987	627	87.2	globlastp
2279	LYD1 94	nasturtium 10v1 GH161629_ P1	5988	627	87.2	globlastp
2280	LYD1 94	oak 10v1 DN950139_P1	5989	627	87.2	globlastp
2281	LYD1 94	orobanche 10v1 SRR023495 S0014225_P1	5990	627	87.2	globlastp
2282	LYD1 94	chestnut gb170 SRR006295S 0000066_P1	5989	627	87.2	globlastp
2283	LYD1 94	cotton 10v1 CO096638_P1	5991	627	87.2	globlastp
2284	LYD1 94	cotton gb164 CO096638_P1	5991	627	87.2	globlastp
2285	LYD1 94	cowpea gb166 FC456727_P 1	5992	627	87.2	globlastp
2286	LYD1 94	lotus 09v1 AI967422_P1	5993	627	87.2	globlastp
2287	LYD1 94	monkeyflower 09v1 GR0091 99_P1	5994	627	87.2	globlastp
2288	LYD1 94	monkeyflower 10v1 GO9607 37_P1	5994	627	87.2	globlastp
2289	LYD1 94	oak gb170 DN950139_P1	5989	627	87.2	globlastp
2290	LYD1 94	sunflower gb162 BU019187 _P1	5995	627	87.2	globlastp
2291	LYD1 94	tobacco gb162 CV018430_P 1	5990	627	87.2	globlastp
2292	LYD1 94	tobacco gb162 EB683810_P 1	5990	627	87.2	globlastp
2293	LYD1 94	artemisia 10v1 SRR019254S 0578500_T1	5996	627	87.18	glotblastn
2294	LYD1 94	cucumber 09v1 AI563048_P 1	5997	627	85.9	globlastp
2295	LYD1 94	melon 10v1 AM715786_P1	5998	627	85.9	globlastp
2296	LYD1 94	nasturtium 10v1 GH161507_ P1	5999	627	85.9	globlastp
2297	LYD1 94	basilicum gb157.3 DY32218 1_P1	6000	627	85.9	globlastp
2298	LYD1 94	bean gb167 CA911581_T1	6001	627	85.9	glotblastn
2299	LYD1 94	cassava 09v1 DV449827_P1	6002	627	85.9	globlastp
2300	LYD1 94	cassava gb164 DV449827_P 1	6002	627	85.9	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2301	LYD1 94	chickpeal09v2 AJ012688_P1	6003	627	85.9	globlastp
2302	LYD1 94	kiwilgb166 FG431941_P1	6004	627	85.9	globlastp
2303	LYD1 94	liquoricelgb171 FS239342_P 1	6005	627	85.9	globlastp
2304	LYD1 94	melon gb165 AM715786_P1	5998	627	85.9	globlastp
2305	LYD1 94	peanut 10v1 EE126745_P1	6006	627	85.9	globlastp
2306	LYD1 94	peanut gb171 EE126745_P1	6006	627	85.9	globlastp
2307	LYD1 94	pepper gb171 BM065729_P 1	6007	627	85.9	globlastp
2308	LYD1 94	petunialgb171 CV293086_P 1	6008	627	85.9	globlastp
2309	LYD1 94	petunialgb171 DY395819_P 1	6009	627	85.9	globlastp
2310	LYD1 94	poppy gb166 FE967024_P1	6010	627	85.9	globlastp
2311	LYD1 94	rose 10v1 BQ106036_P1	6011	627	85.9	globlastp
2312	LYD1 94	rose gb157.2 BQ106036_P1	6011	627	85.9	globlastp
2313	LYD1 94	soybean gb168 BE239639_P 1	6012	627	85.9	globlastp
2314	LYD1 94	spruce gb162 CO225902_P1	6013	627	85.9	globlastp
2315	LYD1 94	sunflower gb162 DY958076 _P1	6014	627	85.9	globlastp
2316	LYD1 94	tripphysarial10v1 DR170795_ T1	6015	627	85.9	glotblastn
2317	LYD1 94	tripphysarialgb164 DR170795 _T1	6016	627	85.9	glotblastn
2318	LYD1 94	zamialgb166 DY033353_P1	6017	627	85.9	globlastp
2319	LYD1 94	basilicum 10v1 DY322181_ P1	6000	627	85.9	globlastp
2320	LYD1 94	salvial10v1 SRR014553S000 6174_T1	6018	627	84.62	glotblastn
2321	LYD1 94	sunflower gb162 CF089569_ T1	6019	627	84.62	glotblastn
2322	LYD1 94	eggplant 10v1 FS001058_P1	6020	627	84.6	globlastp
2323	LYD1 94	eschschozial10v1 CK75462 2_P1	6021	627	84.6	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2324	LYD1 94	oakl10v1 DN949808_P1	6022	627	84.6	globlastp
2325	LYD1 94	orobanche 10v1 SRR023189 S0001513_P1	6023	627	84.6	globlastp
2326	LYD1 94	pigeonpeal10v1 SRR054580 S0170685_P1	6024	627	84.6	globlastp
2327	LYD1 94	salvial10v1 CV165022_P1	6025	627	84.6	globlastp
2328	LYD1 94	salvial10v1 CV170012_P1	6026	627	84.6	globlastp
2329	LYD1 94	canola gb161 EE501998_P1	6027	627	84.6	globlastp
2330	LYD1 94	chestnut gb170 SRR006295S 0007568_P1	6022	627	84.6	globlastp
2331	LYD1 94	citrus gb166 BQ624729_P1	6028	627	84.6	globlastp
2332	LYD1 94	citrus gb166 CB610588_P1	6029	627	84.6	globlastp
2333	LYD1 94	cottonl10v1 DW507921_P1	6030	627	84.6	globlastp
2334	LYD1 94	cycas gb166 CB092434_P1	6031	627	84.6	globlastp
2335	LYD1 94	grape gb160 CA816369_P1	6032	627	84.6	globlastp
2336	LYD1 94	oak gb170 DN949808_P1	6022	627	84.6	globlastp
2337	LYD1 94	poplarl10v1 AI166137_P1	6033	627	84.6	globlastp
2338	LYD1 94	poplar gb170 AI166137_P1	6033	627	84.6	globlastp
2339	LYD1 94	poplarl10v1 BI125869_P1	6034	627	84.6	globlastp
2340	LYD1 94	poplar gb170 BU815949_P1	6035	627	84.6	globlastp
2341	LYD1 94	poplar gb170 CV243434_P1	6036	627	84.6	globlastp
2342	LYD1 94	potato 10v1 BQ117694_P1	6037	627	84.6	globlastp
2343	LYD1 94	potato gb157.2 BQ117694_P 1	6037	627	84.6	globlastp
2344	LYD1 94	solanum_phureja 09v1 SPH BG133573_P1	6037	627	84.6	globlastp
2345	LYD1 94	soybean gb168 AW350181_ P1	6038	627	84.6	globlastp
2346	LYD1 94	soybean gb168 CA911585_P 1	6039	627	84.6	globlastp

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2347	LYD1 94	strawberry gb164 CO379357_P1	6040	627	84.6	globlastp
2348	LYD1 94	tamarix gb166 CF199285_P1	6041	627	84.6	globlastp
2349	LYD1 94	tomato 09v1 BG133573_P1	6042	627	84.6	globlastp
2350	LYD1 94	tomato gb164 BG133573_P1	6043	627	84.6	globlastp
2351	LYD1 94	walnuts gb166 CV196224_P1	6044	627	84.6	globlastp
2352	LYD1 94	sunflower gb162 EL461916_P1	6045	627	83.5	globlastp
2353	LYD1 94	heritiera 10v1 SRR005795S0018549_T1	6046	627	83.33	glotblastn
2354	LYD1 94	cotton gb164 DW507921_T1	6047	627	83.33	glotblastn
2355	LYD1 94	poplar 10v1 BU886510_T1	6048	627	83.33	glotblastn
2356	LYD1 94	potato gb157.2 BG596893_T1	6049	627	83.33	glotblastn
2357	LYD1 94	canola 10v1 EE501998_P1	6050	627	83.3	globlastp
2358	LYD1 94	cyamopsis 10v1 EG978606_P1	6051	627	83.3	globlastp
2359	LYD1 94	ipomoea_batatas 10v1 DV037875XX1_P1	6052	627	83.3	globlastp
2360	LYD1 94	prunus 10v1 BU573631_P1	6053	627	83.3	globlastp
2361	LYD1 94	salvia 10v1 FE536036_P1	6054	627	83.3	globlastp
2362	LYD1 94	apple gb171 CN489087_P1	6055	627	83.3	globlastp
2363	LYD1 94	apple gb171 CN490842_P1	6055	627	83.3	globlastp
2364	LYD1 94	avocado 10v1 FD503400_P1	6056	627	83.3	globlastp
2365	LYD1 94	avocado gb164 FD503400_P1	6056	627	83.3	globlastp
2366	LYD1 94	basilicum gb157.3 DY323895_P1	6057	627	83.3	globlastp
2367	LYD1 94	bean gb167 FD794659_P1	6058	627	83.3	globlastp
2368	LYD1 94	cassava 09v1 FF534508_P1	6059	627	83.3	globlastp
2369	LYD1 94	cassava gb164 DB931786_P1	6059	627	83.3	globlastp

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<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2370	LYD1 94	coffeal10v1 DV667171_P1	6060	627	83.3	globlastp
2371	LYD1 94	coffealgb157.2 DV667171_P 1	6060	627	83.3	globlastp
2372	LYD1 94	cottonlgb164 BE053050_P1	6061	627	83.3	globlastp
2373	LYD1 94	cottonlgb164 DR457498_P1	6061	627	83.3	globlastp
2374	LYD1 94	ipomoealgb157.2 DV037875 _P1	6052	627	83.3	globlastp
2375	LYD1 94	kiwilgb166 FG487691_P1	6062	627	83.3	globlastp
2376	LYD1 94	maizelgb170 AW438182_P1	6063	627	83.3	globlastp
2377	LYD1 94	oil_palm lgb166 EL691360_ P1	6064	627	83.3	globlastp
2378	LYD1 94	pinel10v1 AA739705_P1	6065	627	83.3	globlastp
2379	LYD1 94	pinel10v1 AL750053_P1	6065	627	83.3	globlastp
2380	LYD1 94	prunus gb167 BU043372_P1	6055	627	83.3	globlastp
2381	LYD1 94	prunus gb167 CB819316_P1	6055	627	83.3	globlastp
2382	LYD1 94	soybean gb168 AI967422_P 1	6066	627	83.3	globlastp
2383	LYD1 94	switchgrass gb167 DN14803 5_P1	6067	627	83.3	globlastp
2384	LYD1 94	prunus 10v1 BU043372_P1	6055	627	83.3	globlastp
2385	LYD1 94	maizel10v1 AW438182_P1	6063	627	83.3	globlastp
2386	LYD1 94	antirrhinum lgb166 AJ78733 6_P1	6068	627	82.5	globlastp
2387	LYD1 94	bananal10v1 FF560086_P1	6069	627	82.3	globlastp
2388	LYD1 94	barley 10v1 BE412562_P1	6070	627	82.1	globlastp
2389	LYD1 94	ginsengl10v1 DV553491_P1	6071	627	82.1	globlastp
2390	LYD1 94	ipomoea_nill10v1 BJ554752 _P1	6072	627	82.1	globlastp
2391	LYD1 94	pigeonpeal10v1 GW352154_ P1	6073	627	82.1	globlastp
2392	LYD1 94	bananal10v1 FL659021_P1	6074	627	82.1	globlastp

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2393	LYD1 94	bananalgb167 FL659021_P1	6074	627	82.1	globlastp
2394	LYD1 94	beanlgb167 CA910834_P1	6075	627	82.1	globlastp
2395	LYD1 94	cassaval09v1 DV441811_P1	6076	627	82.1	globlastp
2396	LYD1 94	cassavalgb164 DV441811_P 1	6076	627	82.1	globlastp
2397	LYD1 94	ipomoealgb157.2 BJ554752_ P1	6072	627	82.1	globlastp
2398	LYD1 94	liquoricelgb171 FS241175_P 1	6077	627	82.1	globlastp
2399	LYD1 94	liriodendronlgb166 CK7578 11_P1	6078	627	82.1	globlastp
2400	LYD1 94	lotus 09v1 GO022193_P1	6079	627	82.1	globlastp
2401	LYD1 94	maizelgb170 LLEC884141_ P1	6080	627	82.1	globlastp
2402	LYD1 94	nupharlgb166 CK745724_P1	6081	627	82.1	globlastp
2403	LYD1 94	oil_palm lgb166 EY398455_ P1	6082	627	82.1	globlastp
2404	LYD1 94	papayalgb165 EX252933_P1	6083	627	82.1	globlastp
2405	LYD1 94	peanutlgb171 CX127962_P1	6084	627	82.1	globlastp
2406	LYD1 94	pseudoroegnerialgb167 FF34 4954_P1	6070	627	82.1	globlastp
2407	LYD1 94	ryelgb164 BE587111_P1	6070	627	82.1	globlastp
2408	LYD1 94	sesamel10v1 BU669421_P1	6085	627	82.1	globlastp
2409	LYD1 94	sesamelgb157.2 BU669421_ P1	6085	627	82.1	globlastp
2410	LYD1 94	sorghuml09v1 SB01G03184 0_P1	6086	627	82.1	globlastp
2411	LYD1 94	sugarcanelgb157.3 BQ53544 7_P1	6087	627	82.1	globlastp
2412	LYD1 94	sugarcanelgb157.3 CA19841 0_P1	6087	627	82.1	globlastp
2413	LYD1 94	tobacco lgb162 CV016265_P 1	6088	627	82.1	globlastp
2414	LYD1 94	sugarcanel10v1 BQ535447_ P1	6087	627	82.1	globlastp
2415	LYD1 94	cotton 10v1 BE053050_P1	6089	627	82.1	globlastp

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2416	LYD1 94	pigeonpeal10v1 SRR054580 S0180637_T1	6090	627	82.05	glotblastn
2417	LYD1 94	cleome_spinosal10v1 GR931 202_P1	6091	627	81	globlastp
2418	LYD1 94	beech gb170 SRR006293S00 02103_P1	6092	627	81	globlastp
2419	LYD1 94	monkeyflower 09v1 GO9827 68_P1	6093	627	81	globlastp
2420	LYD1 94	monkeyflower 10v1 DV2064 69_P1	6093	627	81	globlastp
2421	LYD1 94	blueberry 10v1 CF811639_P 1	6094	627	80.8	globlastp
2422	LYD1 94	cucumber 09v1 AM719428_ P1	6095	627	80.8	globlastp
2423	LYD1 94	cucumber 09v1 DV632453_ P1	6096	627	80.8	globlastp
2424	LYD1 94	eggplant 10v1 FS001750_P1	6097	627	80.8	globlastp
2425	LYD1 94	melon 10v1 DV632453_P1	6096	627	80.8	globlastp
2426	LYD1 94	oat 10v2 CN814648_P1	6098	627	80.8	globlastp
2427	LYD1 94	b_juncealgb164 EVGN0077 7512133168_P1	6099	627	80.8	globlastp
2428	LYD1 94	beet gb162 BQ585430_P1	6100	627	80.8	globlastp
2429	LYD1 94	castorbean 09v1 XM002510 070_P1	6101	627	80.8	globlastp
2430	LYD1 94	castorbean 09v1 XM002533 116_P1	6102	627	80.8	globlastp
2431	LYD1 94	cowpealgb166 DR068342_P 1	6103	627	80.8	globlastp
2432	LYD1 94	cryptomer gb166 BW9946 67_P1	6104	627	80.8	globlastp
2433	LYD1 94	fescue gb161 CK803222_P1	6105	627	80.8	globlastp
2434	LYD1 94	ginger gb164 DY354931_P1	6106	627	80.8	globlastp
2435	LYD1 94	lolium 09v1 AU246760_P1	6105	627	80.8	globlastp
2436	LYD1 94	lolium 10v1 AU246760_P1	6105	627	80.8	globlastp
2437	LYD1 94	melon gb165 DV632453_P1	6096	627	80.8	globlastp
2438	LYD1 94	nuphar gb166 CD475546_P1	6107	627	80.8	globlastp

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2439	LYD1 94	rice gb170 OS07G02340_P1	6108	627	80.8	globlastp
2440	LYD1 94	soybean gb168 CA910834_P 1	6109	627	80.8	globlastp
2441	LYD1 94	antirrhinum gb166 AJ78864 1_T1	6110	627	80.77	glotblastn
2442	LYD1 94	eucalyptus gb166 CT983755 _T1	6111	627	80.77	glotblastn
2443	LYD1 94	medicago 09v1 BE239639_P 1	6112	627	80	globlastp
2444	LYD1 95	potato 10v1 BG096397_P1	6113	628	99.6	globlastp
2445	LYD1 95	potato gb157.2 BG096397_P 1	6113	628	99.6	globlastp
2446	LYD1 95	solanum_phureja 09v1 SPH AI483451_P1	6113	628	99.6	globlastp
2447	LYD1 95	tobacco gb162 AF022775_P 1	6114	628	91.8	globlastp
2448	LYD1 95	tobacco gb162 EB424611_P 1	6115	628	91.8	globlastp
2449	LYD1 95	eggplant 10v1 FS008855_P1	6116	628	90.2	globlastp
2450	LYD1 95	tobacco gb162 AJ344574_P1	6117	628	89.9	globlastp
2451	LYD1 95	pepper gb171 BM062010_P 1	6118	628	89.5	globlastp
2452	LYD1 95	potato 10v1 BF459570_P1	6119	628	89.1	globlastp
2453	LYD1 95	potato gb157.2 BF459570_P 1	6119	628	89.1	globlastp
2454	LYD1 95	tomato gb164 BG133462_P1	6120	628	89.1	globlastp
2455	LYD1 95	solanum_phureja 09v1 SPH BG133462_P1	6121	628	88.7	globlastp
2456	LYD1 95	tobacco gb162 CV021257_P 1	6122	628	88.7	globlastp
2457	LYD1 95	petunia gb171 CV293247_P 1	6123	628	88.4	globlastp
2458	LYD1 95	artemisia 10v1 EY055561_P 1	6124	628	88.2	globlastp
2459	LYD1 95	artemisia 10v1 EY078221_P 1	6125	628	88.2	globlastp
2460	LYD1 95	nasturtium 10v1 GH170063_ P1	6126	628	88.2	globlastp
2461	LYD1 95	lettuce 10v1 DW110506_P1	6127	628	87.8	globlastp

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2462	LYD1 95	lettucelgb157.2 DW112190_ P1	6128	628	87.8	globlastp
2463	LYD1 95	lettucel10v1 DW079750_P1	6129	628	87.8	globlastp
2464	LYD1 95	applelgb171 CN489101_P1	6130	628	87.5	globlastp
2465	LYD1 95	centaurealgb166 EH764503_ P1	6131	628	87.3	globlastp
2466	LYD1 95	lettucelgb157.2 DW043694_ P1	6132	628	87.3	globlastp
2467	LYD1 95	lettucelgb157.2 DW079750_ P1	6133	628	87.3	globlastp
2468	LYD1 95	lettucelgb157.2 DW095151_ P1	6134	628	87.3	globlastp
2469	LYD1 95	lettucel10v1 DW043694_P1	6132	628	87.3	globlastp
2470	LYD1 95	dandelion 10v1 DR398855_ P1	6135	628	87	globlastp
2471	LYD1 95	artemisial10v1 EY114017_P 1	6136	628	87	globlastp
2472	LYD1 95	artemisialgb164 EY114017_ P1	6136	628	87	globlastp
2473	LYD1 95	lettucel10v1 DW054823_P1	6137	628	86.9	globlastp
2474	LYD1 95	lettucelgb157.2 DW085965_ P1	6138	628	86.9	globlastp
2475	LYD1 95	seneciolgb170 DY658676_P 1	6139	628	86.9	globlastp
2476	LYD1 95	poplar gb170 AJ224895_P1	6140	628	86.7	globlastp
2477	LYD1 95	dandelion 10v1 DR398892_ P1	6141	628	86.6	globlastp
2478	LYD1 95	dandelionlgb161 DY819202_ P1	6141	628	86.6	globlastp
2479	LYD1 95	centaurealgb166 EH732032_ T1	6142	628	86.53	glotblastn
2480	LYD1 95	lettucelgb157.2 DW078439_ T1	6143	628	86.53	glotblastn
2481	LYD1 95	tragopogon 10v1 SRR02020 5S0001708_P1	6144	628	86.5	globlastp
2482	LYD1 95	centaurealgb166 EH733702_ P1	6145	628	86.5	globlastp
2483	LYD1 95	centaurealgb166 EH780631_ P1	6146	628	86.5	globlastp
2484	LYD1 95	dandelion 10v1 DY816598_ P1	6147	628	86.5	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2485	LYD1 95	dandelion gb161 DY816598_P1	6147	628	86.5	globlastp
2486	LYD1 95	dandelion 10v1 DY828265_P1	6148	628	86.5	globlastp
2487	LYD1 95	dandelion gb161 DY828265_P1	6148	628	86.5	globlastp
2488	LYD1 95	lettuce gb157.2 DW077273_P1	6149	628	86.5	globlastp
2489	LYD1 95	strawberry gb164 AJ001447_P1	6150	628	86.5	globlastp
2490	LYD1 95	sunflower gb162 CF088560_P1	6151	628	86.5	globlastp
2491	LYD1 95	sunflower 10v1 DY925822_P1	6152	628	86.5	globlastp
2492	LYD1 95	sunflower gb162 DY925822_P1	6152	628	86.5	globlastp
2493	LYD1 95	sunflower 10v1 CF088560_P1	6151	628	86.5	globlastp
2494	LYD1 95	poplar 10v1 AJ224895_P1	6153	628	86.3	globlastp
2495	LYD1 95	poplar 10v1 PTU27116_P1	6154	628	86.3	globlastp
2496	LYD1 95	poplar gb170 PTU27116_P1	6154	628	86.3	globlastp
2497	LYD1 95	oak 10v1 EE743854_P1	6155	628	86.2	globlastp
2498	LYD1 95	chestnut gb170 SRR006295S0000995_P1	6156	628	86.2	globlastp
2499	LYD1 95	kiwi gb166 FG418869_P1	6157	628	86.2	globlastp
2500	LYD1 95	oak gb170 EE743854_P1	6156	628	86.2	globlastp
2501	LYD1 95	prunus 10v1 BU044203_P1	6158	628	86.2	globlastp
2502	LYD1 95	prunus gb167 BU044203_P1	6158	628	86.2	globlastp
2503	LYD1 95	tragopogon 10v1 SRR020205S0055567_T1	6159	628	86.12	glotblastn
2504	LYD1 95	lettuce gb157.2 DW075466_T1	6160	628	86.12	glotblastn
2505	LYD1 95	ipomoea_batatas 10v1 BU690759_P1	6161	628	86.1	globlastp
2506	LYD1 95	ipomoea_nill 10v1 CJ738710_P1	6162	628	86.1	globlastp
2507	LYD1 95	b_junceal 10v2 E6ANDIZ01A38JW_P1	6163	628	86.1	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
2508	LYD1 95	ipomoealgb157.2 BU690759_P1	6164	628	86.1	globlastp
2509	LYD1 95	lettucelgb157.2 DW054823_P1	6165	628	86.1	globlastp
2510	LYD1 95	sunflower gb162 CF096542_P1	6166	628	86.1	globlastp
2511	LYD1 95	coffeal10v1 AF534905_P1	6167	628	85.9	globlastp
2512	LYD1 95	coffealgb157.2 AF534905_P1	6167	628	85.9	globlastp
2513	LYD1 95	eucalyptus gb166 AF168780_P1	6168	628	85.9	globlastp
2514	LYD1 95	kiwilgb166 FG421337_P1	6169	628	85.9	globlastp
2515	LYD1 95	flax 09v1 EU926495_P1	6170	628	85.8	globlastp
2516	LYD1 95	centaurealgb166 EH730909_P1	6171	628	85.8	globlastp
2517	LYD1 95	flax 09v1 DQ090002_P1	6172	628	85.8	globlastp
2518	LYD1 95	flax gb157.3 DQ090002_P1	6172	628	85.8	globlastp
2519	LYD1 95	safflower gb162 EL382540_P1	6171	628	85.8	globlastp
2520	LYD1 95	artemisialgb164 EY055561_P1	6173	628	85.7	globlastp
2521	LYD1 95	basilicum gb157.3 DY321549_P1	6174	628	85.7	globlastp
2522	LYD1 95	lettucelgb157.2 BQ986770_P1	6175	628	85.7	globlastp
2523	LYD1 95	lettucelgb157.2 DW107581_P1	6176	628	85.7	globlastp
2524	LYD1 95	lettucelgb157.2 DW110506_P1	6177	628	85.7	globlastp
2525	LYD1 95	lettucelgb157.2 DW136638_P1	6176	628	85.7	globlastp
2526	LYD1 95	zinnialgb171 ZEU13151_P1	6178	628	85.7	globlastp
2527	LYD1 95	lettucel10v1 DW063228_P1	6176	628	85.7	globlastp
2528	LYD1 95	b_junceal10v2 E6ANDIZ01A37PS_P1	6179	628	85.6	globlastp
2529	LYD1 95	b_juncealgb164 EVGN00576715131914_P1	6180	628	85.5	globlastp
2530	LYD1 95	triphysarial10v1 BE574803_P1	6181	628	85.5	globlastp

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2531	LYD1 95	triphysarialgb164 EX990149_P1	6181	628	85.5	globlastp
2532	LYD1 95	soybeanlgb168 AI974778_P1	6182	628	85.4	globlastp
2533	LYD1 95	soybeanlgb168 AW350997_P1	6183	628	85.4	globlastp
2534	LYD1 95	ipomoealgb157.2 EE875282_T1	6184	628	85.31	glotblastn
2535	LYD1 95	lettucelgb157.2 DW063228_P1	6185	628	85.3	globlastp
2536	LYD1 95	melonl10v1 AM722923_P1	6186	628	85.1	globlastp
2537	LYD1 95	monkeyflowerl10v1 DV206851_P1	6187	628	85.1	globlastp
2538	LYD1 95	orobanche 10v1 SRR023189S0001619_P1	6188	628	85.1	globlastp
2539	LYD1 95	cowpealgb166 FF383224_P1	6189	628	85.1	globlastp
2540	LYD1 95	artemisial10v1 EY062910_P1	6190	628	85	globlastp
2541	LYD1 95	dandelionl10v1 DR400849_P1	6191	628	85	globlastp
2542	LYD1 95	cichoriumlgb171 EH681911_P1	6192	628	84.9	globlastp
2543	LYD1 95	dandelionl10v1 DY822859_P1	6193	628	84.9	globlastp
2544	LYD1 95	dandelionlgb161 DY822859_P1	6193	628	84.9	globlastp
2545	LYD1 95	pepperlgb171 BM062476_P1	6194	628	84.9	globlastp
2546	LYD1 95	pepperlgb171 GD052907_P1	6195	628	84.9	globlastp
2547	LYD1 95	potatolgb157.2 AB061268_P1	6196	628	84.9	globlastp
2548	LYD1 95	potatol10v1 CK259364_P1	6197	628	84.9	globlastp
2549	LYD1 95	potatolgb157.2 CK259364_P1	6197	628	84.9	globlastp
2550	LYD1 95	safflowerlgb162 EL401429_P1	6198	628	84.9	globlastp
2551	LYD1 95	catharanthuslgb166 FD416177_P1	6199	628	84.7	globlastp
2552	LYD1 95	peanutlgb171 EG029550_P1	6200	628	84.7	globlastp
2553	LYD1 95	safflowerlgb162 EL401924_T1	6201	628	84.68	glotblastn

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2554	LYD1 95	cacao gb167 CF972935_P1	6202	628	84.6	globlastp
2555	LYD1 95	cotton gb164 BQ409901_P1	6203	628	84.6	globlastp
2556	LYD1 95	cynara gb167 GE585761_P1	6204	628	84.6	globlastp
2557	LYD1 95	artemisia gb164 EY062910_ T1	6205	628	84.55	glotblastn
2558	LYD1 95	basilicum 10v1 DY321550_ P1	6206	628	84.5	globlastp
2559	LYD1 95	aquilegia 10v1 DR940223_P 1	6207	628	84.5	globlastp
2560	LYD1 95	basilicum 10v1 DY322646_ P1	6208	628	84.5	globlastp
2561	LYD1 95	basilicum gb157.3 DY32264 6_P1	6208	628	84.5	globlastp
2562	LYD1 95	aquilegia gb157.3 DR940223 _T1	6209	628	84.49	glotblastn
2563	LYD1 95	lettuce gb157.2 DW046035_ T1	6210	628	84.49	glotblastn
2564	LYD1 95	cucumber 09v1 DQ178939_ P1	6211	628	84.3	globlastp
2565	LYD1 95	bean gb167 CB539234_P1	6212	628	84.3	globlastp
2566	LYD1 95	peanut 10v1 EG029550_P1	6213	628	84.3	globlastp
2567	LYD1 95	walnut gb166 EL893897_P 1	6214	628	84.3	globlastp
2568	LYD1 95	cotton 10v1 BQ409901_P1	6215	628	84.2	globlastp
2569	LYD1 95	sunflower 10v1 DY918862_ P1	6216	628	84.2	globlastp
2570	LYD1 95	sunflower gb162 DY918862 _P1	6216	628	84.2	globlastp
2571	LYD1 95	eggplant 10v1 FS002731_P1	6217	628	84.1	globlastp
2572	LYD1 95	lettuce gb157.2 DW052563_ P1	6218	628	84.1	globlastp
2573	LYD1 95	pepper gb171 BM065108_P 1	6219	628	84.1	globlastp
2574	LYD1 95	petunia gb171 CV293837_P 1	6220	628	84.1	globlastp
2575	LYD1 95	tomato gb164 BG132250_P1	6221	628	84.1	globlastp
2576	LYD1 95	cynara gb167 GE588483_T1	6222	628	84.08	glotblastn

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2577	LYD1 95	onion gb162 BI095707_T1	6223	628	84.08	glotblastn
2578	LYD1 95	lettuce 10v1 DW079335_P1	6224	628	84	globlastp
2579	LYD1 95	lettuce gb157.2 DW079335_P1	6224	628	84	globlastp
2580	LYD1 95	cyamopsis 10v1 EG985137_P1	6225	628	83.9	globlastp
2581	LYD1 95	tragopogon 10v1 SRR020205S0054743_P1	6226	628	83.9	globlastp
2582	LYD1 95	sunflower 10v1 CD849237_P1	6227	628	83.8	globlastp
2583	LYD1 95	sunflower gb162 CD849237_P1	6228	628	83.8	globlastp
2584	LYD1 95	eggplant 10v1 FS074698_P1	6229	628	83.7	globlastp
2585	LYD1 95	grape gb160 CF213537_P1	6230	628	83.7	globlastp
2586	LYD1 95	lettuce gb157.2 DW108949_P1	6231	628	83.7	globlastp
2587	LYD1 95	petunia gb171 CV292827_P1	6232	628	83.7	globlastp
2588	LYD1 95	solanum_phureja 09v1 SPHAI488060_P1	6233	628	83.7	globlastp
2589	LYD1 95	lettuce 10v1 DW052563_P1	6231	628	83.7	globlastp
2590	LYD1 95	sunflower 10v1 DY952631_T1	6234	628	83.67	glotblastn
2591	LYD1 95	dandelion gb161 DY818320_T1	6235	628	83.67	glotblastn
2592	LYD1 95	lettuce gb157.2 DW167480_T1	6236	628	83.67	glotblastn
2593	LYD1 95	lovegrass gb167 DN480953_T1	6237	628	83.67	glotblastn
2593	LYD2 11	lovegrass gb167 DN480953_P1	6237	638	89.3	globlastp
2594	LYD1 95	citrus gb166 BQ623631_P1	6238	628	83.5	globlastp
2595	LYD1 95	grape gb160 CB346952_P1	6239	628	83.4	globlastp
2596	LYD1 95	medicago 09v1 MSU20736_P1	6240	628	83.4	globlastp
2597	LYD1 95	avocado 10v1 CV459964_T1	6241	628	83.33	glotblastn
2598	LYD1 95	avocado gb164 CV459964_T1	6242	628	83.33	glotblastn

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2599	LYD1 95	basilicum gb157.3 DY32142 0_P1	6243	628	83.3	globlastp
2600	LYD1 95	tobacco gb162 NTU62734_P 1	6244	628	83.3	globlastp
2601	LYD1 95	safflower gb162 EL395137_ T1	6245	628	83.27	glotblastn
2602	LYD1 95	wheat gb164 BG605452_T1	6246	628	83.27	glotblastn
2602	LYD2 11	wheat gb164 BG605452_P1	6246	638	86.6	globlastp
2603	LYD1 95	cotton 10v1 CO083019_P1	6247	628	83.1	globlastp
2604	LYD1 95	cotton gb164 CO083019_P1	6247	628	83.1	globlastp
2605	LYD1 95	dandelion 10v1 DY813534_ P1	6248	628	83.1	globlastp
2606	LYD1 95	eucalyptus gb166 Y12228_P 1	6249	628	83	globlastp
2607	LYD1 95	lotus 09v1 AW163940_P1	6250	628	83	globlastp
2608	LYD1 95	cichorium gb171 EH703864 _T1	6251	628	82.93	glotblastn
2609	LYD1 95	b_rapa gb162 BG544230_P1	6252	628	82.9	globlastp
2609	LYD2 11	b_rapa gb162 BG544230_P1	6252	638	81.2	globlastp
2610	LYD1 95	dandelion 10v1 DY811080_ P1	6253	628	82.9	globlastp
2611	LYD1 95	dandelion gb161 DY811080 _P1	6253	628	82.9	globlastp
2612	LYD1 95	ginger gb164 DY345043_P1	6254	628	82.9	globlastp
2613	LYD1 95	radish gb164 EV525011_P1	6255	628	82.9	globlastp
2613	LYD2 11	radish gb164 EV525011_P1	6255	638	80.5	globlastp
2614	LYD1 95	radish gb164 EV525082_P1	6256	628	82.9	globlastp
2614	LYD2 11	radish gb164 EV525082_P1	6256	638	81.2	globlastp
2615	LYD1 95	tobacco gb162 NTU38612_P 1	6257	628	82.9	globlastp
2616	LYD1 95	tomato gb164 EU161983_P1	6258	628	82.9	globlastp
2617	LYD1 95	pseudoroegneria gb167 FF34 4366_T1	6259	628	82.86	glotblastn

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2617	LYD2 11	pseudoroegneria gb167 FF34 4366_P1	6259	638	86.6	globlastp
2618	LYD1 95	wheat gb164 BE499248_T1	6260	628	82.86	glotblastn
2618	LYD2 11	wheat gb164 BE499248_T1	6260	638	85.39	glotblastn
2619	LYD1 95	cleome_spinosal10v1 GR934 613_T1	6261	628	82.8	glotblastn
2620	LYD1 95	papaya gb165 AM903875_P 1	6262	628	82.7	globlastp
2621	LYD1 95	cynodon 10v1 ES293249_T1	6263	628	82.66	glotblastn
2621	LYD2 11	cynodon 10v1 ES293249_P1	6263	638	90.1	globlastp
2622	LYD1 95	b_juncea 10v2 E6ANDIZ01 B5QRG_P1	6264	628	82.6	globlastp
2622	LYD2 11	b_juncea 10v2 E6ANDIZ01 B5QRG_P1	6264	638	81.6	globlastp
2623	LYD1 95	monkeyflower 10v1 GO9833 07_P1	6265	628	82.6	globlastp
2624	LYD1 95	basilicum 10v1 DY326108_ P1	6266	628	82.6	globlastp
2625	LYD1 95	basilicum gb157.3 DY32610 8_P1	6266	628	82.6	globlastp
2626	LYD1 95	canola 10v1 CD832570_P1	6267	628	82.6	globlastp
2626	LYD2 11	canola 10v1 CD832570_P1	6267	638	81.2	globlastp
2627	LYD1 95	canola gb161 CD832570_P1	6267	628	82.6	globlastp
2627	LYD2 11	canola gb161 CD832570_P1	6267	638	81.2	globlastp
2628	LYD1 95	clover gb162 BB903730_P1	6268	628	82.6	globlastp
2629	LYD1 95	radish gb164 EV535109_P1	6269	628	82.6	globlastp
2629	LYD2 11	radish gb164 EV535109_P1	6269	638	80.1	globlastp
2630	LYD1 95	cichorium gb171 EH694888 _P1	6270	628	82.5	globlastp
2631	LYD1 95	brachypodium 09v1 GT8311 68_T1	6271	628	82.45	glotblastn
2631	LYD2 11	brachypodium 09v1 GT8311 68_P1	6271	638	87.1	globlastp
2632	LYD1 95	artemisia 10v1 EY073536_T 1	6272	628	82.45	glotblastn

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2633	LYD1 95	barley 10v1 BF623901_T1	6273	628	82.45	glotblastn
2633	LYD2 11	barley 10v1 BF623901_P1	6273	638	85.3	globlastp
2634	LYD1 95	barley gb157SOLEXA BF62 3901_T1	6273	628	82.45	glotblastn
2634	LYD2 11	barley gb157SOLEXA BF62 3901_P1	6273	638	85.3	globlastp
2635	LYD1 95	brachypodium gb169 BE406 401_T1	6271	628	82.45	glotblastn
2635	LYD2 11	brachypodium gb169 BE406 401_P1	6271	638	87.1	globlastp
2636	LYD1 95	ipomoea_nill 10v1 BJ562028 _P1	6274	628	82.4	globlastp
2637	LYD1 95	citrus gb166 GFXAB035144 X1_P1	6275	628	82.4	globlastp
2638	LYD1 95	cynara gb167 GE593594_P1	6276	628	82.4	globlastp
2639	LYD1 95	ipomoea gb157.2 BJ562028_ P1	6274	628	82.4	globlastp
2640	LYD1 95	lettuce gb157.2 DW154323_ T1	6277	628	82.33	glotblastn
2641	LYD1 95	dandelion 10v1 DR400478_ P1	6278	628	82.3	globlastp
2642	LYD1 95	dandelion gb161 DY802286 _P1	6278	628	82.3	globlastp
2643	LYD1 95	oak 10v1 FP034949_P1	6279	628	82.2	globlastp
2644	LYD1 95	cacao gb167 CU515299_P1	6280	628	82.2	globlastp
2645	LYD1 95	canola 10v1 CD813970_P1	6281	628	82.2	globlastp
2645	LYD2 11	canola 10v1 CD813970_P1	6281	638	80.8	globlastp
2646	LYD1 95	canola gb161 CD813970_P1	6281	628	82.2	globlastp
2646	LYD2 11	canola gb161 CD813970_P1	6281	638	80.8	globlastp
2647	LYD1 95	liquorice gb171 FS288141_P 1	6282	628	82.2	globlastp
2648	LYD1 95	centaurea gb166 EH783138_ T1	6283	628	82.04	glotblastn
2649	LYD1 95	ipomoea_batatas 10v1 EE87 5716_P1	6284	628	82	globlastp
2650	LYD1 95	cichorium gb171 EH700384 _P1	6285	628	82	globlastp

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2651	LYD1 95	cotton gb164 DT568345_P1	6286	628	82	globlastp
2652	LYD1 95	ipomoea gb157.2 EE875716_P1	6284	628	82	globlastp
2653	LYD1 95	acacia 10v1 EU275979_P1	6287	628	81.9	globlastp
2654	LYD1 95	radish gb164 EV539035_P1	6288	628	81.8	globlastp
2654	LYD2 11	radish gb164 EV539035_P1	6288	638	80.1	globlastp
2655	LYD1 95	cassava 09v1 CK644701_P1	6289	628	81.7	globlastp
2656	LYD1 95	cassava gb164 CK644701_P1	6289	628	81.7	globlastp
2657	LYD1 95	lettuce 10v1 DW079459_P1	6290	628	81.7	globlastp
2658	LYD1 95	lettuce gb157.2 DW079459_P1	6290	628	81.7	globlastp
2659	LYD1 95	lettuce gb157.2 DW114772_P1	6291	628	81.7	globlastp
2660	LYD1 95	lettuce 10v1 DW046035_P1	6291	628	81.7	globlastp
2661	LYD1 95	canola gb161 CD817919_T1	6292	628	81.63	glotblastn
2662	LYD1 95	gerbera 09v1 AJ761949_T1	6293	628	81.63	glotblastn
2663	LYD1 95	cotton 10v1 DT568345_P1	6294	628	81.6	globlastp
2664	LYD1 95	poppy gb166 FE964281_P1	6295	628	81.6	globlastp
2665	LYD1 95	wheat gb164 BE406401_T1	6296	628	81.53	glotblastn
2665	LYD2 11	wheat gb164 BE406401_T1	6296	638	86.64	glotblastn
2666	LYD1 95	b_rapa gb162 AT000531_P1	6297	628	81.5	globlastp
2666	LYD2 11	b_rapa gb162 AT000531_P1	6297	638	80.1	globlastp
2667	LYD1 95	canola gb161 CD825507_P1	6297	628	81.5	globlastp
2667	LYD2 11	canola gb161 CD825507_P1	6297	638	80.1	globlastp
2668	LYD1 95	canola gb161 CN827065_P1	6298	628	81.5	globlastp
2669	LYD1 95	castorbean 09v1 XM002518693_P1	6299	628	81.5	globlastp

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2670	LYD1 95	iceplantlgb164 AF053553_P 1	6300	628	81.5	globlastp
2671	LYD1 95	canola 10v1 CD817919_P1	6297	628	81.5	globlastp
2671	LYD2 11	canola 10v1 CD817919_P1	6297	638	80.1	globlastp
2672	LYD1 95	b_juncealgb164 EVGN0020 8909581615_P1	6301	628	81.5	globlastp
2672	LYD2 11	b_juncealgb164 EVGN0020 8909581615_P1	6301	638	80.1	globlastp
2673	LYD1 95	artemisialgb164 EY073536_ P1	6302	628	81.4	globlastp
2674	LYD1 95	thellungiellalgb167 DN7757 57_P1	6303	628	81.4	globlastp
2675	LYD1 95	jatropha 09v1 GO246755_T 1	6304	628	81.38	glotblastn
2676	LYD1 95	cassavalgb164 DV443819_P 1	6305	628	81.3	globlastp
2677	LYD1 95	cryptomerialgb166 BP17613 4_T1	6306	628	81.27	glotblastn
2678	LYD1 95	pinelgb157.2 AF036095_T1	6307	628	81.22	glotblastn
2679	LYD1 95	b_oleracealgb161 AM38546 4_P1	6308	628	81.2	globlastp
2680	LYD1 95	liriodendronlgb166 DT59519 9_P1	6309	628	81.2	globlastp
2681	LYD1 95	gerberal 09v1 AJ762598_P1	6310	628	81	globlastp
2682	LYD1 95	cassaval 09v1 DV448480_T1	6311	628	80.97	glotblastn
2683	LYD1 95	cassaval 09v1 DV443819_P1	6312	628	80.9	globlastp
2684	LYD1 95	spruce lgb162 CO226032_T1	6313	628	80.82	glotblastn
2685	LYD1 95	pinel 10v1 AA556630_T1	6314	628	80.82	glotblastn
2686	LYD1 95	switchgrass lgb167 DN14069 1_T1	6315	628	80.82	glotblastn
2686	LYD2 11	switchgrass lgb167 DN14069 1_P1	6315	638	95.4	globlastp
2687	LYD1 95	switchgrass lgb167 DN14392 7_T1	6316	628	80.82	glotblastn
2687	LYD2 11	switchgrass lgb167 DN14392 7_P1	6316	638	93.9	globlastp
2688	LYD1 95	dandelionlgb161 DY813534 _P1	6317	628	80.8	globlastp

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2689	LYD1 95	arabidopsis_lyratal09v1 JGI AL024592_P1	6318	628	80.7	globlastp
2689	LYD2 11	arabidopsis_lyratal09v1 JGI AL024592_P1	6318	638	80.2	globlastp
2690	LYD1 95	arabidopsis 10v1 AT4G3405 0_P1	6318	628	80.7	globlastp
2690	LYD2 11	arabidopsis 10v1 AT4G3405 0_P1	6318	638	80.2	globlastp
2691	LYD1 95	arabidopsis gb165 AT4G340 50_P1	6318	628	80.7	globlastp
2691	LYD2 11	arabidopsis gb165 AT4G340 50_P1	6318	638	80.2	globlastp
2692	LYD1 95	pinel10v1 AI812878_T1	6319	628	80.41	glotblastn
2693	LYD1 95	pinelgb157.2 AA556630_T1	6320	628	80.41	glotblastn
2694	LYD1 95	pinelgb157.2 AL750465_T1	6321	628	80.41	glotblastn
2695	LYD1 95	artemisia 10v1 EY053286_P 1	6322	628	80.4	globlastp
2696	LYD1 95	cassava gb164 DV448480_T 1	6323	628	80.16	glotblastn
2697	LYD1 95	fescue gb161 DT707061_T1	6324	628	80.08	glotblastn
2697	LYD2 11	fescue gb161 DT707061_P1	6324	638	82.3	globlastp
2698	LYD1 95	castorbean 09v1 XM002523 572_T1	6325	628	80	glotblastn
2699	LYD1 96	sorghum 09v1 SB01G04616 0_T1	6326	629	96.47	glotblastn
2700	LYD1 97	arabidopsis_lyratal09v1 JGI AL031045_P1	6327	630	92.9	globlastp
2701	LYD2 00	canola 10v1 EE435493_P1	6328	631	93.3	globlastp
2702	LYD2 00	canola gb161 EE435493_P1	6328	631	93.3	globlastp
2703	LYD2 00	b_rapa gb162 L35788_P1	6329	631	90	globlastp
2704	LYD2 01	b_oleracea gb161 DY023468 _P1	632	632	100	globlastp
2705	LYD2 01	b_rapa gb162 L33494_P1	632	632	100	globlastp
2706	LYD2 01	canola gb161 CD814222_P1	632	632	100	globlastp
2707	LYD2 01	radish gb164 EV536280_P1	632	632	100	globlastp

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2708	LYD2 01	radish gb164 EV543503_P1	632	632	100	globlastp
2709	LYD2 01	canola 10v1 CN736580_P1	6330	632	99.5	globlastp
2710	LYD2 01	b_rapa gb162 CX266259_P1	6330	632	99.5	globlastp
2711	LYD2 01	canola 10v1 CD814222_P1	6331	632	99.5	globlastp
2712	LYD2 01	canola gb161 CD822065_P1	6331	632	99.5	globlastp
2713	LYD2 01	canola gb161 CN736580_P1	6330	632	99.5	globlastp
2714	LYD2 01	canola 10v1 H74733_P1	6330	632	99.5	globlastp
2715	LYD2 01	canola gb161 H74733_P1	6330	632	99.5	globlastp
2716	LYD2 01	radish gb164 EV535404_P1	6330	632	99.5	globlastp
2717	LYD2 01	arabidopsis_lyrata 09v1 JGI AL000178_P1	6332	632	97.9	globlastp
2718	LYD2 01	arabidopsis_lyrata 09v1 JGI AL023653_P1	6333	632	97.9	globlastp
2719	LYD2 01	arabidopsis 10v1 AT4G0208 0_P1	6334	632	97.9	globlastp
2720	LYD2 01	arabidopsis gb165 AT4G020 80_P1	6334	632	97.9	globlastp
2721	LYD2 01	apple gb171 CN578516_P1	6335	632	96.9	globlastp
2722	LYD2 01	citrus gb166 BE213489_P1	6336	632	96.9	globlastp
2723	LYD2 01	strawberry gb164 CO381157 _P1	6337	632	96.9	globlastp
2724	LYD2 01	cassava 09v1 DB923790_P1	6338	632	96.4	globlastp
2725	LYD2 01	cleome_spinosal 10v1 GR935 463_P1	6339	632	96.4	globlastp
2726	LYD2 01	cucumber 09v1 EB714467_P 1	6340	632	96.4	globlastp
2727	LYD2 01	melon 10v1 EB714467_P1	6341	632	96.4	globlastp
2728	LYD2 01	nasturtium 10v1 GH166857_ P1	6342	632	96.4	globlastp
2729	LYD2 01	apple gb171 CN495817_P1	6343	632	96.4	globlastp
2730	LYD2 01	cassava 09v1 DV456795_P1	6344	632	96.4	globlastp

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2731	LYD2 01	cassava gb164 DV456795_P 1	6344	632	96.4	globlastp
2732	LYD2 01	castorbean 09v1 EE257238_ P1	6345	632	96.4	globlastp
2733	LYD2 01	grape gb160 BQ792627_P1	6346	632	96.4	globlastp
2734	LYD2 01	medicago 09v1 AW329400_ P1	6347	632	96.4	globlastp
2735	LYD2 01	melon gb165 EB714467_P1	6341	632	96.4	globlastp
2736	LYD2 01	cucumber 09v1 AM714944_ P1	6348	632	95.9	globlastp
2737	LYD2 01	millet 10v1 EVO454PM015 862_P1	6349	632	95.9	globlastp
2738	LYD2 01	apple gb171 CN580897_P1	6350	632	95.9	globlastp
2739	LYD2 01	poplar 10v1 AI164063_P1	6351	632	95.9	globlastp
2740	LYD2 01	poplar gb170 AI164063_P1	6351	632	95.9	globlastp
2741	LYD2 01	poplar 10v1 BU821219_P1	6352	632	95.9	globlastp
2742	LYD2 01	poplar gb170 BU821219_P1	6352	632	95.9	globlastp
2743	LYD2 01	jatropha 09v1 GT228862_T1	6353	632	95.85	glotblastn
2744	LYD2 01	brachypodium 09v1 DV4811 00_P1	6354	632	95.3	globlastp
2745	LYD2 01	cleome_gynandra 10v1 SRR 015532S0002941_P1	6355	632	95.3	globlastp
2746	LYD2 01	heritiera 10v1 SRR005794S0 002344_P1	6356	632	95.3	globlastp
2747	LYD2 01	heritiera 10v1 SRR005795S0 007601_P1	6357	632	95.3	globlastp
2748	LYD2 01	melon 10v1 AM714944_P1	6358	632	95.3	globlastp
2749	LYD2 01	melon 10v1 DV635115_P1	6359	632	95.3	globlastp
2750	LYD2 01	millet 10v1 CD725311_P1	6354	632	95.3	globlastp
2751	LYD2 01	oak 10v1 FP041158_P1	6360	632	95.3	globlastp
2752	LYD2 01	apple gb171 CN488933_P1	6361	632	95.3	globlastp
2753	LYD2 01	apple gb171 CN495761_P1	6362	632	95.3	globlastp

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2754	LYD2 01	barley gb157 SOLEXA BE41 1202_P1	6363	632	95.3	globlastp
2755	LYD2 01	brachypodium gb169 BE412 821_P1	6354	632	95.3	globlastp
2756	LYD2 01	cacao gb167 CF972901_P1	6364	632	95.3	globlastp
2757	LYD2 01	castorbean 09v1 EE257230_ P1	6365	632	95.3	globlastp
2758	LYD2 01	cenchrus gb166 EB655029_ P1	6354	632	95.3	globlastp
2759	LYD2 01	chestnut gb170 SRR006295S 0004786_P1	6366	632	95.3	globlastp
2760	LYD2 01	citrus gb166 CF418356_P1	6367	632	95.3	globlastp
2761	LYD2 01	citrus gb166 CF506461_P1	6368	632	95.3	globlastp
2762	LYD2 01	cotton 10v1 AI726023_P1	6369	632	95.3	globlastp
2763	LYD2 01	cotton gb164 AI726023_P1	6369	632	95.3	globlastp
2764	LYD2 01	cotton gb164 DR455589_P1	6370	632	95.3	globlastp
2765	LYD2 01	eucalyptus gb166 ES593417 _P1	6371	632	95.3	globlastp
2766	LYD2 01	grape gb160 BM437739_P1	6372	632	95.3	globlastp
2767	LYD2 01	lolium 09v1 ES699563_P1	6373	632	95.3	globlastp
2768	LYD2 01	lolium 10v1 ES699563_P1	6373	632	95.3	globlastp
2769	LYD2 01	maize 10v1 AW288509_P1	6354	632	95.3	globlastp
2770	LYD2 01	maize 10v1 T14655_P1	6354	632	95.3	globlastp
2771	LYD2 01	maize gb170 T14655_P1	6354	632	95.3	globlastp
2772	LYD2 01	melon gb165 DV635115_P1	6359	632	95.3	globlastp
2773	LYD2 01	oak gb170 DB998925_P1	6360	632	95.3	globlastp
2774	LYD2 01	oak gb170 SRR006307S000 0395_P1	6360	632	95.3	globlastp
2775	LYD2 01	onion gb162 CF446497_P1	6374	632	95.3	globlastp
2776	LYD2 01	sorghum 09v1 SB03G01355 0_P1	6354	632	95.3	globlastp

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2777	LYD2 01	strawberry gb164 EX661290 _P1	6375	632	95.3	globlastp
2778	LYD2 01	sugarcane gb157.3 CA07182 2_P1	6354	632	95.3	globlastp
2779	LYD2 01	sugarcane gb157.3 CA11920 3_P1	6354	632	95.3	globlastp
2780	LYD2 01	switchgrass gb167 DN14383 5_P1	6354	632	95.3	globlastp
2781	LYD2 01	switchgrass gb167 DN14478 1_P1	6354	632	95.3	globlastp
2782	LYD2 01	wheat gb164 BE426680_P1	6376	632	95.3	globlastp
2783	LYD2 01	sugarcane 10v1 CA071822_ P1	6354	632	95.3	globlastp
2784	LYD2 01	oak 10v1 DB998925_T1	6377	632	94.82	glotblastn
2785	LYD2 01	grape gb160 CA815541_T1	6378	632	94.82	glotblastn
2786	LYD2 01	arabidopsis_lyrata 09v1 JGI AL005252_P1	6379	632	94.8	globlastp
2787	LYD2 01	arabidopsis_lyrata 09v1 JGI AL019603_P1	6380	632	94.8	globlastp
2788	LYD2 01	cotton 10v1 DR455589_P1	6381	632	94.8	globlastp
2789	LYD2 01	cucumber 09v1 DV635115_ P1	6382	632	94.8	globlastp
2790	LYD2 01	eggplant 10v1 FS000694_P1	6383	632	94.8	globlastp
2791	LYD2 01	oat 10v2 AF084005_P1	6384	632	94.8	globlastp
2792	LYD2 01	prunus 10v1 AF048825_P1	6385	632	94.8	globlastp
2793	LYD2 01	arabidopsis 10v1 AT1G5633 0_P1	6386	632	94.8	globlastp
2794	LYD2 01	barley 10v1 BE412821_P1	6387	632	94.8	globlastp
2795	LYD2 01	barley gb157 SOLEXA BE41 2821_P1	6387	632	94.8	globlastp
2796	LYD2 01	cotton 10v1 BF277532_P1	6388	632	94.8	globlastp
2797	LYD2 01	cotton 10v1 BQ416087_P1	6389	632	94.8	globlastp
2798	LYD2 01	cowpea gb166 FF386015_P1	6390	632	94.8	globlastp
2799	LYD2 01	ginger gb164 DY349578_P1	6391	632	94.8	globlastp

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2800	LYD2 01	pepper gb171 CO908545_P1	6383	632	94.8	globlastp
2801	LYD2 01	poppy gb166 FE964246_P1	6392	632	94.8	globlastp
2802	LYD2 01	poppy gb166 FE965260_P1	6393	632	94.8	globlastp
2803	LYD2 01	potato 10v1 BG350081_P1	6383	632	94.8	globlastp
2804	LYD2 01	potato gb157.2 BG350081_P 1	6383	632	94.8	globlastp
2805	LYD2 01	prunus 10v1 BU047217_P1	6394	632	94.8	globlastp
2806	LYD2 01	prunus gb167 BU047217_P1	6394	632	94.8	globlastp
2807	LYD2 01	pseudoroegneria gb167 FF34 0041_P1	6395	632	94.8	globlastp
2808	LYD2 01	rose 10v1 BI977245_P1	6396	632	94.8	globlastp
2809	LYD2 01	rose gb157.2 BI977245_P1	6396	632	94.8	globlastp
2810	LYD2 01	solanum_phureja 09v1 SPH BG123382_P1	6383	632	94.8	globlastp
2811	LYD2 01	soybean gb168 CA907801_P 1	6390	632	94.8	globlastp
2812	LYD2 01	strawberry gb164 EX684999 _P1	6397	632	94.8	globlastp
2813	LYD2 01	switchgrass gb167 DN14350 0_P1	6398	632	94.8	globlastp
2814	LYD2 01	tomato 09v1 BG123382_P1	6399	632	94.8	globlastp
2815	LYD2 01	tomato gb164 BG123382_P1	6399	632	94.8	globlastp
2816	LYD2 01	triphysaria 10v1 EY129553_ P1	6400	632	94.8	globlastp
2817	LYD2 01	wheat gb164 BE405729_P1	6401	632	94.8	globlastp
2818	LYD2 01	ipomoea_nil 10v1 BJ556321 _P1	6402	632	94.3	globlastp
2819	LYD2 01	oat 10v2 GO588070_P1	6403	632	94.3	globlastp
2820	LYD2 01	orobanche 10v1 SRR023189 S0020719_P1	6404	632	94.3	globlastp
2821	LYD2 01	rhizophora 10v1 SRR005792 S0001094_P1	6405	632	94.3	globlastp
2822	LYD2 01	apple gb171 CN580370_P1	6406	632	94.3	globlastp

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2823	LYD2 01	apple gb171 CN863209_P1	6407	632	94.3	globlastp
2824	LYD2 01	arabidopsis 10v1 AT3G6256 0_P1	6408	632	94.3	globlastp
2825	LYD2 01	banana 10v1 BBS1216T3_P 1	6409	632	94.3	globlastp
2826	LYD2 01	banana 10v1 FF562066_P1	6410	632	94.3	globlastp
2827	LYD2 01	cacao gb167 CU473711_P1	6411	632	94.3	globlastp
2828	LYD2 01	cacao gb167 CU504692_P1	6412	632	94.3	globlastp
2829	LYD2 01	coffea 10v1 DV663797_P1	6413	632	94.3	globlastp
2830	LYD2 01	coffea gb157.2 DV663797_P 1	6413	632	94.3	globlastp
2831	LYD2 01	cotton 10v1 AI730854_P1	6414	632	94.3	globlastp
2832	LYD2 01	cotton gb164 BF277532_P1	6415	632	94.3	globlastp
2833	LYD2 01	cotton gb164 BQ416087_P1	6416	632	94.3	globlastp
2834	LYD2 01	iceplant gb164 AW053482_ P1	6417	632	94.3	globlastp
2835	LYD2 01	ipomoea gb157.2 BJ556321_ P1	6402	632	94.3	globlastp
2836	LYD2 01	kiwi gb166 FG442511_P1	6418	632	94.3	globlastp
2837	LYD2 01	monkeyflower 09v1 DV2100 70_P1	6419	632	94.3	globlastp
2838	LYD2 01	monkeyflower 10v1 DV2100 70_P1	6419	632	94.3	globlastp
2839	LYD2 01	papaya gb165 EX231956_P1	6420	632	94.3	globlastp
2840	LYD2 01	peal09v1 CD860823_P1	6421	632	94.3	globlastp
2841	LYD2 01	poplar 10v1 BI070125_P1	6422	632	94.3	globlastp
2842	LYD2 01	poplar gb170 BI070125_P1	6422	632	94.3	globlastp
2843	LYD2 01	poplar 10v1 BI126257_P1	6423	632	94.3	globlastp
2844	LYD2 01	prunus 10v1 BU043075_P1	6424	632	94.3	globlastp
2845	LYD2 01	prunus gb167 BU043075_P1	6424	632	94.3	globlastp

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2846	LYD2 01	prunus 10v1 BU047261_P1	6425	632	94.3	globlastp
2847	LYD2 01	prunus gb167 BU047261_P1	6425	632	94.3	globlastp
2848	LYD2 01	rice gb170 OS01G23620_P1	6426	632	94.3	globlastp
2849	LYD2 01	thellungiella gb167 DN7757 26_P1	6427	632	94.3	globlastp
2850	LYD2 01	cucumber 09v1 AM736613_ P1	6428	632	93.8	globlastp
2851	LYD2 01	curcuma 10v1 DY383352_P 1	6429	632	93.8	globlastp
2852	LYD2 01	eggplant 10v1 FS011441_P1	6430	632	93.8	globlastp
2853	LYD2 01	melon 10v1 AM736613_P1	6428	632	93.8	globlastp
2854	LYD2 01	nasturtium 10v1 SRR032558 S0063645_P1	6431	632	93.8	globlastp
2855	LYD2 01	oak 10v1 FP039659_P1	6432	632	93.8	globlastp
2856	LYD2 01	pigeonpea 10v1 GW348949_ P1	6433	632	93.8	globlastp
2857	LYD2 01	salvia 10v1 SRR014553S000 2915_P1	6434	632	93.8	globlastp
2858	LYD2 01	tragopogon 10v1 SRR02020 5S0011036_P1	6435	632	93.8	globlastp
2859	LYD2 01	amborella gb166 CD482203 _P1	6436	632	93.8	globlastp
2860	LYD2 01	banana gb167 FF562066_P1	6437	632	93.8	globlastp
2861	LYD2 01	basilicum 10v1 DY342472_ P1	6438	632	93.8	globlastp
2862	LYD2 01	cassava 09v1 DV458296_P1	6439	632	93.8	globlastp
2863	LYD2 01	cassava gb164 DR085772_P 1	6439	632	93.8	globlastp
2864	LYD2 01	cassava 09v1 DV441309_P1	6440	632	93.8	globlastp
2865	LYD2 01	cassava gb164 DV441309_P 1	6440	632	93.8	globlastp
2866	LYD2 01	castorbean 09v1 EV521574_ P1	6441	632	93.8	globlastp
2867	LYD2 01	chestnut gb170 SRR006295S 0016299_P1	6442	632	93.8	globlastp
2868	LYD2 01	coffea 10v1 CF588658_P1	6443	632	93.8	globlastp

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2869	LYD2 01	coffealgb157.2 CF588658_P 1	6443	632	93.8	globlastp
2870	LYD2 01	cotton 10v1 AI728302_P1	6444	632	93.8	globlastp
2871	LYD2 01	cotton gb164 AI730854_P1	6445	632	93.8	globlastp
2872	LYD2 01	cowpealgb166 FC461231_P 1	6446	632	93.8	globlastp
2873	LYD2 01	eucalyptus gb166 CT980876 _P1	6447	632	93.8	globlastp
2874	LYD2 01	ginger gb164 DY361206_P1	6429	632	93.8	globlastp
2875	LYD2 01	medicagol09v1 LLAJ389002 _P1	6448	632	93.8	globlastp
2876	LYD2 01	melon gb165 AM714944_P1	6449	632	93.8	globlastp
2877	LYD2 01	nuphar gb166 CK746937_P1	6450	632	93.8	globlastp
2878	LYD2 01	oak gb170 SRR006307S001 6171_P1	6451	632	93.8	globlastp
2879	LYD2 01	peanut 10v1 ES722249_P1	6452	632	93.8	globlastp
2880	LYD2 01	pepper gb171 BM059626_P 1	6430	632	93.8	globlastp
2881	LYD2 01	poplar 10v1 BU861778_P1	6453	632	93.8	globlastp
2882	LYD2 01	poplar gb170 BU861778_P1	6453	632	93.8	globlastp
2883	LYD2 01	radish gb164 EX772918_P1	6454	632	93.8	globlastp
2884	LYD2 01	solanum_phurejal09v1 SPH AW034613_P1	6455	632	93.8	globlastp
2885	LYD2 01	sorghum l09v1 SB0111S0020 10_P1	6456	632	93.8	globlastp
2886	LYD2 01	soybean gb168 AW329400_ P1	6457	632	93.8	globlastp
2887	LYD2 01	soybean gb168 BE239992_P 1	6458	632	93.8	globlastp
2888	LYD2 01	sugarcane 10v1 BQ536213_ P1	6456	632	93.8	globlastp
2889	LYD2 01	sugarcane gb157.3 BQ53621 3_P1	6459	632	93.8	globlastp
2890	LYD2 01	sunflower 10v1 DY925572_ P1	6460	632	93.8	globlastp
2891	LYD2 01	sunflower gb162 DY925572 _P1	6460	632	93.8	globlastp

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2892	LYD2 01	switchgrass gb167 FL89034 5_P1	6461	632	93.8	globlastp
2893	LYD2 01	switchgrass gb167 FL92507 1_P1	6462	632	93.8	globlastp
2894	LYD2 01	tomato 09v1 AW034613_P1	6455	632	93.8	globlastp
2895	LYD2 01	tomato gb164 AW034613_P 1	6455	632	93.8	globlastp
2896	LYD2 01	triphysarial 0v1 EX983317_ P1	6463	632	93.8	globlastp
2897	LYD2 01	triphysarial gb164 EX983317 _P1	6463	632	93.8	globlastp
2898	LYD2 01	triphysarial 0v1 EY126729_ P1	6464	632	93.8	globlastp
2899	LYD2 01	triphysarial gb164 EY126729 _P1	6464	632	93.8	globlastp
2900	LYD2 01	triphysarial gb164 EY129553 _P1	6465	632	93.8	globlastp
2901	LYD2 01	canola 10v1 FG554744_P1	6466	632	93.3	globlastp
2902	LYD2 01	cleome_spinosal 0v1 GR931 642_P1	6467	632	93.3	globlastp
2903	LYD2 01	heritieral 10v1 SRR005794S0 007553_P1	6468	632	93.3	globlastp
2904	LYD2 01	ipomoea_nill 0v1 BJ553656 _P1	6469	632	93.3	globlastp
2905	LYD2 01	lettuce 10v1 DW074507_P1	6470	632	93.3	globlastp
2906	LYD2 01	salvia 10v1 CV163233_P1	6471	632	93.3	globlastp
2907	LYD2 01	tea 10v1 GE651401_P1	6472	632	93.3	globlastp
2908	LYD2 01	tragopogon 10v1 SRR02020 5S0016454_P1	6473	632	93.3	globlastp
2909	LYD2 01	antirrhinum gb166 AJ55951 8_P1	6474	632	93.3	globlastp
2910	LYD2 01	apple gb171 AF048825_P1	6475	632	93.3	globlastp
2911	LYD2 01	b_rapa gb162 BCU55036_P 1	6466	632	93.3	globlastp
2912	LYD2 01	canola 10v1 CD812447_P1	6466	632	93.3	globlastp
2913	LYD2 01	canola gb161 CD812447_P1	6466	632	93.3	globlastp
2914	LYD2 01	canola 10v1 DY006847_P1	6466	632	93.3	globlastp

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2915	LYD2 01	canola gb161 DY006847_P1	6466	632	93.3	globlastp
2916	LYD2 01	cassava 09v1 DR085772_P1	6476	632	93.3	globlastp
2917	LYD2 01	cassava gb164 DR086941_P 1	6477	632	93.3	globlastp
2918	LYD2 01	centaurea gb166 EH714735_ P1	6470	632	93.3	globlastp
2919	LYD2 01	centaurea gb166 EH755488_ P1	6470	632	93.3	globlastp
2920	LYD2 01	cichorium gb171 DT212637_ P1	6470	632	93.3	globlastp
2921	LYD2 01	cichorium gb171 EH689329_ P1	6478	632	93.3	globlastp
2922	LYD2 01	cotton gb164 AI728302_P1	6479	632	93.3	globlastp
2923	LYD2 01	cowpea gb166 FC457632_P 1	6480	632	93.3	globlastp
2924	LYD2 01	cynara gb167 GE587803_P1	6470	632	93.3	globlastp
2925	LYD2 01	dandelion 10v1 DR399381_ P1	6470	632	93.3	globlastp
2926	LYD2 01	dandelion gb161 DY807874_ P1	6470	632	93.3	globlastp
2927	LYD2 01	ipomoea gb157.2 BJ553656_ P1	6469	632	93.3	globlastp
2928	LYD2 01	lettuce gb157.2 DW074507_ P1	6470	632	93.3	globlastp
2929	LYD2 01	lettuce gb157.2 DW112970_ P1	6473	632	93.3	globlastp
2930	LYD2 01	lettuce gb157.2 DW145079_ P1	6473	632	93.3	globlastp
2931	LYD2 01	lotus 09v1 LLAI967735_P1	6481	632	93.3	globlastp
2932	LYD2 01	peanut 10v1 ES718834_P1	6482	632	93.3	globlastp
2933	LYD2 01	peanut gb171 EH045041_P1	6482	632	93.3	globlastp
2934	LYD2 01	peanut 10v1 ES721921_P1	6483	632	93.3	globlastp
2935	LYD2 01	potato gb157.2 BF459589_P 1	6484	632	93.3	globlastp
2936	LYD2 01	radish gb164 EV535849_P1	6466	632	93.3	globlastp
2937	LYD2 01	rice gb170 OS01G15010_P1	6485	632	93.3	globlastp

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2938	LYD2 01	rice gb170 OS12G37360_P1	6486	632	93.3	globlastp
2939	LYD2 01	safflower gb162 EL392690_ P1	6470	632	93.3	globlastp
2940	LYD2 01	senecio gb170 DY659667_P 1	6487	632	93.3	globlastp
2941	LYD2 01	solanum_phureja 09v1 SPH BG130022_P1	6484	632	93.3	globlastp
2942	LYD2 01	sunflower gb162 CD852926 _P1	6470	632	93.3	globlastp
2943	LYD2 01	sunflower 10v1 CD852926_ P1	6470	632	93.3	globlastp
2944	LYD2 01	sunflower gb162 EL441563_ P1	6470	632	93.3	globlastp
2945	LYD2 01	tea gb171 CV066987_P1	6472	632	93.3	globlastp
2946	LYD2 01	tomato 09v1 BG130022_P1	6484	632	93.3	globlastp
2947	LYD2 01	tomato gb164 BG130022_P1	6484	632	93.3	globlastp
2948	LYD2 01	lettuce 10v1 DW055345_P1	6473	632	93.3	globlastp
2949	LYD2 01	potato 10v1 BF459589_P1	6484	632	93.3	globlastp
2950	LYD2 01	eucalyptus gb166 CT987357 _T1	6488	632	93.26	glotblastn
2951	LYD2 01	b_junceal 10v2 E6ANDIZ01 BLEAU_P1	6489	632	92.8	globlastp
2952	LYD2 01	b_rapal gb162 ES932634_P1	6489	632	92.8	globlastp
2953	LYD2 01	canola gb161 DY010851_P1	6489	632	92.8	globlastp
2954	LYD2 01	radish gb164 EV543721_P1	6489	632	92.8	globlastp
2955	LYD2 01	radish gb164 EX770221_P1	6489	632	92.8	globlastp
2956	LYD2 01	canola 10v1 DY010851_P1	6489	632	92.8	globlastp
2957	LYD2 01	ipomoea_batatas 10v1 EE88 2235_T1	6490	632	92.75	glotblastn
2958	LYD2 01	pigeonpea 10v1 GW359950_ T1	6491	632	92.75	glotblastn
2959	LYD2 01	pigeonpea 10v1 SRR054580 S0024079_T1	6492	632	92.75	glotblastn
2960	LYD2 01	tripphysaria 10v1 EX999862_ T1	6493	632	92.75	glotblastn

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2961	LYD2 01	melon gb165 AM736613_T1	6494	632	92.75	glotblastn
2962	LYD2 01	aquilegia 10v1 DR922692_P 1	6495	632	92.7	globlastp
2963	LYD2 01	ipomoea_nill 10v1 BJ554402 _P1	6496	632	92.7	globlastp
2964	LYD2 01	nasturtium 10v1 SRR032558 S0002294_P1	6497	632	92.7	globlastp
2965	LYD2 01	triphysaria 10v1 DR172714_ P1	6498	632	92.7	globlastp
2966	LYD2 01	antirrhinum gb166 AJ55952 8_P1	6499	632	92.7	globlastp
2967	LYD2 01	avocado 10v1 CO998056_P1	6500	632	92.7	globlastp
2968	LYD2 01	avocado gb164 CO998056_P 1	6500	632	92.7	globlastp
2969	LYD2 01	basilicum gb157.3 DY34247 2_P1	6501	632	92.7	globlastp
2970	LYD2 01	bean gb167 CA898565_P1	6502	632	92.7	globlastp
2971	LYD2 01	bean gb167 CA907815_P1	6503	632	92.7	globlastp
2972	LYD2 01	bean gb167 CA907901_P1	6504	632	92.7	globlastp
2973	LYD2 01	beet gb162 BQ489381_P1	6505	632	92.7	globlastp
2974	LYD2 01	brachypodium 09v1 DV4842 52_P1	6506	632	92.7	globlastp
2975	LYD2 01	brachypodium gb169 BE405 729_P1	6506	632	92.7	globlastp
2976	LYD2 01	canola gb161 DY010564_P1	6507	632	92.7	globlastp
2977	LYD2 01	chickpea 09v2 GR403699_P 1	6508	632	92.7	globlastp
2978	LYD2 01	cotton 10v1 AI726130_P1	6509	632	92.7	globlastp
2979	LYD2 01	cryptomeria gb166 BJ94028 2_P1	6510	632	92.7	globlastp
2980	LYD2 01	cynara gb167 GE585770_P1	6511	632	92.7	globlastp
2981	LYD2 01	ipomoea gb157.2 BJ554402_ P1	6496	632	92.7	globlastp
2982	LYD2 01	kiwi gb166 FG431590_P1	6512	632	92.7	globlastp
2983	LYD2 01	lettuce gb157.2 DW055345_ P1	6513	632	92.7	globlastp

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2984	LYD2 01	liquorice gb171 FS244269_P 1	6514	632	92.7	globlastp
2985	LYD2 01	lotus 09v1 BP071405_P1	6515	632	92.7	globlastp
2986	LYD2 01	peanut 10v1 EE124259_P1	6516	632	92.7	globlastp
2987	LYD2 01	peanut gb171 EE124259_P1	6516	632	92.7	globlastp
2988	LYD2 01	pepper gb171 CA520057_P1	6517	632	92.7	globlastp
2989	LYD2 01	petunia gb171 CV293121_P 1	6518	632	92.7	globlastp
2990	LYD2 01	poppy gb166 FG607099_P1	6519	632	92.7	globlastp
2991	LYD2 01	potato gb157.2 BG595658_P 1	6520	632	92.7	globlastp
2992	LYD2 01	safflower gb162 EL399824_ P1	6521	632	92.7	globlastp
2993	LYD2 01	soybean gb168 AI967735_P 1	6522	632	92.7	globlastp
2994	LYD2 01	soybean gb168 AJ389002_P 1	6523	632	92.7	globlastp
2995	LYD2 01	soybean gb168 AL375445_P 1	6524	632	92.7	globlastp
2996	LYD2 01	soybean gb168 CF922718_P 1	6525	632	92.7	globlastp
2997	LYD2 01	spurge gb161 DV112769_P1	6526	632	92.7	globlastp
2998	LYD2 01	switchgrass gb167 DN14065 1_P1	6527	632	92.7	globlastp
2999	LYD2 01	switchgrass gb167 DN14117 3_P1	6527	632	92.7	globlastp
3000	LYD2 01	tobacco gb162 BP192482_P 1	6528	632	92.7	globlastp
3001	LYD2 01	tobacco gb162 D87821_P1	6528	632	92.7	globlastp
3002	LYD2 01	tobacco gb162 NTU46928_P 1	6529	632	92.7	globlastp
3003	LYD2 01	walnut gb166 CV195326_P 1	6530	632	92.7	globlastp
3004	LYD2 01	radish gb164 EV528328_P1	6531	632	92.3	globlastp
3005	LYD2 01	chestnut gb170 SRR006295S 0022297_T1	6532	632	92.23	glotblastn
3006	LYD2 01	cassava 09v1 FG805794_P1	6533	632	92.2	globlastp

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3007	LYD2 01	curcumal10v1 DY389286_P 1	6534	632	92.2	globlastp
3008	LYD2 01	milletl10v1 EVO454PM010 619_P1	6535	632	92.2	globlastp
3009	LYD2 01	orobanche10v1 SRR023189 S0005863_P1	6536	632	92.2	globlastp
3010	LYD2 01	tragopogonl10v1 SRR02020 5S0008368_P1	6537	632	92.2	globlastp
3011	LYD2 01	beanlgb167 CA907810_P1	6538	632	92.2	globlastp
3012	LYD2 01	centaurealgb166 EH724820_ P1	6539	632	92.2	globlastp
3013	LYD2 01	centaurealgb166 EH737464_ P1	6540	632	92.2	globlastp
3014	LYD2 01	cowpealgb166 ES884134_P1	6538	632	92.2	globlastp
3015	LYD2 01	lettucel10v1 DW117562_P1	6541	632	92.2	globlastp
3016	LYD2 01	lettucelgb157.2 DW117562_ P1	6541	632	92.2	globlastp
3017	LYD2 01	maizel10v1 AI947720_P1	6542	632	92.2	globlastp
3018	LYD2 01	maizelgb170 AI947720_P1	6542	632	92.2	globlastp
3019	LYD2 01	papayalgb165 EX261772_P1	6543	632	92.2	globlastp
3020	LYD2 01	pinel10v1 BE662420_P1	6544	632	92.2	globlastp
3021	LYD2 01	pinelgb157.2 BE662420_P1	6544	632	92.2	globlastp
3022	LYD2 01	radishlgb164 EV527447_P1	6545	632	92.2	globlastp
3023	LYD2 01	safflowerlgb162 EL384996_ P1	6539	632	92.2	globlastp
3024	LYD2 01	sorghuml09v1 SB03G00976 0_P1	6542	632	92.2	globlastp
3025	LYD2 01	soybeanlgb168 AL370671_P 1	6546	632	92.2	globlastp
3026	LYD2 01	soybeanlgb168 BE659271_P 1	6547	632	92.2	globlastp
3027	LYD2 01	sprucelgb162 CO217770_P1	6548	632	92.2	globlastp
3028	LYD2 01	sunflowerl10v1 CD846865_ P1	6549	632	92.2	globlastp
3029	LYD2 01	sunflowerl10v1 CD848519_ P1	6550	632	92.2	globlastp

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3030	LYD2 01	sunflower gb162 DY912940_P1	6550	632	92.2	globlastp
3031	LYD2 01	tea gb171 GE650564_P1	6551	632	92.2	globlastp
3032	LYD2 01	tobacco gb162 CV017890_P1	6552	632	92.2	globlastp
3033	LYD2 01	tobacco gb162 X97967_P1	6552	632	92.2	globlastp
3034	LYD2 01	tea 10v1 CV067078_T1	6553	632	91.71	glotblastn
3035	LYD2 01	brachypodium 09v1 GT772462_P1	6554	632	91.7	globlastp
3036	LYD2 01	cotton 10v1 BQ406141_P1	6555	632	91.7	globlastp
3037	LYD2 01	dandelion 10v1 DR398699_P1	6556	632	91.7	globlastp
3038	LYD2 01	ipomoea_nill 10v1 BJ562653_P1	6557	632	91.7	globlastp
3039	LYD2 01	pigeonpeal 10v1 SRR054580S0006204_P1	6558	632	91.7	globlastp
3040	LYD2 01	antirrhinum gb166 AJ788613_P1	6559	632	91.7	globlastp
3041	LYD2 01	artemisia 10v1 EY048595_P1	6560	632	91.7	globlastp
3042	LYD2 01	b_junceal 10v2 E6ANDIZ01BI3CE_P1	6561	632	91.7	globlastp
3043	LYD2 01	b_junceal gb164 EVGN00335318190411_P1	6561	632	91.7	globlastp
3044	LYD2 01	b_rapal gb162 CA991946_P1	6561	632	91.7	globlastp
3045	LYD2 01	barley gb157 SOLEXA BE411848_P1	6562	632	91.7	globlastp
3046	LYD2 01	canola 10v1 CD820737_P1	6561	632	91.7	globlastp
3047	LYD2 01	canola gb161 CD820737_P1	6561	632	91.7	globlastp
3048	LYD2 01	cotton gb164 BQ406141_P1	6555	632	91.7	globlastp
3049	LYD2 01	dandelion gb161 DY808686_P1	6556	632	91.7	globlastp
3050	LYD2 01	ipomoeal gb157.2 BJ562653_P1	6563	632	91.7	globlastp
3051	LYD2 01	kiwi gb166 FG404500_P1	6564	632	91.7	globlastp
3052	LYD2 01	lotus 09v1 BW597745_P1	6565	632	91.7	globlastp

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3053	LYD2 01	medicagol09v1 AJ388771_P 1	6566	632	91.7	globlastp
3054	LYD2 01	poplarlgb170 BI126257_P1	6567	632	91.7	globlastp
3055	LYD2 01	pseudoroegneria gb167 FF34 0656_P1	6562	632	91.7	globlastp
3056	LYD2 01	radishlgb164 EV535478_P1	6561	632	91.7	globlastp
3057	LYD2 01	radishlgb164 EV565516_P1	6561	632	91.7	globlastp
3058	LYD2 01	radishlgb164 EW725190_P1	6568	632	91.7	globlastp
3059	LYD2 01	radishlgb164 EX902413_P1	6569	632	91.7	globlastp
3060	LYD2 01	ryelgb164 BE494444_P1	6562	632	91.7	globlastp
3061	LYD2 01	seneciolgb170 DY657889_P 1	6570	632	91.7	globlastp
3062	LYD2 01	seneciolgb170 DY664540_P 1	6571	632	91.7	globlastp
3063	LYD2 01	soybeanlgb168 BI970298_P 1	6572	632	91.7	globlastp
3064	LYD2 01	sugarcanel10v1 BQ530239_ P1	6573	632	91.7	globlastp
3065	LYD2 01	sugarcanelgb157.3 BQ53023 9_P1	6573	632	91.7	globlastp
3066	LYD2 01	sunflowerlgb162 CD846865 _P1	6574	632	91.7	globlastp
3067	LYD2 01	wheatlgb164 BE500854_P1	6562	632	91.7	globlastp
3068	LYD2 01	wheatlgb164 BQ235923_P1	6562	632	91.7	globlastp
3069	LYD2 01	arabidopsis_lyrata 09v1 JGI AL000882_P1	6575	632	91.2	globlastp
3070	LYD2 01	cynodonl10v1 BG322359_P 1	6576	632	91.2	globlastp
3071	LYD2 01	nasturtiuml10v1 SRR032558 S0000930_P1	6577	632	91.2	globlastp
3072	LYD2 01	canolal10v1 CD812048_P1	6578	632	91.2	globlastp
3073	LYD2 01	canolalgb161 CD812048_P1	6578	632	91.2	globlastp
3074	LYD2 01	canolal10v1 EL593228_P1	6579	632	91.2	globlastp
3075	LYD2 01	canolalgb161 EL593228_P1	6579	632	91.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3076	LYD2 01	centaurealgb166 EH755694_ P1	6580	632	91.2	globlastp
3077	LYD2 01	lettucel10v1 DW070398_P1	6581	632	91.2	globlastp
3078	LYD2 01	lettucelgb157.2 DW070398_ P1	6581	632	91.2	globlastp
3079	LYD2 01	liquoricelgb171 FS247073_P 1	6582	632	91.2	globlastp
3080	LYD2 01	monkeyflower 09v1 DV2129 11_P1	6583	632	91.2	globlastp
3081	LYD2 01	monkeyflower 10v1 DV2129 11_P1	6583	632	91.2	globlastp
3082	LYD2 01	spurgelgb161 DV113174_P1	6584	632	91.2	globlastp
3083	LYD2 01	tobacco gb162 NTU46929_P 1	6585	632	91.2	globlastp
3084	LYD2 01	bananalgb167 FF558115_T1	6586	632	91.19	glotblastn
3085	LYD2 01	cynaralgb167 GE585844_T1	6587	632	91.19	glotblastn
3086	LYD2 01	onion gb162 CF435014_T1	6588	632	91.19	glotblastn
3087	LYD2 01	oat 10v2 GO582075_P1	6589	632	90.7	globlastp
3088	LYD2 01	pepper gb171 CA514007_P1	6590	632	90.7	globlastp
3089	LYD2 01	oak 10v1 FN640780_P1	6591	632	90.5	globlastp
3090	LYD2 01	barley 10v1 BE411848_P1	6592	632	90.2	globlastp
3091	LYD2 01	citrus gb166 CX076831_P1	6593	632	90.2	globlastp
3092	LYD2 01	tobacco gb162 EB683024_P 1	6594	632	90.2	globlastp
3093	LYD2 01	beet gb162 BI543263_P1	6595	632	89.8	globlastp
3094	LYD2 01	arabidopsis 10v1 AT1G0918 0_P1	6596	632	89.6	globlastp
3095	LYD2 01	arabidopsis gb165 AT1G091 80_P1	6596	632	89.6	globlastp
3096	LYD2 01	cryptomer algb166 AU29904 1_P1	6597	632	89.6	globlastp
3097	LYD2 01	cycas gb166 CB091054_P1	6598	632	89.6	globlastp
3098	LYD2 01	pine 10v1 AA739841_P1	6599	632	89.6	globlastp

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3099	LYD2 01	pinelgb157.2 AA739841_P1	6599	632	89.6	globlastp
3100	LYD2 01	sprucelgb162 CO238693_P1	6600	632	89.6	globlastp
3101	LYD2 01	triphysarial10v1 EY147779_P1	6601	632	89.6	globlastp
3102	LYD2 01	triphysarialgb164 EY147779_P1	6601	632	89.6	globlastp
3103	LYD2 01	orobanche10v1 SRR023189 S0022597_P1	6602	632	89.1	globlastp
3104	LYD2 01	physcomitrella10v1 BJ1611 16_P1	6603	632	89.1	globlastp
3105	LYD2 01	physcomitrellalgb157 BJ161 116_P1	6603	632	89.1	globlastp
3106	LYD2 01	radishlgb164 EX771703_P1	6604	632	89.1	globlastp
3107	LYD2 01	physcomitrella10v1 BQ827 385_P1	6605	632	88.6	globlastp
3108	LYD2 01	avocadolgb164 FD509067_P 1	6606	632	88.6	globlastp
3109	LYD2 01	gingerlgb164 DY346355_P1	6607	632	88.6	globlastp
3110	LYD2 01	peanutlgb171 ES722249_P1	6608	632	88.6	globlastp
3111	LYD2 01	potatol10v1 BG351944_P1	6609	632	88.6	globlastp
3112	LYD2 01	potatolgb157.2 BG351944_P 1	6609	632	88.6	globlastp
3113	LYD2 01	solanum_phurejal09v1 SPH TOMGTPASE_P1	6609	632	88.6	globlastp
3114	LYD2 01	b_oleracealgb161 AM06252 2_P1	6610	632	88.1	globlastp
3115	LYD2 01	marchantialgb166 C95806_P 1	6611	632	88.1	globlastp
3116	LYD2 01	petunialgb171 CV300582_P 1	6612	632	88.1	globlastp
3117	LYD2 01	tomatol09v1 TOMGTPASE_ P1	6613	632	88.1	globlastp
3118	LYD2 01	tomatolgb164 TOMGTPASE _P1	6613	632	88.1	globlastp
3119	LYD2 01	cassaval09v1 DB922382_T1	-	632	87.56	glotblastn
3120	LYD2 01	gerberal09v1 AJ754374_P1	6614	632	87.2	globlastp
3121	LYD2 01	b_junceal10v2 E6ANDIZ01 B5J2W_P1	6615	632	87	globlastp

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3122	LYD2 01	rhizophoral10v1 SRR005792 S0006460_P1	6616	632	87	globlastp
3123	LYD2 01	canola 10v1 EE502143_P1	6617	632	87	globlastp
3124	LYD2 01	canola gb161 EE502143_P1	6617	632	87	globlastp
3125	LYD2 01	cotton gb164 AI726130_P1	6618	632	87	globlastp
3126	LYD2 01	ipomoea_batatas 10v1 DV03 6611_T1	6619	632	86.53	glotblastn
3127	LYD2 01	acacia 10v1 FS584353_P1	6620	632	86.5	globlastp
3128	LYD2 01	antirrhinum gb166 AJ79013 7_P1	6621	632	86.5	globlastp
3129	LYD2 01	antirrhinum gb166 AJ79360 9_P1	6622	632	86.5	globlastp
3130	LYD2 01	petunia gb171 FN000859_P1	6623	632	86.5	globlastp
3131	LYD2 01	spikemoss gb165 FE450778 _P1	6624	632	86.5	globlastp
3132	LYD2 01	wheat gb164 BG606923_P1	6625	632	86.5	globlastp
3133	LYD2 01	cyamopsis 10v1 EG990518_ T1	6626	632	86.01	glotblastn
3134	LYD2 01	cichorium gb171 EH690632 _P1	6627	632	85.5	globlastp
3135	LYD2 01	fern gb171 DK945400_P1	6628	632	85.5	globlastp
3136	LYD2 01	artemisia 10v1 SRR019254S 0321327_T1	6629	632	85.49	glotblastn
3137	LYD2 01	artemisia gb164 EY061569_ P1	6630	632	85	globlastp
3138	LYD2 01	kiwi gb166 FG404662_P1	6631	632	85	globlastp
3139	LYD2 01	petunia gb171 FN000129_P1	6632	632	85	globlastp
3140	LYD2 01	spikemoss gb165 FE448726 _P1	6633	632	84.5	globlastp
3141	LYD2 01	iceplant gb164 BE033433_T 1	6634	632	84.46	glotblastn
3142	LYD2 01	chickpea 09v2 GR403467_T 1	6635	632	83.94	glotblastn
3143	LYD2 01	physcomitrella 10v1 AW126 671_P1	6636	632	83.9	globlastp
3144	LYD2 01	physcomitrella gb157 AW12 6671_P1	6636	632	83.9	globlastp

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3145	LYD2 01	monkeyflower 10v1 MGJGI 004466_P1	6637	632	83.4	globlastp
3146	LYD2 01	peanut gb171 ES721921_P1	6638	632	83.4	globlastp
3147	LYD2 01	dandelion gb161 DY812100 _T1	6639	632	82.99	glotblastn
3148	LYD2 01	chickpea 09v2 GR402896_P 1	6640	632	82.9	globlastp
3149	LYD2 01	physcomitrella 10v1 BJ1743 10_P1	6641	632	82.9	globlastp
3150	LYD2 01	physcomitrellalgb157 BJ174 310_P1	6641	632	82.9	globlastp
3151	LYD2 01	spikemoss gb165 FE517935 _P1	6642	632	82.9	globlastp
3152	LYD2 01	basilicum 10v1 DY339599_ P1	6643	632	82.3	globlastp
3153	LYD2 01	spikemoss gb165 DN839042 _P1	6644	632	81.9	globlastp
3154	LYD2 01	lovegrass gb167 EH189602_ T1	6645	632	81.87	glotblastn
3155	LYD2 01	zinnia gb171 DV017338_P1	6646	632	81.3	globlastp
3156	LYD2 01	barley 10v1 BE411202_P1	6647	632	81.2	globlastp
3157	LYD2 01	eschscholzia 10v1 CK74799 5_P1	6648	632	80.8	globlastp
3158	LYD2 01	avocado gb164 CK752490_P 1	6649	632	80.8	globlastp
3159	LYD2 01	lolium 09v1 AU245847_P1	6650	632	80.8	globlastp
3160	LYD2 01	lotus 09v1 CB828505_P1	6651	632	80.8	globlastp
3161	LYD2 01	oil_palm gb166 EY411937_ P1	6652	632	80.8	globlastp
3162	LYD2 01	pigeonpea 10v1 SRR054580 S0000341_T1	6653	632	80.31	glotblastn
3163	LYD2 01	lolium 10v1 AU245847_T1	6654	632	80.31	glotblastn
3164	LYD2 01	ostreococcus gb162 XM0014 22553_T1	6655	632	80.31	glotblastn
3165	LYD2 01	ipomoea_batatas 10v1 BU69 1028_P1	6656	632	80.3	globlastp
3166	LYD2 01	avocado 10v1 CK752490_P1	6657	632	80.3	globlastp
3167	LYD2 02	b_oleracea gb161 AM05804 0_P1	6658	633	98.8	globlastp

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3168	LYD2 02	canola gb161 CD843895_P1	6659	633	98.8	globlastp
3169	LYD2 02	canola gb161 EE434181_P1	6658	633	98.8	globlastp
3170	LYD2 02	canola 10v1 CD843895_P1	6658	633	98.8	globlastp
3171	LYD2 02	cleome_gynandra 10v1 SRR 015532S0006952_P1	6660	633	86.7	globlastp
3172	LYD2 02	avocado 10v1 CO998009_P1	6661	633	82.5	globlastp
3173	LYD2 02	avocado gb164 CO998009_P 1	6661	633	82.5	globlastp
3174	LYD2 04	canola 10v1 DW999856_P1	6662	634	98.2	globlastp
3175	LYD2 04	canola gb161 EG019813_P1	6663	634	98.1	globlastp
3176	LYD2 06	canola 10v1 CD827387_P1	6664	635	99.2	globlastp
3177	LYD2 06	canola 10v1 CD822629_P1	6665	635	97.3	globlastp
3178	LYD2 06	b_rapa gb162 BG544285_P1	6666	635	96.2	globlastp
3179	LYD2 06	canola gb161 CD827387_P1	6667	635	96.2	globlastp
3180	LYD2 06	b_oleracea gb161 AM38719 6_P1	6668	635	93.8	globlastp
3181	LYD2 06	canola gb161 CD822629_P1	6669	635	92.9	globlastp
3182	LYD2 06	radish gb164 EV535046_P1	6670	635	88.9	globlastp
3183	LYD2 06	thellungiella gb167 BY8013 44_P1	6671	635	88.3	globlastp
3184	LYD2 06	arabidopsis_lyrata 09v1 JGI AL025591_P1	6672	635	85.3	globlastp
3185	LYD2 06	arabidopsis 10v1 AT4G2513 0_P1	6673	635	84.6	globlastp
3186	LYD2 06	arabidopsis gb165 AT4G251 30_P1	6673	635	84.6	globlastp
3187	LYD2 06	canola 10v1 CN825961_P1	6674	635	82	globlastp
3188	LYD2 06	radish gb164 EW713423_P1	6675	635	82	globlastp
3189	LYD2 06	canola gb161 CN825961_P1	6676	635	80.1	globlastp
3190	LYD2 08	canola 10v1 CD823590_P1	6677	636	99.4	globlastp

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3191	LYD2 08	b_rapalgb162 EF110932_P1	6677	636	99.4	globlastp
3192	LYD2 08	canolalgb161 CD823590_P1	6677	636	99.4	globlastp
3193	LYD2 08	b_nigral09v1 GT069367_P1	6678	636	98.2	globlastp
3194	LYD2 08	b_oleracealgb161 DY027427_P1	6679	636	97.1	globlastp
3195	LYD2 08	canola 10v1 CD822474_P1	6679	636	97.1	globlastp
3196	LYD2 08	canolalgb161 CD822474_P1	6679	636	97.1	globlastp
3197	LYD2 08	canola 10v1 EE468408_P1	6680	636	86	globlastp
3198	LYD2 08	canolalgb161 EE468408_P1	6681	636	84.9	globlastp
3199	LYD2 08	canola 10v1 EE561855_P1	6682	636	83.7	globlastp
3200	LYD2 08	canolalgb161 EE561855_P1	6682	636	83.7	globlastp
3201	LYD2 09	b_rapalgb162 EE520539_P1	637	637	100	globlastp
3202	LYD2 09	canola 10v1 CD817560_P1	637	637	100	globlastp
3203	LYD2 09	canolalgb161 CD817560_P1	637	637	100	globlastp
3204	LYD2 09	canola 10v1 H07613_T1	6683	637	100	glotblastn
3205	LYD2 09	canolalgb161 H07613_T1	6684	637	100	glotblastn
3206	LYD2 09	arabidopsis_lyratal09v1 JGI AL009284_T1	6685	637	98.82	glotblastn
3207	LYD2 09	arabidopsis_lyratal09v1 JGI AL009283_P1	6686	637	98.8	globlastp
3208	LYD2 09	radish gb164 EV552598_P1	6687	637	98.8	globlastp
3209	LYD2 09	radish gb164 EX756792_P1	6687	637	98.8	globlastp
3210	LYD2 09	arabidopsis 10v1 AT3G0889 0_P1	6688	637	98.2	globlastp
3211	LYD2 09	b_oleracealgb161 DY013753_P1	6689	637	98.2	globlastp
3212	LYD2 09	thellungiellalgb167 BY8083 08_P1	6690	637	97.6	globlastp
3213	LYD2 09	cleome_spinosal10v1 GR933 525_P1	6691	637	91.2	globlastp

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3214	LYD2 09	radish gb164 EV528123_P1	6692	637	88.2	globlastp
3215	LYD2 09	nasturtium 10v1 SRR032558 S0012424_P1	6693	637	87.6	globlastp
3216	LYD2 09	cleome_gynandra 10v1 SRR 015532S0013802_P1	6694	637	87.1	globlastp
3217	LYD2 09	arabidopsis 10v1 AT5G3707 0_P1	6695	637	86.5	globlastp
3218	LYD2 09	arabidopsis gb165 AT5G370 70_P1	6695	637	86.5	globlastp
3219	LYD2 09	papaya gb165 EX268088_P1	6696	637	86.5	globlastp
3220	LYD2 09	radish gb164 EW731568_P1	6697	637	85.9	globlastp
3221	LYD2 09	canola gb161 EE464762_P1	6698	637	85.3	globlastp
3222	LYD2 09	canola 10v1 CD833480_P1	6698	637	85.3	globlastp
3223	LYD2 09	arabidopsis_lyrata 09v1 JGI AL019758_P1	6699	637	84.7	globlastp
3224	LYD2 09	canola 10v1 ES900549_P1	6700	637	84.7	globlastp
3225	LYD2 09	canola gb161 CD833480_P1	6701	637	84.7	globlastp
3226	LYD2 09	eucalyptus gb166 CT982262 _P1	6702	637	84.7	globlastp
3227	LYD2 09	radish gb164 EX888617_P1	6703	637	84.7	globlastp
3228	LYD2 09	arabidopsis_lyrata 09v1 JGI AL005254_P1	6704	637	84.1	globlastp
3229	LYD2 09	arabidopsis 10v1 AT5G0161 0_P1	6705	637	84.1	globlastp
3230	LYD2 09	b_oleracea gb161 EH421224 _P1	6706	637	84.1	globlastp
3231	LYD2 09	canola 10v1 CX194506_P1	6707	637	84.1	globlastp
3232	LYD2 09	cotton 10v1 AI729006_P1	6708	637	84.1	globlastp
3233	LYD2 09	cotton gb164 AI729006_P1	6708	637	84.1	globlastp
3234	LYD2 09	ipomoea_nill 10v1 BJ562434 _P1	6709	637	83.5	globlastp
3235	LYD2 09	cassava 09v1 CK642907_P1	6710	637	83.5	globlastp
3236	LYD2 09	ipomoea gb157.2 BJ562434_ P1	6709	637	83.5	globlastp

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3237	LYD2 09	orobanche 10v1 SRR023189 S0000873_P1	6711	637	82.9	globlastp
3238	LYD2 09	cacaolgb167 CU484903_P1	6712	637	82.9	globlastp
3239	LYD2 09	coffeal 10v1 DV673843_P1	6713	637	82.9	globlastp
3240	LYD2 09	coffealgb157.2 DV673843_P 1	6713	637	82.9	globlastp
3241	LYD2 09	liriodendron gb166 DT59969 0_P1	6714	637	82.9	globlastp
3242	LYD2 09	tripphysarial 10v1 EY125780_ P1	6715	637	82.9	globlastp
3243	LYD2 09	cleome_gynandra 10v1 SRR 015532S0000548_P1	6716	637	82.5	globlastp
3244	LYD2 09	flax 09v1 CV478759_P1	6717	637	82.4	globlastp
3245	LYD2 09	cassavalgb164 CK642907_P 1	6718	637	82.4	globlastp
3246	LYD2 09	grapelgb160 CB343986_P1	6719	637	82.4	globlastp
3247	LYD2 09	poplar 10v1 AI162985_P1	6720	637	82.4	globlastp
3248	LYD2 09	poplar gb170 AI162985_P1	6721	637	82.4	globlastp
3249	LYD2 09	tripphysarialgb164 EY125780 _P1	6722	637	82.4	globlastp
3250	LYD2 09	salvia 10v1 FE536769_P1	6723	637	81.8	globlastp
3251	LYD2 09	kiwi gb166 FG437681_P1	6724	637	81.8	globlastp
3252	LYD2 09	pepper gb171 BM064893_P 1	6725	637	81.8	globlastp
3253	LYD2 09	tobacco gb162 EB428951_P 1	6726	637	81.8	globlastp
3254	LYD2 09	tomato 09v1 BG131101_P1	6727	637	81.8	globlastp
3255	LYD2 09	tomato gb164 BG131101_P1	6727	637	81.8	globlastp
3256	LYD2 09	walnuts gb166 CV195525_P 1	6728	637	81.8	globlastp
3257	LYD2 09	ipomoea_batatas 10v1 EE87 5075_T1	6729	637	81.76	glotblastn
3258	LYD2 09	castorbean 09v1 XM002526 627_P1	6730	637	81.2	globlastp
3259	LYD2 09	chestnut gb170 SRR006295S 0007436_P1	6731	637	81.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3260	LYD2 09	peanutl10v1IES720496_P1	6732	637	81.2	globlastp
3261	LYD2 09	peanutlgb171IDQ099062_P1	6732	637	81.2	globlastp
3262	LYD2 09	heritieral10v1ISRR005794S0 004663_T1	6733	637	81.18	glotblastn
3263	LYD2 09	basilicuml10v1IDY332932_ P1	6734	637	80.6	globlastp
3264	LYD2 09	eggplantl10v1IFS000729_P1	6735	637	80.6	globlastp
3265	LYD2 09	oakl10v1IFN759515_P1	6736	637	80.6	globlastp
3266	LYD2 09	oakl10v1IFP038685_P1	6736	637	80.6	globlastp
3267	LYD2 09	rhizophoral10v1ISRR005793 S0022511_P1	6737	637	80.6	globlastp
3268	LYD2 09	oaklgb170ISRR006307S000 5811_P1	6736	637	80.6	globlastp
3269	LYD2 09	poplarl10v1IAI161586_P1	6738	637	80.6	globlastp
3270	LYD2 09	poplarlgb170IAI161586_P1	6738	637	80.6	globlastp
3271	LYD2 09	potatol10v1IBG351980_P1	6739	637	80.6	globlastp
3272	LYD2 09	potatolgb157.2IBG351980_P 1	6739	637	80.6	globlastp
3273	LYD2 09	solanum_phurejal09v1ISPH BG131101_P1	6739	637	80.6	globlastp
3274	LYD2 09	teal10v1ICV014110_P1	6740	637	80.6	globlastp
3275	LYD2 09	tealgb171ICV014110_P1	6740	637	80.6	globlastp
3276	LYD2 09	tobacco gb162 CV020672_P 1	6741	637	80.6	globlastp
3277	LYD2 09	tobacco gb162 EB440426_P 1	6742	637	80.6	globlastp
3278	LYD2 09	tomatol09v1IBG630491_P1	6743	637	80.6	globlastp
3279	LYD2 09	tomatolgb164IBG630491_P1	6743	637	80.6	globlastp
3280	LYD2 09	eggplantl10v1IFS003717_P1	6744	637	80	globlastp
3281	LYD2 09	avocadol10v1ICO996840_T 1	6745	637	80	glotblastn
3282	LYD2 09	medicagol09v1IBF520968_P 1	6746	637	80	globlastp

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3283	LYD2 09	walnutslgb166 EL902338_P 1	6747	637	80	globlastp
3284	LYD2 11	maize 10v1 W59814_P1	6748	638	95.4	globlastp
3285	LYD2 11	maize gb170 W59814_P1	6748	638	95.4	globlastp
3286	LYD2 11	wheat gb164 CA617581_T1	6749	638	93.49	glotblastn
3287	LYD2 11	maize 10v1 AI637136_P1	6750	638	93.2	globlastp
3288	LYD2 11	maize gb170 AI637136_P1	6750	638	93.2	globlastp
3289	LYD2 11	sugarcane 10v1 CA067172_ P1	6751	638	92.3	globlastp
3290	LYD2 11	millet 10v1 OXPM SLX0000 399D1T1_T1	6752	638	88.26	glotblastn
3291	LYD2 11	rice gb170 OS06G06980_P1	6753	638	87	globlastp
3292	LYD2 11	sugarcane 10v1 CA080520_ P1	6754	638	81.2	globlastp
3293	LYD2 12	arabidopsis_lyratal09v1 JGI AL002279_P1	6755	639	83.3	globlastp
3294	LYD2 13	arabidopsis_lyratal09v1 JGI AL005546_P1	6756	640	94	globlastp
3295	LYD2 13	radish gb164 EV528455_P1	6757	640	91	globlastp
3296	LYD2 13	radish gb164 EX896578_P1	6758	640	91	globlastp
3297	LYD2 13	thellungiella gb167 BY8069 01_P1	6759	640	91	globlastp
3298	LYD2 13	canola 10v1 CD823783_P1	6760	640	90.4	globlastp
3299	LYD2 13	canola gb161 CD823783_P1	6760	640	90.4	globlastp
3300	LYD2 13	canola 10v1 EE565774_P1	6761	640	90.4	globlastp
3301	LYD2 13	canola gb161 EE565774_P1	6761	640	90.4	globlastp
3302	LYD2 13	b_oleracealgb161 DY027463 _P1	6762	640	89.8	globlastp
3303	LYD2 13	b_rapa gb162 EX046427_P1	6763	640	83.2	globlastp
3304	LYD2 13	cleome_spinosal10v1 GR935 047_T1	6764	640	81.44	glotblastn
3305	LYD2 13	heritieral10v1 SRR005795S0 007448_T1	6765	640	80.24	glotblastn

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3306	LYD2 13	poplar 10v1 BU837910_P1	6766	640	80	globlastp
3307	LYD2 13	poplar gb170 BU837910_P1	6766	640	80	globlastp
3308	LYD2 14	arabidopsis_lyratal09v1 JGI AL013069_P1	6767	641	85.8	globlastp
3309	LYD2 15	arabidopsis_lyratal09v1 JGI AL015680_P1	6768	642	96.6	globlastp
3310	LYD2 15	thellungiella gb167 BY8259 12_P1	6769	642	81.1	globlastp
3311	LYD2 16	arabidopsis_lyratal09v1 JGI AL008737_P1	6770	643	97.8	globlastp
3312	LYD2 16	canola 10v1 CD812868_P1	6771	643	95.8	globlastp
3313	LYD2 16	canola gb161 CD812868_P1	6771	643	95.8	globlastp
3314	LYD2 16	b_rapa gb162 BG543323_P1	6772	643	95.4	globlastp
3315	LYD2 16	canola 10v1 CD835674_P1	6773	643	95.4	globlastp
3316	LYD2 16	canola gb161 CD835674_P1	6774	643	95.3	globlastp
3317	LYD2 16	radish gb164 EV569880_T1	6775	643	94.54	glotblastn
3318	LYD2 16	arabidopsis_lyratal09v1 JGI AL021535_P1	6776	643	92	globlastp
3319	LYD2 16	oak 10v1 CU656818_P1	6777	643	83.8	globlastp
3320	LYD2 16	peanut 10v1 ES710509_P1	6778	643	83.1	globlastp
3321	LYD2 16	lotus 09v1 AI967690_P1	6779	643	83.1	globlastp
3322	LYD2 16	poplar 10v1 AI163627_P1	6780	643	82.9	globlastp
3323	LYD2 16	poplar gb170 AI163627_P1	6780	643	82.9	globlastp
3324	LYD2 16	grape gb160 CF405689_P1	6781	643	82.7	globlastp
3325	LYD2 16	cassava 09v1 DB925080_P1	6782	643	82.5	globlastp
3326	LYD2 16	poplar 10v1 BU834708_P1	6783	643	82.3	globlastp
3327	LYD2 16	cassava 09v1 DB925255_P1	6784	643	82.1	globlastp
3328	LYD2 16	cucumber 09v1 CK085497_ P1	6785	643	82.1	globlastp

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3329	LYD2 16	pigeonpeal10v1 SRR054580 S0001389_P1	6786	643	82.1	globlastp
3330	LYD2 16	soybean gb168 AW720031_ P1	6787	643	82.1	globlastp
3331	LYD2 16	cowpea gb166 FC457814_P 1	6788	643	82	globlastp
3332	LYD2 16	soybean gb168 AI967690_P 1	6789	643	82	globlastp
3333	LYD2 16	prunus 10v1 BU044770_P1	6790	643	81.8	globlastp
3334	LYD2 16	tripphysarial10v1 EX988561_ P1	6791	643	81.6	globlastp
3335	LYD2 16	castorbean 09v1 EG663398_ P1	6792	643	81.4	globlastp
3336	LYD2 16	monkeyflower 09v1 DV2073 30_P1	6793	643	81.4	globlastp
3337	LYD2 16	monkeyflower 10v1 DV2073 30_P1	6793	643	81.4	globlastp
3338	LYD2 16	monkeyflower 10v1 DV2065 98_P1	6794	643	81.2	globlastp
3339	LYD2 16	cotton 10v1 AI730956_P1	6795	643	81.2	globlastp
3340	LYD2 16	cotton gb164 AI730956_P1	6796	643	81.2	globlastp
3341	LYD2 16	sorghum 09v1 SB05G02247 0_P1	6797	643	81.2	globlastp
3342	LYD2 16	tripphysarial gb164 EX988561 _P1	6798	643	81.1	globlastp
3343	LYD2 16	prunus gb167 BU044770_P1	6799	643	80.9	globlastp
3344	LYD2 16	rice gb170 OS03G59020_P1	6800	643	80.9	globlastp
3345	LYD2 16	sugarcane 10v1 CA064935_ P1	6801	643	80.7	globlastp
3346	LYD2 16	millet 10v1 EVO454PM003 718_P1	6802	643	80.5	globlastp
3347	LYD2 16	maize 10v1 AI438833_P1	6803	643	80.5	globlastp
3348	LYD2 16	maize gb170 AI438833_P1	6803	643	80.5	globlastp
3349	LYD2 16	switchgrass gb167 FE63579 3_P1	6804	643	80.5	globlastp
3350	LYD2 16	orobanche 10v1 SRR023189 S0000892_P1	6805	643	80.3	globlastp
3351	LYD2 16	sugarcane gb157.3 CA06493 5_P1	6806	643	80.3	globlastp

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3352	LYD2 16	tomato gb164 BG123817_P1	6807	643	80.3	globlastp
3353	LYD2 16	cacao gb167 CU508640_P1	6808	643	80.1	globlastp
3354	LYD2 16	maize 10v1 AI461542_P1	6809	643	80.1	globlastp
3355	LYD2 16	maize gb170 AI461542_P1	6809	643	80.1	globlastp
3356	LYD2 16	sunflower 10v1 CD853040_ P1	6810	643	80	globlastp
3357	LYD2 16	sunflower gb162 CD853040 _P1	6810	643	80	globlastp
3358	LYD2 16	tobacco gb162 CV018317_P 1	6811	643	80	globlastp
3359	LYD2 17	arabidopsis_lyrata 09v1 JGI AL008994_P1	6812	644	94	globlastp
3360	LYD2 17	canola 10v1 CD834062_P1	6813	644	82.2	globlastp
3361	LYD2 17	b_oleracealgb161 DY027765 _P1	6814	644	82.2	globlastp
3362	LYD2 17	b_rapalgb162 L46482_P1	6815	644	82.2	globlastp
3363	LYD2 17	canola 10v1 CD823487_P1	6816	644	82.2	globlastp
3364	LYD2 17	canola gb161 CD823487_P1	6816	644	82.2	globlastp
3365	LYD2 17	canola 10v1 DY003791_P1	6817	644	82.2	globlastp
3366	LYD2 17	canola gb161 CD834062_P1	6817	644	82.2	globlastp
3367	LYD2 17	b_junceal10v2 E6ANDIZ01 BQQYN1_P1	6818	644	81.2	globlastp
3368	LYD2 17	radish gb164 EV525090_P1	6819	644	81.2	globlastp
3369	LYD2 17	radish gb164 EV551040_P1	6820	644	81.1	globlastp
3370	LYD2 19	arabidopsis_lyrata 09v1 JGI AL018329_P1	6821	645	96.1	globlastp
3371	LYD2 19	canola gb161 CD824877_T1	6822	645	82.37	glotblastn
3372	LYD2 19	canola 10v1 CD824877_P1	6823	645	82.2	globlastp
3373	LYD2 20	arabidopsis_lyrata 09v1 JGI AL026614_P1	6824	646	97.8	globlastp
3374	LYD2 20	canola 10v1 CX190271_P1	6825	646	92.7	globlastp

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3375	LYD2 20	canola gb161 CX190271_P1	6825	646	92.7	globlastp
3376	LYD2 20	radish gb164 EW716867_P1	6826	646	92.7	globlastp
3377	LYD2 20	canola 10v1 CD829020_P1	6827	646	91.6	globlastp
3378	LYD2 20	canola gb161 CD829020_P1	6827	646	91.6	globlastp
3379	LYD2 20	b_oleracealgb161 ES943495_P1	6828	646	91.1	globlastp
3380	LYD2 20	radish gb164 EW714155_P1	6829	646	91	globlastp
3381	LYD2 20	b_rapalgb162 ES935221_P1	6830	646	82.2	globlastp
3382	LYD2 20	canola 10v1 CN726066_P1	6831	646	82.2	globlastp
3383	LYD2 20	canola gb161 CN726066_P1	6831	646	82.2	globlastp
3384	LYD2 20	canola gb161 CN732719_P1	6832	646	81.7	globlastp
3385	LYD2 20	canola 10v1 CD821217_P1	6832	646	81.7	globlastp
3386	LYD2 20	canola gb161 CD821217_T1	6833	646	81.67	glotblastn
3387	LYD2 20	b_oleracealgb161 DY013876_P1	6834	646	81.1	globlastp
3388	LYD2 21	arabidopsis_lyratal09v1 JGI AL024384_P1	6835	647	97.1	globlastp
3389	LYD2 21	canola 10v1 CX188183_P1	6836	647	88.3	globlastp
3390	LYD2 21	canola gb161 CB686340_P1	6837	647	88.1	globlastp
3391	LYD2 21	b_rapalgb162 CX266123_P1	6838	647	87.9	globlastp
3392	LYD2 21	canola gb161 CD836701_P1	6839	647	87.9	globlastp
3393	LYD2 21	canola 10v1 CB686340_P1	6840	647	87.7	globlastp
3394	LYD2 21	radish gb164 EV538382_P1	6841	647	87.7	globlastp
3395	LYD2 22	arabidopsis_lyratal09v1 JGI AL024369_T1	6842	648	94.64	glotblastn
3396	LYD2 23	arabidopsis_lyratal09v1 JGI AL021005_P1	6843	649	88.6	globlastp
3397	LYD2 23	b_rapalgb162 BQ791203_P1	6844	649	85.8	globlastp

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3398	LYD2 23	canola 10v1 CN728130_P1	6845	649	85.7	globlastp
3399	LYD2 23	canola 10v1 CN727598_P1	6846	649	85.5	globlastp
3400	LYD2 23	canola gb161 CN727598_P1	6846	649	85.5	globlastp
3401	LYD2 23	b_oleracea gb161 AM39164 6_P1	6847	649	85.1	globlastp
3402	LYD2 23	radish gb164 EW717140_P1	6848	649	84.3	globlastp
3403	LYD2 23	radish gb164 EW734029_P1	6849	649	83.5	globlastp
3404	LYD2 24	arabidopsis_lyrata 09v1 JGI AL030393_P1	6850	650	96.2	globlastp
3405	LYD2 24	canola 10v1 CD816983_T1	6851	650	89.25	glotblastn
3406	LYD2 24	canola 10v1 CN726221_P1	6852	650	88.2	globlastp
3407	LYD2 24	canola gb161 CN726221_P1	6852	650	88.2	globlastp
3408	LYD2 24	maize gb170 LLDQ245206_ P1	6852	650	88.2	globlastp
3409	LYD2 24	radish gb164 FD545244_P1	6853	650	88.2	globlastp
3410	LYD2 24	radish gb164 EW717992_P1	6854	650	87.6	globlastp
3411	LYD2 24	canola 10v1 CD823092_P1	6855	650	87.2	globlastp
3412	LYD2 24	canola 10v1 EV083752_P1	6856	650	86.6	globlastp
3413	LYD2 24	b_rapa gb162 BG544824_P1	6856	650	86.6	globlastp
3414	LYD2 24	canola gb161 CD823092_P1	6856	650	86.6	globlastp
3415	LYD2 24	radish gb164 EV568231_P1	6857	650	86.1	globlastp
3416	LYD2 24	radish gb164 EX772197_P1	6858	650	86.1	globlastp
3417	LYD2 24	b_juncea 10v2 E6ANDIZ01 DINO2_T1	6859	650	86.02	glotblastn
3418	LYD2 24	b_juncea 10v2 E6ANDIZ01 D9PQH_P1	6860	650	85.6	globlastp
3419	LYD2 24	b_nigra 09v1 GT069734_P1	6861	650	85	globlastp
3420	LYD2 24	canola 10v1 CD830574_P1	6862	650	85	globlastp

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3421	LYD2 24	b_rapalgb162 BG543212_P1	6862	650	85	globlastp
3422	LYD2 24	canolalgb161 CD830574_P1	6862	650	85	globlastp
3423	LYD2 24	thellungiellalgb167 DN7754 67_P1	6863	650	85	globlastp
3424	LYD2 24	radishlgb164 EV528198_P1	6864	650	84.5	globlastp
3425	LYD2 24	radishlgb164 EV539693_P1	6864	650	84.5	globlastp
3426	LYD2 24	radishlgb164 EW735492_P1	6864	650	84.5	globlastp
3427	LYD2 24	b_rapalgb162 DY008897_P1	6865	650	84.2	globlastp
3428	LYD2 24	b_juncealgb164 EVGN0032 5314303466_P1	6866	650	84	globlastp
3429	LYD2 24	b_oleracealgb161 AM05891 3_P1	6867	650	84	globlastp
3430	LYD2 24	canolal10v1 CD821086_P1	6867	650	84	globlastp
3431	LYD2 24	canolalgb161 CD821086_P1	6867	650	84	globlastp
3432	LYD2 24	b_junceal10v2 BJ1SLX0001 4852D1_P1	6868	650	83.9	globlastp
3433	LYD2 24	radishlgb164 EV568887_P1	6869	650	83.4	globlastp
3434	LYD2 24	b_oleracealgb161 ES947178 _P1	6870	650	82.8	globlastp
3435	LYD2 24	radishlgb164 EX755825_T1	6871	650	82.26	glotblastn
3436	LYD2 24	cleome_spinosal10v1 GR931 469_P1	6872	650	81.7	globlastp
3437	LYD2 24	b_junceal10v2 E6ANDIZ01 BER52_P1	6873	650	81.2	globlastp
3438	LYD2 24	radishlgb164 EV551184_T1	6874	650	80.85	glotblastn
3439	LYD2 24	canolalgb161 CN725816_P1	6875	650	80.6	globlastp
3440	LYD2 24	orobanche 10v1 SRR023189 S0014743_P1	6876	650	80.1	globlastp
3441	LYD2 25	leymuslgb166 EG378671_T 1	6877	651	84.68	glotblastn
3441	LYD2 28	leymuslgb166 EG378671_T 1	6877	653	84.74	glotblastn
3442	LYD2 25	wheatlgb164 BE430129_P1	6878	651	83.4	globlastp

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3442	LYD2 28	wheat gb164 BE430129_P1	6878	653	83.7	globlastp
3443	LYD2 25	wheat gb164 BE493466_P1	6879	651	82.9	globlastp
3443	LYD2 28	wheat gb164 BE493466_P1	6879	653	83.3	globlastp
3444	LYD2 25	wheat gb164 BI751513_P1	6879	651	82.9	globlastp
3444	LYD2 28	wheat gb164 BI751513_P1	6879	653	83.3	globlastp
3445	LYD2 25	barley gb157 SOLEXA BI95 0425_P1	6880	651	81.5	globlastp
3445	LYD2 28	barley gb157 SOLEXA BI95 0425_P1	6880	653	83.4	globlastp
3446	LYD2 25	barley 10v1 BI950425_P1	6880	651	81.5	globlastp
3446	LYD2 28	barley 10v1 BI950425_P1	6880	653	83.4	globlastp
3447	LYD2 25	brachypodium 09v1 DV4736 30_T1	6881	651	81.45	glotblastn
3447	LYD2 28	brachypodium 09v1 DV4736 30_P1	6881	653	82.1	globlastp
3448	LYD2 25	brachypodium gb169 BE430 129_T1	6881	651	81.45	glotblastn
3448	LYD2 28	brachypodium gb169 BE430 129_P1	6881	653	82.1	globlastp
3449	LYD2 25	oat 10v2 GR322675_P1	6882	651	80.8	globlastp
3449	LYD2 28	oat 10v2 GR322675_P1	6882	653	82.3	globlastp
3450	LYD2 27	sugarcane 10v1 BQ533190_ P1	6883	652	95.9	globlastp
3451	LYD2 27	sugarcane gb157.3 BQ53319 0_P1	6883	652	95.9	globlastp
3452	LYD2 27	maize 10v1 AI636982_P1	6884	652	93	globlastp
3453	LYD2 27	cynodon 10v1 ES293243_P1	6885	652	92.4	globlastp
3454	LYD2 27	switchgrass gb167 DN15073 2_P1	6886	652	92.4	globlastp
3455	LYD2 27	millet 10v1 EVO454PM058 462_T1	6887	652	91.81	glotblastn
3456	LYD2 27	switchgrass gb167 FE61780 9_P1	6888	652	91.8	globlastp
3457	LYD2 27	oat 10v2 GO596450_T1	6889	652	90.06	glotblastn

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3458	LYD2 27	pseudoroegneria gb167 FF34 0032_T1	6890	652	88.3	glotblastn
3459	LYD2 27	wheat gb164 BE426355_T1	6891	652	87.72	glotblastn
3460	LYD2 27	wheat gb164 BE499789_T1	6892	652	87.72	glotblastn
3461	LYD2 27	rice gb170 OS03G24380_P1	6893	652	87.7	globlastp
3462	LYD2 27	wheat gb164 BE419519_T1	6894	652	86.55	glotblastn
3463	LYD2 27	fescue gb161 DT680055_P1	6895	652	85.5	globlastp
3464	LYD2 27	brachypodium 09v1 DV4720 62_T1	6896	652	85.38	glotblastn
3465	LYD2 27	brachypodium gb169 BE412 952_T1	6896	652	85.38	glotblastn
3466	LYD2 27	barley 10v1 BE412952_P1	6897	652	85.3	globlastp
3467	LYD2 27	barley gb157 SOLEXA BE41 2952_P1	6897	652	85.3	globlastp
3468	LYD2 27	leymus gb166 CN465857_P 1	6898	652	85.3	globlastp
3469	LYD2 27	rye gb164 BF429400_P1	6899	652	82.5	globlastp
3470	LYD2 27	oat 10v2 GO584438_P1	6900	652	82.4	globlastp
3471	LYD2 28	sugarcane 10v1 BQ537170_ P1	6901	653	98	globlastp
3472	LYD2 28	sugarcane gb157.3 BQ53717 0_P1	6901	653	98	globlastp
3473	LYD2 28	maize 10v1 AI691314_P1	6902	653	95.6	globlastp
3474	LYD2 28	maize gb170 LLAW506702_ P1	6902	653	95.6	globlastp
3475	LYD2 28	millet 10v1 EVO454PM069 124_P1	6903	653	91.2	globlastp
3476	LYD2 28	rice gb170 OS07G08070_P1	6904	653	86.7	globlastp
3477	LYD2 28	cenchrus gb166 EB666958_ P1	6905	653	83.3	globlastp
3478	LYD2 29	maize 10v1 CD995946_P1	6906	654	97.2	globlastp
3479	LYD2 29	maize gb170 CD995946_P1	6906	654	97.2	globlastp
3480	LYD2 29	maize 10v1 CO448545_P1	6907	654	97.2	globlastp

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3481	LYD2 29	maize gb170 CO448545_P1	6908	654	96.8	globlastp
3482	LYD2 29	switchgrass gb167 FL72248 1_P1	6909	654	94.8	globlastp
3483	LYD2 29	barley 10v1 BM368785_P1	6910	654	90.4	globlastp
3484	LYD2 29	brachypodium 09v1 SRR031 795S0033339_P1	6911	654	90.4	globlastp
3485	LYD2 29	brachypodium gb169 BE430 146_P1	6911	654	90.4	globlastp
3486	LYD2 29	wheat gb164 BE430146_P1	6912	654	89.6	globlastp
3487	LYD2 29	rice gb170 OS03G53400_P1	6913	654	88.8	globlastp
3488	LYD2 30	maize 10v1 CF006891_P1	6914	655	86.6	globlastp
3489	LYD2 30	maize gb170 CF006891_P1	6914	655	86.6	globlastp
3490	LYD2 30	switchgrass gb167 DN14117 2_P1	6915	655	84.5	globlastp
3491	LYD2 31	sugarcane gb157.3 BQ53435 2_P1	6916	656	97.3	globlastp
3492	LYD2 31	maize 10v1 AW017610_P1	6917	656	93.2	globlastp
3493	LYD2 31	maize gb170 AW017610_P1	6917	656	93.2	globlastp
3494	LYD2 31	brachypodium 09v1 DV4776 13_P1	6918	656	81.6	globlastp
3495	LYD2 31	rice gb170 OS03G13840_P1	6919	656	81.4	globlastp
3496	LYD2 32	solanum_phureja 09v1 SPH AI774782_P1	6920	657	96.2	globlastp
3497	LYD2 32	pepper gb171 BM066383_P 1	6921	657	88	globlastp
3498	LYD2 32	solanum_phureja 09v1 SPH CRPSP045853_P1	6922	657	83.7	globlastp
3499	LYD2 33	potato 10v1 BI406530_P1	6923	658	97.7	globlastp
3500	LYD2 33	potato gb157.2 BI406530_P1	6923	658	97.7	globlastp
3501	LYD2 33	solanum_phureja 09v1 SPH AW032486_P1	6924	658	97.5	globlastp
3502	LYD2 34	potato gb157.2 BF052303_P 1	6925	659	98.2	globlastp
3503	LYD2 34	solanum_phureja 09v1 SPH BG123219_P1	6926	659	98.2	globlastp

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3504	LYD2 34	potatol10v1 BF052303_P1	6927	659	97.6	globlastp
3505	LYD2 34	pepper gb171 BM063045_P 1	6928	659	90	globlastp
3506	LYD2 34	solanum_phurejal09v1 SPH AI489595_P1	6929	659	82.9	globlastp
3507	LYD2 34	eggplantl10v1 FS038503_P1	6930	659	81.8	globlastp
3508	LYD2 34	tomatol09v1 AI489595_P1	6931	659	81.8	globlastp
3509	LYD2 34	potatol10v1 CK860071_P1	6932	659	81.2	globlastp
3510	LYD2 34	coffeal10v1 DV664407_P1	6933	659	80.6	globlastp
3511	LYD2 34	coffealgb157.2 DV664407_P 1	6933	659	80.6	globlastp
3512	LYD2 34	petunialgb171 CV299482_P 1	6934	659	80	globlastp
3513	LYD2 34	potatolgb157.2 CK860071_T 1	6935	659	80	glotblastn
3514	LYD2 36	potatolgb157.2 BQ512865_P 1	6936	661	98.3	globlastp
3515	LYD2 36	solanum_phurejal09v1 SPH BG629499_P1	6936	661	98.3	globlastp
3516	LYD2 36	potatol10v1 BQ512865_P1	6937	661	97.9	globlastp
3517	LYD2 36	eggplantl10v1 FS012987_P1	6938	661	96.7	globlastp
3518	LYD2 36	tobacco gb162 EB425766_P 1	6939	661	93.4	globlastp
3519	LYD2 36	pepper gb171 BM060326_P 1	6940	661	92.1	globlastp
3520	LYD2 36	petunialgb171 DY396002_P 1	6941	661	91.7	globlastp
3521	LYD2 36	orobanche 10v1 SRR023189 S0003702_P1	6942	661	82.6	globlastp
3522	LYD2 36	nasturtiuml10v1 SRR032558 S0002662_P1	6943	661	82.2	globlastp
3523	LYD2 36	ipomoea_nill10v1 CJ748154 _P1	6944	661	81.4	globlastp
3524	LYD2 36	canola 10v1 CD843095_P1	6945	661	81.4	globlastp
3525	LYD2 36	canolalgb161 CD843095_P1	6945	661	81.4	globlastp
3526	LYD2 36	canola 10v1 CN828945_P1	6946	661	81.4	globlastp

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3527	LYD2 36	canola gb161 CN828945_P1	6946	661	81.4	globlastp
3528	LYD2 36	ipomoea gb157.2 CJ748154_P1	6944	661	81.4	globlastp
3529	LYD2 36	radish gb164 FD968048_P1	6947	661	81.4	globlastp
3530	LYD2 36	monkeyflower 10v1 GR139081_P1	6948	661	81.1	globlastp
3531	LYD2 36	arabidopsis_lyrata 09v1 JGI AL019688_P1	6949	661	81	globlastp
3532	LYD2 36	coffea 10v1 DV680032_P1	6950	661	81	globlastp
3533	LYD2 36	solanum_phureja 09v1 SPH AW930877_T1	6951	661	80.99	glotblastn
3534	LYD2 36	cassava 09v1 JGICASSAVA 24594VALIDM1_P1	6952	661	80.6	globlastp
3535	LYD2 36	arabidopsis 10v1 AT3G63310_P1	6953	661	80.6	globlastp
3536	LYD2 36	arabidopsis gb165 AT3G63310_P1	6953	661	80.6	globlastp
3537	LYD2 36	castorbean 09v1 EG657869_P1	6954	661	80.6	globlastp
3538	LYD2 36	tomato gb164 AW930877_T1	6955	661	80.58	glotblastn
3539	LYD2 36	peanut 10v1 DT044283_P1	6956	661	80.3	globlastp
3540	LYD2 36	cotton 10v1 AI729700_P1	6957	661	80.2	globlastp
3541	LYD2 36	citrus gb166 CF508840_P1	6958	661	80.2	globlastp
3542	LYD2 36	papaya gb165 EX252004_P1	6959	661	80.2	globlastp
3543	LYD2 38	wheat gb164 BE216948_P1	6960	662	92	globlastp
3544	LYD2 38	wheat gb164 BE401874_P1	6961	662	92	globlastp
3545	LYD2 38	wheat gb164 BE402639_P1	6962	662	91.5	globlastp
3546	LYD2 38	wheat gb164 BE399415_P1	6963	662	91.4	globlastp
3547	LYD2 38	rye gb164 BE493975_T1	6964	662	90.23	glotblastn
3548	LYD2 38	wheat gb164 CK161460_P1	6965	662	89.5	globlastp
3549	LYD2 38	barley gb157 SOLEXA BE412540_P1	6966	662	89.1	globlastp

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3550	LYD2 38	barley 10v1 BE412540_P1	6966	662	89.1	globlastp
3551	LYD2 38	barley gb157SOLEXA BF62 5618_P1	6967	662	88.7	globlastp
3552	LYD2 38	oat 10v2 GO583734_P1	6968	662	88.4	globlastp
3553	LYD2 38	rye gb164 BE495984_P1	6969	662	87.9	globlastp
3554	LYD2 38	millet 10v1 EVO454PM015 488_P1	6970	662	86.5	globlastp
3555	LYD2 38	brachypodium gb169 BE216 948_P1	6971	662	86	globlastp
3556	LYD2 38	lolium 10v1 AU245719_P1	6972	662	84.9	globlastp
3557	LYD2 38	wheat gb164 BE516428_P1	6973	662	84.9	globlastp
3558	LYD2 38	sugarcane 10v1 CA065337_ P1	6974	662	84.2	globlastp
3559	LYD2 38	sugarcane gb157.3 CA07183 6_P1	6975	662	83.6	globlastp
3560	LYD2 38	sorghum 09v1 SB04G00033 0_P1	6976	662	83	globlastp
3561	LYD2 38	sugarcane gb157.3 CA07615 5_T1	6977	662	82.58	glotblastn
3562	LYD2 38	cynodon 10v1 ES293159_T1	6978	662	82.02	glotblastn
3563	LYD2 40	wheat gb164 BF200876_P1	6979	663	88.4	globlastp
3564	LYD2 44	arabidopsis_lyrata 09v1 JGI AL007321_P1	6980	664	94.5	globlastp
3565	LYD2 44	b_juncea 10v2 E6ANDIZ01 DG4SQ_P1	6981	664	85.5	globlastp
3566	LYD2 44	b_oleracea gb161 EH415612 _P1	6981	664	85.5	globlastp
3567	LYD2 44	canola 10v1 CD830211_P1	6981	664	85.5	globlastp
3568	LYD2 44	canola gb161 CD830211_P1	6981	664	85.5	globlastp
3569	LYD2 44	canola 10v1 CD830816_P1	6981	664	85.5	globlastp
3570	LYD2 44	canola gb161 CD830816_P1	6981	664	85.5	globlastp
3571	LYD2 44	radish gb164 EV525014_P1	6982	664	83.6	globlastp
3572	LYD2 44	b_juncea 10v2 E6ANDIZ01 EPIVN_P1	6983	664	83	globlastp

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3573	LYD2 44	radishlgb164 EV545064_P1	6984	664	81.8	globlastp
3574	LYD2 44	b_rapalgb162 EX024633_P1	6985	664	80.6	globlastp
3575	LYD2 45	thellungiellalgb167 DN7740 29_P1	6986	665	87	globlastp
3576	LYD2 45	radishlgb164 EX750107_T1	6987	665	84.9	glotblastn
3577	LYD2 45	canolalgb161 EE477076_P1	6988	665	84.5	globlastp
3578	LYD2 45	arabidopsis_lyratal09v1 TM PLEV566587T1_T1	6989	665	84.38	glotblastn
3579	LYD2 45	radishlgb164 EV566587_P1	6990	665	83.9	globlastp
3580	LYD2 46	arabidopsis 10v1 AT4G0858 0_P1	6991	666	98.2	globlastp
3581	LYD2 46	arabidopsis gb165 AT4G085 80_P1	6991	666	98.2	globlastp
3582	LYD2 46	arabidopsis_lyratal09v1 JGI AL021498_P1	6992	666	94.5	globlastp
3583	LYD2 48	b_rapalgb162 BQ790922_P1	6993	667	98.6	globlastp
3584	LYD2 48	canolalgb161 CD816144_P1	6994	667	97.6	globlastp
3585	LYD2 48	canolal10v1 CD816250_P1	6995	667	87.2	globlastp
3586	LYD2 48	canolalgb161 CD816250_P1	6995	667	87.2	globlastp
3587	LYD2 48	b_rapalgb162 CV544898_P1	6996	667	86.6	globlastp
3588	LYD2 48	canolalgb161 CD813767_P1	6997	667	85.8	globlastp
3589	LYD2 48	arabidopsis_lyratal09v1 JGI AL010389_P1	6998	667	85.6	globlastp
3590	LYD2 48	canolal10v1 CD813767_P1	6999	667	85.4	globlastp
3591	LYD2 48	arabidopsis 10v1 AT3G1849 0_P1	7000	667	84.4	globlastp
3592	LYD2 48	canolalgb161 CD820800_P1	7001	667	83.2	globlastp
3593	LYD2 48	canolal10v1 CD820800_P1	7002	667	83	globlastp
3594	LYD2 48	canolal10v1 CD816721_T1	7003	667	82	glotblastn
3595	LYD2 50	canolalgb161 EV168840_P1	7004	668	93	globlastp

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3596	LYD2 50	radish gb164 EX755649_P1	7005	668	93	globlastp
3597	LYD2 50	arabidopsis_lyrata 09v1 JGI AL012240_P1	7006	668	88.4	globlastp
3598	LYD2 50	arabidopsis 10v1 AT2G1773 O_P1	7007	668	86.4	globlastp
3599	LYD2 50	canola 10v1 CD813120_P1	7008	668	84.5	globlastp
3600	LYD2 50	canola gb161 CD813120_P1	7008	668	84.5	globlastp
3601	LYD2 50	canola 10v1 DY023893_P1	7009	668	84.5	globlastp
3602	LYD2 50	canola gb161 DY023893_P1	7009	668	84.5	globlastp
3603	LYD2 50	canola gb161 CD820111_P1	7010	668	83.8	globlastp
3604	LYD2 50	arabidopsis_lyrata 09v1 JGI AL024385_P1	7011	668	83.7	globlastp
3605	LYD2 50	canola 10v1 CD820111_P1	7012	668	83.7	globlastp
3606	LYD2 50	arabidopsis 10v1 AT4G3584 O_P1	7013	668	83.3	globlastp
3607	LYD2 50	radish gb164 EX763901_P1	7014	668	82.8	globlastp
3608	LYD2 50	b_rapa gb162 EE520070_T1	7015	668	81.67	glotblastn
3609	LYD2 50	radish gb164 EW724552_P1	7016	668	80.4	globlastp
3610	LYD2 50	b_rapa gb162 EX039808_P1	7017	668	80	globlastp
3611	LYD2 52	b_junceal 10v2 E6ANDIZ01 D3YNI_P1	7018	669	98.4	globlastp
3612	LYD2 52	b_junceal gb164 EVGN0428 8230702644_P1	7019	669	98.4	globlastp
3613	LYD2 52	b_rapa gb162 CV545283_P1	7018	669	98.4	globlastp
3614	LYD2 52	canola 10v1 CD811728_P1	7018	669	98.4	globlastp
3615	LYD2 52	canola gb161 CD811728_P1	7018	669	98.4	globlastp
3616	LYD2 52	canola 10v1 CD840433_P1	7018	669	98.4	globlastp
3617	LYD2 52	canola gb161 CD818666_P1	7018	669	98.4	globlastp
3618	LYD2 52	canola 10v1 CD832702_P1	7019	669	98.4	globlastp

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3619	LYD2 52	radish gb164 EX761962_P1	7019	669	98.4	globlastp
3620	LYD2 52	radish gb164 EX904863_P1	7020	669	98.4	globlastp
3621	LYD2 52	thellungiella gb167 BY8131 44_P1	7021	669	98.4	globlastp
3622	LYD2 52	b_junceal 10v2 E6ANDIZ01 EDC4C1_P1	7022	669	97.6	globlastp
3623	LYD2 52	canola 10v1 DY012004_P1	7023	669	97.6	globlastp
3624	LYD2 52	b_oleraceal gb161 CO729379 _P1	7024	669	97.6	globlastp
3625	LYD2 52	b_oleraceal gb161 DY027071 _P1	7025	669	97.6	globlastp
3626	LYD2 52	canola 10v1 CD814099_P1	7024	669	97.6	globlastp
3627	LYD2 52	canola gb161 CD814099_P1	7024	669	97.6	globlastp
3628	LYD2 52	canola gb161 CD832702_P1	7026	669	97.6	globlastp
3629	LYD2 52	radish gb164 EV567261_P1	7027	669	97.6	globlastp
3630	LYD2 52	radish gb164 EX748940_P1	7028	669	97.6	globlastp
3631	LYD2 52	b_junceal 10v2 E6ANDIZ01 CCOGE_P1	7029	669	96.8	globlastp
3632	LYD2 52	b_rapal gb162 CX271124_P1	7030	669	96.8	globlastp
3633	LYD2 52	canola 10v1 CD817829_P1	7031	669	96.8	globlastp
3634	LYD2 52	canola gb161 CD817829_P1	7031	669	96.8	globlastp
3635	LYD2 52	b_rapal gb162 CV432392_P1	7032	669	96	globlastp
3636	LYD2 52	b_rapal gb162 CV434073_P1	7032	669	96	globlastp
3637	LYD2 52	arabidopsis lyrata 09v1 JGI AL028037_P1	7033	669	94.4	globlastp
3638	LYD2 52	radish gb164 FD966947_P1	7034	669	93.8	globlastp
3639	LYD2 52	arabidopsis 10v1 AT5G4757 0_P1	7035	669	93.6	globlastp
3640	LYD2 52	arabidopsis gb165 AT5G475 70_P1	7035	669	93.6	globlastp
3641	LYD2 52	cleome_spinosal 10v1 SRR01 5531S0006615_P1	7036	669	91.2	globlastp

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3642	LYD2 52	eucalyptus gb166 CU400330_P1	7037	669	91.2	globlastp
3643	LYD2 52	papaya gb165 EX278970_P1	7038	669	90.4	globlastp
3644	LYD2 52	cleome_spinosa 10v1 GR933959_P1	7039	669	89.6	globlastp
3645	LYD2 52	sesame 10v1 BU667421_P1	7040	669	89.6	globlastp
3646	LYD2 52	sesame gb157.2 BU667421_P1	7040	669	89.6	globlastp
3647	LYD2 52	lettuce gb157.2 DW084867_P1	7041	669	88.8	globlastp
3648	LYD2 52	lettuce gb157.2 DW162422_P1	7041	669	88.8	globlastp
3649	LYD2 52	rhizophora 10v1 SRR005793S0012361_P1	7042	669	88	globlastp
3650	LYD2 52	tragopogon 10v1 SRR020205S0001878_P1	7043	669	88	globlastp
3651	LYD2 52	citrus gb166 CB292761_P1	7044	669	88	globlastp
3652	LYD2 52	lettuce gb157.2 DW107481_P1	7045	669	88	globlastp
3653	LYD2 52	liquorice gb171 FS256375_P1	7046	669	88	globlastp
3654	LYD2 52	lettuce 10v1 DW052883_P1	7045	669	88	globlastp
3655	LYD2 52	oak 10v1 FN740810_P1	7047	669	87.2	globlastp
3656	LYD2 52	salvia 10v1 SRR014553S0000292_P1	7048	669	87.2	globlastp
3657	LYD2 52	bruguiera gb166 BP941272_P1	7049	669	87.2	globlastp
3658	LYD2 52	tea gb171 GE650523_P1	7050	669	87.2	globlastp
3659	LYD2 52	cleome_gynandra 10v1 SRR015532S0001846_P1	7051	669	86.4	globlastp
3660	LYD2 52	tea 10v1 GE650523_P1	7052	669	86.4	globlastp
3661	LYD2 52	antirrhinum gb166 AJ786955_P1	7053	669	86.4	globlastp
3662	LYD2 52	apple gb171 CN496843_P1	7054	669	86.4	globlastp
3663	LYD2 52	cassava 09v1 DV452287_P1	7055	669	86.4	globlastp
3664	LYD2 52	cassava gb164 DV452287_P1	7055	669	86.4	globlastp

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3665	LYD2 52	centaurealgb166 EH782240_P1	7056	669	86.4	globlastp
3666	LYD2 52	grapelgb160 CA816525_P1	7057	669	86.4	globlastp
3667	LYD2 52	poplarl10v1 AI165259_P1	7058	669	86.4	globlastp
3668	LYD2 52	poplarlgb170 AI165259_P1	7058	669	86.4	globlastp
3669	LYD2 52	potatolgb157.2 BF052445_P1	7059	669	86.4	globlastp
3670	LYD2 52	potatolgb157.2 BQ519344_P1	7059	669	86.4	globlastp
3671	LYD2 52	solanum_phurejal09v1 SPH BG133401_P1	7059	669	86.4	globlastp
3672	LYD2 52	tomatol09v1 BG133401_P1	7060	669	86.4	globlastp
3673	LYD2 52	tomatolgb164 BG133401_P1	7060	669	86.4	globlastp
3674	LYD2 52	potatol10v1 BF052445_P1	7059	669	86.4	globlastp
3675	LYD2 52	acacial10v1 FS584402_P1	7061	669	85.6	globlastp
3676	LYD2 52	ipomoea_nill10v1 BJ556249_P1	7062	669	85.6	globlastp
3677	LYD2 52	beetlgb162 BQ592121_T1	7063	669	85.6	glotblastn
3678	LYD2 52	chestnutlgb170 SRR006295S 0021181_P1	7064	669	85.6	globlastp
3679	LYD2 52	cottonl10v1 CO070890_P1	7065	669	85.6	globlastp
3680	LYD2 52	cottonlgb164 AW187773_P1	7065	669	85.6	globlastp
3681	LYD2 52	ipomoealgb157.2 BJ556249_P1	7062	669	85.6	globlastp
3682	LYD2 52	nicotiana_benthamianalgb16 2 CN744797_P1	7066	669	85.6	globlastp
3683	LYD2 52	prunusl10v1 CB819220_P1	7067	669	85.6	globlastp
3684	LYD2 52	prunuslgb167 CB819220_P1	7067	669	85.6	globlastp
3685	LYD2 52	seneciolgb170 SRR006592S 0007335_P1	7068	669	85.6	globlastp
3686	LYD2 52	tobacco gb162 CV020459_T1	7069	669	85.6	glotblastn
3687	LYD2 52	walnutslgb166 CV195294_P1	7070	669	84.9	globlastp

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3688	LYD2 52	dandelion 10v1 DR399370_ P1	7071	669	84.8	globlastp
3689	LYD2 52	sunflower 10v1 CD847361_ P1	7072	669	84.8	globlastp
3690	LYD2 52	cotton 10v1 BF269151_P1	7073	669	84.8	globlastp
3691	LYD2 52	cynara gb167 GE586064_P1	7074	669	84.8	globlastp
3692	LYD2 52	dandelion 10v1 DY817824_ P1	7071	669	84.8	globlastp
3693	LYD2 52	dandelion gb161 DY817824_ P1	7071	669	84.8	globlastp
3694	LYD2 52	liriodendron gb166 FD48956 2_P1	7075	669	84.8	globlastp
3695	LYD2 52	monkeyflower 09v1 GO9638 42_P1	7076	669	84.8	globlastp
3696	LYD2 52	monkeyflower 10v1 GO9638 42_P1	7076	669	84.8	globlastp
3697	LYD2 52	pepper gb171 BM064183_P 1	7077	669	84.8	globlastp
3698	LYD2 52	petunia gb171 DY395455_P 1	7078	669	84.8	globlastp
3699	LYD2 52	sunflower gb162 CD847361_ P1	7072	669	84.8	globlastp
3700	LYD2 52	tobacco gb162 CV020284_P 1	7079	669	84.8	globlastp
3701	LYD2 52	triphysaria 10v1 EX990359_ P1	7080	669	84.8	globlastp
3702	LYD2 52	coffea 10v1 DV673928_P1	7081	669	84	globlastp
3703	LYD2 52	dandelion 10v1 DY835786_ T1	7082	669	84	glotblastn
3704	LYD2 52	eggplant 10v1 FS000144_P1	7083	669	84	globlastp
3705	LYD2 52	centaurea gb166 EH737005_ P1	7084	669	84	globlastp
3706	LYD2 52	cotton gb164 BF269151_P1	7085	669	84	globlastp
3707	LYD2 52	cowpea gb166 FC458079_P 1	7086	669	84	globlastp
3708	LYD2 52	petunia gb171 CV296748_P 1	7087	669	84	globlastp
3709	LYD2 52	soybean gb168 BE320813_P 1	7086	669	84	globlastp
3710	LYD2 52	triphysaria gb164 EX990359_ P1	7088	669	84	globlastp

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3711	LYD2 52	kiwi gb166 FG429909_P1	7089	669	83.7	globlastp
3712	LYD2 52	artemisia 10v1 EY037110_P 1	7090	669	83.2	globlastp
3713	LYD2 52	ipomoea_batatas 10v1 EE88 1968_P1	7091	669	83.2	globlastp
3714	LYD2 52	triphysaria 10v1 EY018432_ P1	7092	669	83.2	globlastp
3715	LYD2 52	artemisia gb164 EY037110_ P1	7090	669	83.2	globlastp
3716	LYD2 52	bean gb167 CA912723_P1	7093	669	83.2	globlastp
3717	LYD2 52	castorbean 09v1 EG667738_ T1	7094	669	83.2	glotblastn
3718	LYD2 52	oil_palm gb166 EL684852_ P1	7095	669	83.2	globlastp
3719	LYD2 52	peanut 10v1 EE125818_P1	7096	669	83.2	globlastp
3720	LYD2 52	peanut gb171 EC365309_P1	7096	669	83.2	globlastp
3721	LYD2 52	pigeonpea gb171 GR471435_ P1	7097	669	83.2	globlastp
3722	LYD2 52	soybean gb168 CA899926_P 1	7098	669	83.2	globlastp
3723	LYD2 52	strawberry gb164 CX662144_ P1	7099	669	83.2	globlastp
3724	LYD2 52	b_juncea 10v2 E6ANDIZ01 BOR0S1_P1	7100	669	82.4	globlastp
3725	LYD2 52	rose 10v1 BQ105459_P1	7101	669	82.4	globlastp
3726	LYD2 52	basilicum gb157.3 DY32343 7_P1	7102	669	82.4	globlastp
3727	LYD2 52	bean gb167 CA899926_P1	7103	669	82.4	globlastp
3728	LYD2 52	bean gb167 EH040312_P1	7103	669	82.4	globlastp
3729	LYD2 52	chickpea 09v2 GR392149_P 1	7104	669	82.4	globlastp
3730	LYD2 52	lettuce gb157.2 DW052883_ T1	7105	669	82.4	glotblastn
3731	LYD2 52	pigeonpea 10v1 GW346529 XX2_T1	7106	669	82.4	glotblastn
3732	LYD2 52	tamarix gb166 EH052332_P 1	7107	669	82.4	globlastp
3733	LYD2 52	b_oleracea gb161 EH421962 _P1	7108	669	81.5	globlastp

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3734	LYD2 52	nasturtium 10v1 SRR032558 S0000551_P1	7109	669	80.8	globlastp
3735	LYD2 52	avocado 10v1 CK759662_T 1	7110	669	80.8	glotblastn
3736	LYD2 52	avocado gb164 CK759662_ T1	7111	669	80.8	glotblastn
3737	LYD2 52	medicago 09v1 BE239635_P 1	7112	669	80.8	globlastp
3738	LYD2 52	oak gb170 SRR006307S000 4113_P1	7113	669	80.8	globlastp
3739	LYD2 52	cucumber 09v1 AB029112_ P1	7114	669	80.3	globlastp
3740	LYD2 52	melon 10v1 AM714236_P1	7114	669	80.3	globlastp
3741	LYD2 52	melon gb165 AM714236_P1	7114	669	80.3	globlastp
3742	LYD2 52	orobanche 10v1 SRR023189 S0009680_P1	7115	669	80	globlastp
3743	LYD2 52	gerbera 09v1 AJ759705_P1	7116	669	80	globlastp
3744	LYD2 53	arabidopsis_lyrata 09v1 JGI AL013828_P1	7117	670	97.4	globlastp
3745	LYD2 53	arabidopsis_lyrata 09v1 JGI AL000784_P1	7118	670	96.1	globlastp
3746	LYD2 53	cacao gb167 CU481903_P1	7119	670	91.3	globlastp
3747	LYD2 53	soybean gb168 BE352739_P 1	7120	670	91	globlastp
3748	LYD2 53	cotton 10v1 AI725856_P1	7121	670	90.7	globlastp
3749	LYD2 53	cotton gb164 AI725856_P1	7121	670	90.7	globlastp
3750	LYD2 53	bean gb167 CA900778_P1	7122	670	90.2	globlastp
3751	LYD2 53	cowpea gb166 FC459485_P 1	7123	670	90	globlastp
3752	LYD2 53	lotus 09v1 BE122579_P1	7124	670	90	globlastp
3753	LYD2 53	peanut 10v1 CD038740_P1	7125	670	90	globlastp
3754	LYD2 53	peanut gb171 CD038740_P1	7125	670	90	globlastp
3755	LYD2 53	ipomoea_nill 10v1 BJ553783 _P1	7126	670	89.7	globlastp
3756	LYD2 53	orobanche 10v1 SRR023189 S0017090_P1	7127	670	89.7	globlastp

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3757	LYD2 53	apple gb171 CN897567_P1	7128	670	89.7	globlastp
3758	LYD2 53	ipomoea gb157.2 BJ566712_P1	7129	670	89.7	globlastp
3759	LYD2 53	pepper gb171 BM064196_P1	7130	670	89.7	globlastp
3760	LYD2 53	tobacco gb162 CV016523_P1	7131	670	89.7	globlastp
3761	LYD2 53	apple gb171 CN489113_P1	7132	670	89.5	globlastp
3762	LYD2 53	potato 10v1 BG597511_P1	7133	670	89.5	globlastp
3763	LYD2 53	potato gb157.2 BG597511_P1	7133	670	89.5	globlastp
3764	LYD2 53	solanum_phureja 09v1 SPH BG126888_P1	7134	670	89.5	globlastp
3765	LYD2 53	tomato 09v1 BG126888_P1	7135	670	89.5	globlastp
3766	LYD2 53	tomato gb164 BG126888_P1	7135	670	89.5	globlastp
3767	LYD2 53	tripphysaria 10v1 BM356747_P1	7136	670	89.5	globlastp
3768	LYD2 53	tripphysaria gb164 BM356747_P1	7136	670	89.5	globlastp
3769	LYD2 53	prunus 10v1 BU039615_P1	7137	670	89.3	globlastp
3770	LYD2 53	nasturtium 10v1 SRR032558 S0017324_P1	7138	670	89.2	globlastp
3771	LYD2 53	orobanche 10v1 SRR023189 S0044816_P1	7139	670	89.2	globlastp
3772	LYD2 53	aquilegia gb157.3 DR917957_P1	7140	670	89.2	globlastp
3773	LYD2 53	prunus gb167 BU039615_P1	7141	670	89	globlastp
3774	LYD2 53	soybean gb168 AW329346_P1	7142	670	88.9	globlastp
3775	LYD2 53	melon 10v1 DV635041_P1	7143	670	88.7	globlastp
3776	LYD2 53	pepper gb171 BM062796_P1	7144	670	88.7	globlastp
3777	LYD2 53	sunflower 10v1 CD849269_P1	7145	670	88.7	globlastp
3778	LYD2 53	sunflower gb162 CD849269_P1	7145	670	88.7	globlastp
3779	LYD2 53	cucumber 09v1 DN909683_P1	7146	670	88.5	globlastp

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3780	LYD2 53	sunflower 10v1 CX946716_ P1	7147	670	88.4	globlastp
3781	LYD2 53	bean gb167 CA901796_P1	7148	670	88.4	globlastp
3782	LYD2 53	artemisia gb164 EY074319_ P1	7149	670	88.2	globlastp
3783	LYD2 53	soybean gb168 BE205188_P 1	7150	670	88	globlastp
3784	LYD2 53	tobacco gb162 DV160802_T 1	7151	670	87.92	glotblastn
3785	LYD2 53	nasturtium 10v1 SRR032558 S0003407_P1	7152	670	87.9	globlastp
3786	LYD2 53	nicotiana_benthamiana gb16 2 AY391715_P1	7153	670	87.9	globlastp
3787	LYD2 53	artemisia 10v1 EY062281_P 1	7154	670	87.7	globlastp
3788	LYD2 53	medicago 09v1 LLAW25668 7_P1	7155	670	87.7	globlastp
3789	LYD2 53	petunia gb171 CV300000_P 1	7156	670	87.7	globlastp
3790	LYD2 53	peanut 10v1 EE125037_P1	7157	670	87.3	globlastp
3791	LYD2 53	clover gb162 BB902680_P1	7158	670	87.2	globlastp
3792	LYD2 53	cowpea gb166 FC459335_P 1	7159	670	87.2	globlastp
3793	LYD2 53	petunia gb171 CV293199_P 1	7160	670	87.2	globlastp
3794	LYD2 53	senecio gb170 DY658575_P 1	7161	670	86.9	globlastp
3795	LYD2 53	artemisia gb164 EY062281_ P1	7162	670	86.5	globlastp
3796	LYD2 53	aquilegia 10v1 DT732268_T 1	7163	670	85.5	glotblastn
3796	LYD2 53	aquilegia gb157.3 DT732268 _T1	7164	670	85.5	glotblastn
3797	LYD2 53	triphysaria 10v1 EX993275_ P1	7165	670	85.1	globlastp
3798	LYD2 53	cryptomeria gb166 AU29875 5_P1	7166	670	84.4	globlastp
3799	LYD2 53	pine 10v1 AA556316_P1	7167	670	83.6	globlastp
3800	LYD2 53	pine gb157.2 AA556316_P1	7167	670	83.6	globlastp
3801	LYD2 53	spruce gb162 CO225443_P1	7168	670	83.3	globlastp

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3802	LYD2 53	barley 10v1 BG299537_P1	7169	670	83	globlastp
3803	LYD2 53	barley gb157SOLEXA AL45 0653_P1	7169	670	83	globlastp
3804	LYD2 53	switchgrass gb167 FL69102 6_P1	7170	670	82.6	globlastp
3805	LYD2 53	medicago 09v1 CRPMT0317 58_T1	7171	670	82.52	glotblastn
3806	LYD2 53	maize gb170 AI372143_P1	7172	670	81.5	globlastp
3807	LYD2 53	maize gb170 LLDR828710_ P1	7172	670	81.5	globlastp
3808	LYD2 53	maize 10v1 AI372143_P1	7172	670	81.5	globlastp
3809	LYD2 53	brachypodium 09v1 DV4788 07_P1	7173	670	81.4	globlastp
3810	LYD2 53	brachypodium gb169 BE414 141_P1	7173	670	81.4	globlastp
3811	LYD2 53	centaurea gb166 EH718869_ T1	7174	670	81.23	glotblastn
3812	LYD2 53	sugarcane gb157.3 CA08416 3_T1	7175	670	80.98	glotblastn
3813	LYD2 53	rice gb170 OS01G73790_P1	7176	670	80.9	globlastp
3814	LYD2 53	sorghum 09v1 SB03G04720 0_P1	7177	670	80.4	globlastp
3815	LYD2 53	millet 10v1 EVO454PM000 133_P1	7178	670	80.2	globlastp
3816	LYD2 53	tobacco gb162 EB428947_P 1	7179	670	80.2	globlastp
3817	LYD2 53	maize 10v1 AI795749_P1	7180	670	80.1	globlastp
3818	LYD2 53	maize gb170 AI795749_P1	7180	670	80.1	globlastp
3819	LYD2 56	arabidopsis 10v1 AT1G7550 0_P1	7181	671	95.9	globlastp
3820	LYD2 56	arabidopsis_lyrata 09v1 JGI AL007823_P1	7182	671	95.7	globlastp
3821	LYD2 56	b_rapa gb162 AT002231_P1	7183	671	95.2	globlastp
3822	LYD2 56	castorbean 09v1 EE256014_ P1	7184	671	80.1	globlastp
3823	LYD2 57	canola gb161 CD825913_P1	7185	672	90.7	globlastp
3824	LYD2 57	b_rapa gb162 EX036030_P1	7186	672	87.5	globlastp

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3825	LYD2 57	radishlgb164 EX773473_P1	7187	672	86.9	globlastp
3826	LYD2 60	radishlgb164 FD571121_T1	7188	673	86.86	glotblastn
3827	LYD2 67	canola 10v1 EL588214_P1	7189	677	97.3	globlastp
3828	LYD2 67	b_rapalgb162 EX090717_P1	7190	677	94.7	globlastp
3829	LYD2 67	canola gb161 EL588214_P1	7191	677	91	globlastp
3830	LYD2 67	arabidopsis 10v1 AT1G6479 0_T1	813	677	88.86	glotblastn
3831	LYD2 67	arabidopsis_lyratal09v1 JGI AL006242_T1	7192	677	88.14	glotblastn
3831	LYD2 67_H 0	arabidopsis_lyratal09v1 JGI AL006242_P1	7192	693	96.9	globlastp
3832	LYD2 67	radishlgb164 EX773772_P1	7193	677	84.3	globlastp
3833	LYD2 71	b_rapalgb162 BG543457_P1	7194	679	93.3	globlastp
3833	LYD2 71_H 0	b_rapalgb162 BG543457_P1	7194	694	91.8	globlastp
3834	LYD2 71	arabidopsis 10v1 AT2G4724 0_P1	694	679	90.6	globlastp
3835	LYD2 71	arabidopsis_lyratal09v1 TM PLAT2G47240T1_P1	7195	679	90.5	globlastp
3835	LYD2 71_H 0	arabidopsis_lyratal09v1 TM PLAT2G47240T1_P1	7195	694	99.8	globlastp
3836	LYD2 71	arabidopsis_lyratal09v1 JGI AL016147_P1	7196	679	90	globlastp
3836	LYD2 71_H 0	arabidopsis_lyratal09v1 JGI AL016147_P1	7196	694	97.7	globlastp
3837	LYD2 71	canola gb161 BQ704756_P1	7197	679	89.7	globlastp
3837	LYD2 71_H 0	canola gb161 BQ704756_P1	7197	694	90.6	globlastp
3838	LYD2 71	canola 10v1 CX189606_P1	7198	679	89.2	globlastp
3838	LYD2 71_H 0	canola 10v1 CX189606_P1	7198	694	90.5	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3839	LYD2 75	b_oleracealgb161 EE535125 _T1	7199	681	100	glotblastn
3840	LYD2 75	b_rapalgb162 CV432945_T1	7200	681	100	glotblastn
3841	LYD2 75	canolal10v1 DW997986_P1	7201	681	98.6	globlastp
3842	LYD2 75	canolalgb161 DW997986_T 1	7202	681	98.57	glotblastn
3843	LYD2 75	canolalgb161 CD811838_T1	7203	681	97.14	glotblastn
3844	LYD2 75	canolal10v1 CD811838_P1	7204	681	97.1	globlastp
3845	LYD2 75	b_nigral09v1 GT069340_P1	7205	681	95.8	globlastp
3846	LYD2 75	radishlgb164 EW726140_P1	7206	681	95.8	globlastp
3847	LYD2 75	thellungiellalgb167 BY8060 64_P1	7207	681	95.7	globlastp
3848	LYD2 75	b_junceal10v2 E6ANDIZ01 B0QZR_P1	7208	681	94.5	globlastp
3849	LYD2 75	radishlgb164 EW715126_T1	7209	681	92.96	glotblastn
3850	LYD2 75	arabidopsis_lyratal09v1 JGI AL011098_T1	7210	681	87.14	glotblastn
3851	LYD2 75	bruguieralgb166 BP941672_ P1	7211	681	86.1	globlastp
3852	LYD2 75	arabidopsislgb165 AT3G241 00_T1	7212	681	85.92	glotblastn
3852	LYD2 75	arabidopsisl10v1 AT3G2410 0_P1	7213	681	85.9	globlastp
3853	LYD2 75	b_junceal10v2 E6ANDIZ01 A1JBJ_P1	7214	681	84.5	globlastp
3854	LYD2 75	b_juncealgb164 EVGN0014 8214090597_P1	7214	681	84.5	globlastp
3855	LYD2 75	cleome_gynandral10v1 SRR 015532S0021751_P1	7215	681	84.3	globlastp
3856	LYD2 75	catharanthuslgb166 EG5549 88_P1	7216	681	84.3	globlastp
3857	LYD2 75	b_juncealgb164 EVGN2100 9617052518_T1	7217	681	84.29	glotblastn
3858	LYD2 75	b_junceal10v2 E6ANDIZ01 A3AK6_P1	7218	681	83.3	globlastp
3859	LYD2 75	b_junceal10v2 E6ANDIZ01 A9VK9_P1	7218	681	83.3	globlastp
3860	LYD2 75	b_juncealgb164 EVGN0005 3230610138_P1	7218	681	83.3	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3861	LYD2 75	b_oleracealgb161 AM05749 8_P1	7218	681	83.3	globlastp
3862	LYD2 75	b_rapalgb162 CV433987_P1	7218	681	83.3	globlastp
3863	LYD2 75	b_rapalgb162 CX270574_P1	7218	681	83.3	globlastp
3864	LYD2 75	b_rapalgb162 L38045_P1	7218	681	83.3	globlastp
3865	LYD2 75	canola 10v1 CD811804_P1	7219	681	83.3	globlastp
3866	LYD2 75	canola gb161 CD811804_P1	7219	681	83.3	globlastp
3867	LYD2 75	canola 10v1 CD812134_P1	7218	681	83.3	globlastp
3868	LYD2 75	canola gb161 CD812134_P1	7218	681	83.3	globlastp
3869	LYD2 75	radish gb164 EV534832_P1	7220	681	83.3	globlastp
3870	LYD2 75	radish gb164 EV544053_P1	7220	681	83.3	globlastp
3871	LYD2 75	arabidopsis 10v1 AT4G1361 5_P1	7221	681	83.1	globlastp
3872	LYD2 75	arabidopsis gb165 AT4G136 15_P1	7221	681	83.1	globlastp
3873	LYD2 75	cleome_spinosal10v1 SRR01 5531S0030693_P1	7222	681	82.9	globlastp
3874	LYD2 75	orobanche 10v1 SRR023189 S0002896_P1	7223	681	82.9	globlastp
3875	LYD2 75	jatropha 09v1 GH295750_P1	7224	681	82.9	globlastp
3876	LYD2 75	lettuce 10v1 DW044456_P1	7225	681	82.9	globlastp
3877	LYD2 75	radish gb164 EW723920_P1	7226	681	82.9	globlastp
3878	LYD2 75	safflower gb162 EL405248_ P1	7227	681	82.9	globlastp
3879	LYD2 75	tea gb171 GH623887_P1	7228	681	82.9	globlastp
3880	LYD2 75	citrus gb166 BQ622948_T1	7229	681	82.86	glotblastn
3881	LYD2 75	cassava 09v1 CK650049_P1	7230	681	81.9	globlastp
3882	LYD2 75	thellungiella gb167 EC59906 8_P1	7231	681	81.7	globlastp
3883	LYD2 75	basilicum 10v1 DY322319_ P1	7232	681	81.4	globlastp

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3884	LYD2 75	centaurealgb166 EH719505_ P1	7233	681	81.4	globlastp
3885	LYD2 75	lettuce 10v1 DW103133_P1	7234	681	81.4	globlastp
3886	LYD2 75	kiwi gb166 FG441257_P1	7235	681	81.4	globlastp
3887	LYD2 75	lettuce 10v1 DW122916_P1	7236	681	81.4	globlastp
3888	LYD2 75	lettuce gb157.2 DW122916_ P1	7236	681	81.4	globlastp
3889	LYD2 75	poplar 10v1 BI123668_P1	7237	681	81.4	globlastp
3890	LYD2 75	poplar gb170 BI123668_P1	7237	681	81.4	globlastp
3891	LYD2 75	poplar 10v1 CN521361_P1	7238	681	80.3	globlastp
3892	LYD2 75	poplar gb170 CN521361_P1	7238	681	80.3	globlastp
3893	LYD2 75	cassava gb164 CK650049_T 1	7239	681	80.28	glotblastn
3894	LYD2 75	cleome_gynandral10v1 SRR 015532S0006496_P1	7240	681	80	globlastp
3895	LYD2 75	cleome_spinosal10v1 SRR01 5531S0002266_P1	7241	681	80	globlastp
3896	LYD2 75	melon 10v1 EB715280_P1	7242	681	80	globlastp
3897	LYD2 75	antirrhinum gb166 AJ78813 7_P1	7243	681	80	globlastp
3898	LYD2 75	gerberal09v1 AJ751325_P1	7244	681	80	globlastp
3899	LYD2 75	melon gb165 EB715280_P1	7242	681	80	globlastp
3900	LYD2 78	canola 10v1 CN830844_P1	7245	683	95.9	globlastp
3901	LYD2 78	canola gb161 CN830844_P1	7245	683	95.9	globlastp
3902	LYD2 78	arabidopsis 10v1 AT4G2848 0_P1	7246	683	83.7	globlastp
3903	LYD2 78	citrus gb166 BQ624949_P1	7247	683	81.3	globlastp
3904	LYD2 78	spurge gb161 BE231328_P1	7248	683	81.2	globlastp
3905	LYD2 78	cassaval09v1 DR084651_P1	7249	683	80.2	globlastp
3906	LYD2 78	cowpea gb166 FC461152_P 1	7250	683	80.2	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3907	LYD2 79	arabidopsis gb165 AT3G107 40_P1	7251	684	90.6	globlastp
3907	LYD2 79	arabidopsis 10v1 AT3G1074 0_P1	7253	684	90.3	globlastp
3908	LYD2 79	arabidopsis_lyratal09v1 JGI AL009496_P1	7252	684	90.5	globlastp
3909	LYD2 82	arabidopsis_lyratal09v1 JGI AL003543_P1	7254	685	83	globlastp
3910	LYD2 83	b_rapa gb162 CA991797_P1	7255	686	99.6	globlastp
3911	LYD2 83	canola 10v1 CN727072_P1	7256	686	99.3	globlastp
3912	LYD2 83	radish gb164 EV535929_P1	7257	686	97	globlastp
3913	LYD2 83	arabidopsis_lyratal09v1 JGI AL016001_P1	7258	686	94.1	globlastp
3914	LYD2 83	canola 10v1 CD814370_P1	7259	686	93.7	globlastp
3915	LYD2 83	arabidopsis 10v1 AT2G4599 0_P1	7260	686	92.6	globlastp
3916	LYD2 83	cleome_spinosal10v1 SRR01 5531S0008712_P1	7261	686	88.1	globlastp
3917	LYD2 83	thellungiellalgb167 BY8067 38_P1	7262	686	83.6	globlastp
3918	LYD2 83	castorbean 09v1 XM002511 832_P1	7263	686	81.4	globlastp
3919	LYD2 83	citrus gb166 CV885783_P1	7264	686	81.4	globlastp
3920	LYD2 83	prunus 10v1 CN862535_P1	7265	686	81.4	globlastp
3921	LYD2 83	prunus gb167 CV047726_P1	7266	686	80.7	globlastp
3922	LYD2 83	nasturtium 10v1 SRR032558 S0041419_P1	7267	686	80.1	globlastp
3923	LYD2 85	canola 10v1 CD811710_P1	7268	687	99.6	globlastp
3924	LYD2 85	canola gb161 CD811710_P1	7268	687	99.6	globlastp
3925	LYD2 85	maize gb170 LLDQ245309_ P1	7268	687	99.6	globlastp
3926	LYD2 85	b_rapa gb162 BG543481_P1	7269	687	98.2	globlastp
3927	LYD2 85	thellungiellalgb167 BY8100 02_P1	7270	687	90.6	globlastp
3928	LYD2 85	arabidopsis_lyratal09v1 JGI AL017442_P1	7271	687	85	globlastp

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3929	LYD2 85	arabidopsis 10v1 AT3G4426 0_P1	7272	687	84.3	globlastp
3930	LYD2 85	arabidopsis_lyratal09v1 JGI AL021902_P1	7273	687	81.2	globlastp
3931	LYD2 85	canola gb161 EV120613_T1	7274	687	81.09	glotblastn
3932	LYD2 85	canola 10v1 EV120613_P1	7275	687	80.7	globlastp
3933	LYD2 85	canola 10v1 EV132851_P1	7276	687	80.4	globlastp
3934	LYD2 86	b_junceal10v2 E6ANDIZ02 GYJJE_T1	7277	688	81.74	glotblastn
3935	LYD2 87	arabidopsis_lyratal09v1 JGI AL020774_P1	7278	689	92.8	globlastp
3936	LYD2 87	thellungiella gb167 BY8084 94_P1	7279	689	87.6	globlastp
3937	LYD2 87	radish gb164 EX896249_P1	7280	689	82.5	globlastp
3938	LYD2 87	radish gb164 EY904290_P1	7281	689	82.5	globlastp
3939	LYD2 87	radish gb164 EV567071_P1	7282	689	81.7	globlastp
3940	LYD2 87	canola 10v1 CD824727_P1	7283	689	81.6	globlastp
3941	LYD2 87	canola gb161 CD824727_P1	7283	689	81.6	globlastp
3942	LYD2 87	b_rapa gb162 EX086492_T1	7284	689	80	glotblastn
3943	LYD2 88	b_juncealgb164 EVGN0007 4614260895_P1	7285	690	93.1	globlastp
3944	LYD2 88	canola 10v1 DY000958_P1	7286	690	92.7	globlastp
3945	LYD2 88	canola gb161 DY000958_P1	7286	690	92.7	globlastp
3946	LYD2 88	canola 10v1 DY002813_P1	7287	690	92.3	globlastp
3947	LYD2 88	b_oleracealgb161 AM38553 8_P1	7288	690	92.3	globlastp
3948	LYD2 88	b_rapa gb162 BQ791265_P1	7289	690	92.3	globlastp
3949	LYD2 88	radish gb164 EV525658_P1	7290	690	91.1	globlastp
3950	LYD2 88	radish gb164 EY926221_P1	7291	690	89.4	globlastp
3951	LYD2 88	canola 10v1 CD819767_P1	7292	690	89	globlastp

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3952	LYD2 88	canola gb161 CD819767_P1	7293	690	89	globlastp
3953	LYD2 88	arabidopsis_lyrata 09v1 JGI AL027537_P1	7294	690	85.4	globlastp
3954	LYD2 88	b_junceal 10v2 E6ANDIZ01 AIU14_P1	7295	690	84.6	globlastp
3955	LYD2 88	thellungiella gb167 BY8265 25_P1	7296	690	84.1	globlastp
3956	LYD2 88	arabidopsis 10v1 AT5G4121 0_P1	7297	690	83.7	globlastp
3957	LYD2 88	arabidopsis 10v1 AT5G4124 0_T1	7298	690	80.89	glotblastn
3958	LYD1 24_H 7	canola 10v1 EE444087_P1	7299	691	98.4	globlastp
3958	LYD1 24	canola 10v1 EE444087_T1	7299	724	89.29	glotblastn
3959	LYD1 24_H 7	b_junceal 10v2 E6ANDIZ01 BWQ1T_P1	7300	691	93.7	globlastp
3959	LYD1 24	b_junceal 10v2 E6ANDIZ01 BWQ1T_P1	7300	724	83.9	globlastp
3960	LYD1 24_H 7	b_junceal 10v2 SEQ3090_P1	7301	691	88.9	globlastp
3960	LYD1 24	b_junceal 10v2 SEQ3090_P1	7301	724	82.3	globlastp
3961	LYD1 24_H 7	b_junceal gb164 EVGN2315 5006653935_P1	7302	691	88.9	globlastp
3961	LYD1 24	b_junceal gb164 EVGN2315 5006653935_T1	7302	724	89.09	glotblastn
3962	LYD1 24_H 7	b_junceal 10v2 SEQ3040_P1	7303	691	87.3	globlastp
3962	LYD1 24	b_junceal 10v2 SEQ3040_P1	7303	724	83.9	globlastp
3963	LYD1 24_H 7	canola 10v1 EE503725_P1	7303	691	87.3	globlastp
3963	LYD1 24	canola 10v1 EE503725_P1	7303	724	83.9	globlastp
3964	LYD1 24_H 7	arabidopsis gb165 AT4G276 54_T1	7304	691	85.71	glotblastn
3964	LYD1 24	arabidopsis gb165 AT4G276 54_T1	7304	724	90.91	glotblastn

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3965	LYD1 24_H 7	arabidopsis 10v1 AT4G2765 4_P1	7305	691	85.7	globlastp
3965	LYD1 24	arabidopsis 10v1 AT4G2765 4_P1	7305	724	80.6	globlastp
3966	LYD1 24_H 7	b_junceal 10v2 BJ1SLX0001 5037D1_P1	7306	691	84.1	globlastp
3966	LYD1 24	b_junceal 10v2 BJ1SLX0001 5037D1_T1	7306	724	83.64	glotblastn
3967	LYD1 24_H 7	b_junceal 10v2 BJ1SLX0007 5379D1_P1	7307	691	84.1	globlastp
3967	LYD1 24	b_junceal 10v2 BJ1SLX0007 5379D1_T1	7307	724	83.64	glotblastn
3968	LYD1 24_H 7	b_junceal 10v2 E6ANDIZ02 HWTS1_P1	7308	691	84.1	globlastp
3968	LYD1 24	b_junceal 10v2 E6ANDIZ02 HWTS1_T1	7308	724	83.64	glotblastn
3969	LYD1 24_H 7	canola 10v1 EE413458_P1	7308	691	84.1	globlastp
3969	LYD1 24	canola 10v1 EE413458_T1	7308	724	83.64	glotblastn
3970	LYD1 24_H 7	canola gb161 EE413458_P1	7308	691	84.1	globlastp
3970	LYD1 24	canola gb161 EE413458_T1	7308	724	83.64	glotblastn
3971	LYD1 24_H 7	arabidopsis_lyratal09v1 JGI AL025317_P1	7309	691	82.5	globlastp
3971	LYD1 24	arabidopsis_lyratal09v1 JGI AL025317_T1	7309	724	85.45	glotblastn
3972	LYD1 24_H 7	arabidopsis_lyratal09v1 JGI AL029923_P1	7310	691	82.5	globlastp
3973	LYD1 24_H 7	b_junceal 10v2 BJ1SLX0001 5379D1_P1	7311	691	82.5	globlastp
3973	LYD1 24	b_junceal 10v2 BJ1SLX0001 5379D1_T1	7311	724	81.82	glotblastn
3974	LYD1 24_H 7	b_junceal 10v2 BJ1SLX0004 4885D1_P1	7311	691	82.5	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3974	LYD1 24	b_junceal10v2 BJ1SLX0004 4885D1_T1	7311	724	81.82	glotblastn
3975	LYD1 24_H 7	canola 10v1 DY000500_P1	7312	691	82.5	globlastp
3975	LYD1 24	canola 10v1 DY000500_T1	7312	724	81.82	glotblastn
3976	LYD1 24_H 7	canola gb161 DY000500_P1	7312	691	82.5	globlastp
3976	LYD1 24	canola gb161 DY000500_T1	7312	724	81.82	glotblastn
3977	LYD1 24_H 7	arabidopsis 10v1 AT4G2765 7_P1	7313	691	81	globlastp
3977	LYD1 24	arabidopsis 10v1 AT4G2765 7_T1	7313	724	87.27	glotblastn
3978	LYD1 24_H 7	arabidopsis gb165 AT4G276 57_P1	7313	691	81	globlastp
3978	LYD1 24	arabidopsis gb165 AT4G276 57_T1	7313	724	87.27	glotblastn
3979	LYD8 9_H0	arabidopsis_lyratal09v1 JGI AL006995_P1	7314	695	95.4	globlastp
3980	LYD8 9_H0	soybean gb168 AW684990_ P1	7315	695	81.5	globlastp
3981	LYD8 9_H0	cucumber 09v1 BGI454H00 57707_P1	7316	695	80.9	globlastp
3982	LYD8 9_H0	cotton 10v1 CO073167_P1	7317	695	80.8	globlastp
3983	LYD8 9_H0	cassava 09v1 CK643245_P1	7318	695	80.3	globlastp
3984	LYD8 9_H0	soybean gb168 AW719229_ P1	7319	695	80.3	globlastp
3985	LYM 104	rice gb170 OS11G03070_P1	7320	696	96.5	globlastp
3986	LYM 275	rye gb164 BE586411_P1	7321	697	88.7	globlastp
3987	LYM 275	wheat gb164 CA597846_P1	7322	697	86.7	globlastp
3988	LYM 275	rice gb170 OS07G47750_P1	7323	697	82.1	globlastp
3989	LYD2 9	pigeonpea 10v1 SRR054580 S0018176_T1	7324	699	83.11	glotblastn
3990	LYD2 9	cowpea gb166 FF383388_T1	7325	699	83.11	glotblastn

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
3991	LYD4 5	solanum_phurejal09v1 SPH AW618293_P1	7326	703	87.5	globlastp
3992	LYD4 5	solanum_phurejal09v1 SPH BQ515895_T1	7327	703	80.53	glotblastn
3993	LYD4 9	potatolgb157.2 BF052426_P 1	7328	705	97	globlastp
3994	LYD4 9	solanum_phurejal09v1 SPH BG123989_P1	7329	705	96.7	globlastp
3995	LYD4 9	eggplantl10v1 FS000181_P1	7330	705	84.5	globlastp
3996	LYD5 0	basilicum 10v1 DY337033_ P1	7331	706	94.9	globlastp
3997	LYD5 0	coffeal10v1 CF588621_T1	7332	706	80	glotblastn
3998	LYD5 2	solanum_phurejal09v1 SPH AW928860_T1	7333	707	91.6	glotblastn
3999	LYD5 2	tomatol09v1 AW928860_T1	7334	707	90.11	glotblastn
4000	LYD5 2	potatolgb157.2 CK276712_T 1	7335	707	83.02	glotblastn
4001	LYD5 9	tobacco gb162 EB441545_P 1	7336	709	87.2	globlastp
4002	LYD5 9	potatol10v1 BG599376_T1	7337	709	84.02	glotblastn
4003	LYD5 9	solanum_phurejal09v1 SPH BG131905_T1	7338	709	83.56	glotblastn
4004	LYD6 1	petunialgb171 CV299685_T 1	7339	710	94.17	glotblastn
4005	LYD6 1	monkeyflowerl10v1 SRR037 227S0029500_T1	7340	710	85.44	glotblastn
4006	LYD6 1	pepper gb171 GD092607_P1	7341	710	84.9	globlastp
4007	LYD6 1	citrus gb166 CK665309_T1	7342	710	83.81	glotblastn
4008	LYD6 1	tobacco gb162 DV162428_T 1	7343	710	83.5	glotblastn
4009	LYD6 1	citrus gb166 DN134814_T1	7344	710	82.86	glotblastn
4010	LYD6 1	arabidopsis_lyratal09v1 JGI AL026462_T1	7345	710	82.52	glotblastn
4011	LYD6 1	rhizophoral10v1 SRR005792 S0003855_T1	7346	710	81.55	glotblastn
4012	LYD6 1	arabidopsis 10v1 AT4G1736 0_T1	7347	710	81.55	glotblastn
4013	LYD6 1	arabidopsis gb165 AT4G173 60_T1	7347	710	81.55	glotblastn

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
4014	LYD6 1	papaya gb165 EX266095_T1	7348	710	81.55	glotblastn
4015	LYD6 1	thellungiella gb167 DN7785 20_T1	7349	710	81.55	glotblastn
4016	LYD6 1	arabidopsis_lyrata 09v1 JGI AL028054_T1	7350	710	80.58	glotblastn
4017	LYD6 1	canola 10v1 CD816661_T1	7351	710	80.58	glotblastn
4018	LYD6 1	tomato 09v1 SRR027939S02 70689_T1	7352	710	80.58	glotblastn
4019	LYD6 1	canola gb161 CD816661_T1	7351	710	80.58	glotblastn
4020	LYD6 1	kiwi gb166 FG526349_T1	7353	710	80.58	glotblastn
4021	LYD6 1	poplar 10v1 BU832393_T1	7354	710	80.58	glotblastn
4022	LYD6 1	poplar gb170 BU832393_T1	7354	710	80.58	glotblastn
4023	LYD6 1	radish gb164 EX887273_T1	7355	710	80.58	glotblastn
4024	LYD6 5	solanum_phureja 09v1 SPH CV491883_T1	7356	712	88.24	glotblastn
4025	LYD6 5	pepper gb171 CA516488_T1	7357	712	85.71	glotblastn
4026	LYD6 5	tobacco gb162 EB679001_T 1	7358	712	81.82	glotblastn
4027	LYD7 4	petunia gb171 CV296742_T 1	7359	714	89.72	glotblastn
4028	LYD7 4	ipomoea gb157.2 BM878729 _T1	7360	714	86.11	glotblastn
4029	LYD7 4	ipomoea gb157.2 BJ554139_ T1	7361	714	85.71	glotblastn
4030	LYD7 4	cotton gb164 AI727586_T1	7362	714	85.45	glotblastn
4031	LYD7 4	rose 10v1 EC586509_T1	7363	714	85.05	glotblastn
4032	LYD7 4	salvia 10v1 SRR014553S000 1681_T1	7364	714	84.65	glotblastn
4033	LYD7 4	banana gb167 DN238032_T 1	7365	714	84.04	glotblastn
4034	LYD7 4	bruguiera gb166 BP939059_ T1	7366	714	83.1	glotblastn
4035	LYD7 4	cleome_gynandra 10v1 SRR 015532S0000664_T1	7367	714	83.03	glotblastn
4036	LYD7 4	banana 10v1 DN238553_P1	7368	714	81.7	globlastp

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4037	LYD7 4	chickpeal09v2 DY475430_T 1	7369	714	80.37	glotblastn
4038	LYD7 4	onion gb162 CF436119_P1	7370	714	80.1	globlastp
4039	LYD7 4	curcumal10v1 DY385612_T 1	7371	714	80.09	glotblastn
4040	LYD7 4	ginger gb164 DY346269_T1	7371	714	80.09	glotblastn
4041	LYD1 06	arabidopsis_lyratal09v1 JGI AL028447_T1	7372	718	86.61	glotblastn
4042	LYD1 18	canola 10v1 CX280679_T1	7373	720	93.94	glotblastn
4043	LYD1 18	b_oleracealgb161 AM05789 1_P1	7374	720	92.1	globlastp
4044	LYD1 19	canola 10v1 ES266621_T1	7375	721	98.07	glotblastn
4045	LYD1 19	canola gb161 CD824955_T1	7376	721	98.07	glotblastn
4046	LYD1 19	radish gb164 EV548773_T1	7377	721	98.07	glotblastn
4047	LYD1 19	canola 10v1 CD824955_T1	7378	721	98.07	glotblastn
4048	LYD1 19	thellungiellalgb167 DN7730 15_T1	7379	721	96.62	glotblastn
4049	LYD1 19	canola gb161 EE490115_P1	7380	721	91.4	globlastp
4050	LYD1 19	b_rapalgb162 DN966501_P1	7381	721	90.8	globlastp
4051	LYD1 19	cleome_spinosal10v1 SRR01 5531S0005496_T1	7382	721	88.1	glotblastn
4052	LYD1 19	cucumber 09v1 AM722352_ T1	7383	721	86.96	glotblastn
4053	LYD1 19	nasturtium 10v1 SRR032558 S0086509_T1	7384	721	86.96	glotblastn
4054	LYD1 19	iceplant gb164 AA962851_T 1	7385	721	86.96	glotblastn
4055	LYD1 19	pine 10v1 AA556728_T1	7386	721	85.99	glotblastn
4056	LYD1 19	orobanche 10v1 SRR023189 S0019360_T1	7387	721	85.71	glotblastn
4057	LYD1 19	bean gb167 CB542468_T1	7388	721	85.71	glotblastn
4058	LYD1 19	soybean gb168 BU090151_T 1	7389	721	85.71	glotblastn
4059	LYD1 19	spruce gb162 CO215773_T1	7390	721	85.51	glotblastn

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4060	LYD1 19	spruce gb162 CO217277_T1	7391	721	85.51	glotblastn
4061	LYD1 19	tragopogon 10v1 SRR02020 5S0067472_T1	7392	721	85.24	glotblastn
4062	LYD1 19	soybean gb168 BI968126_T 1	7393	721	85.24	glotblastn
4063	LYD1 19	oak 10v1 SRR039735S0121 091_P1	7394	721	85.2	globlastp
4064	LYD1 19	tea 10v1 GO254991_P1	7395	721	85.2	globlastp
4065	LYD1 19	tea gb171 GO254991_P1	7395	721	85.2	globlastp
4066	LYD1 19	brachypodium 09v1 GT7634 70_T1	7396	721	85.02	glotblastn
4067	LYD1 19	peanut 10v1 ES709558_T1	7397	721	84.76	glotblastn
4068	LYD1 19	cichorium gb171 EH675630 _T1	7398	721	84.76	glotblastn
4069	LYD1 19	cowpea gb166 FF547244_T1	7399	721	84.76	glotblastn
4070	LYD1 19	sunflower 10v1 BQ914563_ T1	7400	721	84.76	glotblastn
4071	LYD1 19	triphysaria 10v1 DR174364_ T1	7401	721	84.76	glotblastn
4072	LYD1 19	prunus gb167 AJ823038_T1	7402	721	84.29	glotblastn
4073	LYD1 19	sunflower gb162 BQ914563 _T1	7403	721	84.29	glotblastn
4074	LYD1 19	triphysaria gb164 DR174364 _T1	7404	721	84.29	glotblastn
4075	LYD1 19	tomato 09v1 BG124992_T1	7405	721	84.21	glotblastn
4076	LYD1 19	switchgrass gb167 DW1773 36_T1	7406	721	84.06	glotblastn
4077	LYD1 19	pigeonpea 10v1 SRR054580 S0026667_T1	7407	721	83.81	glotblastn
4078	LYD1 19	sunflower gb162 DY908134 _T1	7408	721	83.81	glotblastn
4079	LYD1 19	triphysaria 10v1 EX984488_ T1	7409	721	83.81	glotblastn
4080	LYD1 19	triphysaria gb164 EX984488 _T1	7410	721	83.81	glotblastn
4081	LYD1 19	monkeyflower 09v1 GO9815 62_T1	7411	721	83.73	glotblastn
4082	LYD1 19	monkeyflower 10v1 GO9460 42_T1	7412	721	83.73	glotblastn

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4083	LYD1 19	acacial10v1IFS585672_T1	7413	721	83.57	glotblastn
4084	LYD1 19	potatol10v1IBF154054_T1	7414	721	83.33	glotblastn
4085	LYD1 19	potatolgb157.2IBF154054_T 1	7415	721	83.33	glotblastn
4086	LYD1 19	tomatolgb164IBG631453_P1	7416	721	83.3	globlastp
4087	LYD1 19	seneciolgb170IDY664721_P 1	7417	721	83.1	globlastp
4088	LYD1 19	ricelgb170IOS12G33080_T1	7418	721	83.09	glotblastn
4089	LYD1 19	pinel10v1IBX251835_T1	7419	721	82.86	glotblastn
4090	LYD1 19	artemisialgb164IEY036735_ T1	7420	721	82.86	glotblastn
4091	LYD1 19	basilicumlgbl57.3IDY33142 4_T1	7421	721	82.86	glotblastn
4092	LYD1 19	peal09v1IEF488072_T1	7422	721	82.86	glotblastn
4093	LYD1 19	solanum_phurejal09v1ISPH BG124992_T1	7423	721	82.86	glotblastn
4094	LYD1 19	heritieral10v1ISRR005794S0 000721_T1	7424	721	82.63	glotblastn
4095	LYD1 19	fernlgb171IDK949251_T1	7425	721	82.61	glotblastn
4096	LYD1 19	strawberrylgb164IEX661600 _P1	7426	721	82.6	globlastp
4097	LYD1 19	peanutl10v1IGO261368_T1	7427	721	82.38	glotblastn
4098	LYD1 19	peanutlgb171IGO261368_T1	7428	721	82.38	glotblastn
4099	LYD1 19	oatl10v2IGO586892_T1	7429	721	81.9	glotblastn
4100	LYD1 19	milletl10v1IEVO454PM004 600_T1	7430	721	81.64	glotblastn
4101	LYD1 19	brachypodiumlgbl69IBE402 785_T1	7431	721	81.64	glotblastn
4102	LYD1 19	ipomoea_nil10v1ICJ765444 _P1	7432	721	81.6	globlastp
4102	LYD1 19	ipomoealgb157.2ICJ765444_ P1	7432	721	81.6	globlastp
4103	LYD1 19	pepperlgbl171IBM067160_P 1	7433	721	81.6	globlastp
4104	LYD1 19	barleyl10v1IBE437611_T1	7434	721	81.43	glotblastn

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4105	LYD1 19	barley gb157SOLEXA BE43 7611_T1	7435	721	81.43	glotblastn
4106	LYD1 19	wheat gb164 BE402785_T1	7436	721	81.43	glotblastn
4107	LYD1 19	spikemoss gb165 FE432753 _T1	7437	721	80.95	glotblastn
4108	LYD1 19	wheat gb164 CA676597_T1	7438	721	80.95	glotblastn
4109	LYD1 19	physcomitrella 10v1 BJ1570 18_T1	7439	721	80.48	glotblastn
4110	LYD1 19	cynara gb167 GE593403_P1	7440	721	80.4	globlastp
4111	LYD1 19	ipomoea_nill 10v1 BJ567558 _P1	7441	721	80.3	globlastp
4111	LYD1 19	ipomoea gb157.2 BJ567558_ P1	7441	721	80.3	globlastp
4112	LYD1 19	maize 10v1 AW066569_T1	7442	721	80	glotblastn
4113	LYD1 19	maize gb170 AW066569_T1	7442	721	80	glotblastn
4114	LYD1 19	sorghum 09v1 SB08G01663 0_T1	7443	721	80	glotblastn
4115	LYD1 20	radish gb164 EV543892_T1	7444	722	94.35	glotblastn
4116	LYD1 20	b_junceal 10v2 E6ANDIZ01 DKBDZ_P1	7445	722	84.1	globlastp
4117	LYD1 20	arabidopsis_lyrata 09v1 JGI AL029406_T1	7446	722	83.06	glotblastn
4118	LYD1 20	arabidopsis 10v1 AT5G5010 0_T1	7447	722	83.06	glotblastn
4119	LYD1 20	arabidopsis gb165 AT5G501 00_T1	7448	722	83.06	glotblastn
4120	LYD1 23	canola gb161 EE461239_T1	7449	723	94.33	glotblastn
4121	LYD1 23	radish gb164 FD539059_T1	7450	723	86.11	glotblastn
4122	LYD1 24	arabidopsis_lyrata 09v1 JGI AL025319_T1	7451	724	83.64	glotblastn
4123	LYD1 24	canola gb161 EE503725_T1	7452	724	81.82	glotblastn
4124	LYD1 24	radish gb164 EY911939_T1	7453	724	80	glotblastn
4125	LYD1 24	thellungiella gb167 BY8333 71_T1	7454	724	80	glotblastn
4126	LYD1 27	soybean gb168 FD780693_T 1	7455	725	96.84	glotblastn

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4127	LYD1 27	bean gb167 CB540262_T1	7456	725	95.57	glotblastn
4128	LYD1 27	pigeonpea 10v1 SRR054580 S0015649_T1	7457	725	93.67	glotblastn
4129	LYD1 27	sunflower 10v1 CF081741_ T1	7458	725	89.87	glotblastn
4130	LYD1 27	sunflower gb162 CF081741_ T1	7459	725	89.87	glotblastn
4131	LYD1 27	sunflower 10v1 EE608363_ T1	7460	725	89.87	glotblastn
4132	LYD1 27	artemisia 10v1 EY101060_T 1	7461	725	89.24	glotblastn
4133	LYD1 27	tea gb171 EF218618_T1	7462	725	89.24	glotblastn
4134	LYD1 27	poplar gb170 BI123464_T1	7463	725	88.61	glotblastn
4135	LYD1 27	cassava 09v1 DB951700_T1	7464	725	87.97	glotblastn
4136	LYD1 27	cassava 09v1 JGICASSAVA 6286VALIDM1_T1	7465	725	87.97	glotblastn
4137	LYD1 27	cleome_gynandra 10v1 SRR 015532S0009046_T1	7466	725	87.97	glotblastn
4138	LYD1 27	nasturtium 10v1 SRR032558 S0021243_T1	7467	725	87.97	glotblastn
4139	LYD1 27	prunus 10v1 CB822008_T1	7468	725	87.97	glotblastn
4140	LYD1 27	poplar 10v1 BI123464_T1	7469	725	87.97	glotblastn
4141	LYD1 27	poplar 10v1 CV268483_T1	7470	725	87.97	glotblastn
4142	LYD1 27	poplar gb170 CV268483_T1	7470	725	87.97	glotblastn
4143	LYD1 27	sunflower gb162 EL415366_ T1	7471	725	87.97	glotblastn
4144	LYD1 27	tragopogon 10v1 SRR02020 5S0045666_T1	7472	725	87.65	glotblastn
4145	LYD1 27	cleome_spinosal 10v1 GR932 411_T1	7473	725	86.71	glotblastn
4146	LYD1 27	antirrhinum gb166 AJ78783 1_T1	7474	725	86.71	glotblastn
4147	LYD1 27	apple gb171 CN864453_T1	7475	725	86.71	glotblastn
4148	LYD1 27	castorbean 09v1 XM002510 467_T1	7476	725	86.71	glotblastn
4149	LYD1 27	oak 10v1 FP038114_T1	7477	725	86.08	glotblastn

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4150	LYD1 27	lettucelgb157.2 DW089878_ T1	7478	725	85.8	glotblastn
4151	LYD1 27	cucumber 09v1 AM725987_ T1	7479	725	85.44	glotblastn
4152	LYD1 27	spurgelgb161 DV123737_T1	7480	725	85.44	glotblastn
4153	LYD1 27	lettucel10v1 DW089878_T1	7481	725	85.19	glotblastn
4154	LYD1 27	arabidopsis_lyrata 09v1 JGI AL002097_T1	7482	725	84.81	glotblastn
4155	LYD1 27	aquilegal10v1 DR925552_T 1	7483	725	84.81	glotblastn
4156	LYD1 27	aquilegalgb157.3 DR925552 _T1	7484	725	84.81	glotblastn
4157	LYD1 27	arabidopsis 10v1 AT1G1992 0_T1	7485	725	84.81	glotblastn
4158	LYD1 27	arabidopsis gb165 AT1G199 20_T1	7485	725	84.81	glotblastn
4159	LYD1 27	canola 10v1 DY022321_T1	7486	725	84.18	glotblastn
4160	LYD1 27	canola gb161 EV195140_T1	7487	725	84.18	glotblastn
4161	LYD1 27	monkeyflower 09v1 DV2122 28_T1	7488	725	84.18	glotblastn
4162	LYD1 27	b_oleracealgb161 AF195511 _T1	7489	725	83.54	glotblastn
4163	LYD1 27	b_rapalgb162 ES929820_T1	7490	725	83.54	glotblastn
4164	LYD1 27	monkeyflower 10v1 DV2122 28_T1	7491	725	83.54	glotblastn
4165	LYD1 27	centaurealgb166 EL933253_ T1	7492	725	83.44	glotblastn
4166	LYD1 27	dandelion 10v1 DQ160054_ T1	7493	725	83.33	glotblastn
4167	LYD1 27	canola 10v1 CD825050_T1	7494	725	82.91	glotblastn
4168	LYD1 27	coffeal10v1 DV671705_T1	7495	725	81.65	glotblastn
4169	LYD1 27	canola gb161 CD812541_T1	7496	725	81.65	glotblastn
4170	LYD1 27	switchgrass gb167 FL71842 8_T1	7497	725	81.65	glotblastn
4171	LYD1 27	rice gb170 OS04G02050_T1	7498	725	80.5	glotblastn
4172	LYD1 27	brachypodium 09v1 GT7735 09_T1	7499	725	80.38	glotblastn

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4173	LYD1 27	maize 10v1 AW927833_T1	7500	725	80.38	glotblastn
4174	LYD1 27	brachypodium gb169 BE411 414_T1	7501	725	80.38	glotblastn
4175	LYD1 27	radish gb164 EV525366_T1	7502	725	80.38	glotblastn
4176	LYD1 27	spruce gb162 CO219290_T1	7503	725	80.38	glotblastn
4177	LYD1 42	eggplant 10v1 FS049767_T1	7504	726	80.34	glotblastn
4178	LYD1 85	b_juncea gb164 EVGN0021 0423251166_P1	7505	730	84.5	globlastp
4179	LYD1 85	b_juncea gb164 EVGN0329 5430561543_P1	7506	730	84.2	globlastp
4180	LYD1 85	radish gb164 EW713565_T1	7507	730	83.59	glotblastn
4181	LYD1 85	b_juncea gb164 EVGN0110 4525990565_T1	7508	730	82.56	glotblastn
4182	LYD1 85	canola gb161 CX196125_T1	7509	730	82.05	glotblastn
4183	LYD1 85	b_juncea 10v2 E6ANDIZ01 C91Z3_P1	7510	730	80.3	globlastp
4184	LYD2 12	arabidopsis_lyrata 09v1 JGI AL028662_P1	7511	733	99.7	globlastp
4185	LYD2 31	sugarcane 10v1 CA081528_ T1	7512	734	93.13	glotblastn
4186	LYD2 31	switchgrass gb167 DN14504 2_P1	7513	734	86.7	globlastp
4187	LYD2 32	nicotiana_benthamiana gb16 2 CK286359_T1	7514	735	85.82	glotblastn
4188	LYD2 35	potato 10v1 AJ487407_P1	7515	736	98.2	globlastp
4189	LYD2 35	potato gb157.2 AJ487407_P 1	7515	736	98.2	globlastp
4190	LYD2 35	potato gb157.2 BG589356_P 1	7515	736	98.2	globlastp
4191	LYD2 35	solanum_phureja 09v1 SPH BG132066_P1	7515	736	98.2	globlastp
4192	LYD2 35	eggplant 10v1 FS034595_P1	7516	736	97	globlastp
4193	LYD2 35	pepper gb171 BM062225_P 1	7517	736	95.9	globlastp
4194	LYD2 35	tobacco gb162 AB041518_P 1	7518	736	92.9	globlastp
4195	LYD2 35	cotton 10v1 AF037051_P1	7519	736	91.8	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
4196	LYD2 35	petunia gb171 CV295395_P 1	7520	736	90.5	globlastp
4197	LYD2 35	petunia gb171 FN000529_P1	7521	736	87.1	globlastp
4198	LYD2 35	petunia gb171 DY395977_P 1	7522	736	85.2	globlastp
4199	LYD2 35	flax 09v1 CV478944_P1	7523	736	82.8	globlastp
4200	LYD2 35	rhizophora 10v1 SRR005792 S0007720_P1	7524	736	81.7	globlastp
4201	LYD2 35	cassava gb164 DV444983_P 1	7525	736	81.7	globlastp
4202	LYD2 35	coffea 10v1 DQ123923_P1	7526	736	81.7	globlastp
4203	LYD2 35	spurge gb161 DV112714_P1	7527	736	81.7	globlastp
4204	LYD2 35	prunus 10v1 BU039316_P1	7528	736	81.2	globlastp
4205	LYD2 35	prunus gb167 BU039316_P1	7528	736	81.2	globlastp
4206	LYD2 35	coffea gb157.2 DQ123923_P 1	7529	736	81.1	globlastp
4207	LYD2 35	kiwi gb166 FG428858_P1	7530	736	81.1	globlastp
4208	LYD2 35	cotton 10v1 AI055041_P1	7531	736	80.5	globlastp
4209	LYD2 35	foxtail_millet 09v1 AY5416 94_P1	7532	736	80.5	globlastp
4210	LYD2 35	cassava gb164 CK641649_P 1	7533	736	80.5	globlastp
4211	LYD2 35	castorbean 09v1 T15094_P1	7534	736	80.5	globlastp
4212	LYD2 35	cenchrus gb166 EB654968_ P1	7535	736	80.5	globlastp
4213	LYD2 35	grape gb160 BM436942_P1	7536	736	80.5	globlastp
4214	LYD2 35	monkeyflower 09v1 GR0144 68_P1	7537	736	80.5	globlastp
4215	LYD2 35	monkeyflower 10v1 GR0144 68_P1	7537	736	80.5	globlastp
4216	LYD2 35	poplar 10v1 BI072985_P1	7538	736	80.5	globlastp
4217	LYD2 35	poplar gb170 BI072985_P1	7538	736	80.5	globlastp
4218	LYD2 35	poplar 10v1 BI125787_P1	7539	736	80.5	globlastp

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
4219	LYD2 35	poplar gb170 BI125787_P1	7539	736	80.5	globlastp
4220	LYD2 35	pseudoroegneria gb167 FF34 0959_P1	7540	736	80.5	globlastp
4221	LYD2 35	sorghum 09v1 SB06G02492 0_P1	7535	736	80.5	globlastp
4222	LYD2 35	sugarcane gb157.3 BQ53381 2_P1	7535	736	80.5	globlastp
4223	LYD2 35	sugarcane gb157.3 BQ53590 3_P1	7535	736	80.5	globlastp
4224	LYD2 35	switchgrass gb167 DN14302 5_P1	7541	736	80.5	globlastp
4225	LYD2 35	switchgrass gb167 DN14505 9_P1	7542	736	80.5	globlastp
4226	LYD2 35	sugarcane 10v1 BQ533812_ P1	7535	736	80.5	globlastp
4227	LYD2 35	ginseng 10v1 CN845955_T1	7543	736	80.47	glotblastn
4228	LYD2 48	b_juncea 10v2 E6ANDIZ01 AWPC7_P1	7544	737	97.2	globlastp
4229	LYD2 48	canola 10v1 CX190543_T1	7545	737	96.73	glotblastn
4230	LYD2 48	b_oleracea gb161 DY014208 _T1	7546	737	96.73	glotblastn
4231	LYD2 48	b_oleracea gb161 AM06113 6_P1	7547	737	88.3	globlastp
4232	LYD2 48	b_rapa gb162 EX046027_T1	7548	737	85.12	glotblastn
4233	LYD2 48	cleome_gynandra 10v1 SRR 015532S0001842_T1	7549	737	80.84	glotblastn
4234	LYD2 50	canola 10v1 EV168840_T1	7550	738	98.81	glotblastn
4235	LYD2 50	pigeonpea 10v1 SRR054580 S0022117_T1	7551	738	82.14	glotblastn
4236	LYD2 50	cowpea gb166 FF385901_T1	7552	738	82.14	glotblastn
4237	LYD2 50	b_juncea 10v2 BJ1SLX0018 7033D1_T1	7553	738	80.95	glotblastn
4238	LYD2 50	cassava 09v1 CK646994_T1	7554	738	80.95	glotblastn
4239	LYD2 50	heritiera 10v1 SRR005794S0 006421_T1	7555	738	80.95	glotblastn
4240	LYD2 50	prunus 10v1 CN489066_T1	7556	738	80.95	glotblastn
4241	LYD2 50	bean gb167 CA910825_T1	7557	738	80.95	glotblastn

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
4242	LYD2 50	chestnut gb170 SRR006295S 0000380_T1	7558	738	80.95	glotblastn
4243	LYD2 50	grape gb160 CB973883_T1	7559	738	80.95	glotblastn
4244	LYD2 60	arabidopsis 10v1 AT5G6400 0_T1	7560	739	80.13	glotblastn
4245	LYD2 60	arabidopsis gb165 AT5G640 00_T1	7560	739	80.13	glotblastn
4246	LYD2 61	b_oleracealgb161 EH415860 _T1	7561	740	97.2	glotblastn
4247	LYD2 61	canola 10v1 EE431858_T1	7562	740	94.08	glotblastn
4248	LYD2 61	canola gb161 DY023542_T1	7563	740	93.77	glotblastn
4249	LYD2 61	canola 10v1 EE551454_P1	7564	740	90.5	globlastp
4250	LYD2 61	radish gb164 EV567697_P1	7565	740	88.5	globlastp
4251	LYD2 61	b_rapalgb162 EX040521_T1	7566	740	88.47	glotblastn
4252	LYD2 61	arabidopsis_lyrata 09v1 JGI AL004392_T1	7567	740	87.85	glotblastn
4253	LYD2 61	cleome_gynandra 10v1 SRR 015532S0011521_T1	7568	740	81.62	glotblastn
4254	LYD2 68	canola 10v1 EV039640_T1	7569	742	92.68	glotblastn
4255	LYD2 68	b_junceal 10v2 SEQ2714_T1	7570	742	84.15	glotblastn
4256	LYD2 68	thellungiellalgb167 DN7754 35_T1	7571	742	81.71	glotblastn
4257	LYD2 68	arabidopsis 10v1 AT4G0161 0_T1	7572	742	80.49	glotblastn
4258	LYD2 68	arabidopsis gb165 AT4G016 10_T1	7572	742	80.49	glotblastn
4259	LYD2 68	b_oleracealgb161 AM39587 1_T1	7573	742	80.49	glotblastn
4260	LYD2 68	b_rapalgb162 CV523184_T1	7574	742	80.49	glotblastn
4261	LYD2 68	canola 10v1 CD811685_T1	7575	742	80.49	glotblastn
4262	LYD2 68	canola gb161 CD811685_T1	7575	742	80.49	glotblastn
4263	LYD2 68	canola 10v1 CD814272_T1	7576	742	80.49	glotblastn
4264	LYD2 68	canola gb161 CD814272_T1	7576	742	80.49	glotblastn

<i>Polynuc l. SEQ ID NO:</i>	<i>Homo log to Gene Name</i>	<i>cluster name</i>	<i>Polype p. SEQ ID NO:</i>	<i>Homolo g. To polypep. SEQ ID NO:</i>	<i>% global identity</i>	<i>Algor.</i>
4265	LYD2 71	canola 10v1 CX193148_T1	7577	743	95.45	glotblastn
4266	LYD2 71	canola gb161 CX193148_T1	7578	743	95.45	glotblastn
4267	LYD2 71	canola 10v1 BQ704756_T1	7579	743	93.18	glotblastn
4268	LYD2 71	radish gb164 EX763829_T1	7580	743	92.05	glotblastn
4269	LYD2 71	thellungiella gb167 BY8151 88_T1	7581	743	90.91	glotblastn
4270	LYD2 71	b_junceal 10v2 E6ANDIZ01 D350E_T1	7582	743	85.23	glotblastn
4271	LYD2 71	canola 10v1 ES981471_T1	7583	743	82.95	glotblastn
4272	LYD2 71	b_rapal gb162 EX040706_T1	7584	743	82.95	glotblastn
4273	LYD2 71	radish gb164 EV537391_T1	7585	743	82.95	glotblastn
4274	LYD2 71	b_oleraceal gb161 EH419147 _T1	7586	743	80.68	glotblastn
4275	LYD2 73	canola gb161 ES950584_T1	7587	744	100	glotblastn
4276	LYD2 73	radish gb164 EV536786_T1	7588	744	100	glotblastn
4277	LYD2 73	thellungiella gb167 BY8060 71_T1	7589	744	100	glotblastn
4278	LYD2 73	cleome_spinosal 10v1 SRR01 5531S0023838_T1	7590	744	97.96	glotblastn
4279	LYD2 73	canola 10v1 ES950584_T1	7591	744	95.92	glotblastn
4280	LYD2 73	b_rapal gb162 CV432099_T1	7592	744	93.88	glotblastn
4281	LYD2 73	pigeonpeal 10v1 SRR054580 S0008538_T1	7593	744	87.76	glotblastn
4282	LYD2 73	cacaol gb167 CU473348_T1	7594	744	87.76	glotblastn
4283	LYD2 73	citrus gb166 CX674860_T1	7595	744	87.76	glotblastn
4284	LYD2 73	cowpeal gb166 FF395622_T1	7596	744	87.76	glotblastn
4285	LYD2 73	peanut 10v1 EE127736_T1	7597	744	87.76	glotblastn
4286	LYD2 73	poplar gb170 CA925799_T1	7598	744	87.76	glotblastn
4287	LYD2 73	soybean gb168 AL369908_T 1	7599	744	87.76	glotblastn

DEMANDE OU BREVET VOLUMINEUX

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

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 321

NOTE : Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

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

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 321

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

NOM DU FICHER / FILE NAME :

NOTE POUR LE TOME / VOLUME NOTE:

WHAT IS CLAIMED IS:

1. A method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide at least 80 % identical to SEQ ID NO: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8090 or 8091, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.
2. A method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.
3. A method of increasing oil content, fiber yield and/or fiber quality 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: 5470, 5476, or 5481, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.
4. A method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4850 or 4851, thereby increasing the

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

5. A method of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant, comprising expressing within the plant an exogenous polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644, thereby increasing the yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of the plant.

6. A method of increasing oil content, fiber yield and/or fiber quality of a plant, comprising expressing within the plant an exogenous polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 1627, 1629, or 1631, thereby increasing the oil content, fiber yield and/or fiber quality of the plant.

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: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8090 or 8091, wherein said amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

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: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

9. An isolated polynucleotide comprising a nucleic acid sequence at least 80 % identical to SEQ ID NO: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626,

1632-1642, 1645-4850 or 4851, wherein said nucleic acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

10. An isolated polynucleotide comprising the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

11. A nucleic acid construct comprising the isolated polynucleotide of claim 7, 8, 9 or 10, and a promoter for directing transcription of said nucleic acid sequence in a host cell.

12. An isolated polypeptide comprising an amino acid sequence at least 80 % homologous to SEQ ID NO: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8090 or 8091, wherein said amino acid sequence is capable of increasing yield, biomass, growth rate, vigor, oil content, fiber yield, fiber quality, abiotic stress tolerance, and/or nitrogen use efficiency of a plant.

13. An isolated polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NOs: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

14. A plant cell exogenously expressing the polynucleotide of claim 7, 8, 9 or 10, or the nucleic acid construct of claim 11.

15. A plant cell exogenously expressing the polypeptide of claim 12 or 13.

16. The method of claim 1 or 4, the isolated polynucleotide of claim 7, the nucleic acid construct of claim 11 or the plant cell of claim 14, wherein said nucleic acid sequence encodes an amino acid sequence selected from the group consisting of SEQ ID NOs: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-

8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

17. The method of claim 1, 2, 4 or 5, the isolated polynucleotide of claim 7, 8, 9 or 10, the nucleic acid construct of claim 11 or the plant cell of claim 14, wherein said nucleic acid sequence is selected from the group consisting of SEQ ID NOs: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

18. The method of claim 1, 2, 4 or 5, the isolated polynucleotide of claim 7, 8, 9 or 10, the nucleic acid construct of claim 11 or the plant cell of claim 14, wherein said polynucleotide consists of the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

19. The method of claim 1, the isolated polynucleotide of claim 9, or the nucleic acid construct of claim 11, wherein said nucleic acid sequence encodes the amino acid sequence selected from the group consisting of SEQ ID NOs: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

20. The plant cell of claim 14 or 15, wherein said plant cell forms part of a plant.

21. The method of claim 1, 2, 4, 5, 16, 17, 18 or 19, further comprising growing the plant expressing said exogenous polynucleotide under the abiotic stress.

22. The method of claim 1, 2, 4, 5 or 21, the isolated polynucleotide of claim 7 or 9, or the nucleic acid construct of claim 11, the isolated polypeptide of claim 12, the plant cell of claim 14 or 15, wherein said abiotic stress is selected from the group consisting of salinity, drought, water deprivation, flood, etiolation, low temperature,

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high temperature, heavy metal toxicity, anaerobiosis, nutrient deficiency, nutrient excess, atmospheric pollution and UV irradiation.

23. The method of claim 1, 2, 4 or 5, the isolated polynucleotide of claim 7 or 9, or the nucleic acid construct of claim 11, the isolated polypeptide of claim 12, or the plant cell of claim 14 or 15, wherein the yield comprises seed yield or oil yield.

24. The nucleic acid construct of claim 11, the plant cell of claim 14, 20, 22 or 23, the method of claim 16, 17, 18, 19, 20, 22, or 23, wherein said promoter is set forth by SEQ ID NO: 8096.

25. An isolated polynucleotide comprising the nucleic acid sequence set forth by SEQ ID NO: 8096.

26. A nucleic acid construct comprising the isolated polynucleotide of claim 25.

27. The nucleic acid construct of claim 26, further comprising at least one heterologous polynucleotide operably linked to the isolated polynucleotide.

28. The nucleic acid construct of claim 27, wherein said at least one heterologous polynucleotide is a reporter gene.

29. The nucleic acid construct of claim 27, wherein said at least one heterologous polynucleotide comprises the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

30. A transgenic cell comprising the nucleic acid construct of claim 26, 27, 28 or 29.

31. The transgenic cell of claim 30, being a plant cell.

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32. A transgenic plant comprising the nucleic acid construct of claim 26, 27, 28 or 29.

33. A method of producing a transgenic plant, comprising transforming a plant with the isolated polynucleotide of claim 25 or with the nucleic acid construct of claim 26, 27, 28 or 29.

34. A method of expressing a polypeptide of interest in a cell comprising transforming the cell with a nucleic acid construct which comprises a polynucleotide sequence encoding the polypeptide of interest operably linked to the isolated polynucleotide of claim 25, thereby expressing the polypeptide of interest in the cell.

35. The method of claim 34, wherein said polypeptide of interest comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 799, 488-798, 800-813, 4852-5453, 5460, 5461, 5484, 5486-5550, 5553, 5558-8091, 5454-5459, 5462-5469, 5471-5475, 5477-5480, 5482, 5483, 5485, 5551, 5552, and 5554-5557.

36. The method of claim 34, wherein said polynucleotide encoding the polypeptide of interest comprises the nucleic acid sequence selected from the group consisting of SEQ ID NOs: 460, 1-459, 461-487, 814-1598, 1600-1603, 1605-1626, 1632-1642, 1645-4851, 1599, 1604, 1628, 1630, and 1644.

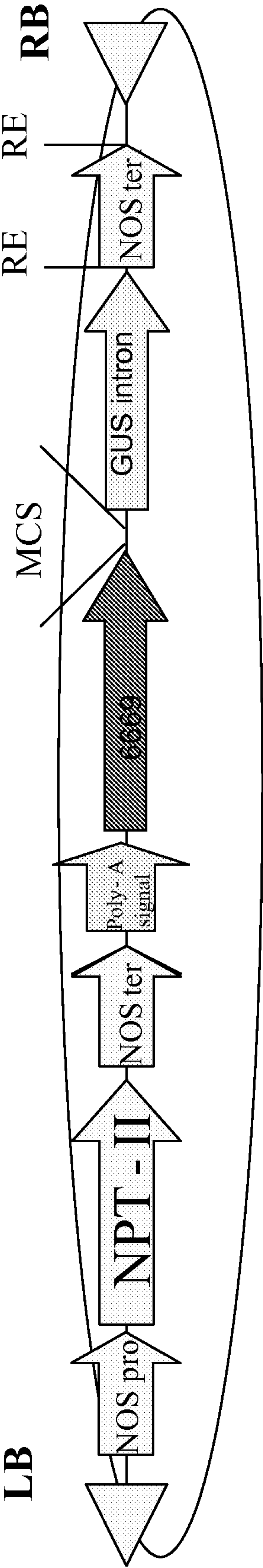


FIG. 1

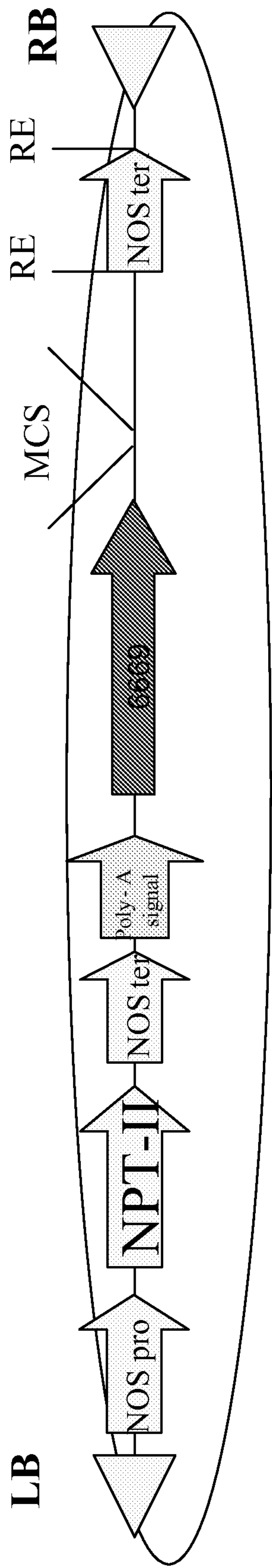


FIG. 2

Nitrogen limiting
conditions

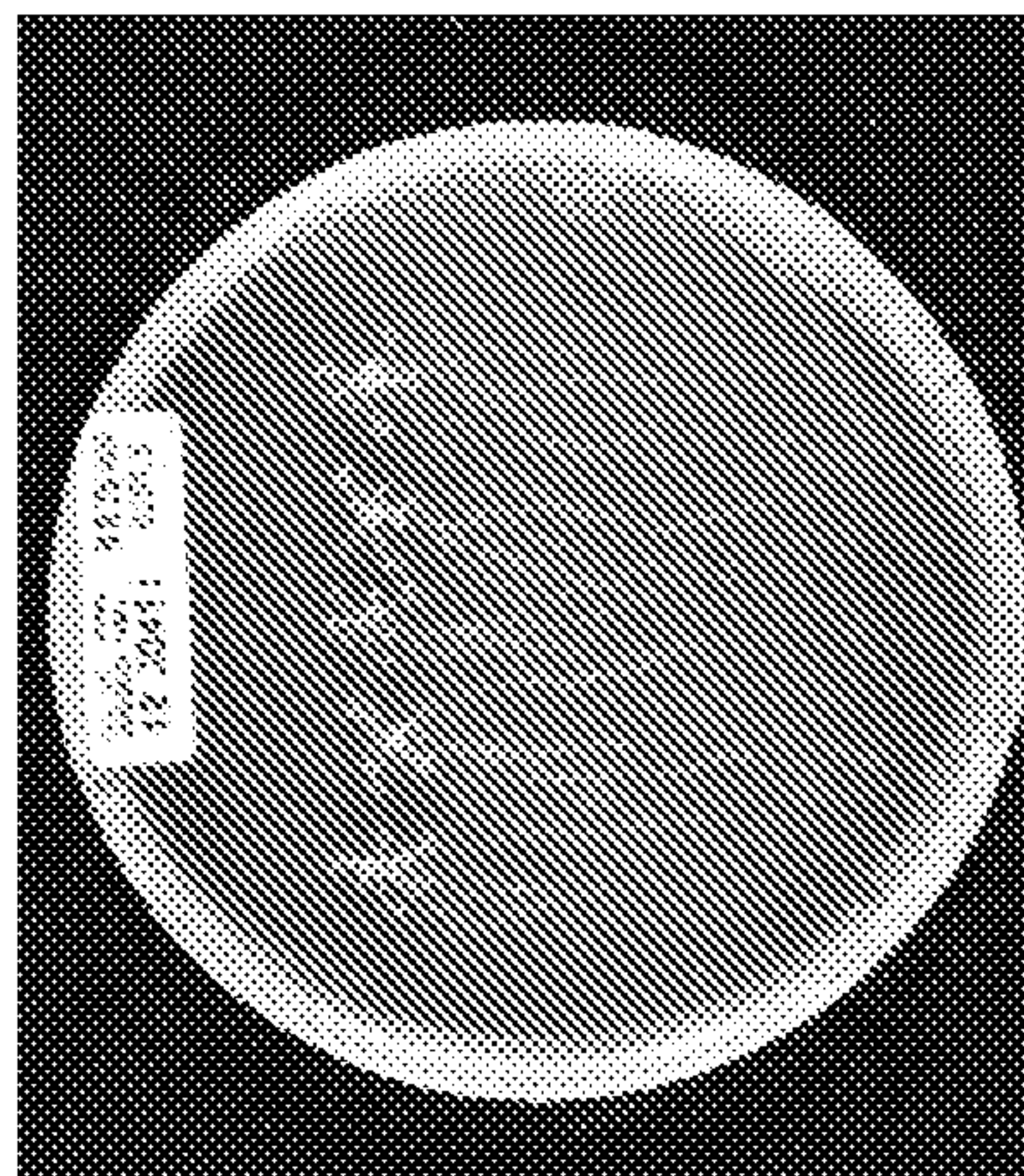


FIG. 3E

Osmotic stress
(15 % PEG)

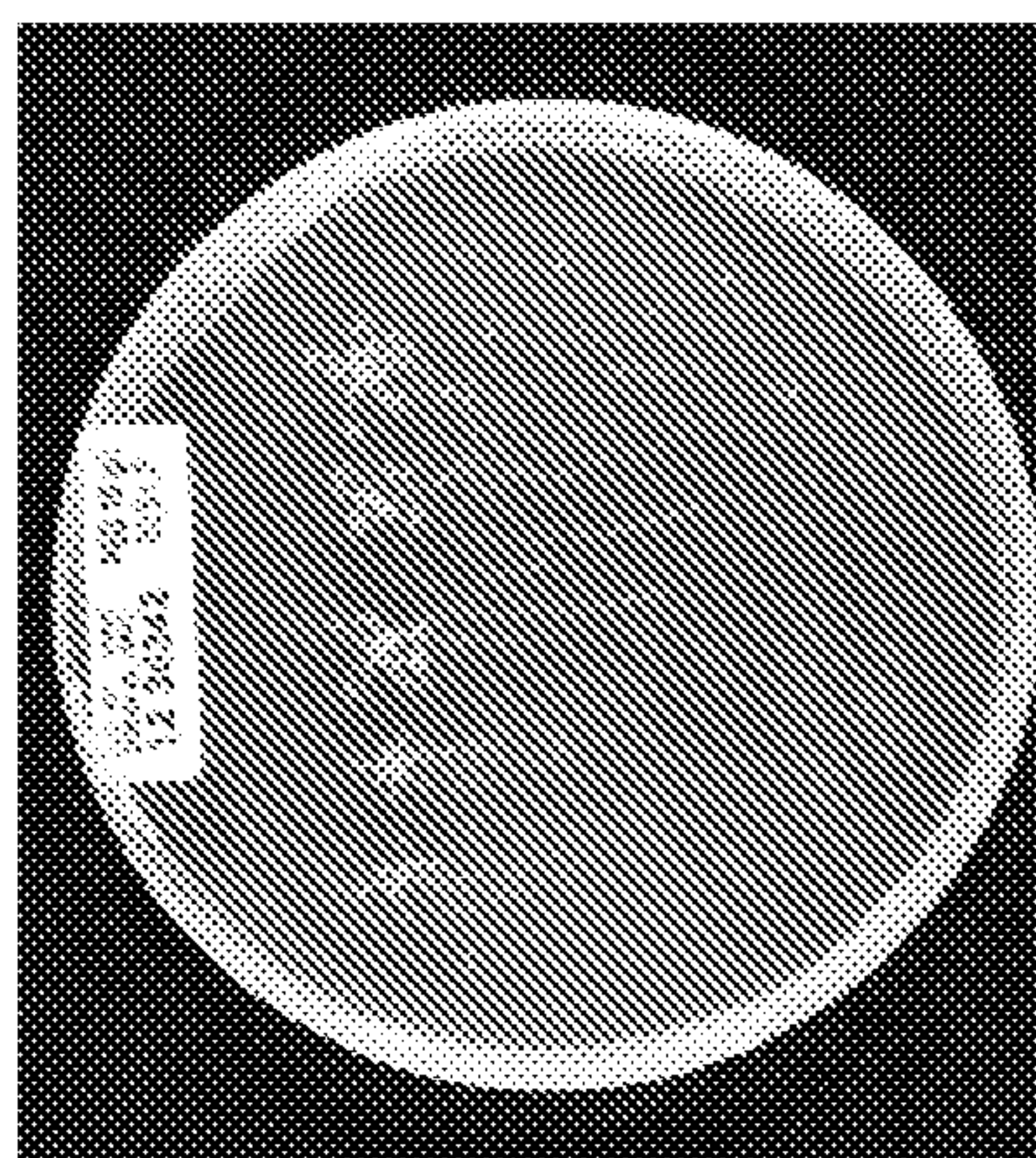


FIG. 3C

Normal conditions

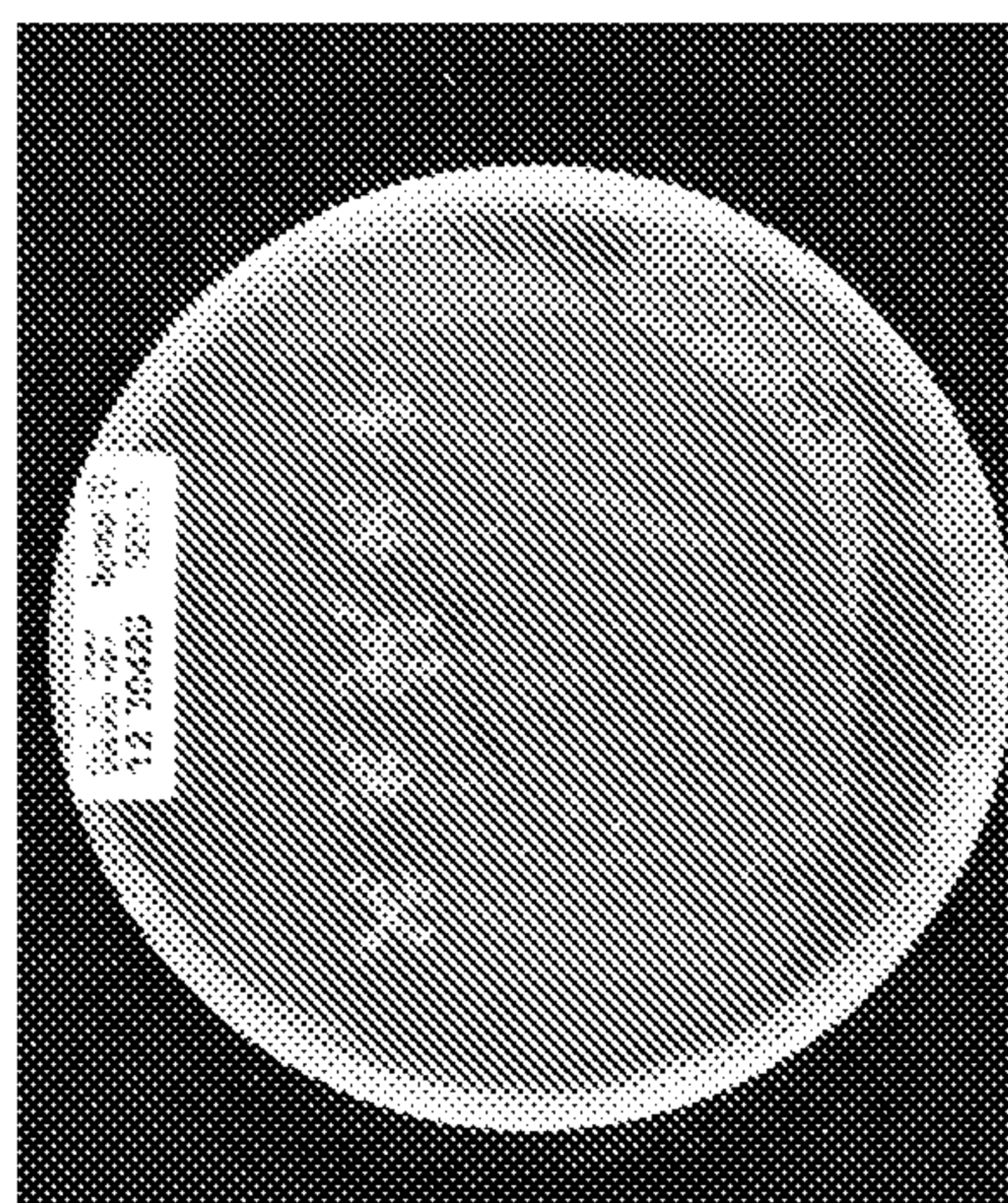


FIG. 3A

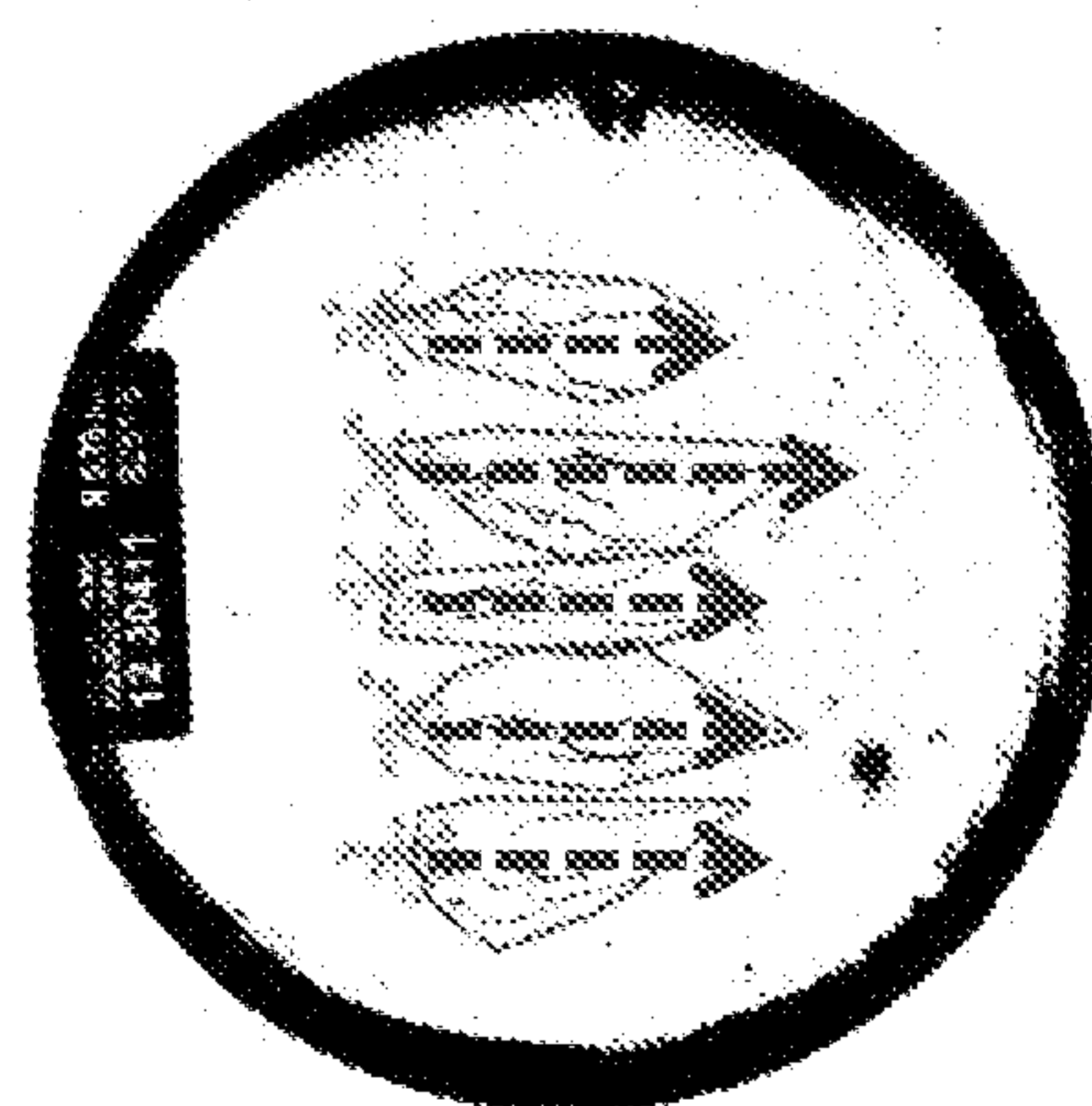


FIG. 3F

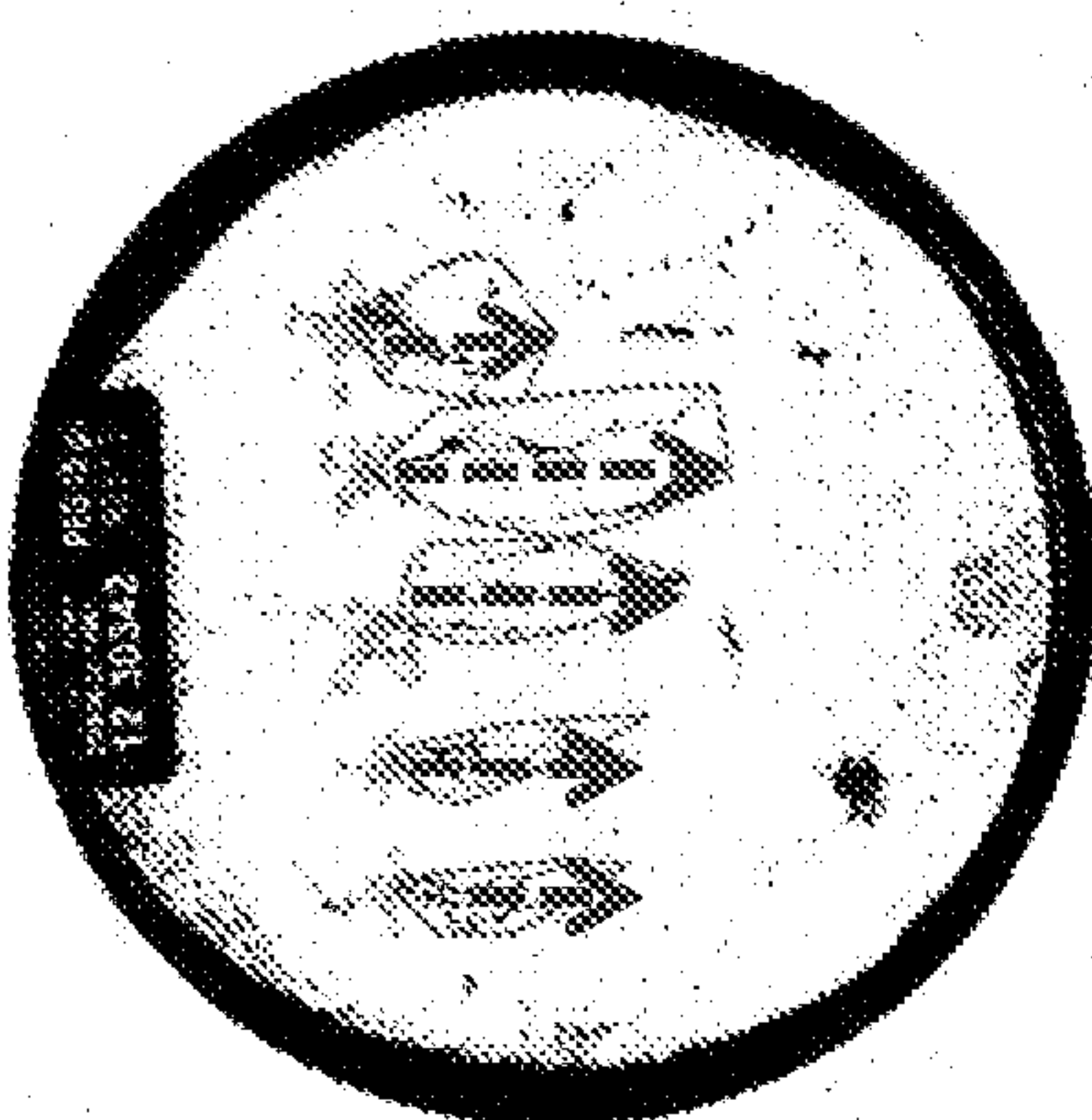


FIG. 3D

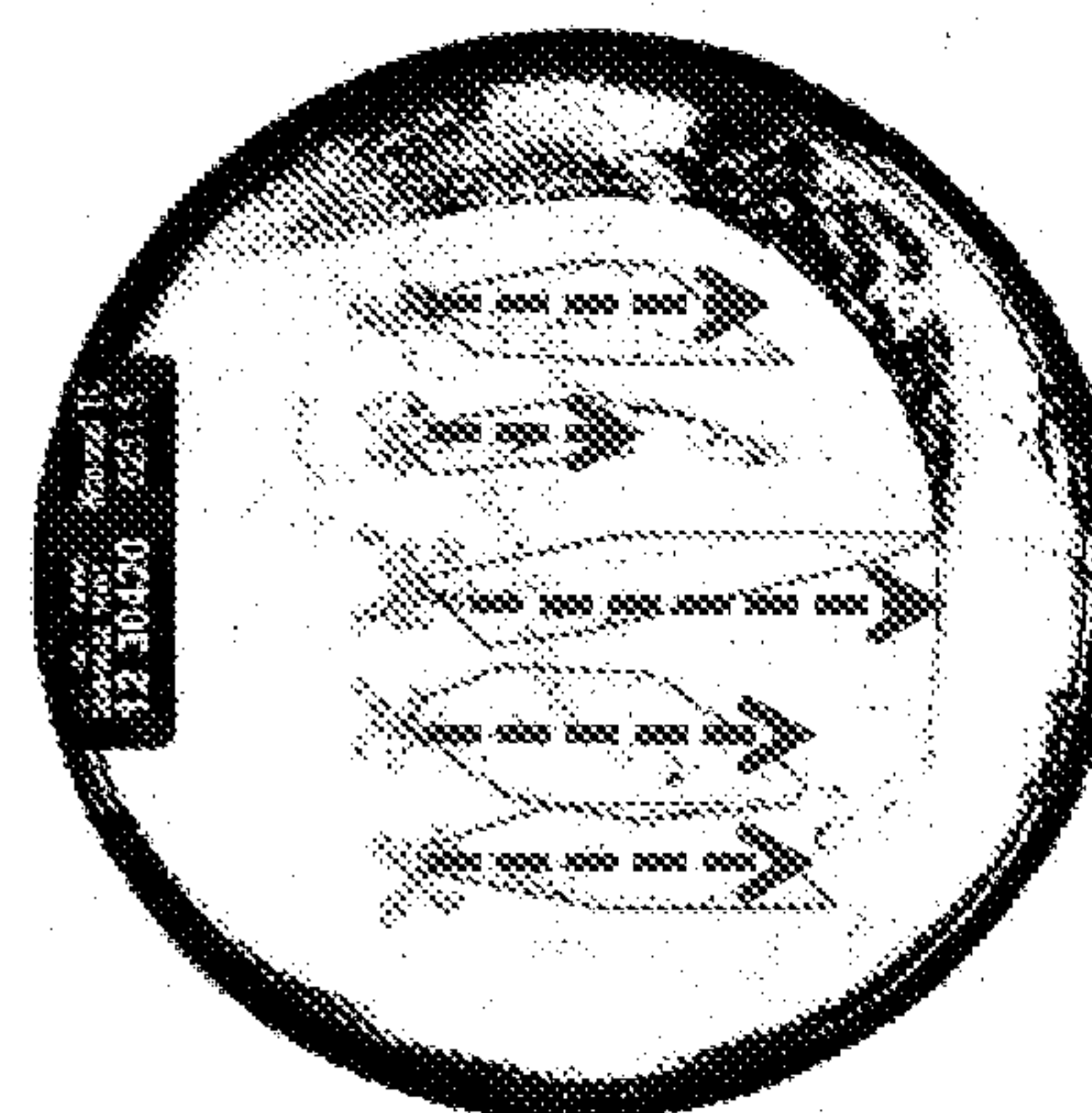


FIG. 3B

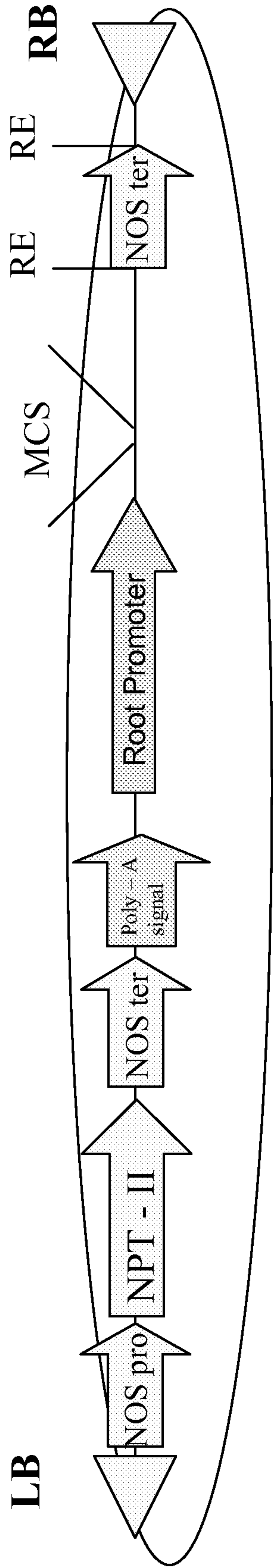


FIG. 4

SEQ ID NO: 8093

SEQ ID NO: 8096

1	AAGCTTTAAGCTCCAAGCCACATCTATGCACCTTCAACATATCTTTTCTAGATGAGTTGGTAAAGTAGAAAAAGATATGATGATTTTAAATTTGTTTC	100
1	AAGCTTTAAGCTCCAAGCCACATCTATGCACCTTCAACATATCTTTTCTAGATGAGTTGGTAAAGTAGAAAAAGATATGATGATTTTAAATTTGTTTC	100
101	TATTTATATGTGTTTCATCGAAACTTCATTTTCTAGTTTAAATAGAGAGTTTATATGACTTTTAAAAATTGATTTAAAACTGTGTCAAAAATTAAAGG	200
101	TATTTATATGTGTTTCATCGAAACTTCATTTTCTAGTTTAAATAGAGAGTTTATATGACTTTTAAAAATTGATTTAAAACTGTGTCAAAAATTAAAGG	200
201	ACAAATAAAAAATTGTCATACAAACCGAAAAATACTTATATTTAGACAAGAAAAATAATACTTTGTGATGCTAATTTTATTTATATATATCATGAATCATG	300
201	ACAAATAAAAAATTGTCATACAAACCGAAAAATACTTATATTTAGACAAGAAAAATAATACTTTGTGATGCTAATTTTATTTATATATATCATGAATCATG	300
301	ATCATCCAATTTTCCGGATAAGCCAAAAGTCAAAAATGATGGGTTCCCCCTAAATCTTTTATGCTGAGAAAATAGATGTATATTTCTTAGATAGTAATATAAAAT	400
301	ATCATCCAATTTTCCGGATAAGCCAAAAGTCAAAAATGATGGGTTCCCCCTAAATCTTTTATGCTGAGAAAATAGATGTATATTTCTTAGATAGTAATATAAAAT	400
401	TGGGTTAAAGAAATGATGATTCGATTATAGCCTCAACTAGAAGATACGTGTAGTGCAGGTGTGTAGTTAACTGGTGGTAGTGGCAGACAAACCAGATTAGGA	500
401	TGGGTTAAAGAAATGATGATTCGATTATAGCCTCAACTAGAAGATACGTGTAGTGCAGGTGTGTAGTTAACTGGTGGTAGTGGCAGACAAACCAGATTAGGA	500
501	GTAAATAAAAGCCTTTAGATTTGAGAGATTGAAATATTCGATTGGAACCTTTTCTAGATTTTACAGCCATCTAAAAATTAGATGCAGATCACCTACTACCA	600
501	GTAAATAAAAGCCTTTAGATTTGAGAGATTGAAATATTCGATTGGAACCTTTTCTAGATTTTACAGCCATCTAAAAATTAGATGCAGATCACCTACTACCA	600
601	TTCAAAAAATGAACAAAAATAATTTTCATTTACATTTTCCCTAGCATAAGATATAATAATAAATAGTCTCATTTTAAATTACTTTTCTAAATATTTTTCGTTA	700
601	TTCAAAAAATGAACAAAAATAATTTTCATTTACATTTTCCCTAGCATAAGATATAATAATAAATAGTCTCATTTTAAATTACTTTTCTAAATATTTTTCGTTA	700
701	TTTTAAATTTTGCTGTCTATACTCTACAGCTCATTTAATAACGGAAACAAAAATAATTGCAGGGATACGGATGGGTAGCTTTCAAAACTTACATCATCT	800
701	TTTTAAATTTTGCTGTCTATACTCTACAGCTCATTTAATAACGGAAACAAAAATAATTGCAGGGATACGGATGGGTAGCTTTCAAAACTTACATCATCT	800
801	TCTGTTTCTTGAGATCAACTATTTTTGGAGCTTTGTCTCAATCGTACCAAAGGATAATGGTCCTACCTCCTTTTGCATTTCTTAACTTTATCTTCTCTACT	900
801	TCTGTTTCTTGAGATCAACTATTTTTGGAGCTTTGTCTCAATCGTACCAAAGGATAATGGTCCTACCTCCTTTTGCATTTCTTAACTTTATCTTCTCTACT	900
901	TATTTCTTTTTTGGGATTTTGGGGGTATTATTTATCTTTTGTAGATATACACATTGATTTACTACAAAACGTATATACTACTATCCATCTTCAACTCTTCG	1000
901	TATTTCTTTTTTGGGATTTTGGGGGTATTATTTATCTTTTGTAGATATACACATTGATTTACTATAAAACGTATATACTACTATCCATCTTCAACTCTTCG	1000
1001	GAATATGATTTTCGAAAAAACTATGAAGATTAAACGGGTATCTTAAACATGTTAAGATACACCGGACAAATTTTCATTTTAGAAGAAATTGATATGCAATTAACA	1100
1001	GAATATGATTTTCGAAAAAACTATGAAGATTAAACGGGTATCTTAAACATGTTAAGATACACCGGACAAATTTTCATTTTAGAAGAAATTGATATGCAATTAACA	1100
1101	ATAAATAGTTGATGATCTTTTAGTTTTGAAGATGTCGGTTAAGACTTAAGCGTGTGGTAAACAAGGTGGGACTCGGGCAACGCAAGCCTTGTAGAGTCCA	1200
1101	ATAAATAGTTGATGATCTTTTAGTTTTGAAGATGTCGGTTAAGACTTAAGCGTGTGGTAAACAAGGTGGGACTCGGGCAACGCAAGCCTTGTAGAGTCCA	1200
1201	CTTGCTCAACTTGCTCTTTCTTTTATCTCTTTTCCAAAGTCTCAAGATTCAATGAACTCCGTGTAACACAAAAACGCCCCATAGATGAGCTCATTTTGGGTAT	1300
1201	CTTGCTCAACTTGCTCTTTTCTTTTATCTCTTTTCCAAAGTCTCAAGATTCAATGAACTCCGTGTAACACAAAAACGCCCCATAGATGAGCTCATTTTGGGTAT	1300

FIG. 5

1301 TTCCAATATTGCCACTCCCATGATAATATCATCTAGGGATGGGGTTCAATTTTGAATCTCAACAAATCTCGTCGATTCTAACACACATGATTGATTT
1301 TTCCAATATTGCCACTCCCATGATAATATCATCTAGGGATGGGGTTCAATTTTGAATCTCAACAAATCTCGTCGATTCTAACACACATGATTGATTT
1401 GTTACTTACTTGAAAGTTGGCAACTATCTGGGATTAAATTTATCTTTTTCTACTGCTAGCTAGCAATCTATATATGTTAGCCTAAATACGTGGAAGA
1401 GTTACTTACTTGAAAGTTGGCAACTATCTGGGATTAAATTTATCTTTTTCTACTGCTAGCTAGCAATCTATATATGTTAGCCTAAATACGTGGAAGA
1501 TGTCAATTGCTAATAATGGCTAAAGATGTGTATTAATTTTCTCTTTTTCTGACATAAACTATGCTGTCAAAAATGTGTAGAA
1501 TGTCAATTGCTAATAATGGCTAAAGATGTGTATTAATTTTCTCTTTTTCTGACATAAACTATGCTGTCAAAAATGTGTAGAA
1601 TCTTTTACATAAAATCATTCCTGTTACACACTAAAGGTTACAAACGGACGATTGTATTGGACTTCCAGATCATAAACCATGCAAAACCTGAAACACCA
1601 TCTTTTACATAAAATCATTCCTGTTACACACTAAAGGTTACAAACGGACGATTGTATTGGACTTCCAGATCATAAACCATGCAAAACCTGAAACACCA
1701 AGAATAATTAGTTCTAACTTTAGAACGTTTCGTACGTGTTTCATGTTCAAAAAGCGTCAATTATAAAAAGTTGGGAAATTACTTTTGAGTTTGACATTTCT
1701 AGAATAATTAGTTCTAACTTTAGAACGTTTCGTACGTGTTTCATGTTCAAAAAGCGTCAATTATAAAAAGTTGGGAAATTACTTTTGAGTTTGACATTTCT
1801 AAGGACAGTCAAAATATGACAACATTGGGATGCAACTTACCTTGTTAACTTATTTGTTATAAAACCATATATTACATATTTTAAAGGGTTGATAAATA
1801 AAGGACAGTCAAAATATGACAACATTGGGATGCAACTTACCTTGTTAACTTATTTGTTATAAAACCATATATTACATATTTTAAAGGGTTGATAAATA
1901 ATCAAAATATACCAAAACATAGCTTTTCAATATATTTGTAAACACAGTTTGGTCTACTAGCTAATTATGAGAACATTTGTTCAATGCATGATTATCTAGTA
1901 ATCAAAATATACCAAAACATAGCTTTTCAATATATTTGTAAACACAGTTTGGTCTACTAGCTAATTATGAGAACATTTGTTCAATGCATGATTATCTAGTA
2001 TCTACTAGTGGATTATGAAAAATTAGATATTTTCATTGTCATGATTATCTTCCATATATAGTGATAACATCAAAAAGAACTACACACCAATTATTGCAATTTTTT
2001 TCTACTAGTGGATTATGAAAAATTAGATATTTTCATTGTCATGATTATCTTCCATATATAGTGATAACATCAAAAAGAACTACACACCAATTATTGCAATTTTTT
2101 CATTATATAATAAGCACTAAACTGTAAAAATTATATTTCAGCCACCCCAACCATGACAAAATCACCTTAAAGGCTTAAACACATAACAGCCATTACGAGTCAC
2101 CATTATATAATAAGCACTAAACTGTAAAAATTATATTTCAGCCACCCCAACCATGACAAAATCACCTTAAAGGCTTAAACACATAACAGCCATTACGAGTCAC
2201 AGGTAAGGGTATAATAGTAAAGAAATCAATCTATATAATATACGACCCACCCCTTTCTCATTTCTTCTGGAGAGTAACATCGAGACAAAGAACTAA
2201 AGGTAAGGGTATAATAGTAAAGAAATCAATCTATATAATATACGACCCACCCCTTTCTCATTTCTTCTGGAGAGTAACATCGAGACAAAGAACTAA
2301 AAAAGAGAACCCCAAA 2316 (SEQ ID NO: 8093)
2301 AAAAGAGAACCCCAAGAA 2318 (SEQ ID NO: 8096)

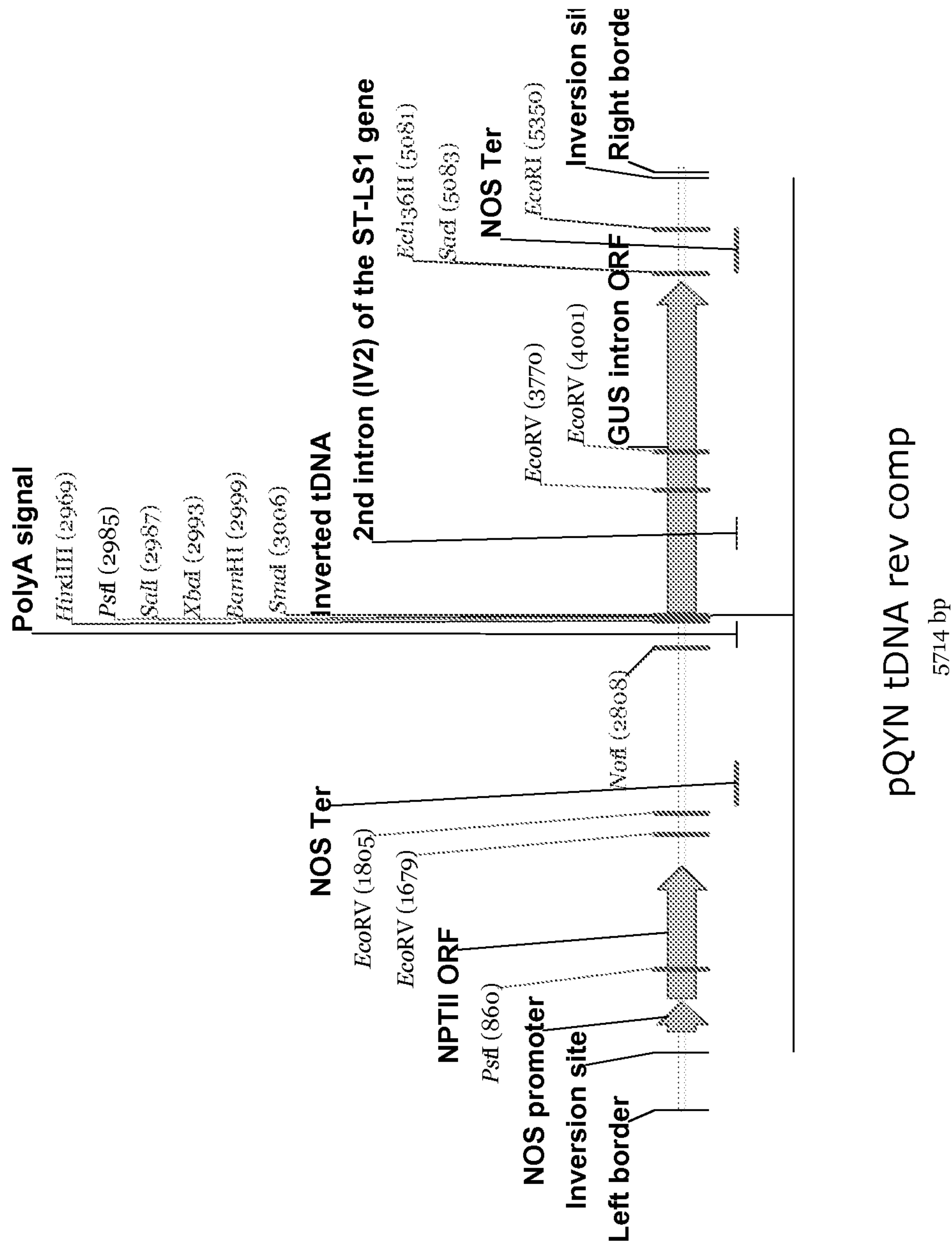
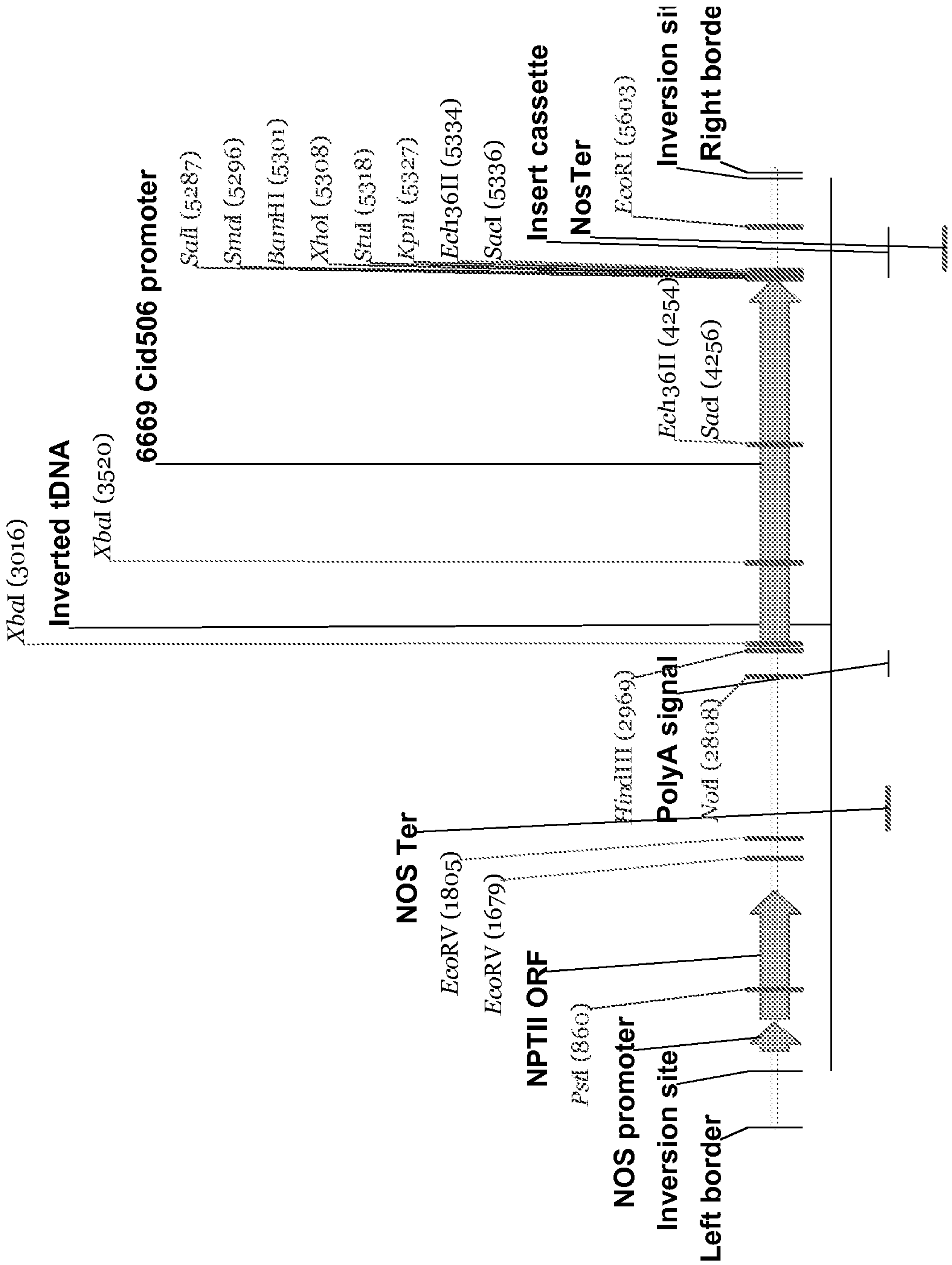
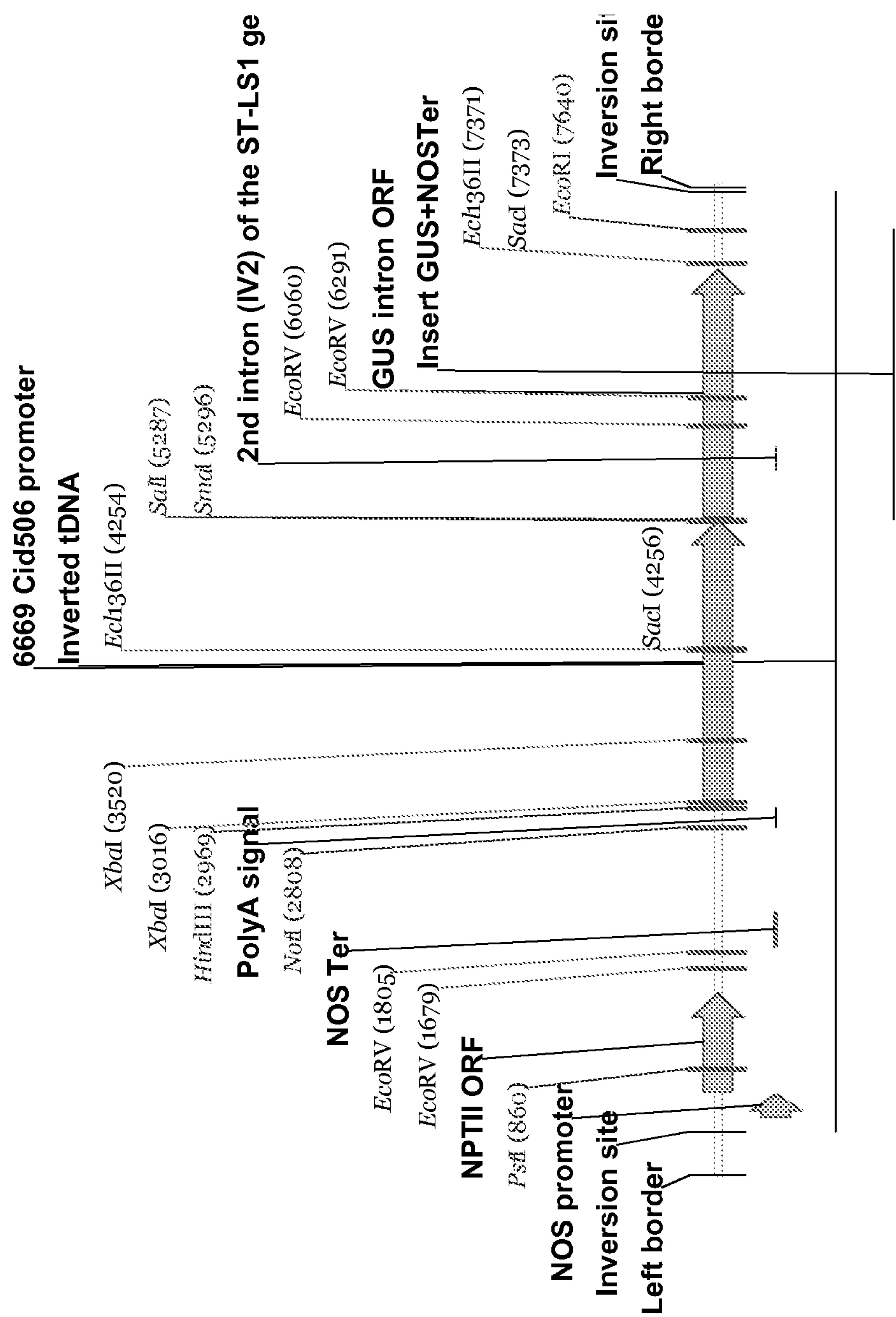


FIG. 6



pQFN
5967 bp

FIG. 7



pQFYN
8004 bp

FIG. 8

FIG. 9A

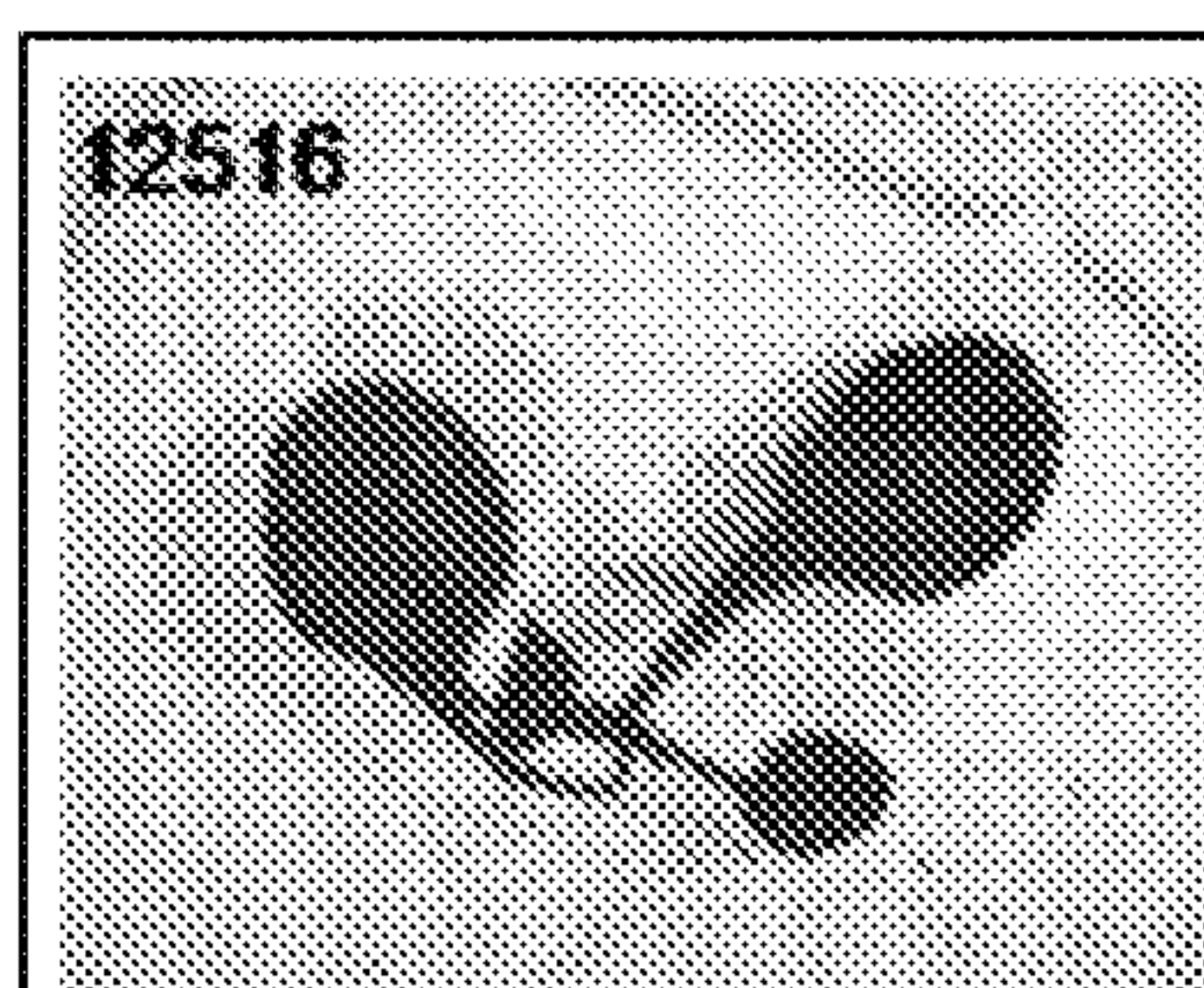


FIG. 9B

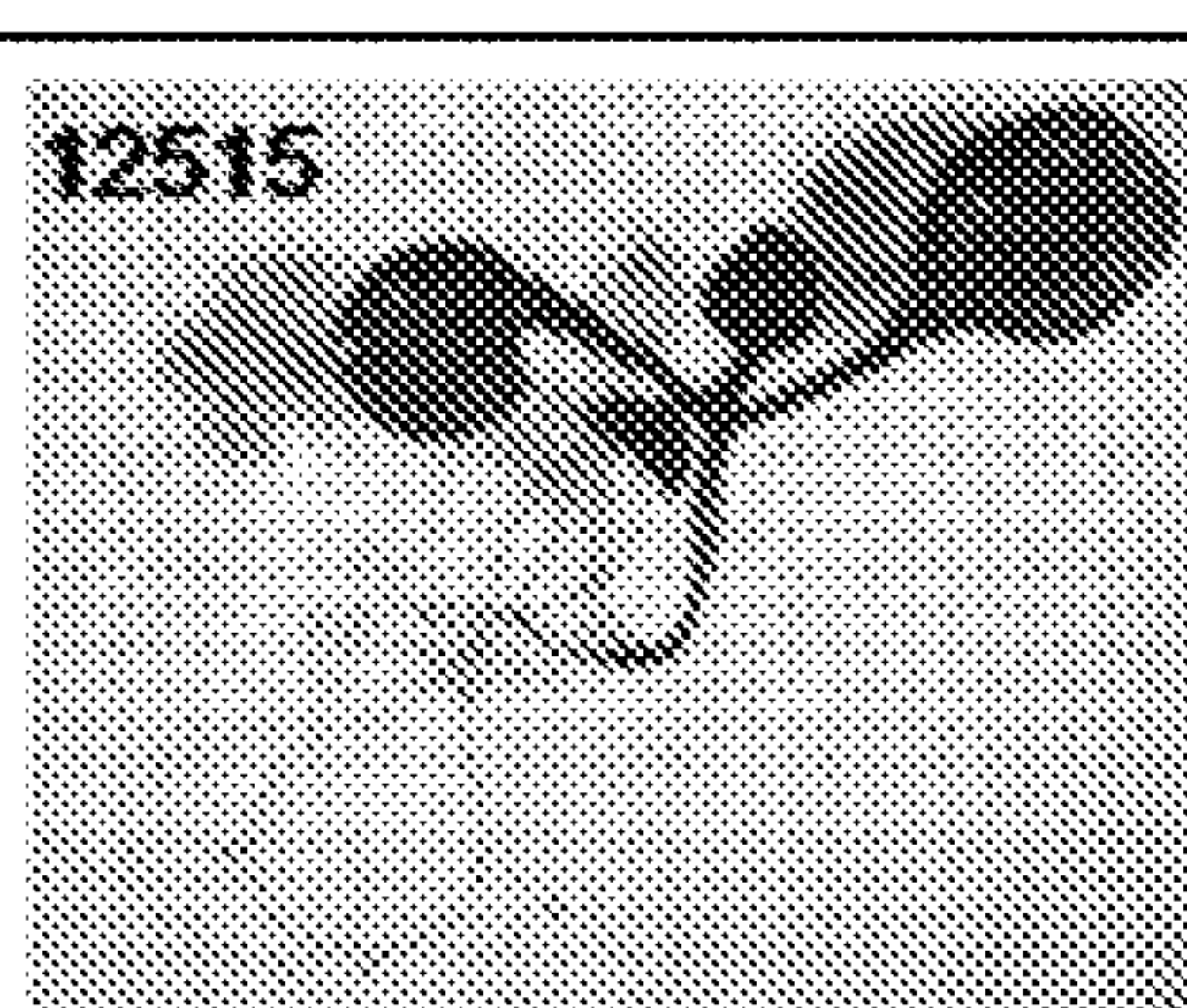


FIG. 9C

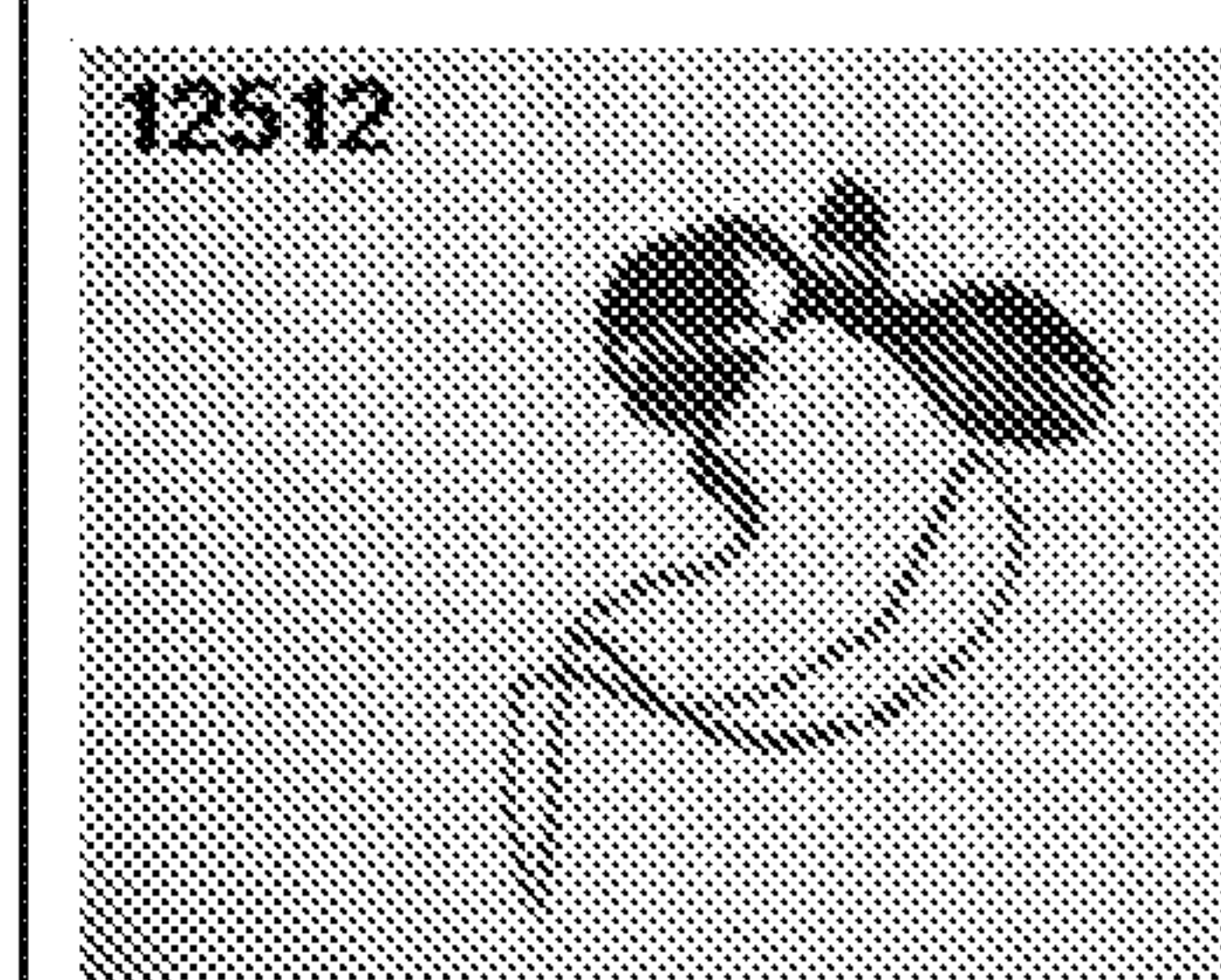


FIG. 9D

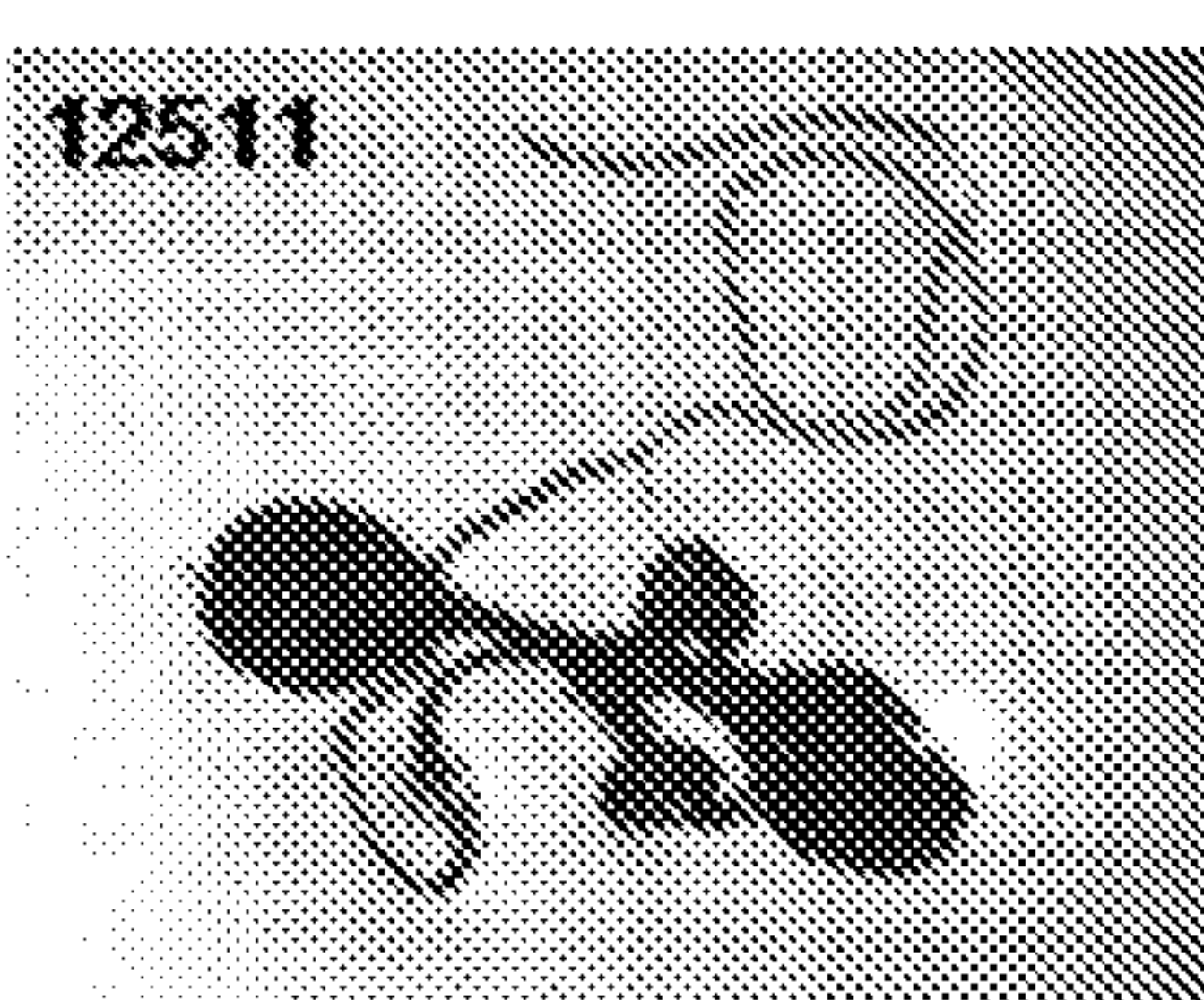


FIG. 10A

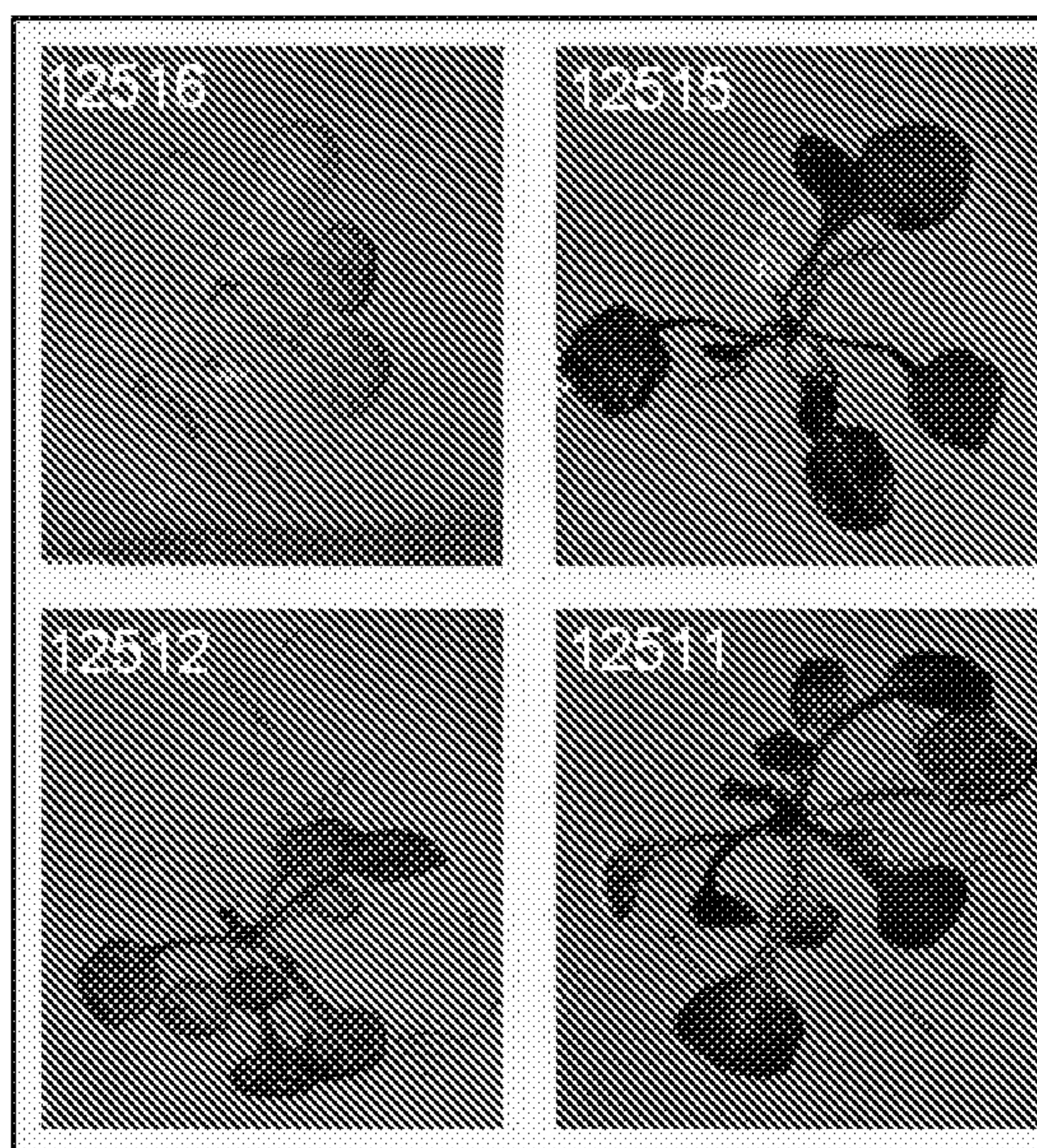
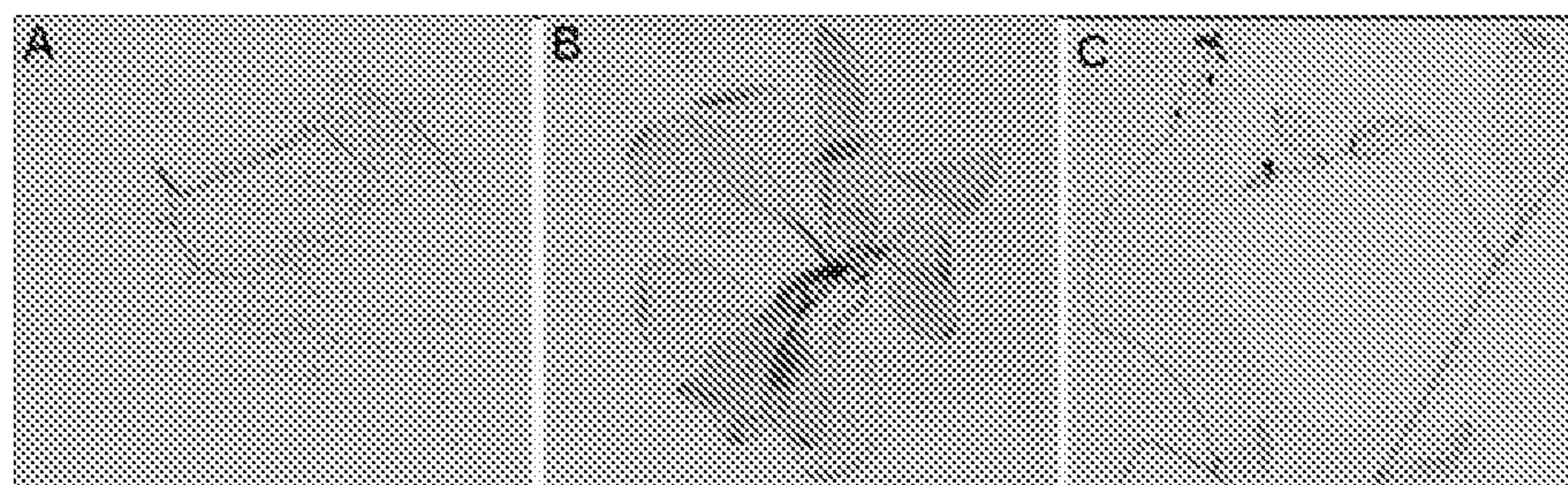


FIG. 10B

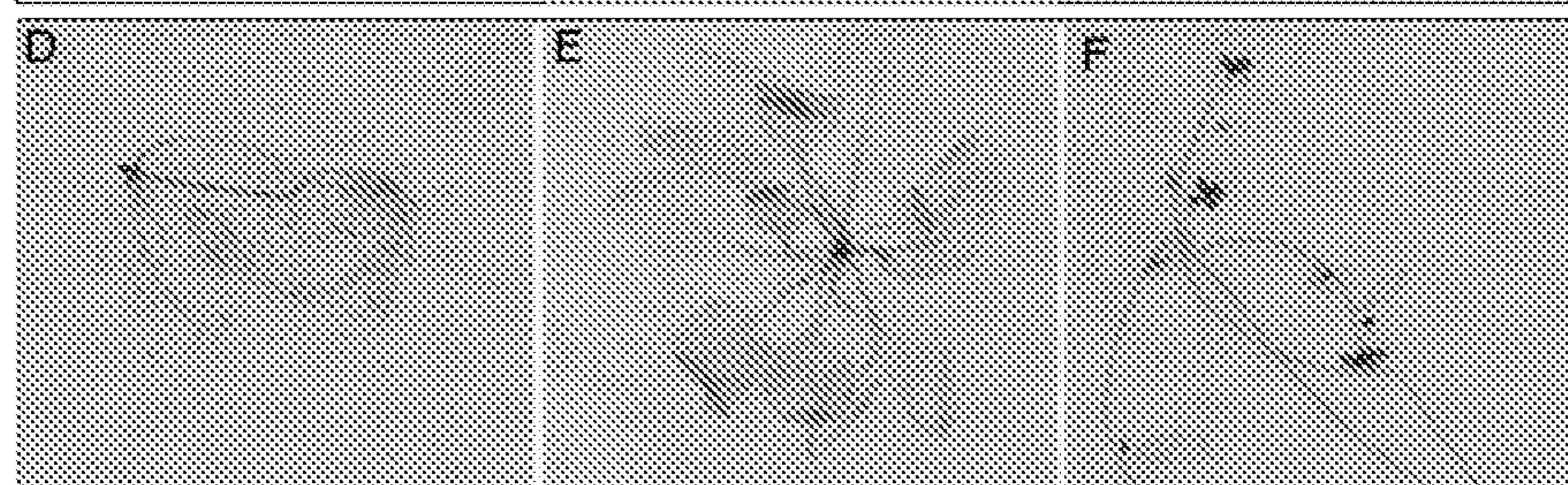
FIG. 10C

FIG. 10D

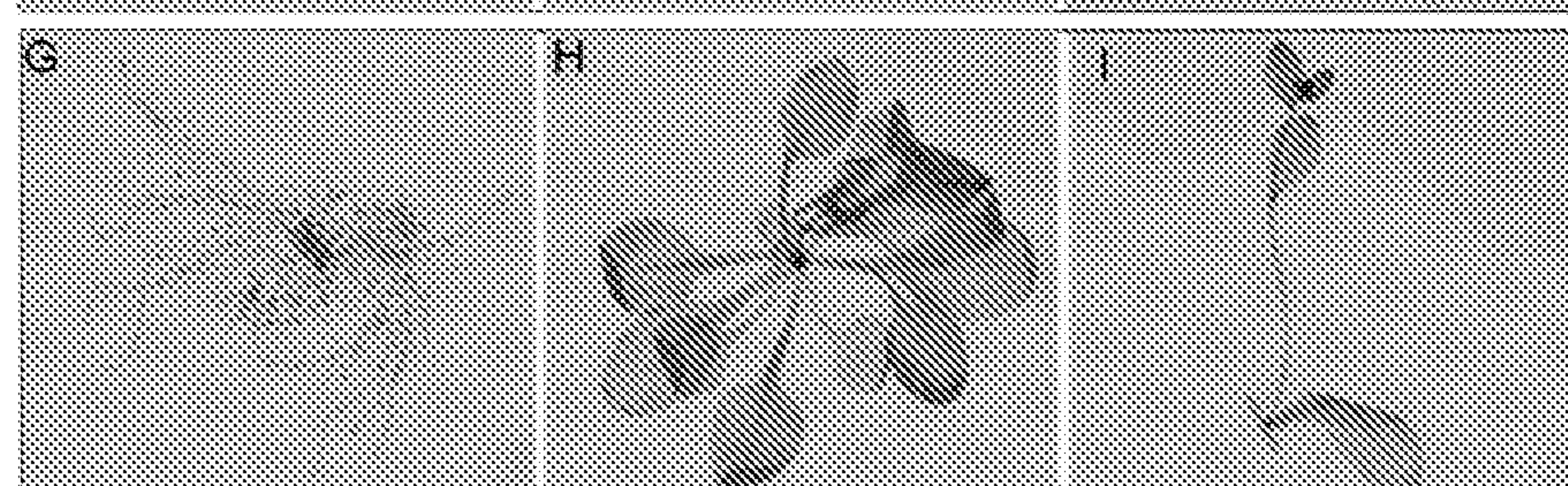
FIGs. 11A-C



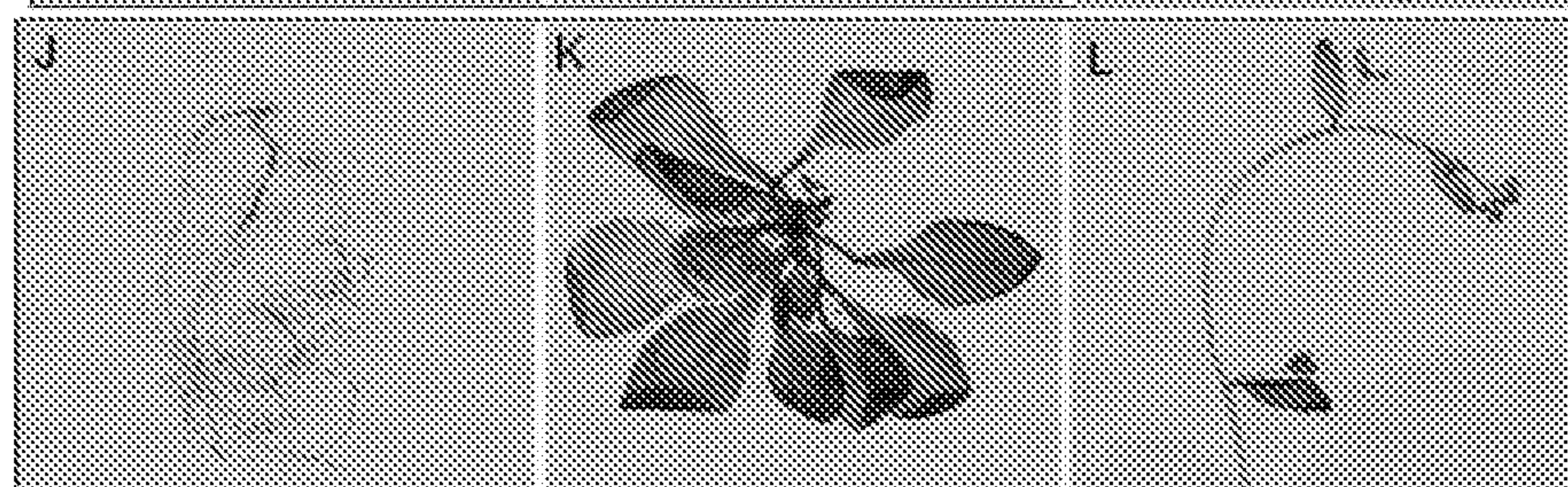
FIGs. 11D-F



FIGs. 11G-I



FIGs. 11J-L



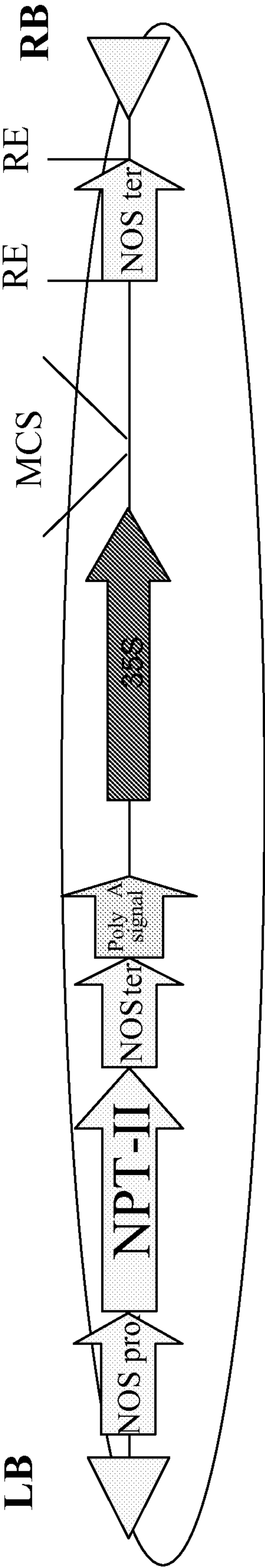


FIG. 12